Package ‘meshes’

January 31, 2017

Title MeSH Enrichment and Semantic analyses

Version 1.0.0

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
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 5.0.1
NeedsCompilation no

Author Guangchuang Yu [aut, cre]
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

R topics documented:

  enrichMeSH .................................................................  2
geneSim ...............................................................  3
gseMeSH .................................................................  3
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’
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')
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", "average", "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")

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
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

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

Description
semantic similarity between two MeSH term vectors

Usage

```r
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")
```

mesh_term_table

Description
These datasets are used in meshes
Index

*Topic datasets*
  mesh_term_table, 5

enrichMeSH, 2

geneSim, 3
gseMeSH, 3

hsamd(mesh_term_table), 5

mesh_term_table, 5
meshdata, 4
meshSim, 5
meshtbl(mesh_term_table), 5