Package ‘NCP’

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Title Network Change Point Detection Using Spectral Clustering
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Description This package detects the change points in terms of network structures. Spectral clustering is used to extract network structure, principal angles are the criterion for change points, and stationary bootstrap is used to test the significance of the change points chosen by exhaustive search.
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R topics documented:

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NCP-package       Network Change Point Detection Using Spectral Clustering

Description

This package detects the change points in terms of network structures. Spectral clustering is used to extract network structure, principal angles are the criterion for change points, and stationary bootstrap is used to test the significance of the change points chosen by exhaustive search.
Details

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References


Examples

### generate data
t  = 100
s.p  = 200
gen.k  = 2
n.tot  = gen.k * s.p
rho  = 0.5
Sigma1  = group.corr(smaller.n = s.p, rho = rho, p = n.tot)
reorder  = sample(c(1:n.tot), n.tot)
Sigma2  = Sigma1[reorder, reorder]
set.seed(1)
Y1  = mvrnorm(n = t, mu = rep(0, n.tot), Sigma = Sigma1)
Y2  = mvrnorm(n = t, mu = rep(0, n.tot), Sigma = Sigma2)
y  = rbind(Y1, Y2)

### set arguments
changepointsplot = 2
network  = 1
T  = 200
quantile_1  = 0.025
quantile_2  = 0.975
K  = 5
thres  = 0.3
core.limit  = 2
# by R policy, the examples cannot use more than 2 cores
# in practice, just leave this argument missing
# all the cores will be used then

### run
spectralfunction(y = y, K = K, core.limit = core.limit)
### four files are automatically saved in the working directory from the previous function
group.corr

```r
## three of them are required to proceed the following function
# ncpplots(y = y, changepointsplot = changepointsplot, network = network, K = K, thres = thres)
```

---

**group.corr**

*Generate a correlation matrix with a group structure.*

**Description**

Used in generating the example data. For a \( p \times p \) correlation matrix with group structure, the off-diagonal entries within each group is \( \rho \) and 0 otherwise.

**Usage**

```r
group.corr(small.n, rho, p)
```

**Arguments**

- `small.n`: group size – a positive integer.
- `rho`: the within group correlation – a real value in \([0, 1]\).
- `p`: the matrix dimension – a positive integer greater than or equal to `small.n`.

**Value**

A \( p \times p \) correlation matrix.

**Author(s)**

Ivor Cribben and Yi Yu

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**ncpplots**

*Network change plots.*

**Description**

`ncpplots` is the main function to plot the change points against time and the undirected graphs, results thereof are provided by `spectral.clustering.plot` and `network.cluster.plot`.

**Usage**

```r
ncpplots(y, changepointsplot, network = 0, quantile_1 = 0.025, quantile_2 = 0.975, actualcps = 'ActualCPs', bootcps = 'BootCPs', signcps = 'SignCPs', K, thres = 0.3)
spectral.clustering.plot(ny, nK)
network.cluster.plot(datay, K, thres = 0.3)
```
spectral.clustering

Arguments

- **y**
  - input matrix – `n.timepoints x n.voxels`, used in `ncpplots`.
- **datay**
  - the input matrix – an `n.timepoints x n.voxels` matrix, used in `network.cluster.plot`.
- **ny**
  - the input matrix – an `n.timepoints x n.voxels` matrix, used in `network.cluster.plot`.
- **nk**
  - number of communities – a positive integer, used in `spectral.clustering.plot`.
- **changepointsplot**
  - the number of significant change points – a positive integer.
- **network**
  - number of networks to plot – a positive integer. If no network to plot, `network = 0`. The default is 0.
- **quantile_1**
  - the lower quantile for change points. The default is 0.025.
- **quantile_2**
  - the upper quantile for change points. The default is 0.975.
- **actualcps**
  - the output file containing actual change points from `spectralfunction`.
- **bootscps**
  - the output file containing stationary bootstrap change points from `spectralfunction`.
- **signncps**
  - the output file containing significant bootstrap change points from `spectralfunction`.
- **K**
  - number of communities – a positive integer, used in `ncpplots` and `network.cluster.plot`.
- **thres**
  - the threshold on the correlation used to construct an adjacency matrix – a real value in [0,1]. The default is 0.3.

Value

A plot is given with x-axis being the time points and y-axis being the cosine values of the angles at the change points.

Author(s)

Ivor Cribben and Yi Yu

References


See Also

`spectralfunction`.

Description

Different from the conventional spectral clustering, the output of this function is a centroid matrix. After a K-dimensional embedding, replacing each node by its corresponding centroid.

Usage

`spectral.clustering(Y, K, t.min = 1, t.max)`
spectralfunction

Arguments

- **Y**: input matrix – an `n.timepoints x n.voxels` matrix.
- **K**: the pre-specified community number – a positive integer.
- **t.min**: the first time point of interest. The default is 1.
- **t.max**: the last time point of interest. If missing, the last point available is set.

Value

- A `n.voxels x K` correlation matrix.

Author(s)

Ivor Cribben and Yi Yu

References


Examples

```r
### generate data
t  = 100
s.p = 200
gen.k = 2
n.tot = gen.k * s.p
rho = 0.5
Sigma = group.cor(small.n = s.p, rho = rho, p = n.tot)
y = mvrnorm(n = t, mu = rep(0, n.tot), Sigma = Sigma)

### set arguments
K  = 5

### run
fit = spectral.clustering(Y = y, K = K)
```

---

**spectralfunction**

*Network change points detection using spectral clustering.*

Description

The main function in this package.

Usage

```r
spectralfunction(y, K, lower = 0, upper, maxn = 50, quan = 0.9, n.boot = 100, block = 0.05,
quantile_1 = 0.025, quantile_2 = 0.975, actualcps = 'ActualCPs',
bootcps = 'BootCPs', signcps = 'SignCPs', core.limit)
```
spectralfunction

Arguments

- **y**
  - dataset to be analysed – a n.timepoints x n.voxels matrix.
- **K**
  - the pre-specified number of communities – a positive integer.
- **lower**
  - first time point for the algorithm. The default is 0.
- **upper**
  - last time point for the algorithm. If missing, then the default is the last time point in y.
- **maxn**
  - minimum number of time points to construct a network. The default choice is 50.
- **quan**
  - quantile threshold – used in detect outliers in the criterion values. The default choice is 0.9.
- **n.boot**
  - number of iterations used in the stationary bootstrap. The default choice is 100.
- **block**
  - size of average block length for stationary bootstrap. The default is 0.05.
- **quantile_1**
  - the lower quantile for testing, used in the stationary bootstrap. The default is 0.025.
- **quantile_2**
  - the upper quantile for testing, used in the stationary bootstrap. The default is 0.975.
- **actualcps**
  - the name of the file containing the actual change points. The default is 'Actual-CPs'.
- **bootscps**
  - the name of the file containing the actual change points. The default is 'BootCPs'.
- **signcps**
  - the name of the file containing the actual change points. The default is 'SignCPs'.
- **core.limit**
  - the upper limit of the cores could be used. If missing, all the cores detected will be used.

Details

The smaller the criterion value is, the more significant the corresponding change point is.

Value

- **ActualCPs**
  - a plain text file containing the change points and their corresponding criterion values by exhaustive search.
- **BootCPs**
  - a plain text file containing the stationary bootstrap results on the change points detected by exhaustive search.
- **SignCPs**
  - a plain text file containing the significant change points and their corresponding criterion values after stationary bootstrap inference.

Author(s)

Ivor Cribben and Yi Yu

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