

Package ‘neaGUI’

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Type Package

Title An R package to perform the network enrichment analysis (NEA).

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Description neaGUI is an easy to use R package developed to perform the network enrichment analysis (NEA) proposed by Alexeyenko et al. (2012). The NEA method extends the overlap statistics in GSEA to network links between genes in the experimental set and those in the functional categories by exploiting biological information in terms of gene interaction network. The neaGUI requires the following R packages: tcltk, KEGG.db, GO.db, reactome.db, org.Hs.eg.db, AnnotationDbi, and hwriter.

Depends tcltk

Imports hwriter

Suggests AnnotationDbi, org.Hs.eg.db, KEGG.db, GO.db, reactome.db, RUnit, GOstats, hwriter

biocViews Microarray, DifferentialExpression, GUI

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IsoGeneGUI-package *IsoGeneGUI Graphical User Interface for the IsoGene package*

Description

neaGUI is an easy to use R package developed to perform the network enrichment analysis (NEA) proposed by Alexeyenko et al. (2012). The NEA method extends the overlap statistics in GSEA to network links between genes in the experimental set and those in the functional categories by exploiting biological information in terms of gene interaction network.

Details

The Network Enrichment Analysis Graphical User Interface (neaGUI) is a user friendly interface for network enrichment analysis (NEA).

Author(s)

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Examples

```
## Not run:  
library(neagui)  
neaGUI()  
  
## End(Not run)
```

nea *Network Enrichment Analysis*

Description

nea performs network enrichment analysis. The number of network links between a novel altered gene set (AGS) and a known functional gene set (FGS) is computed and assessed by the number of network links obtained from randomly permuted network where the degree distribution is kept. As a measure of activation of the FGS, we provide the z-score.

manypnet generates a specified number of randomly permuted networks.

Usage

```
nea(ags, fgs, fgslib = NULL, network, pnet = NULL, nperm = 50, stat="F", seed = NULL)
```

Arguments

ags	A vector of altered genes. Gene symbols (upper case) are used as a default.
fgs	A list defined by user or a character to specify GO ontologies or KEGG pathway. User can provide their own functional gene sets as a list. Options to specify GO ontologies or KEGG pathways or Reactome pathways are "CC", "BP", "MF", "KEGG", "Reactome" (cellular component, biological process, molecular function and KEGG pathway).
fgslib	A character of the name of annotation data. To use GO terms, KEGG pathways or Reactome pathways, a specific annotation data should be specified. For GO, KEGG and Reactome are, respectively, "GO.db", "KEGG.db" and "reactome.db".
network	A vector of gene pairs or a list representing the network link. For the vector case, each element has a combined name of two gene symbols with separation ". For example, "7SK ALDOA". The number of network links is computed with respect to this network.
pnet	A list of randomly permuted networks. This is the output of manypnet. If you do not specify this, the permutation procedure for the network automatically performed.
nperm	The number of permutations
stat	Two types of network enrichment statistic: FNEA and MNEA. FNEA (stat="F") depends on the size of ags while MNEA (Stat="M") avoids the dependence by taking the largest statistic across AGS. Default is FNEA.
seed	A seed number for the permutation procedure

Value

MainResult	A matrix (the length of fgs by the number of permutation) of the imputed FGS (pathways) (fgs names are shown as rownames). The FGS are shown (sorted by on te p-values) with corresponding number of observed and expected network links, number of genes, number of AGS genes, z-score, p-values based on network permutations, and the false discovery rate (FDR).
geneinfgs	A vector containing genes from AGS which are in the FGS
fgslist	A list of gene symbols for each FGS
pnetout	A list of permuted network matrix. It can be used for other analysis.

Author(s)

Woojoo Lee, Setia Pramana and Yudi Pawitan

References

Setia Pramana, Woojoo Lee, Andrey Alexeyenko, and Yudi Pawitan (2013). neaGUI: A Graphical User Interface for Network Enrichment Analysis. The R Journal.

Examples

```
## Not run:
## Example 1: artifical data.

AGS<-c("A","B","C","D","E")
FGS<-list(FGS1=c("B","E","F","G","H"),FGS2=c("F","C"))
NETWORK<-c("A B","A F","E C","Q R","S T","U V")

res<-nea(ags=AGS, fgs = FGS, fgslib = NULL, network=NETWORK, pnet = NULL, nperm = 50, stat="F", seed = 1234)
res$MainResult

## End(Not run)
## Example 2: use of annotaion data.
## We use gene symbols (upper case)

## Not run:
AGS<-c("AIFM3","DIMIT1L","ADNP","AHCYL1","EIF4H","RGL1","SEC23IP","EIF4A1","CSNK2B","NOS3")
NETWORK<-c("DNAJC6 RGL1","C1ORF156 NCBP2","AHCYL1 RTN3","PLK4 SKIV2L2","C22ORF28 MESDC2","TINP1 UTP23",
"HEATR3 MVD","WBP11 XAB2","CSNK2B PA2G4","GCN1L1 RRM2","DIMIT1L SMC1A","GPN3 THOC3",
"DLG3 GPHN","C19ORF29 EXOSC4","AIFM3 SFXN5","HSPA1L RUVBL2","DLAT EIF4A1","ADNP XRCC5",
"NOS2 NOS3","CIZ1 TLK2","MRPL49 RPS7","GSPT1 SLK","LUC7L2 SEC23IP","DHX8 IGF2BP3",
"CNTROB SASS6","MRPS12 RPLP2","DHODH EIF4H","GINS3 KIF23","ANXA5 TGFBI","CDK5 PMM1")

res<-nea(ags=AGS, fgs = "KEGG", fgslib = "KEGG.db", network=NETWORK, pnet = NULL, nperm = 5, stat="F", seed = 1234)
res$MainResult

## End(Not run)
```

neaGUI

neaGUI

Description

This function will load the neaGUI package.

Usage

```
neaGUI()
```

Details

To run the package, we use the function: neaGUI().

Author(s)

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Examples

```
## Not run:  
library(neaGUI)  
neaGUI()  
  
## End(Not run)
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