Package ‘meshes’

November 5, 2018

Title MeSH Enrichment and Semantic analyses

Version 1.8.0

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 (>= 3.4.0)

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

RoxygenNote 6.1.0

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

git_branch RELEASE_3_8

git_last_commit c84c001

git_last_commit_date 2018-10-30

Date/Publication 2018-11-04

Author Guangchuang Yu [aut, cre]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>
R topics documented:

enrichMeSH

genSim

gseMeSH

meshdata

meshSim

mesh_term_table

Index

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)

Arguments

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

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

## 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
```
## hsamd <- meshdata("MeSH.Hsa eg.db", category='A', computeIC=T, database="gendoo")
data(hsamd)
meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")
```

---

**mesh_term_table**  
**DATA Sets**

**Description**
These datasets are used in meshes
Index

*Topic datasets
  mesh_term_table, 6

enrichMeSH, 2

geneSim, 3
gseMeSH, 4

hsamd(mesh_term_table), 6

mesh_term_table, 6
meshdata, 5
meshSim, 5
meshtbl(mesh_term_table), 6