Package ‘bifurcatingr’

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Title  Bifurcating Autoregressive Models
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Description  Estimation of bifurcating autoregressive models of any order, p, BAR(p) as well as several types of bias correction for the least squares estimators of the autoregressive parameters as described in Zhou and Basawa (2005) <doi:10.1016/j.spl.2005.04.024> and Elbayoumi and Mostafa (2020) <doi:10.1002/sta4.342>. Currently, the bias correction methods supported include bootstrap (single, double and fast-double) bias correction and linear-bias-function-based bias correction. Functions for generating and plotting bifurcating autoregressive data from any BAR(p) model are also included.

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**bfa.boot1.ls**

*Single Bootstrap of Least Squares Estimators of BAR(p) Models*

**Description**

This function performs single bootstrapping of the least squares estimators of the autoregressive coefficients in a bifurcating autoregressive (BAR) model of any order \( p \) as described in Elbayoumi & Mostafa (2020).

**Usage**

```r
bfa.boot1.ls(z, p, burn = 5, B, boot.est = TRUE, boot.data = FALSE)
```

**Arguments**

- `z` a numeric vector containing the tree data
- `p` an integer determining the order of bifurcating autoregressive model to be fit to the data
- `burn` number of tree generations to discard before starting the bootstrap sample (replicate)
- `B` number of bootstrap samples (replicates)
- `boot.est` a logical that determines whether the bootstrapped least squares estimates of the autoregressive coefficients should be returned. Defaults to TRUE.
- `boot.data` a logical that determines whether the bootstrap samples should be returned. Defaults to FALSE.

**Value**

- `boot.est` a matrix containing the bootstrapped least squares estimates of the autoregressive coefficients
- `boot.data` a matrix containing the bootstrap samples used

**References**

Examples

```r
z <- bfa.tree.gen(31, 1, 1, 1, 0.5, 0.5, 0, 10, c(0.7))
bfa.boot1.ls(z, p=1, B=999)
```

---

**bfa.boot2.ls**  
*Double Bootstrap of Least Squares Estimators of BAR(p) Models*

**Description**

This function performs double bootstrapping of the least squares estimators of the autoregressive coefficients in a bifurcating autoregressive (BAR) model of any order $p$ as described in Elbayoumi & Mostafa (2020).

**Usage**

```r
bfa.boot2.ls(z, p, burn = 5, B1, B2)
```

**Arguments**

- `z`: a numeric vector containing the tree data
- `p`: an integer determining the order of bifurcating autoregressive model to be fit to the data
- `burn`: number of tree generations to discard before starting the bootstrap sample (replicate)
- `B1`: number of bootstrap samples (replicates) used in first round of bootstrapping
- `B2`: number of bootstrap samples (replicates) used in second round of bootstrapping

**Value**

- `boot.est`: a matrix containing the first-stage bootstrapped least squares estimates of the autoregressive coefficients
- `boot2`: a matrix containing the second-stage bootstrapped least squares estimates of the autoregressive coefficients

**References**


**Examples**

```r
z <- bfa.tree.gen(31, 1, 1, 1, 0.5, 0.5, 0, 10, c(0.7))
bfa.boot2.ls(z, p=1, B1=99, B2=9)
```
bfa.boot2fast.ls

Fast Double Bootstrap of Least Squares Estimators of BAR(p) Models

Description

This function performs fast double bootstrapping of the least squares estimators of the autoregressive coefficients in a bifurcating autoregressive (BAR) model of any order \( p \) as described in Elbayoumi & Mostafa (2020).

Usage

bfa.boot2fast.ls(z, p, burn = 5, B)

Arguments

- **z**: a numeric vector containing the tree data
- **p**: an integer determining the order of bifurcating autoregressive model to be fit to the data
- **burn**: number of tree generations to discard before starting the bootstrap sample (replicate)
- **B**: number of bootstrap samples (replicates) used in first round of bootstrapping

Value

- **boot.est**: a matrix containing the first-stage bootstrapped least squares estimates of the autoregressive coefficients
- **boot2**: a matrix containing the second-stage bootstrapped least squares estimates of the autoregressive coefficients

References


Examples

```r
z <- bfa.tree.gen(31, 1, 1, 1, 0.5, 0.5, 0, 10, c(0.7))
bfa.boot2fast.ls(z, p=1, B=499)
```
**bfa.lbc.ls**

*Linear Function Bias-Corrected Estimators for BAR(p); p=1,2,...,6*

**Description**

This function performs bias correction on the least squares estimators of the autoregressive coefficients in a BAR(p) model based on the assumption that the bias of the least squares estimator is approximately linear as a function of the parameter as described in Elbayoumi & Mostafa (2020).

