Package ‘gsean’

May 29, 2024

**Type**  Package

**Title**  Gene Set Enrichment Analysis with Networks

**Description**  Biological molecules in a living organism seldom work individually. They usually interact each other in a cooperative way. Biological process is too complicated to understand without considering such interactions. Thus, network-based procedures can be seen as powerful methods for studying complex process. However, many methods are devised for analyzing individual genes. It is said that techniques based on biological networks such as gene co-expression are more precise ways to represent information than those using lists of genes only. This package is aimed to integrate the gene expression and biological network. A biological network is constructed from gene expression data and it is used for Gene Set Enrichment Analysis.

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**Maintainer**  Dongmin Jung  <dmdmjung@gmail.com>

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**Suggests**  SummarizedExperiment, pasilla, org.Dm.eg.db, AnnotationDbi, knitr, plotly, WGCNA, rmarkdown

**License**  Artistic-2.0

**biocViews**  Software, StatisticalMethod, Network, GraphAndNetwork, GeneSetEnrichment, GeneExpression, NetworkEnrichment, Pathways, DifferentialExpression

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Gene Set Enrichment Analysis with Networks

Description

Biological molecules in a living organism seldom work individually. They usually interact each other in a cooperative way. Biological process is too complicated to understand without considering such interactions. Thus, network-based procedures can be seen as powerful methods for studying complex process. However, many methods are devised for analyzing individual genes. It is said that techniques based on biological networks such as gene co-expression are more precise ways to represent information than those using lists of genes only. This package is aimed to integrate the gene expression and biological network. A biological network is constructed from gene expression data and it is used for Gene Set Enrichment Analysis.

Details

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Author(s)

Dongmin Jung

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centrality_gsea

Gene Set Enrichment Analysis with centrality measure

Description

GSEA is performed with centrality measure

Usage

centrality_gsea(geneset, x, adjacency, pseudo = 1, nperm = 1000,
   centrality = function(x) rowSums(abs(x)),
   weightParam = 1, minSize = 1, maxSize = Inf,
   gseaParam = 1, nproc = 0, BPPARAM = NULL)

Arguments

geneset list of gene sets
x Named vector of gene-level statistics. Names should be the same as in gene sets.
adjacency adjacency matrix
pseudo pseudo number for log2 transformation (default: 1)
nperm number of permutations (default: 1000)
centrality centrality measure, degree centrality or node strength is default
weightParam weight parameter value for the centrality measure, equally weight if weightParam = 0 (default: 1)
minSize minimal size of a gene set (default: 1)
maxSize maximal size of a gene set (default: Inf)
gseaParam GSEA parameter value (default: 1)
nproc see fgsea::fgsea
BPPARAM see fgsea::fgsea

Value

GSEA result

Author(s)

Dongmin Jung

See Also

fgsea::fgsea
Examples

```r
data(examplePathways)
data(exampleRanks)
exampleRanks <- exampleRanks[1:100]
adjacency <- diag(length(exampleRanks))
rownames(adjacency) <- names(exampleRanks)
set.seed(1)
result.GSEA <- centrality_gsea(examplePathways, exampleRanks, adjacency)
```

exprs2adj

Convert gene expression data to adjacency matrix by using correlation coefficients

Description

A biological network is constructed from gene expression data and it is used for Gene Set Enrichment Analysis.

Usage

`exprs2adj(x, pseudo = 1, ...)`

Arguments

- `x` gene expression data
- `pseudo` pseudo number for log2 transformation (default: 1)
- `...` additional parameters for correlation; see WGCNA::cor

Value

adjacency matrix

Author(s)

Dongmin Jung

See Also

fgsea::fgsea, WGCNA::cor

Examples

```r
data(exampleRanks)
Names <- names(exampleRanks)
exprs <- matrix(rnorm(10*length(exampleRanks)), ncol = 10)
adjacency <- exprs2adj(exprs)
```
**GO_dme**  
*Gene Ontology terms with gene ID for Drosophila melanogaster*

**Description**

The data set contains all Gene Ontology terms for Drosophila melanogaster and genes are identified by gene ID. There are 2823 categories.

