

# Package ‘Omisc’

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**Type** Package

**Title** Univariate Bootstrapping and Other Things

**Version** 0.1.4

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**Description** Primarily devoted to implementing the Univariate Bootstrap (as well as the Traditional Bootstrap). In addition there are multiple functions for DeFries-Fulker behavioral genetics models. The univariate bootstrapping functions, DeFries-Fulker functions, regression and traditional bootstrapping functions form the original core. Additional features may come online later, however this software is a work in progress. For more information about univariate bootstrapping see: Lee and Rodgers (1998) and Beasley et al (2007) <doi:10.1037/1082-989X.12.4.414>.

**License** GPL-3

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about	<i>Title</i>
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---

**Description**

Title

**Usage**

about(boot)

**Arguments**

boot                    a vector of bootstrap resample statistics to use to calculate the acceleration parameter.

**Value**

a vector of acceleration parameters for use in BCa bootstrap intervals

**Examples**

```
data<-DFSimulated()
boots<-NaiveBoot(data, groups="Rs", keepgroups=TRUE)
boots<-bootAnalysis(boots, cbind, DFanalysis, 1,2,3, robust=FALSE)
boots<-t(boots)
aboot(boots)
```

---

aCalc

*aCalc*

---

**Description**

This function calculates the actual "a" estimate from the jackknife approximation of a used in BCa CI's

**Usage**

```
aCalc(X)
```

**Arguments**

X                    A vector of jackknife results

**Value**

An estimate of a for use in BCa.

**Examples**

```
X<-rchisq(100,2)
aCalc(X)
```

add                      *add*

---

**Description**

add

**Usage**

add(x)

**Arguments**

x                      a list to be summed. Useful for doing elementwise summation of a list of matrices.

**Value**

returns a single summed object (e.g., a matrix)

**Examples**

```
x<-list(matrix(c(1:4),nrow=2),matrix(c(1:4),nrow=2))
add(x)
```

---

ajack                      *ajack*

---

**Description**

ajack

**Usage**

ajack(data, FUN, ...)

**Arguments**

data                      data to get the bias parameter (a) for  
FUN                      a function to be applied to the data  
...                      additional arguments passed to FUN

**Value**

a vector of acceleration parameters for use in BCa bootstrap intervals

**Examples**

```
data<-DFSimulated()
ajack(data,DFanalysis, betasonly=TRUE, robust=FALSE)
```

---

AllBootResults	<i>AllBootResults</i>
----------------	-----------------------

---

**Description**

AllBootResults

**Usage**

```
AllBootResults(boot, lower = 0.025, upper = 0.975, data, FUN, ...)
```

**Arguments**

boot	A matrix of bootstrap results
lower	the lower alpha
upper	the upper alpha
data	the data used for analysis
FUN	the function used for analysis
...	additional arguments to pass to FUN

**Value**

a matrix of results. Includes the baseline results, all output from standardBootIntervals, all results from BCa for both the jackknife and bootstrap acceleration methods. The bootstrap acceleration method is experimental.

**Examples**

```
data<-DFSimulated()
boots<-NaiveBoot(data, groups="Rs", keepgroups=TRUE)
boots<-bootAnalysis(boots, cbind, DFanalysis, 1,2,3, robust=FALSE)
AllBootResults(boots, .025,.975, data, DFanalysis, 1,2,3, robust=FALSE)
```

---

BarebonesBetas	<i>BarebonesBetas</i>
----------------	-----------------------

---

**Description**

Gives just the beta weights from a linear model.

**Usage**

```
BarebonesBetas(data, Y = NULL, RHS = NULL)
```

**Arguments**

data	Data to be analyzed. Dependent variable MUST BE THE FIRST VARIABLE.
Y	optional. The dependent variable
RHS	option. The right hand side of the model, in R's model formulation (i.e., ~ X1+X2+etc)

**Value**

A vector of beta coefficients

**Examples**

```
Data<-TestData()
BarebonesBetas(Data)
```

---

BCa	<i>BCa</i>
-----	------------

---

**Description**

BCa

**Usage**

```
BCa(
  boot,
  data,
  alphalower = 0.025,
  alphaupper = 0.975,
  acceleration = "jack",
  FUN,
  ...
)
```