**Usage**

\[ \text{bfa.lbc.ls}(z, p) \]

**Arguments**

- **z**: a numeric vector containing the tree data
- **p**: an integer determining the order of bifurcating autoregressive model to be fit to the data

**Value**

- **coef.lbc**: linear-bias-function-based bias-corrected least squares estimates of the autoregressive coefficients

**References**


**Examples**

```r
z <- bfa.tree.gen(127, 1, 1, 1, 0.5, 0.5, 0, 10, c(0.7))
bfa.lbc.ls(z, p=1)
z <- bfa.tree.gen(127, 2, 1, 1, 0.5, 0.5, 0, 10, c(0.5, 0.3))
bfa.lbc.ls(z, p=2)
```

---

**bfa.ls**

*Least Squares Estimation of Bifurcating Autoregressive Models*

**Description**

This function performs Least Squares estimation of bifurcating autoregressive (BFA) models of any order as described in Zhou & Basawa (2005).
bfa.ls(  
  z,  
  p,  
  x.data = FALSE,  
  y.data = FALSE,  
  resid = FALSE,  
  error.cor = TRUE,  
  error.var = FALSE,  
  cov.matrix = FALSE,  
  conf = FALSE,  
  conf.level = 0.95,  
  p.value = FALSE  
)

Arguments

z      a numeric vector containing the tree data
p      an integer determining the order of bifurcating autoregressive model to be fit to the data
x.data a logical that determines whether the x data used in fitting the model should be returned. Defaults to FALSE.
y.data a logical that determines whether the y data used in fitting the model should be returned. Defaults to FALSE.
resid  a logical that determines whether the model residuals should be returned. Defaults to FALSE.
error.cor a logical that determines whether the estimated correlation between pairs of model errors \( (e_{2t}, e_{2t+1}) \) should be returned. Defaults to TRUE.
error.var a logical that determines whether the estimated variance of the model errors should be returned. Defaults to FALSE.
cov.matrix a logical that determines whether the estimated variance-covariance matrix of the least squares estimates should be returned. Defaults to FALSE.
conf a logical that determines whether confidence intervals for model coefficients should be returned. Defaults to FALSE. If TRUE, normal confidence intervals are calculated using cov.matrix.
conf.level confidence level to be used in computing the normal confidence intervals for model coefficients when conf=TRUE. Defaults to 0.95.
p.value a logical that determines whether p-values for model coefficients should be returned. Defaults to FALSE. If TRUE, p-values are computed from normal distribution using estimated coefficients and cov.matrix.

Value

coef a matrix containing the least squares estimates of the autoregressive coefficients
error.cor  the least squares estimate of the correlation between pairs of model errors \((e_{2t}, e_{2t+1})\). Only returned if error.cor=TRUE

x  a matrix containing the x data used in fitting the model. Only returned if x.data=TRUE

y  a vector containing the y data used in fitting the model. Only returned if y.data=TRUE

resids  the model residuals. Only returned if resids=TRUE

error.var  the estimated variance of the model errors. Only returned if error.var=TRUE

cov.matrix  the estimated variance-covariance matrix of the least squares coefficients. Only returned if cov.matrix=TRUE

conf  a matrix of normal confidence intervals for model coefficients. Only returned if conf=TRUE

p.value  a matrix of two-sided p-values for testing the significance of model coefficients. Computed from normal distribution and using the estimated covariance matrix cov.matrix. Only returned if p.value=TRUE

References

Examples
z <- bfa.tree.gen(127, 1, 1, 1, -0.9, -0.9, 0, 10, c(0.7))
bfa.ls(z, p=1)
bfa.ls(z, p=1, conf=TRUE, cov.matrix = TRUE, conf.level = 0.9, p.value=TRUE)

---

**bfa.ls.bc**  
Bias-Corrected Least Squares Estimators for Bifurcating Autoregressive Models

**Description**
This function performs bias correction on the least squares estimators of the autoregressive coefficients in a BAR(p) model using single, double and fast-double bootstrapping, and the linear-bias-function approach as described in Elbayoumi & Mostafa (2020).

