Package ‘meshes’

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Title MeSH Enrichment and Semantic analyses

Version 1.4.0

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 (>= 3.3.1), DOSE (>= 2.11.7)

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

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

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

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

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

biocViews Annotation, Clustering, MultipleComparison, Software

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

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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)

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

data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = "MeSH.Hsa.eg.db", database='gendoo', category = 'C')
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

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

Description

Gene Set Enrichment Analysis of MeSH

Usage
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'

- **category**

- **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
data(geneList, package="DOSE")
## y <- gseMeSH(geneList, MeSHDb = "MeSH.Hsa.eg.db", database = 'gene2pubmed', category = "G")
```

### 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
**meshSim**

**Value**

a GOSemSimDATA object

**Author(s)**

Guangchuang Yu

**Examples**

```
meshdata("MeSH.Cel.eg.db", category='A', computeIC=FALSE, database="gene2pubmed")
```

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

**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**

```
## 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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