# Package 'deltaGseg'

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**Type** Package

**Title** deltaGseg

**Version** 1.38.0

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**Author** Diana Low, Efthymios Motakis

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**Description** Identifying distinct subpopulations through multiscale time series analysis

**License** GPL-2

**Depends** R (>= 2.15.1), methods, ggplot2, changepoint, wavethresh,
tseries, pvclust, fBasics, grid, reshape, scales

**Suggests** knitr

**VignetteBuilder** knitr

**biocViews** Proteomics, TimeCourse, Visualization, Clustering

**Collate** AllClasses.R AllGenerics.R show-methods.R plot-methods.R
pvclust-mods.R helpers.R

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## R topics documented:

1

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chooseBreaks                          *Choose a given number of breakpoints in a set of trajectories.*

---

## Description

This function automatically chooses a subset of breakpoints from all the estimated breakpoints of
function splitTraj

## Usage

```
chooseBreaks(breakpoints, numbreaks)
```

## Arguments

breakpoints    Numeric list, output from splitTraj.

numbreaks      Integer. Number of breakpoints to be returned per trajectory. Breakpoints chosen will be evenly spaced from those defined by splitTraj.

## Details

None.

## Value

Returns a numeric list of breakpoints, one list per trajectory.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## See Also

[splitTraj](#)

## Examples

```
data(deltaGseg)
all_breakpoints<-splitTraj(traj1) #default splits=15 (i.e. 16 segments).
all_breakpoints
chooseBreaks(all_breakpoints,numbreaks=3)
```

---

chooseBreaks-methods    *chooseBreaks*

---

## Description

Choose evenly spaced breakpoints from a list of breakpoints.

## Methods

signature(breakpoints="list",numbreaks="numeric") Returns a sublist of breakpoints of length numbreaks.

## Author(s)

Diana H.P. Low, Efthimios Motakis

---

clusterPV                          *clusterPV*

---

## Description

Wrapper for modified pvclust function.

## Usage

```
clusterPV(object,bootstrap=500)
```

## Arguments

object          An object of class 'SegTrajectories'.

bootstrap       Integer. Number of bootstraps to run.

## Details

This is a wrapper to call the pvclust function that has been modified to suit our deltaGseg computation.

## Value

Returns an object of class "pvclust". For use in [clusterSegments](#) when running the pvclust option.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

Shimodaira, H. (2004). Approximately unbiased tests of regions using multistep-multiscale bootstrap resampling, Annals of Statistics 32, 2616-2641.

## See Also

[clusterSegments](#)]

## Examples

```
data(deltaGseg)
clusterPV(traj1.denoise)
```

---

clusterPV-methods          *clusterPV*

---

### Description

Returns a pvclust values for object of class "SegTrajectories")

### Methods

signature(object = "SegSeriesTrajectories") Returns an object of class "pvclust".

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### See Also

[transformSeries](#)

### Examples

```
#data(deltaGseg)
#clusterPV(td2)
```

---

clusterSegments          *clusterSegments*

---

### Description

The function does hierarchical clustering of the segmented (and joined) series by hclust and performs one of the "intervention" methods (see the respective parameter below) to identify subpopulations. The hierarchical clustering is performed by Euclidean distances using "average" linkage method.

### Usage

```
clusterSegments(object, intervention = "groups",pv=NULL,graphics=NULL)
```

## Arguments

| | |
|---|---|
| `object` | An object of class 'SegTrajectories' |
| `intervention` | intervention: Character. One of "groups","heights" or "pvclust". Option pvclust performs simple hierarchical clustering by hclust and then assesses the uncertainty in the clustering by the bootstrap probability values computed via multiscale bootstrap resampling. Option "groups" asks the user to input the number of subpopulations we want to identify (interactive). Option "heights" asks the user to interactively set a threshold T (a horizontal line on the tree plot) that defines the number of subpopulations. |
| `pv` | Supplied p-values for intervention=pvclust. See [clusterPV](clusterPV) |
| `graphics` | Character vector. Optional parameter defining the colors for plotting (each color indicates a different subpopulation). Must be at least the length of total number of subpopulations defined. |

## Details

The algorithm offers several alternatives for subpopulation estimation that, ultimately, they lead to similar solutions. The user should first visualize the segmented data to get a rough idea of the possible subpopulations (plots generated by the algorithm). Option "pvclust" computes the hierarchical clustering tree with the p-values. The subpopulations are defined interactively by the user (point and click based on the R function identify(); see help(identify)). Alternatively, option "groups" asks the user to input the number of subpopulations or define them interactively in option "height" (point and click at the desired height in the tree). The final plot shows the number of estimated subpopulations.

