

Package ‘meshes’

October 16, 2025

Title MeSH Enrichment and Semantic analyses

Version 1.34.0

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

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

git_url <https://git.bioconductor.org/packages/meshes>

git_branch RELEASE_3_21

git_last_commit 1bdb588

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-10-15
Author Guangchuang Yu [aut, cre]
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Contents

meshes-package	2
enrichMeSH	3
geneSim	4
gseMeSH	5
meshdata	6
meshSim	7
mesh_term_table	8
reexports	8
Index	9

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

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>

`enrichMeSH`*enrichMeSH*

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>
---------	----------------

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>
----------	-----------------

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>
-----------------	------------------

Description

These datasets are used in meshes

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

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](#)

Index

- * **datasets**
 - mesh_term_table, 8
- * **internal**
 - meshes-package, 2
 - reexports, 8
- cnetplot, 8
- cnetplot (reexports), 8
- dotplot, 8
- dotplot (reexports), 8
- emapplot, 8
- emapplot (reexports), 8
- enrichMeSH, 3
- geneID, 8
- geneID (reexports), 8
- geneInCategory, 8
- geneInCategory (reexports), 8
- geneSim, 4
- gseaplot, 8
- gseaplot (reexports), 8
- gseMeSH, 5
- heatplot, 8
- heatplot (reexports), 8
- hsamd (mesh_term_table), 8
- mesh_term_table, 8
- meshdata, 6
- meshes (meshes-package), 2
- meshes-package, 2
- meshSim, 7
- meshtbl (mesh_term_table), 8
- reexports, 8
- ridgeplot, 8
- ridgeplot (reexports), 8