aboot

Description

Title

Usage

aboot(boot)
aCalc

Arguments

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

Value

  a vector of accelleration parameters for use in BCa bootstrap intervals

Examples

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

Description

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

Usage

```r
aCalc(X)
```

Arguments

  X  A vector of jackknife results

Value

  An estimate of a for use in BCa.

Examples

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

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

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

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

### Description

**AllBootResults**

### Usage

```r
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

```r
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

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

Description
BCa

Usage
BCa(
  boot,
  data,
  alphalower = 0.025,
  alphaupper = 0.975,
  accelleration = "jack",
  FUN,
  ... )
Arguments

boot A vector of bootstrap estimates of Theta
data The data that was analyzed via the bootstrap
alpha_lower The lower alpha for CI creation
alpha_upper The upper alpha for CI creation
accelleration can currently take two values, "jack" and "bootstrap". "jack" returns the jack-knife estimate of the accelleration parameter. "boot" is an experimental function that uses the bootstrap estimates in the calculation of the accelleration 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 accelleration 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, accelleration="bootstrap", DFanalysis, 1,2,3, robust=FALSE)

bias

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<thead>
<tr>
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<td>bias</td>
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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

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

Description

`bootAnalysis`

Usage

```r
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

```r
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**

**bootsample**

**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

**Description**

cent

**Usage**

cent(X)

**Arguments**

X:

vector to be centered

**Value**

Returns a centered vector

**Examples**

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

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
cholcovs

Examples

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

cholcovs

Description

cholcovs

Usage

```r
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

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

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).
DFanalysis

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
DFSimulated

Examples

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

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

Description

DFSimulatedChisq

Usage

DFSimulatedChisq(MZ = 250, DZ = 250, a2 = 0.3, c2 = 0.3, df = 10)
DFSimulatedChisqNew

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

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

---

**Description**

DFSimulatedChisqNew

**Usage**

```r
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**

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

DoubleEnter

**Usage**

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

**Arguments**

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

**Value**

A dataframe

**Examples**

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

---

**Description**

This is an implementation of the YHY bootstrap covariance matrix.

**Usage**

```r
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 interactions.

Examples

```r
require(Omisc)
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

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

Grouping_function
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

**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

**Description**

jackknife

**Usage**

jackknife(data)

**Arguments**

- **data**: The data to jackknife

**Value**

a list of jackknife datasets
justBetas

Examples

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

justBetas

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))
**Description**

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

**Usage**

```r
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 each other).
- `n` : The number of objects in each group. Currently each group must consist of the same number of objects.

**Value**

`lapply` index, `lbind`, `alist`, 3

**Examples**

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

---

**leave1out**

**Description**

leave1out

**Usage**

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

**Arguments**

- `x` : Which row(s) of data to leave out.
- `data` : A dataframe or matrix.
**MyLM**

**Value**

The reduced dataframe or matrix

**Examples**

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

---

**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
resample

Value

a list of bootstrap resamples

Examples

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

resample

resample

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

RK

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

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

**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**

```r
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**

```r
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

**Description**

Simple function for creating a dataset of two related variables.

**Usage**

```r
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

```r
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

```r
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?
unibootsample

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

unibootsample

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

\[
X \leftarrow c(0:9) \\
Y \leftarrow c(20:29) \\
Z \leftarrow \text{cbind}(X, Y) \\
\text{unibootsample}(Z, 1)
\]

---

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

\[
X \leftarrow c(1,2) \\
times \leftarrow 100 \\
\text{unibootVar}(X, \text{times}) \\
\text{var}(X)
\]

---

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)
### Description

Title

### Usage

\[
\text{zScore}(X, \text{reps} = 1)
\]

### 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

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

### Description

centerData

### Usage

\[
\text{zScoreData}(\text{data})
\]

### Arguments

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

### Value

Data converted to z scores

### Examples

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