## Value

An object of class SegSeriesTrajectories.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

Shimodaira, H. (2004) Approximately unbiased tests of regions using multistep-multiscale bootstrap resampling, Annals of Statistics, 32, 2616-2641.

## Examples

```
## Not run:
## interactive!
data(deltaGseg)
traj1.ss<-clusterSegments(traj1.denoise, intervention = "groups") #define clusters by number of groups formed.

## End(Not run)
```

---

clusterSegments-methods

*clusterSegments*

---

## Description

Performs the function `clusterSegments` on an object of class "SegTrajectories".

## Methods

signature(object = "SegTrajectories") Returns an object of class "SegSeriesTrajectories"

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None

## Examples

```
#data(deltaGseg)
#st<-clusterSegments(dt)
```

---

deltaGseg *deltaGseg*

---

## Description

deltaGseg

## Details

| | |
|---|---|
| Package: | deltaGseg |
| Type: | Package |
| Version: | 0.99.0 |
| Date: | 2013-02-04 |
| License: | GPL-2 |

**Author(s)**

Diana H.P. Low, Efthimios Motakis

Maintainer: Diana H.P. Low <dlow@imcb.a-star.edu.sg>

**References**

Zhou W., Motakis E., Fuentes G., Verma C.S. (2012) Macrostate identification from biomolecular simulations through time series analysis. J Chem Inf Model. 2012 Sep 24;52(9):2319-24. Epub 2012 Sep 5.

Dickey, D.A. and W.A. Fuller (1979), Distribution of the Estimators for Autoregressive Time Series with a Unit Root. Journal of the American Statistical Association, 74, p. 427-431.

Nason, G.P. (2008) Wavelet methods in Statistics with R. Springer, New York.

Auger, I. E.; Lawrence, C. E. Algorithms for the optimal identification of segment neighborhoods. Bull. Math.Biol. 1989, 51(1), 39-54.

Shimodaira, H. (2004) Approximately unbiased tests of regions using multistep-multiscale bootstrap resampling, Annals of Statistics, 32, 2616-2641.

D'Agostino R.B., Pearson E.S. (1973); Tests for Departure from Normality, Biometrika 60, 613-22.

---

denoiseSegments                     *Wavelet denoising of trajectory series (segments)*

---

**Description**

This function computes Augmented Dickey-Fuller test for weak-stationarity and carries out segmentation and wavelets denoising.

**Usage**

```
denoiseSegments(object,seg_method="BinSeg",maxQ=15,fn=1,factor=0.8,thresh_level=TRUE,minobs=200)
```

**Arguments**

object          An object of class "Trajectories" or "TransTrajectories". (the output of functions
                parseTraj or transformSeries, respectively).

seg_method      Character. One of "SegNeigh" or "BinSeg". By default it performs the Segment
                Neighborhood (SegNeigh) method to find multiple changes in mean for data that
                is assumed to be normally distributed. The value returned is the result of finding
                the optimal location of up to Q changepoints using the log of the likelihood ratio
                statistic. Once all changepoint locations have been calculated, the optimal num-
                ber of changepoints is decided using k*pen as the penalty function where k is the
                number of changepoints tested (k in (1,Q)). In very large series, the memory de-
                manding "SegNeigh" can be replaced by "BinSeg"" (Binary Segmentation). The
                segmenation is performed only if the Augmented Dickey-Fuller test P-value is
                significant at alpha=0.05. If not, an error message appears indicating the need
                of series splitting or differentiation (see transformSeries).

| maxQ | Integer. The maximum number of Q changepoints to be estimated. |
|------|---|
| fn | Integer. It specifies the degree of smoothness of the wavelet that you want to use in the decomposition. It takes values from 1 (coarsest/hard smoothing, i.e. Haar's step function) to 10 (finest/soft smoothing). Put simply, the fitted (wavelet denoised/estimated) data of segment q with fn=1 have lower variance than the fitted data of q under fn=10. The former data will resemble a step function over time while the latter will be much closer to the original data. |
| factor | Numeric. Between 0.6 and 1 used for re-scaling the denoising threshold. |
| thresh_level | Logical. If FALSE then a global threshold is computed on and applied to all scale levels. If TRUE a threshold is computed and applied separately to each scale level (for serious residuals autocorrelation). |
| minobs | Integer. The minimum number of observations a segment should consist of to be accepted |

## Value

An object of class "SegTrajectories"

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

Dickey, D.A. and W.A. Fuller (1979), Distribution of the Estimators for Autoregressive Time Series with a Unit Root, Journal of the American Statistical Association, 74, p. 427-431.

