# Package: gsean (via r-universe)

<center>September 22, 2024</center>

**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.

**Version** 1.25.0

**Date** 2023-05-24

**Author** Dongmin Jung

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

**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

**RemoteSha** aa9b841aa892d43d5f92b5c1fe3474f94619dc11

# Contents

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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**

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

**Author(s)**

Dongmin Jung

Maintainer: Dongmin Jung <dmdmjung@gmail.com>

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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 weight-Param = 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 | *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

```
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 propagtion (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"))
```

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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