**Arguments**

boot	A vector of bootstrap estimates of Theta
data	The data that was analyzed via the bootstrap
alphalower	The lower alpha for CI creation
alphaupper	The upper alpha for CI creation
acceleration	can currently take two values, "jack" and "bootstrap". "jack" returns the jack-knife estimate of the acceleration parameter. "boot" is an experimental function that uses the bootstrap estimates in the calculation of the acceleration parameter. "boot" is many times faster (approximately n times faster where n is the number of observations).
FUN	The function used to get estimates of Theta
...	Additional arguments to FUN

**Value**

A matrix of BCa bootstrap CI's, the bias parameter and the acceleration parameter

**Examples**

```
data<-DFSimulated()
boot<-NaiveBoot(data, groups="Rs", keepgroups=TRUE)
boot<-bootAnalysis(boot, cbind, DFanalysis, 1,2,3, robust=FALSE)
BCa(boot, data, .025,.975, acceleration="bootstrap", DFanalysis, 1,2,3, robust=FALSE)
```

---

bias

*Title*

---

**Description**

Title

**Usage**

```
bias(boot, theta)
```

**Arguments**

boot	A vector of bootstrap estimates of theta
theta	the sample estimate of theta

**Value**

z0 the bias parameter for BCa CI

**Examples**

```
X<-data.frame(rnorm(1000))
theta<-mean(X)
boot<-NaiveBoot(X)
boot<-lapply(boot, mean)
boot<-do.call(rbind, boot)
bias(boot, theta)
```

---

bootAnalysis

*bootAnalysis*


---

**Description**

bootAnalysis

**Usage**

```
bootAnalysis(boot, collapse = cbind, FUN, ...)
```

**Arguments**

boot	A list of bootstrap resamples from NaiveBoot or uniboot.
collapse	Should the results be collapsed from list form. Can take values of NULL, cbind or rbind
FUN	The function to apply to the bootstrap resamples
...	additional arguments to be passed to FUN

**Value**

A list or matrix of results

**Examples**

```
data<-DFSimulated()
data<-doubleEnter(data[,1],data[,2],data[,3])
boots<-uniboot(data, 1000, "Rs", TRUE, .5, NULL)
results<-bootAnalysis(boots, cbind, FUN=DFanalysis, 1,2,3,TRUE,FALSE,FALSE,TRUE,FALSE)
```



---

bootsample	<i>bootsample</i>
------------	-------------------

---

**Description**

bootsample

**Usage**

```
bootsample(data, size = 1)
```

**Arguments**

data	a dataset to be bootstrapped
size	the size of the bootstrap sample relative to the original sample

**Value**

a dataset

**Examples**

```
X<-TestData()  
Y<-bootsample(X)
```

---

cent	<i>cent</i>
------	-------------

---

**Description**

cent

**Usage**

```
cent(X)
```

**Arguments**

X	vector to be centered
---	-----------------------

**Value**

Returns a centered vector

**Examples**

```
X<-c(1:10)  
cent(X)
```

centerData

*centerData*

---

**Description**

centerData

**Usage**

centerData(data)

**Arguments**

data            The data to be centered

**Value**

The centered data

**Examples**

```
X<-data.frame(X=c(1:4),Y=c(6:9))
centerData(X)
```

---

cholcors*cholcors*

---

**Description**

cholcors

**Usage**

cholcors(X, use = "everything")

**Arguments**

X            A matrix of data.

use            the missing data type to use for the correlation. Default is R's default "everything".

**Value**

This function returns the cholesky decomposition of the correlation matrix of the data

**Examples**

```
X<-stats::rnorm(100)
Y<-stats::rnorm(100)+X
Z<-cbind(X,Y)
cholcovs(Z)
```

---

 cholcovs

*cholcovs*


---

**Description**

cholcovs

**Usage**

```
cholcovs(X, use = "everything")
```

**Arguments**

X	A matrix of data.
use	the missing data type to use for the correlation. Default is R's default "everything".