Nason, G.P. (2008) Wavelet methods in Statistics with R. Springer, New York.

Auger, I. E.; Lawrence, C. E. Algorithms for the optimal identification of segment neighborhoods. Bull. Math.Biol. 1989, 51(1), 39-54.

## See Also

[transformSeries](transformSeries)

## Examples

```
data(deltaGseg)
traj1.denoise<-denoiseSegments(traj1.tr,seg_method="BinSeg",maxQ=15,fn=1,factor=0.8,thresh_level=TRUE,minobs=2
```

---

denoiseSegments-methods
                            *denoiseSegments*

---

### Description

Performs the function `denoiseSegments` on an object of either class "Trajectories" or "TransTrajectories" (classUnion="TrajORTransTraj").

### Methods

signature(object = "Trajectories")  Returns an object of class "SegTrajectories"

signature(object = "TransTrajectories")  Returns an object of class "SegTrajectories"

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### Examples

```
#data(deltaGseg)
#dt<-denoiseSegments(tt)
```

---

 diagnosticPlots            *diagnosticPlots*

---

### Description

This function generates the diagnostic plots of the wavelet denoising model residuals. The assumptions are that the residuals autocorrelation is not significant and that the residuals distribution is approximately normal or, at least, symmetric around 0. We provide plots and test to verify these assumptions (depends on R package fBasics).

### Usage

```
diagnosticPlots(object, norm.test="KS",single.series = FALSE)
```

## Arguments

object        An object of class "SegSeriesTrajectories".

norm.test     Character. One of "KS", "Shapiro", "Agost". Test for residuals normality accepting "KS" (Kolmogorov Smirnov test with Lilliefors correction), "Shapiro"" (Shapiro test for normality) and "Agost"" (D'Agostino test for normality using the skewness and kurtosis of the data ; also gives the skewness and kurtosis p-values for the hypothesis that the respective estimated measures differ from the theoretical values under the normal distribution).

single.series  Logical. If FALSE (default) the residuals of each series are independently analyzed.

## Details

The function outputs the standard autocorrelation plots for viewing the residuals autocorrelation, histograms for checking the normality assumptions and the respective P-values to test the normality assumption.

## Value

A series of plots with printed P-values for the autocorrelation and normality tests.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

D'Agostino R.B., Pearson E.S. (1973); Tests for Departure from Normality, Biometrika 60, 613-22.

## Examples

```
data(deltaGseg)
diagnosticPlots(traj1.ss,norm.test="KS",single.series=TRUE)
```

---

```
diagnosticPlots-methods
```
                         *diagnosticPlots*

---

## Description

Performs the function `diagnosticPlots` on an object of class "SegSeriesTrajectories".

## Methods

signature(object = "SegSeriesTrajectories") Returns histogram and acf plots of series

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### Examples

```
#data(deltaGseg)
#diagnosticPlots(st)
```

---

getAVD                                        *getAVD*

---

### Description

Accessor of Trajectories or TransTrajectories object to retrieve adf p-values.

### Usage

```
getAVD(object)
```

### Arguments

object              An object of class 'Trajectories' or 'TransTrajectories'.

### Value

Returns a vector (of pvalues) for each trajectory defined in the object.

### Note

None.

### Author(s)

Diana H.P. Low, Efthimios Motakis

### See Also

[parseTraj](#),[transformSeries](#)

### Examples

```
data(deltaGseg)
getAVD(traj1)
```

---

getAVD-methods          getAVD

---

### Description

Returns numeric vector from the slot @avd in an object of class "Trajectories", or @tavd in an object of class "TransTrajectories."

### Methods

signature(object = "Trajectories") Numeric vector of length equal to series length.

signature(object = "TransTrajectories") Numeric vector of length equal to series length.

### See Also

[getAVD](),[parseTraj](),[transformSeries]()

---

getBreaks          *getBreaks*

---

### Description

Accessor of TransTrajectories object to retrieve computed breakpoints.

### Usage

getBreaks(object)

### Arguments

object          An object of class 'TransTrajectories'.

### Details

None.

### Value

Returns a list (of numerical breakpoint values) for each trajectory defined in an object of class 'Trajectories'.

