Package: meshes (via r-universe)

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Title MeSH Enrichment and Semantic analyses

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Description Provides tools for MeSH (Medical Subject Headings) enrichment and semantic similarity analysis. The package uses MeSH term annotations linked to Entrez Gene identifiers through gendoo, gene2pubmed and RBBH, enabling over-representation analysis, gene set enrichment analysis and semantic comparison of gene lists or ranked expression profiles. It implements Resnik, Schlicker, Jiang, Lin and Wang similarity methods for comparing MeSH terms, genes and gene groups across more than 70 species.

Depends R (>= 4.1.0)

Imports enrichit (>= 0.2.2), gson, AnnotationDbi, GOSemSim (> 2.37.0), methods, utils, AnnotationHub, MeSHDbi, yulab.utils (>= 0.1.5)

Suggests knitr, quarto

VignetteBuilder quarto

ByteCompile true

License Artistic-2.0

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

BugReports https://github.com/YuLab-SMU/meshes/issues

biocViews Annotation, Clustering, MultipleComparison, Software

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`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"))
## inspect qr_hsa and select the organism-specific MeSHDb resource
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"))
## ## inspect qr_hsa and select the organism-specific MeSHDb resource
## 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,
```

```
  eps = 1e-10,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  verbose = TRUE,
  seed = FALSE,
  ...
)
```

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
eps	boundary for calculating the p value in multilevel mode
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
seed	random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see `enrichit::gsea()` for details.
...	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"))
## inspect qr_hsa and select the organism-specific MeSHDb resource
```

```
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"))
## inspect qr_hsa and select the organism-specific MeSHDb resource
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"))
## ## inspect qr_hsa and select the organism-specific MeSHDb resource
## 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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