**Usage**

`GO_dme`

**Format**

a list of gene sets

**Value**

GO gene sets

**Author(s)**

Dongmin Jung

**Source**

http://www.go2msig.org/cgi-bin/prebuilt.cgi?taxid=7227

**Examples**

```r
load(system.file("data", "GO_dme.rda", package = "gsean"))
```

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**gsean**  
*Gene Set Enrichment Analysis with Networks*

**Description**

GSEA or ORA is performed with networks from gene expression data

**Usage**

```r
gsean(geneset, x, exprs, pseudo = 1, threshold = 0.99, nperm = 1000,  
  centrality = function(x) rowSums(abs(x)), weightParam = 1,  
  minSize = 1, maxSize = Inf, gseaParam = 1, nproc = 0,  
  BPPARAM = NULL, corParam = list(), tmax = 10, ...)
```
Arguments

- **geneset**: list of gene sets
- **x**: Named vector of gene-level statistics for GSEA or set of genes for ORA. Names should be the same as in gene sets.
- **exprs**: gene expression data
- **pseudo**: pseudo number for log2 transformation (default: 1)
- **threshold**: threshold of correlation for nodes to be considered neighbors for ORA (default: 0.99)
- **nperm**: number of permutations (default: 1000)
- **centrality**: centrality measure, degree centrality or node strength is default
- **weightParam**: weight parameter value for the centrality measure, equally weight if weightParam = 0 (default: 1)
- **minSize**: minimal size of a gene set (default: 1)
- **maxSize**: maximal size of a gene set (default: Inf)
- **gseaParam**: GSEA parameter value (default: 1)
- **nproc**: see fgsea::fgsea
- **BPPARAM**: see fgsea::fgsea
- **corParam**: additional parameters for correlation; see WGCNA::cor
- **tmax**: maximum number of iterations for label propagation (default: 10)
- **...**: additional parameters for label propagation; see RANKS::label.prop

Value

GSEA result

Author(s)

Dongmin Jung

See Also

exprs2adj, label_prop_gsea, centrality_gsea

Examples

data(examplePathways)
data(exampleRanks)
exampleRanks <- exampleRanks[1:100]
Names <- names(exampleRanks)
exprs <- matrix(rnorm(10*length(exampleRanks)), ncol = 10)ownames(exprs) <- names(exampleRanks)
set.seed(1)
result.GSEA <- gsean(examplePathways, exampleRanks, exprs)
**Description**

The data set contains 186 KEGG pathways for Drosophila melanogaster and genes are identified by gene symbol.

**Usage**

```r
KEGG_hsa
```

**Format**

a list of gene sets

**Value**

KEGG gene sets

**Author(s)**

Dongmin Jung

**Source**

http://software.broadinstitute.org/gsea/msigdb/collections.jsp

**Examples**

```r
load(system.file("data", "KEGG_hsa.rda", package = "gsean"))
```

---

**label_prop_gsea**

*Over-representation analysis with the label propagation algorithm*

**Description**

ORA is performed by GSEA with the label propagation algorithm

**Usage**

```r
label_prop_gsea(geneset, x, adjacency, threshold = 0.99, nperm = 1000, 
minSize = 1, maxSize = Inf, gseaParam = 1, nproc = 0, 
BPPARAM = NULL, ...)
```
Arguments

geneset               list of gene sets
x                     set of genes
adjacency             adjacency matrix
threshold             threshold of correlation for nodes to be considered neighbors (default: 0.99)
nperm                 number of permutations (default: 1000)
minSize               minimal size of a gene set (default: 1)
maxSize               maximal size of a gene set (default: Inf)
gseaParam             GSEA parameter value (default: 1)
nproc                 see fgsea::fgsea
BPPARAM               see fgsea::fgsea
...                   additional parameters for label propagation; see RANKS::label.prop

Value

GSEA result

Author(s)

Dongmin Jung

See Also

fgsea::fgsea

Examples

data(examplePathways)
data(exampleRanks)
exampleRanks <- exampleRanks[1:100]
geneNames <- names(exampleRanks)
set.seed(1)
x <- sample(geneNames, 10)
adjacency <- diag(length(exampleRanks))
rownames(adjacency) <- geneNames
result.GSEA <- label_prop_gsea(examplePathways, x, adjacency)
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