Package ‘meshes’

May 11, 2024

Title MeSH Enrichment and Semantic analyses
Version 1.30.0

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 (>= 4.1.0)
Imports AnnotationDbi, DOSE, enrichplot, GOSemSim, methods, utils, AnnotationHub, MeSHDbi, yulab.utils
Suggests knitr, rmarkdown, prettydoc
VignetteBuilder knitr
ByteCompile true
License Artistic-2.0


BugReports https://github.com/GuangchuangYu/meshes/issues
biocViews Annotation, Clustering, MultipleComparison, Software
Encoding UTF-8

LazyData true

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**enrichMeSH**

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## Contents

<table>
<thead>
<tr>
<th>Description</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>MeSH term enrichment analysis</td>
<td>2</td>
</tr>
</tbody>
</table>

**Usage**

```r
enrichMeSH(
    gene, 
    MeSHDb, 
    database = "gendoo", 
    category = "C", 
    pvalueCutoff = 0.05, 
    pAdjustMethod = "BH", 
    universe, 
    qvalueCutoff = 0.2, 
    minGSSize = 10, 
    maxGSSize = 500, 
    meshdbVersion = NULL
)
```

**Arguments**

- `gene` : a vector of entrez gene id
- `MeSHDb` : MeSHDb
- `database` : one of 'gendoo', 'gene2pubmed' or 'RBBH'

**Description**

MeSH term enrichment analysis

**Usage**

```r
enrichMeSH(
    gene, 
    MeSHDb, 
    database = "gendoo", 
    category = "C", 
    pvalueCutoff = 0.05, 
    pAdjustMethod = "BH", 
    universe, 
    qvalueCutoff = 0.2, 
    minGSSize = 10, 
    maxGSSize = 500, 
    meshdbVersion = NULL
)
```
geneSim

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
meshdbVersion  version of MeSH.db. If NULL (the default), use the latest version.

Value
An enrichResult instance.

Author(s)
Guangchuang Yu

See Also
class?enrichResult

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = db, database='gendoo', category = 'C')

## End(Not run)

geneSim  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", "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
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(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

```r
gseMeSH(
  geneList,
  MeSHDb,
  database = "gendoo",
  category = "C",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
)```
gseMeSH

pAdjustMethod = "BH",
verbose = TRUE,
seed = FALSE,
by = "fgsea",
meshdbVersion = NULL,
...
)

Arguments

geneList          order ranked geneList
MeSHDb            MeSHDb
database          one of 'gendoo', 'gene2pubmed' or 'RBBH'
exponent          weight of each step
minGSSize          minimal size of each geneSet for analyzing
maxGSSize          maximal size of genes annotated for testing
eps               This parameter sets the boundary for calculating the p value.
pvalueCutoff       pvalue Cutoff
pAdjustMethod      pvalue adjustment method
verbose           print message or not
seed              logical
by                one of 'fgsea' or 'DOSE'
meshdbVersion     version of MeSH.db. If NULL (the default), use the latest version.
...                other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDb::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
y <- gseMeSH(geneList, MeSHDb = db, database = 'gene2pubmed', category = "G")

## End(Not run)
Description

construct annoData for semantic measurement

Usage

meshdata(MeSHDb = NULL, database, category, computeIC = FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>MeSHDb</td>
<td>MeSHDb package</td>
</tr>
<tr>
<td>database</td>
<td>one of supported database</td>
</tr>
<tr>
<td>category</td>
<td>one of supported category</td>
</tr>
<tr>
<td>computeIC</td>
<td>logical value</td>
</tr>
</tbody>
</table>

Value

a GOSemSimDATA object

Author(s)

Guangchuang Yu

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDb::MeSHDb(filepath_hsa)
hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")

## End(Not run)
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**

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
data(hsamd)
meshSim("D000009", "D000130", semData=hsamd, measure="Resnik")
```

---

**Description**

These datasets are used in meshes
**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

- **DOSE**  
  *geneID, geneInCategory*
- **enrichplot**  
  *cnetplot, dotplot, emapplot, gseaplot, heatplot, ridgeplot*
Index

* datasets
  mesh_term_table, 7
* internal
  reexports, 8

cnetplot, 8
cnetplot(reexports), 8
dotplot, 8
dotplot(reexports), 8
emapplot, 8
emapplot(reexports), 8
enrichMeSH, 2
geneID, 8
geneID(reexports), 8
geneInCategory, 8
geneInCategory(reexports), 8
geneSim, 3
gseaplot, 8
gseaplot(reexports), 8
gseMeSH, 4

heatplot, 8
heatplot(reexports), 8
hsamd(mesh_term_table), 7

mesh_term_table, 7
meshdata, 6
meshSim, 7
meshtbl(mesh_term_table), 7

reexports, 8
ridgeplot, 8
ridgeplot(reexports), 8