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### See Also

[splitTraj](#),[transformSeries](#)

### Examples

```
data(deltaGseg)
getBreaks(traj1.tr)
```

---

getBreaks-methods          *getBreaks*

---

### Description

Returns a list from the @breakpoints slot for object of class "TransTrajectories")

### Methods

signature(object = "SegSeriesTrajectories") List of breakpoints per series after transformation of series data using transformSeries

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### See Also

[transformSeries](#)

### Examples

```
#data(deltaGseg)
#getBreaks(traj1.tr)
```

```
getIntervals            getIntervals
```

## Description

Helper function to retrieve subpopulations and computes the intervals for each subpopulation after segmentation and clustering.

## Usage

```
getIntervals(object)
```

## Arguments

object          An object of class 'SegSeriesTrajectories'.

## Details

None.

## Value

Returns a list of subpopulations and the intervals.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None

## See Also

[clusterSegments](clusterSegments)

## Examples

```
data(deltaGseg)
getIntervals(traj1.ss)
```

---

getIntervals-methods    *getIntervals*

---

### Description

Returns a list of subpopulations and the intervals of the segmented series.)

### Methods

signature(object = "SegSeriesTrajectories") Returns a list of subpopulations and the intervals of the segmented series from segmentationWithinSeries

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### See Also

[transformSeries](transformSeries)

### Examples

```
#data(deltaGseg)
#getIntervals(traj1.ss)
```

---

getSegments    *getSegments*

---

### Description

Accessor of SegTrajectories or SegSeriesTrajectories object to retrieve segment matrix.

### Usage

```
getSegments(object)
```

### Arguments

object    Object of class "SegTrajectories"" or "SegSeriesTrajectories"

### Value

A matrix with segment information including quantiles.

## Note

None.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None.

## See Also

denoiseSegments, clusterSegments

## Examples

```
data(deltaGseg)
segments<-getSegments(traj1.denoise)
```

---

getSegments-methods          *getSegments*

---

## Description

Returns a matrix from the @smatrix slot (for object of class "SegTrajectories") or @ssmatrix slot (for object of class "SegSeriesTrajectories")

## Methods

signature(object = "SegSeriesTrajectories") Matrix is a result of the function clusterSegments

signature(object = "SegTrajectories") Matrix is a result of the function denoiseSegments

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None

## Examples

```
#data(deltaGseg)
#getSegments(traj1.denoise)
```

---

getTNames                    *getTNames*

---

## Description

Accessor of Trajectories and TransTrajectories object to retrieve filename(s) used in trajectory computation.

## Usage

```
getTNames(object)
```

## Arguments

object            An object of class 'Trajectories' or 'TransTrajectories'.

## Details

None.

## Value

Returns character vector of filenames.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None.

## Examples

```
data(deltaGseg)
getTNames(traj1)
```

---

getTNames-methods *Retrieve filenames of trajectories*

---

### Description

Returns a vector from the @filenames or @tfilenames slot.

### Details

Returns a vector of filename(s) values.

### Methods

signature(object = "Trajectories") Returns the original filenames of series read by parse-Traj.

signature(object = "TransTrajectories") Returns filenames generated by the transformSeries function if the originial series has been split into subseries. Subseries names are denoted by an underscore after the original names, eg. FILE1_1, FILE1_2.

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### Examples

```
#data(deltaGseg)
#getTNames(traj1)
```

---

getTraj *getTraj*

---

### Description

Accessor of Trajectories or TransTrajectories object to retrieve trajectories.

### Usage

```
getTraj(object)
```

### Arguments

object          An object of class "Trajectories" or "TransTrajectories"

## Details

None.

## Value

List of length equal to number of trajectories, each containing matrix with 2 columns. 1: time points, 2: free energy values.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None.

## Examples

```
data(deltaGseg)
alltrajectories<-getTraj(traj1)
```

---

getTraj-methods                 *getTrajectories*

---

## Description

Returns a list of matrices from the @trajlist slot (for object of class "Trajectories") or @ttrajlist slot (for object of class "TransTrajectories")

## Methods

signature(object = "Trajectories") Returns the original trajectories used for computation.

signature(object = "TransTrajectories") Returns the transformed trajectories generated by the function `transformSeries`

## Author(s)

Diana H.P. Low, Efthimios Motakis

---

parseTraj                    *Reads in files containing trajectory data*

---

## Description

Reads in files with 2-column, space-separated numerical values containing 1:time points, 2:trajectory(free binding energies).

## Usage

```
parseTraj(path = getwd(), files = NULL,fromfile=TRUE)
```

## Arguments

| | |
|---|---|
| path | Directory containing trajectory files. |
| files | Character vector of filenames to read. If not provided, will read all files in given directory and treat them as a set. Can also be used to read in variables if given as list. |
| fromfile | Logical. If set to FALSE, the files parameter will be used to read in variables. |

## Details

This is an initialization function for the deltaGseg package. It reads the trajectory files (input) and reports the a short description of the file, the Augmented Dickey-Fuller test p-values for each trajectory in the set and the data plot. The input files should be in tab delimited form with 2 columns: the first column contains the time points 1, 2, ..., T and the second the free binding energies at each time point.

