Package: meshes (via r-universe)

June 18, 2026

Title MeSH Enrichment and Semantic analyses

Version 1.38.0

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 enrichit, gson, AnnotationDbi, GOSemSim (> 2.37.0), 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 7.3.3

Config/pak/sysreqs cmake make libicu-dev libpng-dev libuv1-dev libssl-dev zlib1g-dev

Repository https://bioc-release.r-universe.dev

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RemoteUrl https://github.com/bioc/meshes

RemoteRef RELEASE_3_23

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Contents

`enrichMeSH` *enrichMeSH*

Description

MeSH term enrichment analysis

Usage

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

Arguments

`gene`	a vector of entrez gene id
`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"
`pvalueCutoff`	Cutoff value of pvalue.

pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
qvalueCutoff	qvalue cutoff
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)
```

---

geneSim *geneSim*

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 *gseMeSH*

Description

Gene Set Enrichment Analysis of MeSH

Usage

```
gseMeSH(
  geneList,
  MeSHDb,
  database = "gendoo",
  category = "C",
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
```

```
  pAdjustMethod = "BH",
  verbose = TRUE,
  ...
)
```

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"
nPerm	number of permutations.
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
...	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)
```

mesh_term_table *DATA Sets*

Description

These datasets are used in meshes

meshdata *meshdata*

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 *meshSim*

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")
```

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