

# Package ‘meshes’

September 26, 2024

**Title** MeSH Enrichment and Semantic analyses

**Version** 1.30.0

**Description** MeSH (Medical Subject Headings) is the NLM controlled vocabulary used to manually index articles for MEDLINE/PubMed. MeSH terms were associated by Entrez Gene ID by three methods, gendoo, gene2pubmed and RBBH. This association is fundamental for enrichment and semantic analyses. meshes supports enrichment analysis (over-representation and gene set enrichment analysis) of gene list or whole expression profile. The semantic comparisons of MeSH terms provide quantitative ways to compute similarities between genes and gene groups. meshes implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively and supports more than 70 species.

**Depends** R (>= 4.1.0)

**Imports** AnnotationDbi, DOSE, enrichplot, GOSemSim, methods, utils, AnnotationHub, MeSHDbi, yulab.utils

**Suggests** knitr, rmarkdown, prettydoc

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**URL** <https://yulab-smu.top/biomedical-knowledge-mining-book/>

**BugReports** <https://github.com/GuangchuangYu/meshes/issues>

**biocViews** Annotation, Clustering, MultipleComparison, Software

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.2

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enrichMeSH	<i>enrichMeSH</i>
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## Description

MeSH term enrichment analysis

## Usage

```
enrichMeSH(
  gene,
  MeSHDb,
  database = "gendo",
  category = "C",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  qvalueCutoff = 0.2,
  minGSSize = 10,
  maxGSSize = 500,
  meshdbVersion = NULL
)
```

## Arguments

gene	a vector of entrez gene id
MeSHDb	MeSHDb
database	one of 'gendo', 'gene2pubmed' or 'RBBH'

category	one of "A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L", "M", "N", "V", "Z"
pvalueCutoff	Cutoff value of pvalue.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
qvalueCutoff	qvalue cutoff
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
meshdbVersion	version of MeSH.db. If NULL(the default), use the latest version.

**Value**

An `enrichResult` instance.

**Author(s)**

Guangchuang Yu

**See Also**

`class?enrichResult`

**Examples**

```
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = db, database='gendoo', category = 'C')

## End(Not run)
```

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geneSim

*geneSim*

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**Description**

semantic similarity between two gene vector

**Usage**

```
geneSim(geneID1, geneID2 = NULL, measure = "Wang", combine = "BMA", semData)
```

**Arguments**

geneID1	gene ID vector
geneID2	gene ID vector
measure	one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
combine	One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.
semData	gene annotation data for semantic measurement

**Value**

score matrix

**Author(s)**

Guangchuang Yu

**Examples**

```
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
data(hsamd)
geneSim("241", "251", semData=hsamd, measure="Wang", combine="BMA")
```

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gseMeSH

*gseMeSH*

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**Description**

Gene Set Enrichment Analysis of MeSH

**Usage**

```
gseMeSH(
  geneList,
  MeSHDb,
  database = "gendoo",
  category = "C",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
```

```

    pAdjustMethod = "BH",
    verbose = TRUE,
    seed = FALSE,
    by = "fgsea",
    meshdbVersion = NULL,
    ...
)

```

## Arguments

geneList	order ranked geneList
MeSHDb	MeSHDb
database	one of 'gendo', 'gene2pubmed' or 'RBBH'
category	one of "A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L", "M", "N", "V", "Z"
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
eps	This parameter sets the boundary for calculating the p value.
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'
meshdbVersion	version of MeSH.db. If NULL(the default), use the latest version.
...	other parameter

## Value

gseaResult object

## Author(s)

Yu Guangchuang

## Examples

```

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
y <- gseMeSH(geneList, MeSHDb = db, database = 'gene2pubmed', category = "G")

## End(Not run)

```

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meshdata	<i>meshdata</i>
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### Description

construct annoData for semantic measurement

### Usage

```
meshdata(MeSHDb = NULL, database, category, computeIC = FALSE)
```

### Arguments

MeSHDb	MeSHDb package
database	one of supported database
category	one of supported category
computeIC	logical value

### Value

a GOSemSimDATA object

### Author(s)

Guangchuang Yu

### Examples

```
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")

## End(Not run)
```

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meshSim	<i>meshSim</i>
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---

**Description**

semantic similarity between two MeSH term vectors

**Usage**

```
meshSim(meshID1, meshID2, measure = "Wang", semData)
```

**Arguments**

meshID1	MeSH term vector
meshID2	MeSH term vector
measure	one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
semData	annotation data for semantic measurement, output by meshdata function

**Value**

score matrix

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

**Examples**

```
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category='A', computeIC=T, database="gendo")
data(hsamd)
meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")
```

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mesh_term_table	<i>DATA Sets</i>
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**Description**

These datasets are used in meshes

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reexports

*Objects exported from other packages*

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### **Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**DOSE** [geneID](#), [geneInCategory](#)

**enrichplot** [cnetplot](#), [dotplot](#), [emapplot](#), [gseaplot](#), [heatplot](#), [ridgeplot](#)



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