**Value**

This function returns the cholesky decomposition of the correlation matrix of the data

**Examples**

```
X<-stats::rnorm(100)
Y<-stats::rnorm(100)+X
Z<-cbind(X,Y)
cholcovs(Z)
```

---

 DFanalysis

*DFanalysis*


---

**Description**

There are three possible models to be fit. The default is the Rodgers and Kohler formulation of the DF model (Rodgers & Kohler, 2005). The non-default (if RK=F), is to fit the original DeFries-Fulker model. The third option is only used when dominance coefficients are provided, and is based on the formulation by Waller (Waller 1994).

**Usage**

```
DFanalysis(
  data = NULL,
  proband,
  sibling,
  Rs,
  Ds = NULL,
  RK = T,
  robust = T,
  DE = T,
  betasonly = F,
  typicalSE = F
)
```

**Arguments**

data	A dataframe. This is not necessary as the variables can be passed directly via the other arguments.
proband	Called "proband" for historical reasons this is the variable on the left hand side of the regression.
sibling	The right hand side version of proband. This would be the matched sibling scores.
Rs	This is the vector of relatedness coefficients
Ds	A vector of dominance coefficients. 1 for MZ twins, .25 for DZ twins and full siblings. The default is null, and no value should be provided if using the ACE model. This should only have a non-null value when fitting an ADE model. There is an RK version of this model, however it is not based on published work. The RK version uses double entered (and mean centered) data in order to drop the intercept term and the extraneous regression coefficient (both of which can be constrained to 0 when the phenotypic mean is 0). Initial simulations suggest that this formulation provides accurate parameter estimates, however the original formulation can be used by simply setting RK=F. It is assumed that, if RK=T, that DE=T (i.e., do NOT double enter data prior to analysis if using the ADE model).
RK	Use the Rodgers and Kohler simplified version of the DF model (recommended). Data should not be double entered prior to analysis.
robust	Use the Kohler and Rodgers robust standard errors (recommended when using double entered data)
DE	Will the data need to be double entered?
betasonly	If TRUE only the beta weights from the regression analysis will be returned.
typicalSE	Should the typical regression standard errors be used? Default is false.

**Value**

The results from MyLM

**Examples**

```
TwinData<-DFSImulated(2000,2000,.3,.3)
p<-TwinData[,1]
s<-TwinData[,2]
r<-TwinData[,3]
DFanalysis(data=NULL, p,s,r)
```

---

DFSImulated

*DFSImulated*


---

**Description**

DFSImulated

**Usage**

```
DFSImulated(MZ = 250, DZ = 250, a2 = 0.3, c2 = 0.3)
```

**Arguments**

MZ	Number of MZ twins to simulate
DZ	Number of DZ twins to simulate
a2	Heritability (proportion of variance)
c2	Shared environment (proportion of variance)

**Value**

A dataframe

**Examples**

```
TwinData<-DFSImulated(200,200,.3,.3)
```

---

DFSImulatedChisq

*DFSImulatedChisq*


---

**Description**

DFSImulatedChisq

**Usage**

```
DFSImulatedChisq(MZ = 250, DZ = 250, a2 = 0.3, c2 = 0.3, df = 10)
```

**Arguments**

MZ	Number of MZ twins to simulate
DZ	Number of DZ twins to simulate
a2	Heritability (proportion of variance)
c2	Shared environment (proportion of variance)
df	Total degrees of freedom for the Chi-Square variable

**Value**

A dataframe of Chi-Square distributed outcome observations for MZ and DZ twins

**Examples**

```
TwinData<-DFSimulatedChisq(200,200,.3,.3, 10)
```

---

```
DFSimulatedChisqNew  DFSimulatedChisqNew
```

---

**Description**

DFSimulatedChisqNew

**Usage**

```
DFSimulatedChisqNew(MZ = 250, DZ = 250, a2 = 0.3, c2 = 0.3, df = 5)
```

**Arguments**

MZ	Number of MZ twins to simulate
DZ	Number of DZ twins to simulate
a2	Heritability (proportion of variance)
c2	Shared environment (proportion of variance)
df	Total degrees of freedom for the Chi-Square variable

