Package 'QtAC'

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Type Package

Title Quantifying the Adaptive Cycle

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Author Hannah Schrenk and Nico Schreiber and Carlos Garcia-Perez

Maintainer <hannah-schrenk@arcor.de>

Description

QtAC provides tools to analyze the maturation process of complex systems in the sense of Gunderson's and Holling's adaptive cycle metaphor (see e.g. Holling 2001). Using time series of a system's components' abundance data, the dynamics of information transfer among the components are estimated. On the basis of the resulting information networks, potential, connectedness, and resilience can be computed. The development of these three variables defines the system's course through the adaptive cycle. In addition to the functions needed to carry out the just described calculations, the package offers several options to visualize the results. The main function requires a transfer entropy estimator being included in the JIDT toolkit (Lizier 2014). Besides, functions of the packages pracma, rJava, igraph, and rgl are used.

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NeedsCompilation no

R topics documented:

QtAC   *QtAC (Main function)*

Description

This function calculates the transfer entropy between two species each for shifting time windows of fixed length or local values. The output is a list of adjacency matrices and the corresponding significance matrices.

Usage

```
QtAC(
  data,
  num_timepoints,
  javapath,
  noise_level = "1e-20",
  num_permcheck = 1000L,
  k = 1L,
  k_tau = 1L,
  l = 1L,
  l_tau = 1L,
  delay = 1L,
  mode = c("average", "local"),
  save = FALSE,
  filename = "result_QtAC"
)
```

Arguments

data	data array containing time series of the system's components' abundance data
num_timepoints	length of the time windows of abundance data serving as basis of the transfer entropy estimations
javapath	path of the file "MTinfodynamics.jar"
noise_level	amount of random Gaussian noise added in the estimation
num_permcheck	number of surrogate samples to bootstrap to generate the distribution in the significance test
k	embedding length of destination past history to consider
k_tau	embedding delay for the destination variable
l	embedding length of source past history to consider
l_tau	embedding delay for the source variable
delay	time lag between last element of source and destination next value
mode	Active information storage is either averaged over time windows ("average") or local values are estimated ("local"). In the latter case, the value of num_timepoints is ignored.
save	If save=TRUE, the output is saved in a file called filename.

Value

list of two lists (adjacency and corresponding significance matrices)

```
QtAC.2dmixplot          2dmixplot
```

Description

This function plots two selected systemic variables w.r.t. each other. A curve is interpolated via a piecewise cubic spline.

Usage

```
QtAC.2dmixplot(
  mat,
  prop1,
  prop2,
  save = FALSE,
  filename = paste("2dmixplot_", prop1, "_", prop2)
)
```

Arguments

prop1	variable on x-axis ("potential","connectedness","resilience")
prop2	variable on y-axis ("potential","connectedness","resilience")
save	If Save = TRUE, the 2D plot will be saved in a PNG file.
filename	If Save = TRUE, the network will be saved in a file called filename.
Mat	data frame containing a time series of systemic variables

Value

2D plot and, if Save = TRUE, a PNG file containing the plot

```
QtAC.2dplot             2dplot
```

Description

This function plots potential, connectedness and resilience with respect to time. Curves are interpolated via a piecewise cubic spline.

Usage

```
QtAC.2dplot(
  mat,
  prop = NULL,
  time_int = NULL,
  time = "time",
  save = FALSE,
  filename = "2dplot"
)
```

Arguments

mat	dataframe containing a time series of systemic variables
prop	If prop = NULL, the three systemic variables are plotted w.r.t time in one plot each. If prop = "potential", "connectedness", or "resilience", only the selected systemic variable is plotted w.r.t time.
time_int	vector containing start time, end time, and step size to define the xaxis
time	unit (i.e. "years", "steps",...)
save	If save = TRUE, the 2D plot will be saved in a PNG file.
filename	If save = TRUE, the network will be saved in a file called filename.

Value

2D plot and, if save = TRUE, a PNG file containing the plots.

QtAC.3dplot   *3dplot*

Description

3D plot of the three systemic variables w.r.t each other. A curve is interpolated via a piecewise cubic spline.

Usage

```
QtAC.3dplot(mat, mat_points = FALSE)
```

Arguments

mat_points	If mat_points = TRUE, the maturation points are visible.
Mat	data frame containing a time series of the three systemic variables

Value

3D plot

QtAC.maturation   *maturation*

Description

This function computes the three systemic variables (potential, connectedness, and resilience) of each adjacency matrix.

Usage

```
QtAC.maturation(result_mtx, res_stand = "maxweight")
```

Arguments

`result_mtx`	list of adjacency matrices and significance matrices
`res_stand`	standardization constant c of the Laplacian matrices ("none", "maxweight", "nodes", "maxweightnodes"). Let N be the number of nodes of the underlying graph and M its maximal edge weight. If res_stand = "none", $c = 1$. If res_stand = "maxweight", $c = \frac{1}{\sqrt{M}}$. If res_stand = "nodes", $c = \frac{\sqrt{N-1}}{N}$. If res_stand = "maxweightnodes", $c = \frac{\sqrt{N-1}}{N \cdot \sqrt{M}}$.

Value

dataframe containing the three systemic variables (potential, connectedness, and resilience) of each adjacency matrix

---

`QtAC.network`	*network*

Description

This function plots a selected adjacency matrix as network.