## Value

A 'Trajectories' object.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None.

## See Also

[Trajectories-class](Trajectories-class)

## Examples

```
traj1<-parseTraj(path=system.file("extdata",package="deltaGseg"),files=c("D_GBTOT1","D_GBTOT2","D_GBTOT3"))
traj1  #prints summary of traj1 object

# using parseTraj for existing variables ##
subtraj<-getTraj(traj1)[[1]] #extracts first trajectory in the above series
traj2<-parseTraj(files=list(subtraj),fromfile=FALSE)
traj2
```

---

plot-methods                *Plot Trajectories-related objects*

---

### Description

Plot "Trajectories" objects and customizes output.

### Methods

signature(x = "Trajectories") plot(object,name='all',breakpoints=NULL)

> name: Character. Name of sub-series, or if all, plots the whole series.
> breakpoints: List. Supply breakpoints generated by splitTraj.

signature(x = "TransTrajectories") plot(object,labelling=TRUE)

> labelling: Logical. Writes labels. May be turned off to prevent overcrowding of plot.

signature(x = "SegTrajectories") plot(object)

signature(x = "SegSeriesTrajectories") plot(object)

---

plotDiff                    *plotDiff*

---

### Description

Plots (sub)series before and after transformation.

### Usage

```
plotDiff(object,name=NULL)
```

### Arguments

| | |
|---|---|
| object | An object of class 'TransTrajectories'. |
| name | Character. Name of (sub)series. |

## Details

None.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None

## See Also

[transformSeries](#)

## Examples

```
data(deltaGseg)
plotDiff(simtraj.tr2,name="1_2")
```

---

```
plotDiff-methods        plotDiff
```

---

## Description

Plots differentiated (sub)series in object of class "TransTrajectories")

## Methods

signature(object = "TransTrajectories") Plots (sub)series before and after transformation.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

None

## See Also

[transformSeries](#)

## Examples

```
#data(deltaGseg)
#plotDiff(traj1.tr,'D_GBTOT3_1')
```

---

| pvals | *pvalues data* |
|---|---|

---

### Description

pvals is the bootstrapped pvalues obtained via [pvclust](#) for [clusterSegments](#)

### Usage

```
data(deltaGseg)
```

### Format

class pvclust

### Source

internal

---

SegSeriesTrajectories-class

*Class* "SegSeriesTrajectories"

---

### Description

Objects of this class is a product of the clusterSegments function.

### Objects from the Class

Objects can be created by calls of the form new("SegSeriesTrajectories", ...).

### Slots

ssmatrix: Object of class "data.frame" The output is a data.frame with the following information (in columns): the observed data ("observed"), the estimated, wavelet denoised data ("estimated"), the residuals of the estimation ("residuals"), the estimated subpopulations IDs ("subpopulations"), the series IDs/filenames ("seriesID")

ssparams: Object of class "character" Parameters used to run the clustering algorithm, [clusterSegments](#).

sparams: Object of class "character" Parameters used to run the segmentation algorithm, [denoiseSegments](#).

smatrix: Object of class "matrix" A matrix containing the preliminary results from segmentation/denoising for each (sub)series generated by [transformSeries](#). Each list element contains the following information in matrix form (in columns): the observed data (1st column), the estimated, wavelet denoised data (2nd column), the residuals of the estimation (3rd column), the starting/ending time points of each segment (4th/5th columns), the estimated segment IDs (6th column), the quantiles of the estimated data [minimum, 5%, 10%, 15%, ..., 95%, maximum] (from columns 7th to 27th) and the series IDs (28th column)

path: Object of class "character" Inherited from Trajectories-class

filenames: Object of class "character" Inherited from Trajectories-class

trajlist: Object of class "list" Trajectories. Inherited from Trajectories-class

avd: Object of class "numeric" adf p-values. Inherited from Trajectories-class

tmethod: Object of class "character" Transformation method. Inherited from TransTrajectories-class

breakpoints: Object of class "list" breakpoints, if used.

tavd: Object of class "numeric" adf p-values after transformation, if used. Inherited from TransTrajectories-class

ttrajlist: Object of class "list" Transformed trajectories. Inherited from TransTrajectories-class

tfilenames: Object of class "character" Transformed trajectories names. Inherited from TransTrajectories-class

ct: Object of class "numeric" Grouping information.