**Value**

A dataframe of Chi-Square distributed outcome observations for MZ and DZ twins

**Examples**

```
TwinData<-DFSimulatedChisqNew(200,200,.3,.3, 10)
```

---

doubleEnter	<i>DoubleEnter</i>
-------------	--------------------

---

**Description**

DoubleEnter

**Usage**

```
doubleEnter(proband, sibling, Rs)
```

**Arguments**

proband	The proband scores
sibling	The matched sibling scores
Rs	The relatedness coefficients

**Value**

A dataframe

**Examples**

```
X<-DFSimulated(10,10,.2,.2)
Y<-doubleEnter(X[, "proband"], X[, "sibling"], X[, "Rs"])
```

---

findSa	<i>findSa</i>
--------	---------------

---

**Description**

This is an implementation of the YHY bootstrap covariance matrix.

**Usage**

```
findSa(S, fitted, p, a = 0.5, df, n, tau = NULL, tol = 1e-07)
```

**Arguments**

S	Sample covariance matrix
fitted	The fitted covariance matrix
p	the number of columns in the covariance matrix
a	the starting value for the a parameter
df	the degrees of freedom in the model

n	the number of participants in the model
tau	the population tau. If no tau is provided, the estimated tau from the model will be used
tol	the difference between ga and tau at which the function will converge

**Value**

a list of the "a" adjusted covariance matrix, Sa, the tau, ga, and the number of iterations.

**Examples**

```
require(0misc)
require(lavaan)
set.seed(2^7-1)
modelTest<-'
LV1=~ .7*x1+.8*x2+.75*x3+.6*x4
LV2=~ .7*y1+.8*y2+.75*y3+.6*y4
LV1~~.3*LV2
LV1~~1*LV1
LV2~~1*LV2
'

modelFit<-'
LV1=~ x1+x2+x3+x4
LV2=~ y1+y2+y3+y4
LV1~~start(.5)*LV2
LV1~~1*LV1
LV2~~1*LV2
'

testdata<-simulateData(modelTest, sample.nobs = 250)
fit<-cfa(modelFit, testdata)

fitted<-fitted(fit)$cov
fitted<-fitted[,1:ncol(fitted)]
S<-cov(testdata)
p<-8
a<-.5
n<-250
df<-21
findSa(S, fitted, p, .5, df, n)
```

---

Group\_function

*Grouping\_function*


---

**Description**

originally from the ParallelTree package. If data argument is Null, takes a variable "x" and a matrix or dataframe of level identifiers (e.g., mother and then child IDs). Level variables should be included in order from highest level to the lowest. Listwise deletes missing data. Otherwise grabs variables from entered dataframe Group\_function



**Usage**

```
Group_function(
  data = NULL,
  x,
  levels,
  func = mean,
  center = FALSE,
  nested = TRUE,
  append = FALSE,
  funcName = "Mean"
)
```

**Arguments**

data	a data frame with the x and level variables included. Default is NULL.
x	If data = NULL a dataframe of scores to have the function applied to. If data != NULL, a vector of string(s) naming the variable(s) in data to use.
levels	If data = NULL, a dataframe of grouping variables. If data != NULL, a vector of strings naming the variables in data to use. levels should be ordered from the highest level to the lowest. Group and case identifiers should be unique, if they are not unique, cases with non-unique identifiers will be grouped together.
func	A function to apply at each group. Default is mean.
center	If set to true variables will be group/person mean centered. Note that the grand mean remains unchanged by this operation. If this output is to be passed directly to Parallel_Tree the grand mean should be set to 0.
nested	Are level variables nested? Default is TRUE. If set to FALSE means will be calculated for level variable independently. FALSE may be useful in cases of crossed designs. Note that if data are nested but all identifiers are unique both within and across groups nested = FALSE and nested = TRUE will return the same result.
append	If set to true, the original data will be returned along with all created variables.
funcName	Provides way to name function used. This is used when creating names for created variables. Default is "Mean".

**Value**

This function returns a dataframe with variables labeled according to the level at which the function was applied. Assumed function is mean, and all variables are labeled accordingly. If an alternative function is used labels should be manually changed to reflect function used.