Usage

```
QtAC.network(
  result_mtx,
  num_mtx = 1,
  edge_label = FALSE,
  dec = 2,
  layout = "nicely",
  edge_width = 3,
  arrow_width = 5,
  col_node = "palegreen3",
  col_edge = "steelblue3",
  vertex_label = "short",
  title = paste("Network of Adjacency matrix ", times[num_mtx]),
  save = FALSE,
  filename = paste("network_", num_mtx, sep = "")
)
```

Arguments

`result_mtx`	list of adjacency matrices and significance matrices
`num_mtx`	number of the adjacency matrix you want to plot (default = 1)
`edge_label`	If edge_label = TRUE, the weight of the edges are plotted next to the edges.
`dec`	number of decimal digits in the edge labels
`layout`	layout format ("circle","star","fruchterman.reingold","grid","nicely")
`edge_width`	muliplicator for the width of the edges
`arrow_width`	muliplicator for the width of the arrows
`col_node`	color of the vertices

col_edge	color of the edges
vertex_label	If vertex_label = "short", the first 4 letters of the components' names will be used as vertex labels, if vertex_label = "long", the whole names will be used as vertex labels. Via vertex_label = c(...), customized names can be used as vertex labels.
title	title of the network
save	If save = TRUE, the network will be saved as a PNG file.
filename	If save = TRUE, the network will be saved in a file called filename.

Value

network plot and, if save = TRUE, a PNG file containing the plot

---

QtAC.signfactor   *signfactor*

Description

This function sets all entries in the adjacency matrices to 0 whose p-value is above the predefined significance level.

Usage

```
QtAC.signfactor(result_mtx, signfac = 0.05)
```

Arguments

| result_mtx | list of adjacency and significance matrices |
| signfac | significance level |

Value

list of two lists (adjacency matrix containing only significant transfers and significance matrices)

QtAC.signfactor_CTE   *.signfactor_CTE*

Description

This function sets all transfer entropies to 0 whose p-value is above the predefined significance level.

Usage

```
QtAC.signfactor_CTE(result_mtx, signfac = 0.05)
```

Arguments

`result_mtx`	list of matrices containing summands of collective transfer entropies (one row per species) and corresponding significance matrices
`signfac`	significance level

Value

list of two lists (vectors of significant collective transfer entropies and significance matrices)

`QtAC.TXT.reader`	*TXT-reader*

Description

This function is used to import the data in R. The data should be in a tab-separated file with or without column/row names. Columns should contain time points, rows the system's components.

Usage

```
QtAC.TXT.reader(filename, col_names = FALSE, row_names = FALSE)
```

Arguments

`filename`	path of the file you want to import
`col_names`	logical operator. TRUE if the file contains column names, FALSE if it does not
`row_names`	logical operator. TRUE if the file contains row names, FALSE if it does not

Value

data array. If no column or row names were given, column or row names of the form "t_ " and "C_ " respectively are added.

`QtAC_AIS`	*QtAC_AIS*

Description

This function calculates the active information storage of each species for shifting time windows of fixed length or local values. The output is a list of adjacency matrices and the corresponding significance matrices.

Usage

```
QtAC_AIS(
  data,
  num_timepoints,
  javapath,
  noise_level = "1e-20",
  num_permcheck = 1000L,
  k = 1L,
  k_tau = 1L,
  mode = c("average", "local"),
  save = FALSE,
  filename = "result_QtAC"
)
```

Arguments

data	data array containing time series of the system's components' abundance data
num_timepoints	length of the time windows of abundance data serving as basis of the active information storage estimations
javapath	path of the file "MTinfodynamics.jar"
noise_level	amount of random Gaussian noise added in the estimation
num_permcheck	number of surrogate samples to bootstrap to generate the distribution in the significance test
k	embedding length of destination past history to consider
k_tau	embedding delay
mode	Active information storage is either averaged over time windows ("average") or local values are estimated ("local"). In the latter case, the value of num_timepoints is ignored.
save	If save=TRUE, the output is saved in a file called filename.

Value

list of two vectors (AIS of all species and corresponding significance values)

QtAC_CTE   *QtAC_CTE*

Description

This function calculates the collective transfer entropy of each species for shifting time windows of fixed length or local values. The output is a list of adjacency matrices and the corresponding significance matrices.

Usage

```
QtAC_CTE(
  data,
  num_timepoints = 5,
  javapath,
  noise_level = "1e-20",
  num_permcheck = 1000L,
  k = 1L,
  k_tau = 1L,
  l = 1L,
  l_tau = 1L,
  delay = 1L,
  condEmbedDims = 1L,
  cond_taus = 1L,
  cond_delays = 1L,
  mode = c("average", "local"),
  save = FALSE,
  filename = "result_QtAC"
)
```

Arguments

data	data array containing time series of the system's components' abundance data
num_timepoints	length of the time windows of abundance data serving as basis of the collective transfer entropy estimations
javapath	path of the file "MTinfodynamics.jar"
noise_level	amount of random Gaussian noise added in the estimation
num_permcheck	number of surrogate samples to bootstrap to generate the distribution in the significance test
k	embedding length of destination past history to consider
k_tau	embedding delay for the destination variable
l	embedding length of source past history to consider
l_tau	embedding delay for the source variable
delay	time lag between last element of source and destination next value
condEmbedDims	array of embedding lengths for each conditional variable
cond_taus	array of embedding delays for the conditional variables
cond_delays	array of time lags between last element of each conditional variable and destination next value
mode	Transfer entropy is either averaged over time windows ("average") or local values are estimated ("local"). In the latter case, the value of num_timepoints is ignored.
save	If save=TRUE, the output is saved in a file called filename.

Value

list of two lists (adjacency and corresponding significance matrices)

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