Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.18.3

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Description This package implements five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring semantic similarities among DO terms and gene products. Enrichment analyses including hypergeometric model and gene set enrichment analysis are also implemented for discovering disease associations of high-throughput biological data.

Depends R (>= 3.5.0)

Imports AnnotationDbi, BiocParallel, DO.db, fgsea, ggplot2, GOSemSim (>= 2.0.0), methods, qvalue, reshape2, stats, utils

Suggests prettydoc, clusterProfiler, knitr, rmarkdown, org.Hs.eg.db, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

Encoding UTF-8

URL `https://yulab-smu.top/biomedical-knowledge-mining-book/`

BugReports `https://github.com/GuangchuangYu/DOSE/issues`

biocViews Annotation, Visualization, MultipleComparison, GeneSetEnrichment, Pathways, Software

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R topics documented:

`DOSE-package` *Disease Ontology Semantic and Enrichment analysis Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring DO semantic similarities, and hypergeometric test for enrichment analysis.*

Description

This package is designed to estimate DO-based semantic similarity measurement and enrichment analysis.

Details

Package:	DOSE
Type:	Package
Version:	2.3.5
Date:	2-27-2012
biocViews:	Bioinformatics, Annotation
Depends:	
Imports:	methods, AnnotationDbi, DO.db
Suggests:	clusterProfiler, GOSemSim
License:	Artistic-2.0

Author(s)

Guangchuang Yu, Li-Gen Wang

Maintainer: Guangchuang Yu <`guangchuangyu@gmail.com`>

See Also

enrichResult

`clusterSim` *clusterSim*

Description

semantic similarity between two gene clusters

Usage

```
clusterSim(cluster1, cluster2, measure = "Wang", combine = "BMA")
```

Arguments

`cluster1`	a vector of gene IDs
`cluster2`	another vector of gene IDs
`measure`	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
`combine`	One of "max", "avg", "rcmax", "BMA" methods, for combining

Details

given two gene clusters, this function calculates semantic similarity between them.

Value

similarity

Author(s)

Yu Guangchuang

Examples

```
cluster1 <- c("835", "5261","241", "994")
cluster2 <- c("307", "308", "317", "321", "506", "540", "378", "388", "396")
clusterSim(cluster1, cluster2)
```

`compareClusterResult-class`

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Description

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Slots

`compareClusterResult` cluster comparing result

`geneClusters` a list of genes

`fun` one of groupGO, enrichGO and enrichKEGG

`gene2Symbol` gene ID to Symbol

`keytype` Gene ID type

`readable` logical flag of gene ID in symbol or not.

`.call` function call

`termsim` Similarity between term

`method` method of calculating the similarity between nodes

Author(s)

Guangchuang Yu `https://guangchuangyu.github.io`

See Also

`enrichResult`

`computeIC` *compute information content*

Description

compute information content

Usage

```
computeIC(ont = "DO", organism = "human")
```

Arguments

`ont`	"DO"
`organism`	"human"

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

`DataSet` *Datasets*

Description

Information content and DO term to entrez gene IDs mapping

`doSim` *doSim*

Description

measuring similarities between two DO term vectors.

Usage

```
doSim(DOID1, DOID2, measure = "Wang")
```

Arguments

`DOID1`	DO term vector
`DOID2`	DO term vector
`measure`	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".

Details

provide two DO term vectors, this function will calculate their similarities.

Value

score matrix

Author(s)

Guangchuang Yu `https://guangchuangyu.github.io`

`enrichDGN` *Enrichment analysis based on the DisGeNET (`http://www.disgenet.org/`)*

Description

given a vector of genes, this function will return the enrichment NCG categories with FDR control

Usage

```
enrichDGN(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  readable = FALSE
)
```

Arguments

`gene`	a vector of entrez gene id
`pvalueCutoff`	pvalue cutoff
`pAdjustMethod`	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
`universe`	background genes
`minGSSize`	minimal size of genes annotated by NCG category for testing
`maxGSSize`	maximal size of each geneSet for analyzing
`qvalueCutoff`	qvalue cutoff
`readable`	whether mapping gene ID to gene Name

Value

A `enrichResult` instance

Author(s)