**Examples**

```
#the ChickWeight data is from base R
#nested is set to false because Chick and Time are crossed
Means_Chick<-Group_function(data=ChickWeight,x="weight", levels =c("Diet","Chick","Time"),
nested = FALSE, append=TRUE)
```

---

HoffPseudoStandard	<i>HoffPseudoStandard</i>
--------------------	---------------------------

---

**Description**

HoffPseudoStandard

**Usage**

HoffPseudoStandard(betas, SDX, interceptvar)

**Arguments**

betas	A vector of betas from a multilevel model
SDX	A vector of the standard deviations of the X value for each of the X's associated with the bets
interceptvar	A vector of the intercept variances at the level associated with the betas

**Value**

A vector of pseudostandardized coefficients

**Examples**

```
print("none")
```

---

jackknife	<i>jackknife</i>
-----------	------------------

---

**Description**

jackknife

**Usage**

jackknife(data)

**Arguments**

data	The data to jackknife
------	-----------------------

**Value**

a list of jackknife datasets

**Examples**

```
data<-cbind(1:10,1:10)
result<-jackknife(data)
lapply(result,mean)
```

---

justBetas	<i>justBetas</i>
-----------	------------------

---

**Description**

justBetas

**Usage**

```
justBetas(data, Y, X)
```

**Arguments**

data	A data frame
Y	The name or column number of the Y variable
X	The name(s) or column number(s) of the X variables

**Value**

A vector of unstandardized beta weights

**Examples**

```
X<-stats::rnorm(100)
Y<-stats::rnorm(100)+5*(X)
data<-cbind(Y,X)
justBetas(data,1,2)
#if you want an intercept
Y<-stats::rnorm(100)+5*(X)+5
data<-cbind(Y,X,1)
justBetas(data,1,c(2:3))
```

lbind *lbind*

---

**Description**

lbind is meant to be used in conjunction with lapply to combine elements of lists using rbind.

**Usage**

```
lbind(index, alist, n)
```

**Arguments**

index	a list of indexes. This should count the number of items to return in the final list
alist	a list of objects to be passed to rbind. They should be grouped according to which objects will be combined (e.g., if 1,2,3 are to be passed to cbind then they should be adjacent to eachother).
n	The number of objects in each group. Currently each group must consist of the same number of objects.

**Value**

a list

**Examples**

```
alist<-list(c(1,1),c(2,2),c(3,3))
index<-list(1)
n<-3
lapply(index,lbind,alist,3)
```

---

leave1out *leave1out*

---

**Description**

leave1out

**Usage**

```
leave1out(x, data)
```

**Arguments**

x	Which row(s) of data to leave out
data	A dataframe or matrix.

**Value**

The reduced dataframe or matrix

**Examples**

```
data<-cbind(1:10,1:10)
leave1out(5,data)
```

---

MyLM

*MyLM*

---

**Description**

MyLM

**Usage**

```
MyLM(Y, X, robust = F, betasonly = F, typicalSE = T)
```

**Arguments**

Y	The Y variable
X	A matrix of X variables
robust	Should robust standard errors be calculated? Assumes a double entered twin dataset with twins evenly spaced in the dataset.
betasonly	Should only the betas be returned? Good for bootstrapping
typicalSE	Should the typical standard errors be included? Default is true. Can be true when robust is True.

**Value**

Returns a matrix of betas and standard errors

**Examples**

```
X<-DFSimulated(100,100,.4,.4)
Y<-RK(X[,1],X[,2],X[,3])
MyLM(Y[,1],Y[,c(2:3)],TRUE)
```

---

 NaiveBoot

*The Naive Bootstrap*


---

**Description**

The Naive Bootstrap

**Usage**

```
NaiveBoot(data, B = 1000, groups = NULL, keepgroups = F, size = 1)
```

**Arguments**

data	data to be bootstrapped
B	number of bootstrap samples to take
groups	grouping variable if there is one
keepgroups	keep the grouping variable?
size	size of the bootstrap resamples relative to the original sample

