

Package ‘nsiGGM’

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Type Package

Title Node-structured Integrative Gaussian Graphical Model

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Description This package contains functions for nsiGGM.

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LazyData TRUE

Imports doMC, mnormt, igraph

URL <https://sites.google.com/site/sunghwanshome/>

NeedsCompilation no

R topics documented:

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nsiGGM	<i>Node-structured Integrative Gaussian Graphical Model</i>
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Description

This function develops an estimation and variable selection algorithm for node-structured integrative gaussian graphical model (nsiGGM).

Usage

```
nsiGGM(Y, lambda1, lambda2, lambda3, params.in_gr,  
       params.out_gr, params.dummy, params.verbose,  
       penalty = "group", rho = 1, penalize.diagonal = FALSE,  
       maxiter = 50, tol = 1e-5, warm = NULL,  
       truncate = 1e-5, is.Naive.Group = TRUE)
```

Arguments

Please note an example below.

Details

We propose a novel statistical framework called the “node-structured joint Gaussian graphical model”, for fitting joint Gaussian graphical model simultaneously with informative pathways consistently expressed across multiple studies. With an application to simulated and breast cancer genomic data, the proposed model is found to be superior in efficiently capturing transcriptional modules pre-defined by pathway database.

Value

A list contains information on the final model

Author(s)

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Examples

```
library(nsiGGM)
library(doMC)
library(mnormt)
library(igraph)
registerDoMC(10)

# True precision matrix
path1 = system.file("extdata", "TR_PR_mat.Rdata", package = "nsiGGM")
TR_PR_mat = get(load(path1))
# Three data sets generated from the Barabasi Albert algorithm
Y <- list()
n.S <- 3
for(i in 1:n.S){
  Y[[i]] <- rmnorm(100, mean = rep(0,dim(TR_PR_mat)[1]), solve(TR_PR_mat))
}

# Node-group index list that contains a single pathway geneset in the 449th slot in the list.
path2 = system.file("extdata", "out_gr.Rdata", package = "nsiGGM")
out_gr <- get(load(path2))

# Study-group index that captures all involved three studies.
in_gr = list(c(1,2,3))

params.in_gr = in_gr
params.out_gr = out_gr
params.verbose = 1;

lambda1 <- 0.05
lambda2 <- 0.05
lambda3 <- 0.05

rst_nsiJGL <- nsiGGM(Y, lambda1, lambda2, lambda3, params.in_gr = params.in_gr,
  params.out_gr = params.out_gr, params.dummy = 1,
  params.verbose = params.verbose, rho = 1,
  penalize.diagonal = FALSE, maxiter = 50,
```

```
tol = 1e-5, warm = NULL, truncate = 1e-5)  
tmp_theta <- rst_nsJGL$theta
```

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