Guangchuang Yu

References

Janet et al. (2015) DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. *Database* bav028 `http://database.oxfordjournals.org/content/2015/bav028.long`

`enrichDGNv` *enrichDGN*

Description

Enrichment analysis based on the DisGeNET (`http://www.disgenet.org/`)

Usage

```
enrichDGNv(
  snp,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  readable = FALSE
)
```

Arguments

`snp`	a vector of SNP
`pvalueCutoff`	pvalue cutoff
`pAdjustMethod`	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
`universe`	background genes
`minGSSize`	minimal size of genes annotated by NCG category for testing
`maxGSSize`	maximal size of each geneSet for analyzing
`qvalueCutoff`	qvalue cutoff
`readable`	whether mapping gene ID to gene Name

Details

given a vector of genes, this function will return the enrichment NCG categories with FDR control

Value

A `enrichResult` instance

Author(s)

Guangchuang Yu

References

Janet et al. (2015) DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. *Database* bav028 http://database.oxfordjournals.org/content/2015/bav028.long

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`enrichDO` *DO Enrichment Analysis*

Description

Given a vector of genes, this function will return the enrichment DO categories with FDR control.

Usage

```
enrichDO(
  gene,
  ont = "DO",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  readable = FALSE
)
```

Arguments

`gene`	a vector of entrez gene id
`ont`	one of DO or DOLite.
`pvalueCutoff`	pvalue cutoff
`pAdjustMethod`	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
`universe`	background genes
`minGSSize`	minimal size of genes annotated by NCG category for testing
`maxGSSize`	maximal size of each geneSet for analyzing
`qvalueCutoff`	qvalue cutoff
`readable`	whether mapping gene ID to gene Name

Value

A `enrichResult` instance.

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

See Also

`enrichResult-class`

Examples

```
data(geneList)
gene = names(geneList)[geneList > 1]
yy = enrichDO(gene, pvalueCutoff=0.05)
summary(yy)
```

`enricher_internal` *enrich.internal*

Description

interal method for enrichment analysis

Usage

```
enricher_internal(
  gene,
  pvalueCutoff,
  pAdjustMethod = "BH",
  universe = NULL,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  USER_DATA
)
```

Arguments

`gene`	a vector of entrez gene id.
`pvalueCutoff`	Cutoff value of pvalue.
`pAdjustMethod`	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
`universe`	background genes
`minGSSize`	minimal size of genes annotated by Ontology term for testing.
`maxGSSize`	maximal size of each geneSet for analyzing
`qvalueCutoff`	cutoff of qvalue
`USER_DATA`	ontology information

Details

using the hypergeometric model

Value

A `enrichResult` instance.

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

`enrichNCG` *enrichNCG*

Description

Enrichment analysis based on the Network of Cancer Genes database (http://ncg.kcl.ac.uk/)

Usage

```
enrichNCG(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  readable = FALSE
)
```

Arguments

`gene`	a vector of entrez gene id
`pvalueCutoff`	pvalue cutoff
`pAdjustMethod`	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
`universe`	background genes
`minGSSize`	minimal size of genes annotated by NCG category for testing
`maxGSSize`	maximal size of each geneSet for analyzing
`qvalueCutoff`	qvalue cutoff
`readable`	whether mapping gene ID to gene Name

Details

given a vector of genes, this function will return the enrichment NCG categories with FDR control

Value

A `enrichResult` instance

Author(s)

Guangchuang Yu

`enrichResult-class` *Class "enrichResult" This class represents the result of enrichment analysis.*

Description

Class "enrichResult" This class represents the result of enrichment analysis.

Slots

`result`	enrichment analysis
`pvalueCutoff`	pvalueCutoff
`pAdjustMethod`	pvalue adjust method
`qvalueCutoff`	qvalueCutoff
`organism`	only "human" supported
`ontology`	biological ontology
`gene`	Gene IDs
`keytype`	Gene ID type
`universe`	background gene
`gene2Symbol`	mapping gene to Symbol
`geneSets`	gene sets
`readable`	logical flag of gene ID in symbol or not.
`termsim`	Similarity between term
`method`	method of calculating the similarity between nodes

Author(s)