**Value**

a list of bootstrap resamples

**Examples**

```
X<-TestData()
Y<-NaiveBoot(X)
```

---

 NaiveBoot\_dep

*The Naive Bootstrap*


---

**Description**

The Naive Bootstrap

**Usage**

```
NaiveBoot_dep(data, B = 1000, groups = NULL, keepgroups = F, size = 1)
```

**Arguments**

data	data to be bootstrapped
B	number of bootstrap samples to take
groups	grouping variable if there is one
keepgroups	keep the grouping variable?
size	size of the bootstrap resamples relative to the original sample

**Value**

a list of bootstrap resamples

**Examples**

```
X<-TestData()
Y<-NaiveBoot(X)
```

---

resample	<i>resample</i>
----------	-----------------

---

**Description**

resample

**Usage**

```
resample(X, size)
```

**Arguments**

X	A vector to be resamples
size	The size of the resulting vector. Should be a number such that size*nrow(X) is a whole number

**Value**

A vector of resampled X values

**Examples**

```
X<-c(1:10)
resample(X,.5)
```

---

RK	<i>RK</i>
----	-----------

---

**Description**

RK

**Usage**

```
RK(proband, sibling, Rs, DE = T)
```

**Arguments**

proband	column name or number of the proband
sibling	column name or number of the siblings
Rs	column name or number of the relatedness coefficients
DE	Should the data be double entered?

**Value**

A dataframe

**Examples**

```
X<-DFSimulated(100,100,.3,.3)
Y<-RK(X[,1],X[,2],X[,3])
```

---

Sfunc

*Sfunc*

---

**Description**

function for calculating the matrices for the Kohler Rodgers SE

**Usage**

```
Sfunc(X, e)
```

**Arguments**

X	A matrix of X variables
e	A matrix of error terms

**Value**

A matrix

**Examples**

```
print("Nah")
```



---

standardBootIntervals *standardBootIntervals*

---

### Description

This returns the quantiles of the bootstrap samples specified by the user. The quantiles uses the type=4 argument of the quantile function, which appears to function best.

### Usage

```
standardBootIntervals(boot, lower = 0.025, upper = 0.975)
```

### Arguments

boot	A vector of bootstrap results
lower	the lower alpha
upper	the upper alpha

### Value

A matrix of the mean, median, min, max, lower and upper CI values

### Examples

```
data<-DFSImulated()
boots<-NaiveBoot(data, groups="Rs", keepgroups=TRUE, B=100)
boots<-bootAnalysis(boots, cbind, DFanalysis,1,2,3,TRUE,FALSE,TRUE,TRUE,FALSE)
apply(boots,1, standardBootIntervals)
DFanalysis(data,1,2,3)
```

---

TestData	<i>TestData</i>
----------	-----------------

---

### Description

Simple function for creating a dataset of two related variables.

### Usage

```
TestData(nobs = 1000, intercept = 0, beta = 5, meanX = 0, sdX = 1, sdYerr = 1)
```

**Arguments**

nobs	Number of observations, defaults to 1000
intercept	Intercept of the regression. Defaults to 0
beta	Beta for the regression equation, defaults to 5
meanX	Mean of X, defaults to 0
sdX	Standard deviation of X, defaults to 1
sdYerr	Variance of the error term of Y, defaults to 1

**Value**

A dataframe with an X and Y variable produced by the entered parameters

**Examples**

```
X<-TestData()
```

---

 uniboot

*Univariate Bootstrap*


---

**Description**

WARNING: This function can't be used with data that is already fed through the RK function. The correlation matrix will not be positive definite.

**Usage**

```
uniboot(
  data,
  B = 1000,
  groups = NULL,
  keepgroups = F,
  size = 1,
  HIcor = NULL,
  samplefrom = "group",
  use = "everything",
  standardized = T
)
```

**Arguments**

data	The data frame to be resampled
B	The number of bootstrap samples.
groups	A grouping variable name
keepgroups	Should the grouping variable be kept in the final datasets?

size	The size of the bootstrap sample to be returned. Should be as a proportion and must be evenly divided into nrow(data).
HIcor	If a hypothesis imposed correlation matrix is to be used, this argument takes a list of hypothesized correlation matrices. IT MUST BE A LIST OF ONE OR MORE MATRICES. Multiple matrices can be entered in the case of grouped data (one for each group). If the nil-null correlation is to be used an identity matrix can be entered here (the same size as the appropriate correlation matrix).
samplefrom	Takes one of either "group" or "whole". When doing bootstrapping of grouped data this tells uniboot if the whole sample should be used as the sampling frame for each group (whole), or not (group). "group" should be used unless it is believed that all groups share the same underlying marginal distribution for each variable (e.g., the same mean and variance in the case of normally distributed data).
use	The missing data method for cor. Default is R's default "everything".
standardized	should the resampled data be standardized? The default is TRUE. This is computationally more efficient (the data are standardized as a step during the diagonalization procedure).

