Package ‘meshes’

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Title MeSH Enrichment and Semantic analyses

Version 1.6.1

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 (>= 3.4.0)

Imports AnnotationDbi, DOSE (>= 3.5.1), enrichplot, GOSemSim (>= 1.99.3), MeSH.db, methods, rvcheck

Suggests knitr, MeSH.Cel.eg.db, MeSH.Hsa.eg.db, prettydoc

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

URL https://guangchuangyu.github.io/software/meshes

BugReports https://github.com/GuangchuangYu/meshes/issues

biocViews Annotation, Clustering, MultipleComparison, Software

Encoding UTF-8

LazyData true

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R topics documented:

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gseMeSH

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mesh_term_table

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)

Arguments

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

Value

An enrichResult instance.

Author(s)

Guangchuang Yu

See Also

class?enrichResult
Examples

```r
## Not run:
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = "MeSH.Hsa.eg.db", database='gendoo', category = 'C')

## End(Not run)
```

Description

semantic similarity between two gene vector

Usage

```r
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

```r
## hsamd <- meshdata("MeSH.Hsa.eg.db", category='A', computeIC=T, database="gendoo")
data(hsamd)
geneSim("241", "251", semData=hsamd, measure="Wang", combine="BMA")
```
### gseMeSH

**Description**

Gene Set Enrichment Analysis of MeSH

**Usage**

```r
gseMeSH(geneList, MeSHDb, database = "gendoo", category = "C",
exponent = 1, nPerm = 1000, minGSSize = 10, maxGSSize = 500,
pvalueCutoff = 0.05, pAdjustMethod = "BH", verbose = TRUE,
seed = FALSE, by = "fgsea")
```

**Arguments**

- `geneList`: order ranked geneList
- `MeSHDb`: MeSHDb
- `database`: one of 'gendoo', 'gene2pubmed' or 'RBBH'
- `exponent`: weight of each step
- `nPerm`: permutation numbers
- `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
- `seed`: logical
- `by`: one of 'fgsea' or 'DOSE'

**Value**

`gseaResult` object

**Author(s)**

Yu Guangchuang

**Examples**

```r
## Not run:
data(geneList, package="DOSE")
y <- gseMeSH(geneList, MeSHDb = "MeSH.Hsa.eg.db", database = 'gene2pubmed', category = "G")
## End(Not run)
```
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
meshdata("MeSH.Cel.eg.db", category='A', computeIC=FALSE, database="gene2pubmed")

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](https://guangchuangyu.github.io)

**Examples**

```r
## hsamd <- meshdata("MeSH.Hsa.eg.db", category="A", computeIC=T, database="gendoo")
data(hsamd)
meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")
```

**Description**

These datasets are used in meshes
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