Package ‘meshes’

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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>

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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"
uuniverse 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="Var", 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")
```

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**meshSim**

**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")
```

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**mesh_term_table**

**DATA Sets**

**Description**

These datasets are used in meshes
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