**Value**

A list of bootstrap samples

**Examples**

```
data<-TestData()
X<-uniboot(data,1000)
```

---

unibootsample	<i>unibootsample</i>
---------------	----------------------

---

**Description**

unibootsample

**Usage**

```
unibootsample(data, size)
```

**Arguments**

data	A dataframe or matrix to be univariately bootstrapped
size	size of each bootstrap sample as a fraction of the total sample size. Total sample size must be evenly divisible by "size".

**Value**

A matrix or dataframe with nrow=nrow(X)\*size

**Examples**

```
X<-c(0:9)
Y<-c(20:29)
Z<-cbind(X,Y)
uniboosample(Z,1)
```

---

unibootVar

*unibootVar*


---

**Description**

unibootVar

**Usage**

```
unibootVar(X, times)
```

**Arguments**

X	The variable
times	The number of times the variable is repeated in the univariate sampling frame. This is going to be equal to the number of variables being univariately sampled

**Value**

The variance of the variable in the univariate sampling frame

**Examples**

```
X<-c(1,2)
times<-100
unibootVar(X,times)
var(X)
```

---

uniboot\_dep

*Univariate Bootstrap*


---

**Description**

**WARNING:** This function can't be used with data that is already fed through the RK function. The correlation matrix will not be positive definite.

**Usage**

```
uniboot_dep(
  data,
  B = 1000,
  groups = NULL,
  keepgroups = F,
  size = 1,
  HIcor = NULL,
  samplefrom = "group",
  use = "everything"
)
```

**Arguments**

data	The data frame to be resampled
B	The number of bootstrap samples. Alternatively "sampleframe" which will return the univariate sampling frame. "samplefrom" is not advised when there are many observations and/or many variables as the returned dataframe will be quite large.
groups	A grouping variable name
keepgroups	Should the grouping variable be kept in the final datasets?
size	The size of the bootstrap sample to be returned. Should be as a proportion and must be evenly divided into nrow(data).
HIcor	If a hypothesis imposed correlation matrix is to be used, this argument takes a list of hypothesized correlation matrices. IT MUST BE A LIST OF ONE OR MORE MATRICES. Multiple matrices can be entered in the case of grouped data (one for each group). If the nil-null correlation is to be used an identity matrix can be entered here (the same size as the appropriate correlation matrix).
samplefrom	Takes one of either "group" or "whole". When doing bootstrapping of grouped data this tells uniboot if the whole sample should be used as the sampling frame for each group (whole), or not (group). "group" should be used unless it is believed that all groups share the same underlying marginal distribution for each variable (e.g., the same mean and variance in the case of normally distributed data).
use	The missing data method for cor. Default is R's default "everything".

**Value**

A list of bootstrap samples

**Examples**

```
data<-TestData()
X<-uniboot(data,1000)
```

---

zScore	<i>Title</i>
--------	--------------

---

**Description**

Title

**Usage**

```
zScore(X, reps = 1)
```

**Arguments**

X	The vector to be turned into z scores
reps	The number of reps the vector is to be repeated. This will only be used in univariate bootstrapping. The default is 1.

**Value**

A vector of z scores.

**Examples**

```
X<-c(1:10)
zScore(X)
```

---

zScoreData	<i>centerData</i>
------------	-------------------

---

**Description**

centerData

**Usage**

```
zScoreData(data)
```

**Arguments**

data	The data to be converted to z scores
------	--------------------------------------

**Value**

Data converted to z scores

**Examples**

```
X<-data.frame(X=c(1:4),Y=c(6:9))
zScoreData(X)
```

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