Package ‘meshes’

November 20, 2016

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

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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')
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**

**DATA Sets**

**Description**

These datasets are used in meshes
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