Package 'NeighborNet'

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Title Neighbor_net analysis

Version 1.16.0

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Description Identify the putative mechanism explaining the active interactions between genes in the investigated phenotype.

biocViews Software, GeneExpression, StatisticalMethod, GraphAndNetwork

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Depends methods

Imports graph, stats

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R topics documented:

neighborNet	*Neighbor Net: An approach to infer putative disease-specific mechanisms using neighboring gene networks.*

Description

Neighbor Net: An approach to infer putative disease-specific mechanisms using neighboring gene networks.

Usage

```
neighborNet(de, ref, listofgenes, threshold = 0.1, minsize = 2)
```

Arguments

de	a vector including the differentially expressed genes; de must use the same id's as ref and the genes in the listofgenes
ref	the reference vector for all genes in the analysis
listofgenes	a list representing the neighbor networks associated to each gene; the name of the list must be the same as genes in the de
threshold	a threshold of choosing significant neighbor networks (default is 0.1)
minsize	minimum size of the neighbor networks that should be considered in the analysis (default is 2)

Details

See details in the cited articles.

Value

An object of class graphNEL.

Author(s)

Sahar Ansari and Sorin Draghici

References

Sahar Ansari, Michele Donato, Nafiseh Saberian, Sorin Draghici; An approach to infer putative disease-specific mechanisms using neighboring gene networks, Bioinformatics, Volume 33, Issue 13, 1 July 2017, Pages 1987–1994

Examples

```
# load multiple colorectal cancer study (public data available in GEO
# ID: GSE4183, GSE9348, GSE21510, GSE32323, GSEl8671)
# These files contains the tables, produced by the limma package with
# added gene information.
# The table contains the expression fold change and signficance of each
# probe set comparing colorectal cancer disease and normal.
load(system.file("extdata/dataColorectal4183.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal9348.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal21510.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal32323.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal8671.RData", package = "NeighborNet"))
head(dataColorectal4183)

load(system.file("extdata/listofgenes.RData", package = "NeighborNet"))
head(listofgenes)

# select differentially expressed genes for each data set at p-value below 1%
# and absolute value for more than 1.5 and save their entrez ID in a vector de1 to de5
pvThreshold <- 0.01
foldThreshold <- 1.5
de1 <- dataColorectal4183$EntrezID [
  dataColorectal4183$adj.P.Val < pvThreshold &
  abs(dataColorectal4183$logFC) > foldThreshold]
de2 <- dataColorectal9348$EntrezID [
  dataColorectal9348$adj.P.Val < pvThreshold &
  abs(dataColorectal9348$logFC) > foldThreshold]
de3 <- dataColorectal21510$EntrezID [
  dataColorectal21510$adj.P.Val < pvThreshold &
  abs(dataColorectal21510$logFC) > foldThreshold]
de4 <- dataColorectal32323$EntrezID [
  dataColorectal32323$adj.P.Val < pvThreshold &
  abs(dataColorectal32323$logFC) > foldThreshold]
de5 <- dataColorectal8671$EntrezID [
  dataColorectal8671$adj.P.Val < pvThreshold &
  abs(dataColorectal8671$logFC) > foldThreshold]
all <- unique( c(dataColorectal4183$EntrezID, dataColorectal9348$EntrezID,
  dataColorectal21510$EntrezID, dataColorectal32323$EntrezID,
  dataColorectal8671$EntrezID))
de <- unique( c(de1,de2,de3,de4,de5))

sig_net <- neighborNet (de, all, listofgenes)
```

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