

# Package ‘meshes’

November 17, 2025

**Title** MeSH Enrichment and Semantic analyses

**Version** 1.37.0

**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 (>= 2.31.2), methods, utils, AnnotationHub, MeSHDbi, yulab.utils (>= 0.1.5)

**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

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**LazyData** true

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|                |                                                      |
|----------------|------------------------------------------------------|
| meshes-package | <i>meshes: MeSH Enrichment and Semantic analyses</i> |
|----------------|------------------------------------------------------|

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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.

Author(s)

**Maintainer:** Guangchuang Yu <guangchuangyu@gmail.com>

See Also

- Useful links:
- <https://yulab-smu.top/biomedical-knowledge-mining-book/>
  - Report bugs at <https://github.com/GuangchuangYu/meshes/issues>

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`enrichMeSH`*enrichMeSH*

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**Description**

MeSH term enrichment analysis

**Usage**

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

**Arguments**

|                            |                                                                                       |
|----------------------------|---------------------------------------------------------------------------------------|
| <code>gene</code>          | a vector of entrez gene id                                                            |
| <code>MeSHDb</code>        | MeSHDb                                                                                |
| <code>database</code>      | one of 'gendoo', 'gene2pubmed' or 'RBBH'                                              |
| <code>category</code>      | one of "A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L", "M", "N", "V", "Z" |
| <code>pvalueCutoff</code>  | Cutoff value of pvalue.                                                               |
| <code>pAdjustMethod</code> | one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"          |
| <code>universe</code>      | background genes                                                                      |
| <code>qvalueCutoff</code>  | qvalue cutoff                                                                         |
| <code>minGSSize</code>     | minimal size of genes annotated by Ontology term for testing.                         |
| <code>maxGSSize</code>     | maximal size of genes annotated for testing                                           |
| <code>meshdbVersion</code> | 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)
```

---

|         |                |
|---------|----------------|
| geneSim | <i>geneSim</i> |
|---------|----------------|

---

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")
```

---

|         |                |
|---------|----------------|
| gseMeSH | <i>gseMeSH</i> |
|---------|----------------|

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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 'gendoo', '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)
```

---

|          |                 |
|----------|-----------------|
| 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)
```

---

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

---

**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="gendoo")
data(hsamd)
meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")
```

---

|                 |                  |
|-----------------|------------------|
| mesh_term_table | <i>DATA Sets</i> |
|-----------------|------------------|

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Description

These datasets are used in meshes

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|           |                                             |
|-----------|---------------------------------------------|
| reexports | <i>Objects exported from other packages</i> |
|-----------|---------------------------------------------|

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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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