Package ‘GOGANPA’

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Description

Accounting for genes’ functional-non-equivalence within pathways in classical Gene-set-analysis.

Details
getGNET

Description

Construct a gene network by linking gene-pairs with GO similarity above a chosen threshold.

Usage

getGNET(simMat, rho)

Arguments

<table>
<thead>
<tr>
<th>simMat</th>
<th>The GO-similarity matrix. Missing and negative entries are not allowed. The gene names should be assigned to the row and column names.</th>
</tr>
</thead>
<tbody>
<tr>
<td>rho</td>
<td>The threshold, chosen e.g. by selectRho. Gene-pairs with similarity above the threshold will be linked.</td>
</tr>
</tbody>
</table>

Value

A list, where each element contains the names of the genes connected to the corresponding gene indicated by the element-header.
Note

Note that certain GO-similarity measures are unbounded (e.g. the Resnik similarity). This code will not normalize the similarity matrix, and rho should therefore be chosen according to the range of the GO-similarity values inside simMat.

Author(s)

Billy Chang

References


See Also

selectRho

Examples

# Not to Run
data("simMatSmall",package="GOGANPA")
gNET <- gNET(simMatSmall,rho=0.7)
hist(sapply(gNET,length)) # network connectivities (excluding unconnected genes)
Arguments

gExprs.obj: Gene expression experiment data object

gsets: A list of gene sets.

gNET: A gene association network stored in a list.

simMat: The GO-similarity matrix. Missing and negative entries are not allowed. The gene names should be assigned to the row and column names.

rho: The threshold, chosen e.g. by selectRho. If NULL, then chosen automatically by selectRho.

msp.groups: A list of multi-subunit-proteins-coding genes.

check.exprs: Logical (TRUE by default). Check and correct the missing values and scaling in the gExprs.obj. If the scale is natural, it will be converted to log2.

msp.correction: Logical (TRUE). Whether to do a correction for multi-subunit proteins in gene weighting.

size.min: Minimum size of gene sets used for analysis. By default 15 genes.

size.max: Maximum size of gene sets used for analysis. By default 500 genes.

permN: Sample permutation times. By default 2000 times.

randN: Gene randomization times. Can be set smaller (say, 30) if you do not care randomization-based significance so as to be faster.

permFDR.cutoff: Sample permutation FDR cutoff. A number between 0 and 1. Set it larger if wish to see the significance of more gene sets.

output.label: A label to name output files.

Details

Exactly one of gNET and simMat must be NULL. If simMat and rho are provided, getGNET will be called to obtain the gene network. If simMat is provided but rho is missing, then selectRho will also be called to provide an automatic choice of rho. This code is based on GANPA (Fang et al. 2011), the gene network, gNET, whether supplied or derived from simMat, will be fed into gSE.Test.Main in the package GANPA for weighted Gene-Set-Analysis.

Value

A .csv file containing various statistics.

Author(s)

Billy Chang

References


See Also

getGNET, selectRho

Examples

# Not to Run
require(GANPA)
data("simMatSmall", package="GOGANPA")
data("gExprs.p53", "gsets.msigdb.pnas", "msp.groups", package="GANPData")
set.seed(10000)
GOGANPA(gExprs.obj=gExprs.p53, gsets=gsets.msigdb.pnas, gNET=NULL, simMat=simMatSmall, rho=NULL,
   msp.groups=msp.groups, check.exprs=TRUE, msp.correction=TRUE,
   size.min=15, size.max=500, permN=2000, randN=30,
   permFDR.cutoff=0.15, output.label="GOGANPAresult")

selectRho

Choosing a threshold based on the Scale-Free-Topology-Criterion

Description

Determine the threshold parameter which will result in a network with optimal scale-free fitness.

Usage

selectRho(simMat, rhovec = NULL)

Arguments

simMat The GO-similarity matrix. Missing and negative entries are not allowed. The
gene names should be assigned to the row and column names.

rhovec a vector of candidate thresholds, or if NULL, a set of thresholds chosen according
to the range of the similarity matrix.

Details

The scale-free fitness measure is based on linear-regression-based R-squared goodness-of-fit mea-
asure.

Value

A list, with elements:

criterion a summary table of the candidate thresholds’ resulting fits.
bestrho The candidate threshold with the highest R-squared.
**simMatSmall**

**Note**

Note that certain GO-similarity measures are unbounded (e.g. the Resnik similarity). This code will not normalize the similarity matrix, and rhovec, if supplied, should be chosen according to the range of the GO-similarity values inside simMat.

**Author(s)**

Billy Chang

**References**


**See Also**

getGNET

**Examples**

```r
# Not to Run
data("simMatSmall", package="GOGANPA")
fit <- selectRho(simMatSmall)
plot(fit$criterion[,1],fit$criterion[,2])
abline(v=fit$bestrho,col=2)
```

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**Description**

A Resnik Similarity Matrix (normalized) for 2000 human genes sampled from 14173 annotated human genes.

**Details**

The similarity matrix was computed using the R package csbl.go (http://csbi.ltdk.helsinki.fi/csbl.go/), using a GO term specificity table computed using GO BP annotations for all human Entrez Genes available in the Bioconductor package org.Hs.eg.db, version 2.6.4 (not the default table provided csbl.go).

**Note**

This matrix is provided for test-running GOGANPA only. Although it is sampled from the similarity matrix used in Chang et. al. (2012), it cannot be used to reproduce the results presented in Chang et. al. (2012).
Author(s)

Billy Chang

References


Examples

#Not to Run
data("simMatSmall",package='GOGANPA')
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