

Package ‘WaveCD’

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Type Package

Title Wavelet change point detection for array CGH data

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Description Detects change points

License GPL (>= 2)

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 WaveCD-package

Detects and plots change points in a series

Description

It finds and plots change points in a series using wavelet method. We compare the wavelet coefficients obtained at highest order resolution with Wang's threshold to detect change points. Double implementation of MODWT confirms the presence of break points in the series.

Details

Package: WaveCD
 Type: Package
 Version: 1.0
 Date: 2010-05-15
 License: GPL (>= 2)

Author(s)

M. Shahidul Islam Maintainer: <islam@stats.uwo.ca>

References

M.S. Islam (2008). Periodicity, Change Detection and Prediction in Microarrays. Ph.D. Thesis, University of Western Ontario.

Examples

```
# Finding break points in the series
set.seed(123)
x<-c(rnorm(150, sd=0.1), rnorm(250, 0.8, sd=0.1), rnorm(150, sd=0.1))
BreakPoints(x)

# Graphical displa of break points
phi<-0.8
SigE<- 0.12
ex.c1<- c(rep(0, 80), rep(-0.7,30), rep(0,40))+ SimulateError(phi, SigE, 150)
ex.c2<- c(rep(0,40), rep(0.7, 30), rep(0, 50))+ SimulateError(phi, SigE, 120)
ex.c<-c(ex.c1, ex.c2)
PlotBreakPoints(ex.c, c(rep(1, 150),rep(2, 120)))
```

`arrayCGH`*A real array-CGH data*

Description

In CGH array, 2400 BAC clones were measured each with three replicates (Snijders et al., 2001). Measurements for log base 2 intensity ratio are provided.

Usage

```
data(arrayCGH)
```

Format

A data frame with 1040 observations on the following 2 variables.

value a numeric vector

chromosome a numeric vector

Source

Snijders, A. M., Nowak, N., Segreaves, R., Blackwood, S., Brown N., Conroy, J., Hamilton, G., Hindle, A. K, Huey, B., Kimura, K., Law, S., Myambo, K., Palmer, J., Ylstra, B., Yue, J. P., Gray, J. W., Jain, A. N., Pinkel, D. and Albertson, D. (2001) Assembly of microarrays for genome-wide measurement of DNA copy number. *Nature Genetics* 29, 263 - 264.

Examples

```
data(arrayCGH)
names(arrayCGH)
```

`BreakPoints`*Find break points in a given series*

Description

This function applies maximum overlap discrete wavelet transform (MODWT) to find break points in a series. We compare the wavelet coefficients obtained at highest order resolution with Wang's threshold to detect change points. Double application of the process distinguishes noise from a real jump.

Usage

```
BreakPoints(x)
```

Arguments

x a series

Details

Uses MODWT to detect breakpoints. See Islam (2008).

Value

list of break points (end points not included)

Author(s)

M.Shahidul Islam

References

M.S. Islam (2008). Periodicity, Change Detection and Prediction in Microarrays. Ph.D. Thesis, University of Western Ontario.

See Also

[PlotBreakPoints](#)

Examples

```
set.seed(123)
x<-c(rnorm(150), rnorm(250, 1), rnorm(200))
BreakPoints(x)
```

PlotBreakPoints *Plot the series and detected jump points*

Description

A lattice style plot is used to show break points for each chromosome

Usage

```
PlotBreakPoints(x, Chromosome, layout = c(length(unique(Chromosome)),1), ...)
```

Arguments

x any series of observations
Chromosome chromosome corresponding to data in x
layout the layout of the lattice plot
... arguments that can be passed to plot command

Details

Uses MODWT method described in Islam (2008).

Value

lattice plot

Author(s)

M. Shahidul Islam

References

M.S. Islam (2008). Periodicity, Change Detection and Prediction in Microarrays. Ph.D. Thesis, University of Western Ontario.

See Also

[BreakPoints](#)

Examples

```
# Example-1: Data simulated from AR(1) process with phi=0.8
phi<-0.8
SigE<- 0.12
ex.c1<- c(rep(0, 80), rep(-0.7,30), rep(0,40))+ SimulateError(phi, SigE, 150)
ex.c2<- c(rep(0,40), rep(0.7, 30), rep(0, 50))+ SimulateError(phi, SigE, 120)
ex.c<-c(ex.c1, ex.c2)
PlotBreakPoints(ex.c, c(rep(1, 150),rep(2, 120)))
```

```
# Example-2: seven jump points
```

```
fx<-function(x){ifelse(x<50,0,
ifelse(x>=50 && x<60,1,
  ifelse(x>=60 && x<92,0,
    ifelse(x>=92 && x<106,-1,
      ifelse(x>=106 && x<145,0,
        ifelse(x>=145 && x<169,1,
          ifelse(x>=169 && x<=180,2, 0)))))))+rnorm(1,0,0.1)}
```

```
set.seed(123)
y<-sapply(1:200,fx)
PlotBreakPoints(y, c(rep(1, length(y))), type="l", lwd=1.7)
```

```
#
# CGH Data
#
data(arrayCGH)
```

```
# Plotting first 12 chromosomes
PlotBreakPoints(arrayCGH[1:765,1], arrayCGH[1:765,2], type="l",layout=c(3,4))
# Plotting rest of the chromosomes
PlotBreakPoints(arrayCGH[766:1040,1], arrayCGH[766:1040,2], type="l",layout=c(3,4))
```

SimulateError

Simulate AR(p) error series

Description

This function finds an AR(P) error series with given length, coefficients and error standard deviation.

Usage

```
SimulateError(phi, SigE, n)
```

Arguments

phi	Vector of AR(p) coefficients.
SigE	Standard deviation of errors in an AR(p) series.
n	Length of series.

Value

Simulated series with AR(p) process.

Author(s)

M. Shahidul Islam

References

M.S. Islam (2008). Periodicity, Change Detection and Prediction in Microarrays. Ph.D. Thesis, University of Western Ontario.

`SymmetricMA`*Make a series smooth using moving average*

Description

It makes the data smooth using moving average of specified window size.

Usage

```
SymmetricMA(x, w = 5)
```

Arguments

<code>x</code>	Array-CGH data
<code>w</code>	Window size.

Value

Smoothed version of original data.

Author(s)

M. Shahidul Islam

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