Package 'JEGN'

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Type Package

Title JEGN

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Author Xiao-Fei Zhang

Maintainer Xiao-Fei Zhang <zhangxf@mail.ccnu.edu.cn>

Description JEGN is a graphical model for joint estimation of gene networks across multiple subpopulations and data types. JGNI can deal with both Gaussian and nonparanormal data.

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Imports Matrix, stats

R topics documented:

JEGN *Joint gene network inference across multiple subpopulations and data types*

Description

The complete procedure for reconstructin gene networks from gene expression data using JEGN (Algorithm 2 in the Supplementary Information). For details, refer to Supplementary Section S3.4.

Usage

```
JEGN(X, lambda, alpha, model = "Gaussian", weights = "equal",
  penalize.diagonal = FALSE)
```

Arguments

X	A matrix ($K \times G$) of list of data matrices ($n_g \times p$), where K is the number of data types and G is the number of subpopulations. The (k,g)-th element is a $n_g \times p$ data matrix corresponding to the k-th data type and the g-th subpopulation.
lambda	The tuning parameter for controlling the level of sparsity of the estimated networks.
alpha	The tuning parameter for controlling the extend of similarity among the estimated subpopulation-specific networks.
model	A character string indicating which model is used to fit the data. "Gaussian" (default) and "nonparanormal" can be used. If model == "Gaussian", the Gaussian graphical model will be used. If model == "nonparanormal", the nonparanormal graphical model will be used.
weights	Determines the putative sample size of each subpopulation's data. Allowed values: a vector with length equal to the number of subpopulations; "equal", giving each subpopulation weight 1; "sample.size", giving each subpopulation weight corresponding to its sample size.
penalize.diagonal	Determines whether the sparsity penalty is applied to the diagonal.

Value

a list with the following components

Omega.hat	A matrix ($K \times G$) of list of estimated precision matrices.
R.hat	A matrix ($K \times 1$) of list of estimated common components.
M.hat	A matrix ($K \times G$) of list of estimated subpopulation-unique components.
Omega.bar	A matrix ($1 \times G$) of list of estimated gene networks.
R.bar	A matrix of estimated common subnetworks.
M.bar	A matrix ($1 \times G$) of list of estimated subpopulation-unique subnetworks.

Author(s)

Xiao-Fei Zhang <zhangxf@mail.ccnu.edu.cn>

References

Xiao-Fei Zhang, Le Ou-Yang, Ting Yan, Xiaohua Hu and Hong Yan (2019), A joint graphical model for inferring gene networks across multiple subpopulations and data types,

Examples

```
data("TCGA.BRCA")
result = JEGN(TCGA.BRCA$X, 0.95, 0.4, model = "nonparanormal", weights = "equal")
```

JEGN.admm *ADMM algorithm for JEGN*

Description

ADMM algorithm for JEGN (Algorithm 1 in the Supplementary Information). For details, refer to Supplementary Section S3.3.

Usage

```
JEGN.admm(S, lambda, alpha, n = NULL, penalize.diagonal = FALSE,
  epsilon = 1e-05, maxiter = 500, rho = 0.1, rho.incr = 1.2,
  rho.max = 1e+10)
```

Arguments

S	A matrix ($K \times G$) of list of sample covariance matrices ($p \times p$), where K is the number of data types and G is the number of subpopulations. The (k,g)-th element is a $p \times p$ sample covariance matrix corresponding to the k-th data type and the g-th subpopulation.
lambda	The tuning parameter for controlling the level of sparsity of networks.
alpha	The tuning parameter for controlling the extend of similarity among subpopulation-specific networks.
n	The sample size. A vector with length equal to the number of subpopulations.
penalize.diagonal	Determines whether the sparsity penalty is applied to the diagonal.
epsilon	The tolerance parameter for convergence criteria.
maxiter	The maximum number of iterations for the ADMM algorithm.
rho	The penalty parameter in the ADMM algorithm.
rho.incr	The increase step parameter for varying penalty parameter rho.
rho.max	The maximum value of rho.

Value

a list with the following components

Omega.hat	A matrix ($K \times G$) of list of estimated precision matrices.
R.hat	A matrix ($K \times 1$) of list of estimated common components.
M.hat	A matrix ($K \times G$) of list of estimated subpopulation-unique components.

Author(s)

Xiao-Fei Zhang <zhangxf@mail.ccnu.edu.cn>

References

Xiao-Fei Zhang, Le Ou-Yang, Ting Yan, Xiaohua Hu and Hong Yan (2019), A joint graphical model for inferring gene networks across multiple subpopulations and data types,

Examples

```
data("TCGA.BRCA")
result = JEGN(TCGA.BRCA$Sigma, 0.95, 0.4, model = "nonparanormal", weights = "equal")
```

TCGA.BRCA *TCGA breast cancer data*

Description

The TCGA breast cancer gene expression data used in our study. The data are obtained from the TCGA database. They are collected from two platforms: mRNA expression (Agilent G450 microarray) and mRNA expression (RNA sequencing). The cancers are grouped into four subtypes: Luminal A, Luminal B, HER2-enriched, and Basal-like. The data only include expression measure of genes that overlap with the breast cancer pathway collected from the Kyoto Encyclopedia of Genes and Genomes database.

Usage

```
TCGA.BRCA
```

Format

An object of class `list` of length 4.

Author(s)

Xiao-Fei Zhang <zhangxf@mail.ccnu.edu.cn>

References

Xiao-Fei Zhang, Le Ou-Yang, Ting Yan, Xiaohua Hu and Hong Yan (2019), A joint graphical model for inferring gene networks across multiple subpopulations and data types,

Examples

```
data("TCGA.BRCA")
```

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