**Usage**
bfa.ls.bc(
  z,
  p,
  method = "boot1",
  burn = 5,
  B1 = 999,
  B2 = 499,
  boot.est = TRUE,
  boot.data = FALSE
)
Arguments

z: a numeric vector containing the tree data
p: an integer determining the order of bifurcating autoregressive model to be fit to the data
method: method of bias correction. Currently, "boot1", "boot2", "boot2fast" and "LBC" are supported and they implement single bootstrap, double bootstrap, fast-double bootstrap, and linear-bias-function bias-correction, respectively.
burn: number of tree generations to discard before starting the bootstrap sample (replicate)
B1: number of bootstrap samples (replicates) used in first round of bootstrapping
B2: number of bootstrap samples (replicates) used in second round of bootstrapping
boot.est: a logical that determines whether the bootstrapped least squares estimates of the autoregressive coefficients should be returned. Defaults to TRUE.
boot.data: a logical that determines whether the bootstrap samples should be returned. Defaults to FALSE.

Value

coef.ls.bc: bias-corrected least squares estimates of the autoregressive coefficients

References


Examples

z <- bfa.tree.gen(63, 1, 1, 1, 0.5, 0.5, 0, 10, c(0.7))
bfa.ls.bc(z, p=1, method="boot1")
z <- bfa.tree.gen(63, 2, 1, 1, 0.5, 0.5, 0, 10, c(0.5, 0.3))
bfa.ls.bc(z, p=2, method="LBC")

bfa.scatterplot Scatterplots for Bifurcating Autoregressive Data

Description

Draw scatterplots between observations at time t and the lagged observations from the given bifurcating autoregressive tree data.

Usage

bfa.scatterplot(z, p, ...)
Arguments

z  a numeric vector containing the tree data
p  an integer determining the order of the bifurcating autoregressive model that is believed to best fit the data
... other graphical parameters that can be passed to plot() or pairs() (see par and pairs)

Value

A single scatterplot when p=1 or a matrix of scatterplots when p>1.

Examples

z <- bfa.tree.gen(63, 1, 2, 0.5, 0.5, 0.2, 10, c(0.7))
bfa.scatterplot(z,1)
z<-bfa.tree.gen(63, 2, 1, 2, 0.5, 0.5, 0.2, 10, c(0.7,0.2))
bfa.scatterplot(z,2)
bfa.scatterplot(z,2,lower.panel=NULL)

bfa.subtree
Subtree Extractor

Description

This function extracts subtree of size $(2^p - 1)$ from the end of a given bifurcating autoregressive tree (model) of order p.

Usage

bfa.subtree(n, p)

Arguments

n  subtree size (integer)
p  an integer determining the order of bifurcating autoregressive model

Value

A numeric vector representing a subtree of size $(2^p - 1)$ from the end of a given bifurcating autoregressive tree.

Examples

bfa.subtree(31, 1)
bfa.subtree(31, 2)
**bfa.tree.gen**  
**Bifurcating Autoregressive Tree generator**

**Description**
This function generates bifurcating autoregressive (BFA) trees of any size based on a BFA model of any order.

**Usage**

```r
bfa.tree.gen(n, p, s1, s2, r1, r2, g, intercept, ar.coef)
```

**Arguments**
- `n`: tree size (integer)
- `p`: an integer determining the order of bifurcating autoregressive model
- `s1`: standard deviation of the errors distribution
- `s2`: standard deviation of the second component of the mixture normal distribution generating contaminated errors. `s2` should be greater than `s1`. `s2` is only effective when `g>0`.
- `r1`: correlation between pairs of errors
- `r2`: is used in combination with `r1` to compute the correlation between pairs of errors in the second component of the mixture normal distribution generating the contaminated errors. `r2` is only effective when `g>0`.
- `g`: proportion of contamination. Defaults to zero producing non-contaminated multivariate normal errors for the tree generation.
- `intercept`: the intercept in the BAR model generating the tree
- `ar.coef`: a vector of length `p` giving the autoregressive coefficients in the BAR model generating the tree

**Value**
A numeric vector representing a bifurcating autoregressive (BFA) tree with `n` observations.

**Examples**

```r
# Non-contaminated BAR(1) tree:
bfa.tree.gen(127, 1, 1, 1, 0.5, 0.5, 0, 10, c(0.7))
# Non-contaminated BAR(2) tree:
bfa.tree.gen(127, 2, 1, 1, 0.5, 0.5, 0, 10, c(0.5, 0.3))
# Contaminated BAR(1) tree:
bfa.tree.gen(127, 1, 1, 2, 0.5, 0.5, 0.2, 10, c(0.7))
```
bfa.tree.plot  

Plotting Bifurcating Autoregressive Trees

Description

This function graphs bifurcating autoregressive (BFA) tree data.

