

Package: hdbinseg (via r-universe)

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Type Package

Title Change-Point Analysis of High-Dimensional Time Series via Binary Segmentation

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Description Binary segmentation methods for detecting and estimating multiple change-points in the mean or second-order structure of high-dimensional time series as described in Cho and Fryzlewicz (2014) <[doi:10.1111/rssb.12079](https://doi.org/10.1111/rssb.12079)> and Cho (2016) <[doi:10.1214/16-EJS1155](https://doi.org/10.1214/16-EJS1155)>.

Depends R (>= 4.2.0)

License GPL (>= 3)

Suggests RcppArmadillo

Imports Rcpp (>= 0.12.10), foreach, iterators, doParallel

LinkingTo Rcpp, RcppArmadillo

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dcbs.alg

*Double CUSUM Binary Segmentation***Description**

Perform the Double CUSUM Binary Segmentation algorithm detecting change points in the mean or second-order structure of the data.

Usage

```
dcbs.alg(
  x,
  cp.type = c(1, 2)[1],
  phi = 0.5,
  thr = NULL,
  trim = NULL,
  height = NULL,
  tau = NULL,
  temporal = TRUE,
  scales = NULL,
  diag = FALSE,
  B = 1000,
  q = 0.01,
  do.parallel = 4
)
```

Arguments

<code>x</code>	input data matrix, with each row representing the component time series
<code>cp.type</code>	<code>cp.type = 1</code> specifies change points in the mean, <code>cp.type = 2</code> specifies change points in the second-order structure
<code>phi</code>	choice of parameter for weights in Double CUSUM statistic; $0 \leq \phi \leq 1$ or $\phi = -1$ allowed with the latter leading to the DC statistic combining $\phi = 0$ and $\phi = 1/2$, see Section 4.1 of Cho (2016) for further details
<code>thr</code>	pre-defined threshold values; when <code>thr = NULL</code> , bootstrap procedure is employed for the threshold selection; when <code>thr != NULL</code> and <code>cp.type = 1</code> , <code>length(thr)</code> should be one, if <code>cp.type = 2</code> , <code>length(thr)</code> should match <code>length(scales)</code>
<code>trim</code>	length of the intervals trimmed off around the change point candidates; <code>trim = NULL</code> activates the default choice (<code>trim = round(log(dim(x)[2]))</code>)
<code>height</code>	maximum height of the binary tree; <code>height = NULL</code> activates the default choice (<code>height = floor(log(dim(x)[2], 2)/2)</code>)
<code>tau</code>	a vector containing the scaling constant for each row of <code>x</code> ; if <code>tau = NULL</code> , a data-driven choice is made which takes into account the presence of possibly multiple mean shifts and temporal dependence when <code>temporal = TRUE</code>

temporal	used when <code>cp.type = 1</code> ; if <code>temporal = FALSE</code> , rows of <code>x</code> are scaled by <code>mad</code> estimates, if <code>temporal = TRUE</code> , their long-run variance estimates are used
scales	used when <code>cp.type = 2</code> ; negative integers representing Haar wavelet scales to be used for computing $nrow(x) * (nrow(x) + 1) / 2$ dimensional wavelet transformation of <code>x</code> ; a small negative integer represents a fine scale
diag	used when <code>cp.type = 2</code> ; if <code>diag = TRUE</code> , only changes in the diagonal elements of the autocovariance matrices are searched for
B	used when <code>is.null(thr)</code> ; number of bootstrap samples for threshold selection
q	used when <code>is.null(thr)</code> ; indicates the quantile of bootstrap test statistics to be used for threshold selection
do.parallel	used when <code>is.null(thr)</code> ; number of copies of R running in parallel, if <code>do.parallel = 0</code> , <code>%do%</code> operator is used, see also <code>foreach</code>

Value

S3 bin. tree object, which contains the following fields:

tree	a <code>list</code> object containing information about the nodes at which change points are detected
mat	matrix concatenation of the nodes of <code>tree</code>
ecp	estimated change points
thr	threshold used to construct the tree

References

H. Cho (2016) change point detection in panel data via double CUSUM statistic. *Electronic Journal of Statistics*, vol. 10, pp. 2000–2038.

Examples

```
x <- matrix(rnorm(10*100), nrow = 10)
dcbs.alg(x, cp.type = 1, phi=.5, temporal = FALSE, do.parallel = 0)$ecp
```

```
x <- matrix(rnorm(100*300), nrow = 100)
x[1:10, 151:300] <- x[1:10, 151:300] + 1
dcbs.alg(x, cp.type = 1, phi=-1, temporal = FALSE, do.parallel = 0)$ecp
```

dcbs.thr

Bootstrapping for threshold selection in DCBS algorithm

Description

Generate thresholds for DCBS algorithm via bootstrapping

Usage

```
dcbs.thr(
  z,
  interval = c(1, dim(z)[2]),
  phi = 0.5,
  cp.type = 1,
  do.clean.cp = FALSE,
  temporal = TRUE,
  scales = NULL,
  diag = FALSE,
  sgn = NULL,
  B = 1000,
  q = 0.01,
  do.parallel = 4
)
```

Arguments

`z` input data matrix, with each row representing the component time series

`interval` a vector of two containing the start and the end points of the interval from which the bootstrap test statistics are to be calculated

`phi`, `cp.type`, `temporal`, `scales`, `diag`, `B`, `q`, `do.parallel`
see [dcbs.alg](#)

`do.clean.cp` if `do.clean.cp = TRUE` pre-change point cleaning is performed

`sgn` if `diag = FALSE`, wavelet transformations of the cross-covariances are computed with the matching signs

Value

a numeric value for the threshold

sbs.alg

Sparsified Binary Segmentation

Description

Perform the Sparsified Binary Segmentation algorithm detecting change-points in the mean or second-order structure of the data.