## Extends

Class "SegTrajectories", directly. Class "TransTrajectories", directly. Class "Trajectories", directly.

## Accessors

In the code snippets below, x is a SegSeriesTrajectories object.

getTNames(x): Retrieves filenames from slot filenames or tfilenames depending on whether the series has been transformed.

getTraj(x): Retrieves trajectories list from slot trajlist or ttrajlist depending on whether the series has been transformed.

getBreaks(x): Retrives breakpoints (if any) from slot breakpoints

getAVD(x): Retrieves adf p-values from slot avd or tavd depending on whether the series has been transformed.

getSegments(x): Retrieves clustered segmentation data from slot smatrix produced by clusterSegments

## Other methods

In the code snippets below, x is a SegSeriesTrajectories object.

diagnosticPlots(x): Generates the diagnostic plots of the wavelet denoising model residuals

getIntervals(x): Helper function to retrieve subpopulations and computes the intervals for each subpopulation after segmentation and clustering.

plot(x): Plots the final clustered segmentation data after clusterSegments

show(x): Displays summary of object, including inherited classes. This helps in recalling the analysis path taken to produce the current results.

## Author(s)

Diana H.P. Low, Efthimios Motakis

## See Also

[SegTrajectories](), [clusterSegments]()

## Examples

```
showClass("SegSeriesTrajectories")
```

---

SegTrajectories-class    *Class* "SegTrajectories"

---

## Description

Objects of this class is a product of the denoiseSegments function.

## Objects from the Class

Objects can be created by calls of the form new("SegTrajectories", ...).

## Slots

sparams: Object of class "character" Parameters used to run the segmentation algorithm.

smatrix: Object of class "matrix" A matrix containing the preliminary results from segmentation/denoising for each (sub)series generated by [transformSeries](). Each list element contains the following information in matrix form (in columns): the observed data (1st column), the estimated, wavelet denoised data (2nd column), the residuals of the estimation (3rd column), the starting/ending time points of each segment (4th/5th columns), the estimated segment IDs (6th column), the quantiles of the estimated data [minimum, 5%, 10%, 15%, ..., 95%, maximum] (from columns 7th to 27th) and the series IDs (28th column)

path: Object of class "character" Inherited from [Trajectories-class]()

filenames: Object of class "character" Inherited from [Trajectories-class]()

trajlist: Object of class "list" Trajectories. Inherited from [Trajectories-class]()

avd: Object of class "numeric" adf p-values. Inherited from [Trajectories-class]()

tmethod: Object of class "character" Transformation method. Inherited from [TransTrajectories-class]()

breakpoints: Object of class "list" breakpoints, if used.

tavd: Object of class "numeric" adf p-values after transformation, if used. Inherited from [TransTrajectories-class]()

ttrajlist: Object of class "list" Transformed trajectories. Inherited from [TransTrajectories-class]()

tfilenames: Object of class "character" Transformed trajectories names. Inherited from [TransTrajectories-class]()

**Extends**

Class *"TransTrajectories"*, directly. Class *"Trajectories"*, directly.

**Accessors**

In the code snippets below, x is a SegTrajectories object.

getTNames(x): Retrieves filenames from slot filenames or tfilenames depending on whether the series has been transformed.

getTraj(x): Retrieves trajectories list from slot trajlist or ttrajlist depending on whether the series has been transformed.

getBreaks(x): Retrives breakpoints (if any) from slot breakpoints

getAVD(x): Retrieves adf p-values from slot avd or tavd depending on whether the series has been transformed.

getSegments(x): Retrieves initial segmentation data from slot smatrix produced by denoiseSegments

**Other methods**

In the code snippets below, x is a SegTrajectories object.

clusterPV(x,bootstrap=500): Computes p-values to be used with method="pvclust" in clusterSegments(x)

clusterSegments(x): clustering of segmented trajectories into similar groups.

plot(x): Plots the initial segmentation data after denoising by denoiseSegments

show(x): Displays summary of object, including inherited classes. This helps in recalling the analysis path taken to produce the current results.

