Package 'meshes'

October 17, 2020

Title MeSH Enrichment and Semantic analyses

Version 1.14.0

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, utils

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 7.0.2

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R topics documented:

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enrichMeSH   *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'
category	one of "A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L","M", "N", "V", "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

```
## 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)
```

---

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

```
## hsamd <- meshdata("MeSH.Hsa.eg.db", category='A', computeIC=T, database="gendoo")
data(hsamd)
geneSim("241", "251", semData=hsamd, measure="Wang", combine="BMA")
```

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gseMeSH   *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'
category	one of "A", "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L","M", "N", "V", "Z"
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)
```

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meshdata	*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")
```

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meshSim	*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>

Examples

```
## 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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