Usage

```
sbs.alg(
  x,
  cp.type = c(1, 2)[1],
  thr = NULL,
  trim = NULL,
```

```

height = NULL,
tau = NULL,
temporal = TRUE,
scales = NULL,
diag = FALSE,
B = 1000,
q = 0.01,
do.parallel = 4
)

```

Arguments

<code>x</code>	input data matrix, with each row representing the component time series
<code>cp.type</code>	<code>cp.type = 1</code> specifies change-points in the mean, <code>cp.type = 2</code> specifies change-points in the second-order structure
<code>thr</code>	pre-defined threshold values; when <code>thr = NULL</code> , bootstrap procedure is employed for the threshold selection; when <code>thr != NULL</code> and <code>cp.type = 1</code> , <code>length(thr)</code> should match <code>nrow(x)</code> , if <code>cp.type = 2</code> , <code>length(thr)</code> should match <code>nrow(x)*(nrow(x)+1)/2*length(s</code>
<code>trim</code>	length of the intervals trimmed off around the change-point candidates; <code>trim = NULL</code> activates the default choice (<code>trim = round(log(dim(x)[2]))</code>)
<code>height</code>	maximum height of the binary tree; <code>height = NULL</code> activates the default choice (<code>height = floor(log(dim(x)[2], 2)/2)</code>)
<code>tau</code>	a vector containing the scaling constant for each row of <code>x</code> ; if <code>tau = NULL</code> , a data-driven choice is made which takes into account the presence of possibly multiple mean shifts and temporal dependence when <code>temporal = TRUE</code>
<code>temporal</code>	used when <code>cp.type = 1</code> ; if <code>temporal = FALSE</code> , rows of <code>x</code> are scaled by <code>mad</code> estimates, if <code>temporal = TRUE</code> , their long-run variance estimates are used
<code>scales</code>	used when <code>cp.type = 2</code> ; negative integers representing Haar wavelet scales to be used for computing <code>nrow(x)*(nrow(x)+1)/2</code> dimensional wavelet transformation of <code>x</code> ; a small negative integer represents a fine scale
<code>diag</code>	used when <code>cp.type = 2</code> ; if <code>diag = TRUE</code> , only changes in the diagonal elements of the autocovariance matrices are searched for
<code>B</code>	used when <code>is.null(thr)</code> ; number of bootstrap samples for threshold selection
<code>q</code>	used when <code>is.null(thr)</code> ; quantile of bootstrap test statistics to be used for threshold selection
<code>do.parallel</code>	used when <code>is.null(thr)</code> ; number of copies of R running in parallel, if <code>do.parallel = 0</code> , <code>%do%</code> operator is used, see also <code>foreach</code>

Value

S3 `bin.tree` object, which contains the following fields:

<code>tree</code>	a <code>list</code> object containing information about the nodes at which change-points are detected
<code>mat</code>	matrix concatenation of the nodes of <code>tree</code>
<code>ecp</code>	estimated change-points
<code>thr</code>	threshold used to construct the tree

References

H. Cho and P. Fryzlewicz (2014) Multiple-change-point detection for high dimensional time series via sparsified binary segmentation. *JRSSB*, vol. 77, pp. 475–507.

Examples

```
x <- matrix(rnorm(20*300), nrow = 20)
sbs.alg(x, cp.type = 2, scales = -1, diag = TRUE, do.parallel = 0)$ecp
```

```
x <- matrix(rnorm(100*300), nrow = 100)
x[1:10, 151:300] <- x[1:10, 151:300]*sqrt(2)
sbs.alg(x, cp.type = 2, scales = -1, diag = TRUE, do.parallel = 0)$ecp
```

sbs.thr

Bootstrapping for threshold selection in SBS algorithm

Description

Generate thresholds for SBS algorithm via bootstrapping

Usage

```
sbs.thr(
  z,
  interval = c(1, dim(z)[2]),
  cp.type = 1,
  do.clean.cp = TRUE,
  scales = NULL,
  diag = FALSE,
  sgn = NULL,
  B = 1000,
  q = 0.01,
  do.parallel = 4
)
```

Arguments

<code>z</code>	input data matrix, with each row representing the component time series
<code>interval</code>	a vector of two containing the start and the end points of the interval from which the bootstrap test statistics are to be calculated
<code>cp.type</code> , <code>scales</code> , <code>diag</code> , <code>B</code> , <code>q</code> , <code>do.parallel</code>	see sbs.alg
<code>do.clean.cp</code>	if <code>do.clean.cp = TRUE</code> pre-change-point cleaning is performed
<code>sgn</code>	if <code>diag = FALSE</code> , wavelet transformations of the cross-covariances are computed with the matching signs

Value

if `cp.type = 1`, a vector of length `nrow(z)`, each containing the threshold applied to the CUSUM statistics from the corresponding coordinate of `z` if `cp.type = 2`, a vector of length `length(scales)*nrow(z)` (when `diag = TRUE`) or `length(scales)*nrow(z)*(nrow(z)+1)/2` (when `diag = FALSE`), each containing the threshold applied to the CUSUM statistics of the corresponding wavelet transformation of `z`

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