**Author(s)**

Diana H.P. Low, Efthimios Motakis

**See Also**

denoiseSegments

**Examples**

showClass("SegTrajectories")

---

show-methods                    *~~ Methods for Function* show *~~*

---

**Description**

~~ Methods for function show ~~

**Methods:**

```
signature(object = "SegSeriesTrajectories")
signature(object = "SegTrajectories")
signature(object = "Trajectories")
signature(object = "TransTrajectories")
```

---

simtraj                    *Sample trajectory series*

---

**Description**

simulated trajectory for appendix example

**Usage**

```
data(deltaGseg)
```

**Format**

class Trajectories

**Source**

internal

---

simtraj.tr *Sample trajectory series*

---

### Description

simulated trajectory for appendix example

### Usage

```
data(deltaGseg)
```

### Format

class Trajectories

### Source

internal

---

simtraj.tr2 *Sample trajectory series*

---

### Description

simulated trajectory for appendix example

### Usage

```
data(deltaGseg)
```

### Format

class Trajectories

### Source

internal

---

splitTraj                    *Identify Breakpoints in a Trajectory*

---

### Description

splitTraj determines the breakpoints to split a given trajectory into a user specified number of segments. This analysis is performed for very long series (more than 20,000 time points) in order to avoid any memory allocation problems in R. Alternatively, it can be used for manual splitting of the series (see transformSeries with method="override_splitting")

### Usage

```
splitTraj(object, segsplits = rep(5,length(object@filenames)))
```

### Arguments

object          An object of class "Trajectories".

segsplits       Numeric vector. The number of breakpoints. The length of segsplits must equal
                the number of trajectory series in the Trajectories object. Each value specifies
                the number of splits we want to impose in our long series in order to make it
                shorter.

### Details

The output of the function is the estimated points that split the series into smaller sub-series. Typically, the plotted series and the estimated splits are further inspected using plots.

### Value

A numeric list of length equal to number of trajectory series, containing the breakpoints for each series.

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### Examples

```
data(deltaGseg)
splitTraj(traj1)
```

---

splitTraj-methods          *splitTraj*

---

### Description

Performs the function splitTraj

### Methods

signature(object = "Trajectories") Returns a list of breakpoints identified in the trajectory
        series.

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### Examples

```
#data(deltaGseg)
#all_breakpoints<-splitTraj(traj1)
```

---

traj1                    *Sample trajectory series*

---

### Description

traj1 is a sample trajectory series from the data files provided in the deltaGseg package

### Usage

```
data(deltaGseg)
```

### Format

class Trajectories

### Source

internal

---

traj1.denoise                    *Sample trajectory series*

---

### Description

traj1.tr is the denoised trajectory after using [denoiseSegments](#)

### Usage

    data(deltaGseg)

### Format

class SegTrajectories

### Source

internal

---

traj1.ss                         *Sample trajectory series*

---

### Description

traj1.ss is the clustered series after using [clusterSegments](#)

### Usage

    data(deltaGseg)

### Format

class SegSeriesTrajectories

### Source

internal

---

traj1.tr *Sample trajectory series*

---

### Description

traj1.tr is the transformed trajectory after using [transformSeries](#)

### Usage

```
data(deltaGseg)
```

### Format

class TransTrajectories

### Source

internal

---

Trajectories-class *Class* "Trajectories"

---

### Description

Objects of this class is a product of the initialization function, parseTraj.

### Objects from the Class

Objects can be created by calls of the form new("Trajectories", ...).

### Slots

path: Object of class "character" Directory where files were read from.

filenames: Object of class "character" Name of files read.

trajlist: Object of class "list" Trajectories.

avd: Object of class "numeric" adf p-values.

### Accessors

In the code snippets below, x is a Trajectories object.

getTNames(x): Retrieves filenames from slot filenames.

getTraj(x): Retrieves trajectories list from slot trajlist.

getBreaks(x): Retrives breakpoints (if any) from slot breakpoints

getAVD(x): Retrieves adf p-values from slot avd.

**Other methods**

In the code snippets below, x is a Trajectories object.

splitTraj(x): Computes likely breakpoints for the series.

transformSeries(x): Apply transformation functions for the series if series is not stationary, or to split long series after determining breakpoints with splitTraj.

plot(x,name='all'): Plots the trajectory series either individually, or combined.

show(x): Displays summary of object, including inherited classes. This helps in recalling the analysis path taken to produce the current results.

**Author(s)**

Diana H.P. Low, Efthimios Motakis

**See Also**

parseTraj

**Examples**

```
showClass("Trajectories")
```

---

transformSeries                   *Transforms a Non-Stationary Series into a Weakly-Stationary one*

---

**Description**

It transforms non-stationary series into weakly stationary (sub)series with three alternative methods (see parameter "methods").

