Package 'chNet'

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Type Package

Title Differential network analysis by simultaneously considering changes in gene interactions and gene expression.

Version 2.0.0

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Description chNet is a method designed for inferring diffferential network that satisfy hierarchichal constraints. chNet can simultaneously take into account the change of gene interactions and gene expression.

Depends R(>= 3.5.1)

Imports MASS, Matrix, igraph, mvtnorm, glmnet

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 6.1.1

License GPL(>= 2)

Encoding UTF-8

LazyData true

R topics documented:

chNet *Differential network analysis by simultaneously considering changes in gene interactions and gene expression*

Description

The complete procedure for estimating differential network using chNet. For details, refer to method (Sections 2.4 and 2.5 in the main text).

Usage

```
chNet (X,group,subsampling,R,lambar,parallel,nCpus)
```

Arguments

X	Data matrix for which the rows represent the samples and the columns represent the genes.
group	Vector which defines two groups of samples under comparison.
subsampling	Logical value to indicate if the process should be run to obtain a weight matrix, default to FALSE.
R	The number of sub-sampled datasets; default is 20.
lambar	The tuning (threshold) parameter controls the sparsity level.
parallel	Logical value to indicate if the process should be run parallelly in multiple threads, default to FALSE.
nCpus	Number of (maximum) cores to use for parallel execution, default to 4.

Details

This function is implemented to infer diffferential network that satisfy hierarchichal constraints. We first define the differential network as the difference of partial correlations from two different conditions, and develop a new test statistic to quantify the change of partial correlations. Then the Student's t-test statistic is used to quantify the changes in expression levels of individual genes. Finally, an optimization model is developed to combine the two different types of test statistics so that the estimated differential networks exhibit the hierarchical structures. A closed-formed solution is derived to solve the optimization model. In addition, based on sub-sampling experiments, a weighted hierarchial differential network can also be inferred.

Value

diff.edge.weight	the estimated weighted differential network.
diff.edge	the adjacency matrix of the estimated differential network.
diff.gene	the adjacency matrix of the estimated differentially expressed genes.
Diff.net	the estimated differential network over all genes.
Diff.net.connected	the estimated differential network over only the connected genes.

Author(s)

Jia-Juan Tu

References

Jia-Juan Tu, Le Ou-Yang, Hong Yan, Hong Qin and Xiao-Fei Zhang (2021), Differential network analysis by simultaneously considering changes in gene interactions and gene expression.

See Also

generate.data, TCGA.BRCA, GSE13159.AML

Examples

```
# Simulation data
data.x= generate.data(p = 100, n = 100, umin = 0.5, umax = 1)
result = chNet(data.x$X,data.x$group, subsampling = FALSE, R= 20,
lambar = 3, parallel = FALSE, nCpus = 4)

# TCGA breast cancer data
data("TCGA.BRCA")
result = chNet(TCGA.BRCA$X,TCGA.BRCA$group,subsampling = FALSE, R= 20,
 lambar = 2.825, parallel = FALSE, nCpus = 4)
# GSE13159 AML
data("GSE13159.AML")
result = chNet(TCGA.BRCA$X,TCGA.BRCA$group,subsampling = FALSE, R= 20,
lambar = 2.8, parallel = FALSE, nCpus = 4)
```

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generate.data *Generate simulated data*

Description

The complete procedure for generating simulated data. For details, refer to simulation study (Supplementary Section 3.3.1).

Usage

```
generate.data (p, n, umin, umax)
```

Arguments

p	The number of genes.
n	The sample size.
umin	The lower limits of the edge values.
umax	The upper limits of the edge values.

Details

The function is used to generate the gene expression datasets.

Value

X	A matrix of sample matrice ($2n \times p$) from two different conditions.
group	A matrix of sample label matrice ($2n \times 1$) from two different conditions.
rho	A list (length = 2) of the partical coefficients matrices ($p \times p$).
hubgene	A set hub genes.

Author(s)

Jia-Juan Tu

References

Jia-Juan Tu, Le Ou-Yang, Hong Yan, Hong Qin and Xiao-Fei Zhang (2021), Differential network analysis by simultaneously considering changes in gene interactions and gene expression.

See Also

chNet, TCGA.BRCA, GSE13159.AML

Examples

```
# Simulation data
data.x = generate.data(p = 100, n = 100, umin = 0.5, umax = 1)
```

GSE13159.AML *Acute myeloid leukemia data (GSE13159)*

Description

Gene expression datasets for acute myeloid leukemia (GSE13159) is download from http://discern-leelab.cs.washington.ed. There are 541 AML and 73 normal samples. The data include expression measurements of genes that overlap with the mTOR signaling pathway (hsa04150) from the Kyoto Encyclopedia of Genes and Genomes databas and 50 non-differentially expressed genes (Student's t-test, p-value > 0.05) with the highest variation AML samples. It includes an expression matrix for which the rows represent the samples and the columns represent the genes, and a vector denoting the group membership of each sample.

Usage

```
data("GSE13159.AML")
```

Format

An object of class `list` of length 2.

Author(s)

Jia-Juan Tu

Source

[1] The Cancer Genome Atlas Research Network (2012), Comprehensive molecular portraits of human breast tumors. Nature. 490 (7418), 61-70. (http://cancergenome.nih.gov/).

References

Jia-Juan Tu, Le Ou-Yang, Hong Yan, Hong Qin and Xiao-Fei Zhang (2021), Differential network analysis by simultaneously considering changes in gene interactions and gene expression.

See Also

generate.data, chNet,TCGA.BRCA

Examples

```
data("GSE13159.AML")
```

TCGA.BRCA *TCGA breast cancer data*

Description

The TCGA breast cancer gene expression dataset used in our case study. The data (level 3, Agilent G450 microarray, version: May 6 2017) is diwnloaded from the TCGA database using the TCGA2STAT R package. It includes gene expression measurements for 231 luminal A cancers and 95 basal-like cancers. The data includes expression measurement of genes that overlap with the breast cancer pathway (hsa05224) collected from the Kyoto Encyclopedia of Genes and Genomes database and 50 non-differentially expressed genes (Student's t-test, p-value > 0.05) with the highest variation across luminal A and basal-like cancers. It includes an expression matrix for which the rows represent the samples and the columns represent the genes, and a vector denoting the group membership of each sample.

Usage

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

Format

An object of class `list` of length 2.

Author(s)

Jia-Juan Tu

Source

[1] The Cancer Genome Atlas Research Network (2012), Comprehensive molecular portraits of human breast tumors. Nature. 490 (7418), 61-70. (http://cancergenome.nih.gov/)

References

Jia-Juan Tu, Le Ou-Yang, Hong Yan, Hong Qin and Xiao-Fei Zhang (2021), Differential network analysis by simultaneously considering changes in gene interactions and gene expression.

See Also

generate.data, TCGA.BRCA, GSE13159.AML

Examples

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

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