

# Package: gsean (via r-universe)

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**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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**Depends** R (>= 3.5), fgsea, PPInfer

**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

**NeedsCompilation** no

**VignetteBuilder** knitr

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/gsean>

**RemoteRef** HEAD

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## Contents

gsean-package . . . . .	2
centrality_gsea . . . . .	3
exprs2adj . . . . .	4
GO_dme . . . . .	5
gsean . . . . .	5
KEGG_hsa . . . . .	7
label_prop_gsea . . . . .	7
<b>Index</b>	<b>9</b>

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gsean-package

*Gene Set Enrichment Analysis with Networks*

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## 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

Maintainer: Dongmin Jung <dmdmjung@gmail.com>

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centrality\_gsea      *Gene Set Enrichment Analysis with centrality measure*

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### 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

```
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)
```

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exprs2adj	<i>Convert gene expression data to adjacency matrix by using correlation coefficients</i>
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## 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

```
data(exampleRanks)
Names <- names(exampleRanks)
exprs <- matrix(rnorm(10*length(exampleRanks)), ncol = 10)
adjacency <- exprs2adj(exprs)
```

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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**

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

---

gsean

*Gene Set Enrichment Analysis with Networks*

---

**Description**

GSEA or ORA is performed with networks from gene expression data

**Usage**

```
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)
rownames(exprs) <- names(exampleRanks)
set.seed(1)
result.GSEA <- gsean(examplePathways, exampleRanks, exprs)
```

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KEGG\_hsa

*KEGG pathways with gene symbol for human*

---

**Description**

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

**Usage**

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**

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

---

label\_prop\_gsea

*Over-representaion analysis with the label propagation algorithm*

---

**Description**

ORA is performed by GSEA with the label propagation algorithm

**Usage**

```
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)
```



# Index

centrality\_gsea, [3](#)

exprs2adj, [4](#)

GO\_dme, [5](#)

gsean, [5](#)

gsean-package, [2](#)

KEGG\_hsa, [7](#)

label\_prop\_gsea, [7](#)