Package 'DiffNetFDR'

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Type Package

Title DiffNetFDR: Differential Network Analysis with False Discovery Rate Control

Version 1.1

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Description DiffNetFDR is an R package which implements two differential network analysis methods. The methods included in DiffNetFD control the overall false discovery rate at a desired level using a multiple testing procedure.

License GPL (>= 2)

Encoding UTF-8

NeedsCompilation no

Depends R (>= 3.0), igraph, glmnet, parallel

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`DiffNet.FDR` *Differential network analysis with false discovery rate control*

Description

This function is implemented to infer diffferential network based on Gaussian graphical models. The differential network can be determined as the difference of partial correlations or the difference of precision matrices. The false discovery rate can be controlled using a multiple testing procedure.

Usage

```
DiffNet.FDR(X, group, alpha = 0.2, test.type = "pcor", parallel = F, nCpus = 4)
```

Arguments

X	data matrix for which the rows represent the samples and the columns represent the variables.
group	vector which defines two groups of samples under comparison.
alpha	desired FDR level ($0 \leq \alpha \leq 1$), default to 0.2. alpha can be a scalar or vetcor. If alpha is a scale, a signle differential network will be generated. If alapha is a vector, multiple differential networks correspoding to different FDR levels will be generated.
test.type	parameter to decide which approach is selected to define the differential network, default to "pcor". If test.type = "pcor", the differential network will be inferred based on the difference of partial correlations. If test.type = "pmat", the differential network will be inferred based on the difference of precicion matrices.
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

If alpha is a vector, a list of multiple differential networks correspoding to different FDR levels will be return.

Value

Diff.edge	the adjacency matrix of the estimated differential network.
W	the values of the statistics.
t	the threshold level such that H0 is rejected.
Diff.net	the estimated differential network over all nodes.
Diff.net.connected	the estimated differential network over only the connected nodes.

Author(s)

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

References

Xiao-Fei Zhang, Le Ou-Yang, Shuo Yang, Xiaohua Hu and Hong Yan, DiffNetFDR: Differential network analysis with false discovery rate control, 2018
Yin Xia, Tianxi Cai and T. Tony Cai, Testing differential networks with applications to the detection of gene-gene interactions, Biometrika, 102(2): 247-266, 2015
Weidong Liu, Structural similarity and difference testing on multiple sparse Gaussian graphical models, Annals of Statistics, 45(6): 2680-2707, 2017.

See Also

TCGA.BRCA, GSE13159.AML

Examples

```
rm(list=ls())
data("TCGA.BRCA")

result = DiffNet.FDR(TCGA.BRCA$X,TCGA.BRCA$group, alpha = 0.2, test.type = "pcor")
Diff.net.connected = result$Diff.net.connected
# Visualize the estimated differential network in an interactive manner.
tkid <- tkplot(Diff.net.connected, vertex.size= degree(Diff.net.connected)*1.2, layout =layout_with_fr,
               vertex.color="red", vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")
# Visualize the estimated differential network in a non-interactive manner.
# grab the coordinates from tkplot
loc <- tkplot.getcoords(tkid)
plot(Diff.net.connected, layout=loc, vertex.size= degree(Diff.net.connected)*1.2, vertex.color="red",
     vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")


rm(list=ls())
data("TCGA.BRCA")
result = DiffNet.FDR(TCGA.BRCA$X,TCGA.BRCA$group, alpha = 0.2, test.type = "pmat")
Diff.net.connected = result$Diff.net.connected
# Visualize the estimated differential network in an interactive manner.
tkid <- tkplot(Diff.net.connected, vertex.size= degree(Diff.net.connected)*1.2, layout =layout_with_fr,
               vertex.color="red", vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")
# Visualize the estimated differential network in a non-interactive manner.
# grab the coordinates from tkplot
loc <- tkplot.getcoords(tkid)
plot(Diff.net.connected, layout=loc, vertex.size= degree(Diff.net.connected)*1.2, vertex.color="red",
     vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")



rm(list=ls())
data("GSE13159.AML")

result = DiffNet.FDR(GSE13159.AML$X,GSE13159.AML$group, alpha = 0.2, test.type = "pcor")
Diff.net.connected = result$Diff.net.connected
# Visualize the estimated differential network in an interactive manner.
tkid <- tkplot(Diff.net.connected, vertex.size= degree(Diff.net.connected)*2, layout =layout_with_fr,
               vertex.color="red", vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")
# Visualize the estimated differential network in a non-interactive manner.
# grab the coordinates from tkplot
loc <- tkplot.getcoords(tkid)
plot(Diff.net.connected, layout=loc, vertex.size= degree(Diff.net.connected)*2, vertex.color="red",
     vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")


rm(list=ls())
data("GSE13159.AML")
result = DiffNet.FDR(GSE13159.AML$X,GSE13159.AML$group, alpha = 0.2, test.type = "pmat")
Diff.net.connected = result$Diff.net.connected
# Visualize the estimated differential network in an interactive manner.
tkid <- tkplot(Diff.net.connected, vertex.size= degree(Diff.net.connected)*2, layout =layout_with_fr,
               vertex.color="red", vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")
# Visualize the estimated differential network in a non-interactive manner.
# grab the coordinates from tkplot
loc <- tkplot.getcoords(tkid)
```

```
plot(Diff.net.connected, layout=loc, vertex.size= degree(Diff.net.connected)*2, vertex.color="red",
     vertex.group.cex=0.8, edge.width =1.2, edge.color="orange")
```

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

Description

Gene expression datasets for acute myeloid leukemia (GSE13159). The data is obtained from http://discern-leelab.cs.washington.edu/. It includes expression measurments for 541 AML cancers and 73 normal samples. The data only include expression measurements of genes that overlap with the acute myeloid leukemia pathway (hsa05221) collected from the Kyoto Encyclopedia of Genes and Genomes databas. 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")
```

Author(s)

Xiao-Fei Zhang

References

Xiao-Fei Zhang, Le Ou-Yang, Shuo Yang, Xiaohua Hu and Hong Yan, DiffNetFDR: An R package for differential network analysis with false discovery rate control, 2018.

Maxim Grechkin, Benjamin A. Logsdon, Andrew J. Gentles and Su-In Lee, Identifying network perturbation in cancer, PLoS Computational Biology, 12(5): e1004888, 2016.

See Also

DiffNet.FDR

Examples

```
data(GSE13159.AML)
## maybe str(GSE13159.AML) ...
```

TCGA.BRCA *TCGA breast cancer data*

Description

The TCGA breast cancer gene expression dataset used in our case study. The dataset (level 3, Agilent G450 microarray, version: May 6 2017) is obtained 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 only includes expression measurement of genes that overlap with the breast cancer pathway (hsa05224) collected from the Kyoto Encyclopedia of Genes and Genomes database. 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")
```

Author(s)

Xiao-Fei Zhang

References

Xiao-Fei Zhang, Le Ou-Yang, Shuo Yang, Xiaohua Hu and Hong Yan, DiffNetFDR: Differential network analysis with false discovery rate control, 2018.

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

See Also

DiffNet.FDR

Examples

```
data(TCGA.BRCA)
## maybe str(TCGA.BRCA) ...
```

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