

Package ‘QtAC’

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Type Package

Title Quantifying the Adaptive Cycle

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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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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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QtAC

*QtAC (Main function)***Description**

This function calculates the transfer entropy between two species each for shifting time windows of fixed length. 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,
  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
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	<i>2dmixplot</i>
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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	<i>2dplot</i>
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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	<i>3dplot</i>
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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	<i>maturation</i>
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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 $\text{res_stand} = \text{"none"}$, $c = 1$. If $\text{res_stand} = \text{"maxweight"}$, $c = \frac{1}{\sqrt{M}}$. If $\text{res_stand} = \text{"nodes"}$, $c = \frac{\sqrt{N-1}}{N}$. If $\text{res_stand} = \text{"maxweightnodes"}$, $c = \frac{\sqrt{N-1}}{N \cdot \sqrt{M}}$.

Value

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

QtAC.network	<i>network</i>
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Description

This function plots a selected adjacency matrix as network.

Usage

```
QtAC.network(
  result_mtx,
  num_mtx,
  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
edge_label	If $\text{edge_label} = \text{TRUE}$, 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	multiplicator for the width of the edges
arrow_width	multiplicator 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	<i>signfactor</i>
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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.TXT.reader	<i>TXT-reader</i>
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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.

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