

Package ‘SCFA’

June 7, 2024

Title Community Detection and Semi-confirmatory Factor Analysis
Version 0.1.0.9002
Description This package provides tools for performing community detection and semi-confirmatory factor analysis in statistical computing environments.
License MIT + file LICENSE
Encoding UTF-8
Roxygen list(markdown = TRUE)
RoxygenNote 7.2.3
Depends R (>= 2.10)
LazyData true
Suggests knitr,
rmarkdown
VignetteBuilder knitr

R topics documented:

get_sigmau	1
get_vectorform	2
greedy	3
greedy_peeling	3
param_tuning_sigmau	4
plotMatrix	5
sim	6

get_sigmau	<i>Calculate Σ_u, the unexplained residual</i>
------------	--

Description

This function calculates Σ_u and its Frobenius norm, given the data and subnetwork detection results.

Usage

```
get_sigmau(data, cid, clist)
```

Arguments

data	A data matrix.
cid	A vector of cluster sizes.
clist	A vector of cluster assignments.

Value

A list containing the SigmaU matrix (sigma_u) and its Frobenius norm (sigma_u_norm).

Examples

```
data <- matrix(runif(200), nrow = 20)
cid <- c(5, 5)
clist <- sample(1:2, 20, replace = TRUE)
result <- sigmau(data, cid, clist)
print(result)
```

get_vectorform

Convert a Square-Form Matrix to a Vector

Description

Given a distance matrix, this function converts it into a half-vector form, (a vector of the upper triangular part excluding the diagonal).

Usage

```
get_vectorform(dist)
```

Arguments

dist	A square symmetric matrix.
------	----------------------------

Value

A vector containing the upper triangular part of the matrix.

Examples

```
data(sim)
get_vectorform(sim)

mat <- matrix(1:6, nrow = 3)
get_vectorform(mat)
```

greedy	<i>Greedy algorithm</i>
--------	-------------------------

Description

A greedy version of the greedy peeling algorithm.

Usage

greedy(Wp, threshold_DSD, lambda)

Arguments

- Wp Adjacency matrix
- threshold_DSD Threshold value for filtering edges
- lambda Parameter for greedy peeling algorithm

Details

The algorithm finds a cluster at each time until the average value in the remainder adjacency matrix is below the mean of the input cluster.

Value

A list containing the resulting adjacency matrix W_DSD_greedy, cluster list Clist, and cluster ID list CID.

Examples

greedy()

greedy_peeling	<i>Greedy Peeling</i>
----------------	-----------------------

Description

A simple implementation of the greedy algorithm from the "Denser than the Densest subgraph" paper (Tsourakakis 2013) using the generalized objective function (Shuo 2023).

Usage

greedy_peeling(Wp_DSD, lambda)

Arguments

- Wp_DSD Input adjacency matrix
- lambda Parameter for the objective function

Details

Note that this function only extracts ONE dense subgraph.

Value

A list containing:

W_DSD_greedy	Reordered adjacency matrix
Clist	Cluster list
Node_Seq	A vector of reordered nodes
removing_node	Nodes to be removed

Examples

```
data(sim)
greedy_peeling(sim, 1.4)
greedy_peeling(sim, 1.6)
```

param_tuning_sigmau *Parameter Tuning for SigmaU*

Description

This function tunes parameters for the SigmaU function by evaluating different combinations of lambda and cut-off values.

Usage

```
param_tuning_sigmau(Wp, data, prctile_vec, lam_vec)
```

Arguments

Wp	A symmetric matrix representing pairwise potentials (weights).
data	A data matrix used in the SigmaU function.
prctile_vec	A vector of percentiles for the pairwise potentials to consider.
lam_vec	A vector of lambda values to test.

Value

A list containing the optimal lambda value (lambda_out) and the corresponding cut-off value (cut_out).

Examples

```
Wp <- matrix(runif(100), nrow = 10)
data <- matrix(runif(200), nrow = 20)
prctile_vec <- c(10, 20, 30)
lam_vec <- c(0.1, 0.5, 1.0)
result <- param_tuning_sigmau(Wp, data, prctile_vec, lam_vec)
print(result)
```

plotMatrix

*Visualize a matrix as a heatmap and save it to a file***Description**

This function creates a heatmap to visualize a numeric matrix. The heatmap is saved to a file at the specified filepath in one of several supported formats.

Usage

```
plotMatrix(
  data,
  filepath,
  width = 850,
  height = 800,
  palette = "viridis",
  format = "tiff"
)
```

Arguments

data	A numeric matrix.
filepath	The output file path.
width	Width of the output image in pixels, default is 850.
height	Height of the output image in pixels, default is 800.
palette	Type of color palette to use: "jet" or "viridis", default is "viridis".
format	File format for saving the image, default is "tiff". Supported formats: "tiff", "png", "jpeg", "svg".

Value

Nothing is explicitly returned; an image file is saved to the designated file path.

Examples

```
mat <- matrix(rnorm(100), nrow = 10)
plotMatrix(mat, "heatmap.tiff")
```

sim	<i>Simulated adjacency matrix</i>
-----	-----------------------------------

Description

details to be filled in

Usage

sim

Format

sim:
A data frame with 100 subjects and 200 variables:
V1
V2
V3 ...

Source

null