Usage

bfa.tree.plot(
  z,
  digits,
  shape = "none",
  vertex.size = 10,
  text.size = 1,
  text.color = "black",
  vertex.color = "gold",
  arrow.size = 0.5,
  arrow.width = 0.5,
  arrow.color = "black",
  plot.margin = -0.3
)

Arguments

z an numeric vector containing the tree data

digits an integer indicating the number of decimal places to be displayed in vertex labels

shape the shape of the vertex. Currently “circle”, “square”, “csquare”, “rectangle”, “crectangle”, “vrectangle”, and “none” are supported. Defaults to “none” which does not display the vertices at all.

vertex.size a numeric scalar or vector defining the size of the vertex or vertices. If a vector is supplied, vertex sizes may differ. Defaults to 10.

text.size the font size of vertex labels. Defaults to 1.

text.color the color of vertex labels. If it is a character vector, then it may either contain integer values, named colors or RGB specified colors with three or four bytes. Defaults to “black”.

vertex.color the fill color of the vertex. If you don’t want some or all vertices to have any color, supply NA. The default is “gold”. See also the options in text.color.

arrow.size the size of the arrows. The default value is 0.5.

arrow.width the width of the arrows. The default value is 0.5.

arrow.color the color of the arrows. The default is “black”. See also the options in text.color.

plot.margin the amount of empty space around the plot, it is a numeric vector of length four. Usually values between 0 and 0.5 are meaningful, but negative values are also possible and in that case it will make the plot zoom in to a part of the graph. If it is shorter than four, recycling will occur. The default value is -0.3.
Details

For more details about the graph options see igraph.plotting.

Value

A binary tree displaying the BFA data.

Examples

```r
z <- bfa.tree.gen(31, 1, 1, 1, 0.5, 0.5, 0, 10, c(0.7))
bfa.tree.plot(z)
bfa.tree.plot(z, shape = "circle")
bfa.tree.plot(z, shape = "circle", text.color = "white", vertex.color = "darkgrey")
```

---

table:<
<table>
<thead>
<tr>
<th>ecoli</th>
<th>Lifetimes (in minutes) of lineage E. coli cells.</th>
</tr>
</thead>
</table>

Description

A real cell lineage dataset taken from Cowan and Staudte (1986). The values represent the lifetimes in minutes of lineage E. coli cells. It contains 31 observations making which can be described by a bifurcating autoregressive tree with 4 generations.

Usage

dati

disa

Format

A data frame with 31 rows and 1 variable:

- **lifetime** E. coli cells lifetime, in minutes

Source

**Description**

This function generates contaminated multivariate normal errors that are used in the generation of the Bifurcating autoregressive tree.

**Usage**

```r
rcontmnorm(
  n,
  d = 2,
  mu1 = rep(0, d),
  sigma1 = diag(d),
  mu2 = rep(0, d),
  sigma2 = diag(d),
  g
)
```

**Arguments**

- `n` sample size
- `d` dimension. Defaults to 2 for bivariate normal errors.
- `mu1` mean vector for first multivariate normal distribution. Defaults to the zero vector.
- `sigma1` variance-covariance matrix for first multivariate normal distribution. Defaults to the d by d identity matrix, where d is the dimension.
- `mu2` mean vector for second multivariate normal distribution. Defaults to the zero vector.
- `sigma2` variance-covariance matrix for second multivariate normal distribution. Defaults to the d by d identity matrix, where d is the dimension.
- `g` proportion of contamination. Defaults to zero producing non-contaminated multivariate normal data.

**Value**

An n by d contaminated multivariate normal matrix.

**Examples**

```r
# Non-contaminated bivariate normal:
rcontmnorm(10, sigma2=2^2*matrix(c(1,0,0,1),nrow=2) , g=0)
# Contaminated bivariate normal with 20% contamination:
rcontmnorm(10, sigma2=2^2*matrix(c(1,0,0,1),nrow=2) , g=0.2)
```
**rmnorm**  
*Multivariate Normal Generator*

**Description**
This function generates multivariate normal errors that are used in the generation of the Bifurcating autoregressive tree.

**Usage**
```r
rmnorm(n, d = 2, mu = rep(0, d), sigma = diag(d))
```

**Arguments**
- `n` sample size
- `d` dimension. Defaults to 2 for bivariate normal errors.
- `mu` mean vector. Defaults to the zero vector.
- `sigma` variance-covariance matrix. Defaults to the d by d identity matrix, where d is the dimension.

**Value**
An n by d multivariate normal matrix.

**Examples**
```r
rmnorm(10)
rmnorm(10, 3)
```
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