**Usage**

```
transformSeries(object, method = "splitting", breakpoints = 1)
```

**Arguments**

| | |
|---|---|
| object | An object of class "Trajectories". |
| method | Character. One of "differentiation","override_splitting","splitting". See details. |
| breakpoints | Integer (for method="splitting") or numeric vector (for method="override_splitting"). See details. |

## Details

(i) method="differentiation": first differences B[t]-B[t-1] are calculated and the first differentiated series is used for further analysis (segmentation and clustering). This option is needed in special cases, only when the series exhibits a trend-like behavior that cannot be removed by splitting. The first differentiations with remove the trend completely (see Appendix in the manual).

(ii) method="splitting": the series are split by automatic data segmentation to subseries. This option divides a non-stationary series to a number of subseries that are weakly stationary;

(iii) method="override_splitting": the series are split into subseries by user-defined cut-offs obtained from the numerical output of the splitTraj function. This option is for long stationary series that cannot be analyzed due to memory limitations. It can be also used for manual splitting when "splitting" option is not satisfactory. Typically, "splitting"" and "override_splitting" generate new data files of subseries.

Determining breakpoints for method (i) "splitting": an integer specifying the number of split points. This number (a single value applied to all series) denotes the number of subseries that the original series should be divided into. (ii) "override_splitting": the parameter takes the exact values (time points coordinates) of split points (a list of length equal to the number of series; see manual). One can derive and manually insert these split points after inspecting the output of the splitTraj function (see manual). The user should select a few splits so that the original series is not divided into too many subseries (difficult to process because many new files are generated). Alternatively, function chooseBreaks automatically chooses a subset of breakpoints (not recommended to keep those without inspection)

## Value

An object of class "TransTrajectories".

## Author(s)

Diana H.P. Low, Efthimios Motakis

## References

Dickey, D.A. and W.A. Fuller (1979). Distribution of the Estimators for Autoregressive Time Series with a Unit Root. Journal of the American Statistical Association 74, 427-431.

## See Also

parseTraj,splitTraj,chooseBreaks

## Examples

```
data(deltaGseg)
trans_series<-transformSeries(traj1,method='splitting',breakpoints=1)
```

---

transformSeries-methods

*transformSeries*

---

### Description

Returns a matrix from the @smatrix slot (for object of class "SegTrajectories") or @ssmatrix slot (for object of class "SegSeriesTrajectories")

### Methods

signature(object = "Trajectories") Returns an object of class "TransTrajectories"

### Author(s)

Diana H.P. Low, Efthimios Motakis

### References

None

### Examples

```
#data(deltaGseg)
#breakpoints<-chooseBreaks(all_breakpoints,3)
#tt<-transformSeries(traj1,breakpoints=breakpoints)
```

---

TransTrajectories-class

*Class "TransTrajectories"*

---

### Description

Object of this class is a product of the transformSeries function.

### Objects from the Class

Objects can be created by calls of the form new("TransTrajectories", ...).

## Slots

tmethod: Object of class "character" Transformation method.

breakpoints: Object of class "list" breakpoints, if used.

tavd: Object of class "numeric" adf p-values after transformation.

ttrajlist: Object of class "list" Transformed trajectories.

difftraj: Object of class "list" Differentiated trajectories. These trajectories may be produced if transformSeries was used with method="differentiation". The original trajectory will be kept in ttrajlist its differentiated version (used only for computation, not presentation) will be stored in this slot. The plotting function plotDiff enables the user to compare the original and differentiated versions of the subseries.

tfilenames: Object of class "character" Transformed trajectories names.

path: Object of class "character" Inherited from Trajectories-class

filenames: Object of class "character" Inherited from Trajectories-class

trajlist: Object of class "list" Trajectories. Inherited from Trajectories-class

avd: Object of class "numeric" adf p-values. Inherited from Trajectories-class

## Extends

Class "Trajectories", directly.

## Accessors

In the code snippets below, x is a TransTrajectories object.

getTNames(x): Retrieves filenames from slot tfilenames.

getTraj(x): Retrieves trajectories list from slot ttrajlist.

getBreaks(x): Retrives breakpoints (if any) from slot breakpoints

getAVD(x): Retrieves adf p-values from slot tavd.

## Other methods

In the code snippets below, x is a TransTrajectories object.

denoiseSegments(x): denoising and initial segmentation of trajectory series.

plotDiff(x,name='diff_object_name'): Plots the original and differentiated subseries (one at a time) if method="differentiation" was used in transformSeries

plot(x): Plots the transformed series after transformSeries

show(x): Displays summary of object, including inherited classes. This helps in recalling the analysis path taken to produce the current results.

## Author(s)

Diana H.P. Low, Efthimios Motakis

**See Also**

transformSeries

**Examples**

    showClass("TransTrajectories")

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