Guangchuang Yu `https://guangchuangyu.github.io`

See Also

`enrichDO`

`EXTID2NAME` *EXTID2NAME*

Description

mapping gene ID to gene Symbol

Usage

```
EXTID2NAME(OrgDb, geneID, keytype)
```

Arguments

`OrgDb`	OrgDb
`geneID`	entrez gene ID
`keytype`	keytype

Value

gene symbol

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

`gene2DO` *convert Gene ID to DO Terms*

Description

provide gene ID, this function will convert to the corresponding DO Terms

Usage

```
gene2DO(gene)
```

Arguments

`gene`	entrez gene ID

Value

DO Terms

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

`geneID` *geneID generic*

Description

geneID generic

Usage

```
geneID(x)
```

Arguments

`x`	enrichResult object

Value

'geneID' return the 'geneID' column of the enriched result which can be converted to data.frame via 'as.data.frame'

Examples

```
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichDO(de)
geneID(x)
```

`geneInCategory` *geneInCategory generic*

Description

geneInCategory generic

Usage

```
geneInCategory(x)
```

Arguments

`x`	enrichResult

Value

'geneInCategory' return a list of genes, by spliting the input gene vector to enriched functional categories

Examples

```
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichDO(de)
geneInCategory(x)
```

`geneSim` *geneSim*

Description

measuring similarities bewteen two gene vectors.

Usage

```
geneSim(geneID1, geneID2 = NULL, measure = "Wang", combine = "BMA")
```

Arguments

`geneID1`	entrez gene vector
`geneID2`	entrez gene 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.

Details

provide two entrez gene vectors, this function will calculate their similarity.

Value

score matrix

Author(s)

Guangchuang Yu `http://ygc.name`

`gseaResult-class` *Class "gseaResult" This class represents the result of GSEA analysis*

Description

Class "gseaResult" This class represents the result of GSEA analysis

Slots

`result`	GSEA anaysis
`organism`	organism
`setType`	setType
`geneSets`	geneSets
`geneList`	order rank geneList
`keytype`	ID type of gene
`permScores`	permutation scores
`params`	parameters
`gene2Symbol`	gene ID to Symbol
`readable`	whether convert gene ID to symbol

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

`GSEA_internal` *GSEA_internal*

Description

generic function for gene set enrichment analysis

Usage

```
GSEA_internal(
  geneList,
  exponent,
  minGSSize,
  maxGSSize,
  eps,
  pvalueCutoff,
  pAdjustMethod,
  verbose,
  seed = FALSE,
```

```
  USER_DATA,
  by = "fgsea",
  ...
)
```

Arguments

`geneList`	order ranked geneList
`exponent`	weight of each step
`minGSSize`	minimal size of each geneSet for analyzing
`maxGSSize`	maximal size of each geneSet for analyzing
`eps`	This parameter sets the boundary for calculating the p value.
`pvalueCutoff`	p value Cutoff
`pAdjustMethod`	p value adjustment method
`verbose`	print message or not
`seed`	set seed inside the function to make result reproducible. FALSE by default.
`USER_DATA`	annotation data
`by`	one of 'fgsea' or 'DOSE'
`...`	other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

`gseDGN` *DisGeNET Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseDGN(
  geneList,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
```

```
  verbose = TRUE,
  seed = FALSE,
  by = "fgsea",
  ...
)
```

Arguments

`geneList`	order ranked geneList
`exponent`	weight of each step
`minGSSize`	minimal size of each geneSet for analyzing
`maxGSSize`	maximal size of each geneSet for analyzing
`pvalueCutoff`	pvalue Cutoff
`pAdjustMethod`	p value adjustment method
`verbose`	print message or not
`seed`	logical
`by`	one of 'fgsea' or 'DOSE'
`...`	other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

`gseDO` *DO Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseDO(
  geneList,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  verbose = TRUE,
  seed = FALSE,
  by = "fgsea",
  ...
)
```

Arguments

`geneList`	order ranked geneList
`exponent`	weight of each step
`minGSSize`	minimal size of each geneSet for analyzing
`maxGSSize`	maximal size of each geneSet for analyzing
`pvalueCutoff`	pvalue Cutoff
`pAdjustMethod`	p value adjustment method
`verbose`	print message or not
`seed`	logical
`by`	one of 'fgsea' or 'DOSE'
`...`	other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

`gseNCG` *NCG Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseNCG(
  geneList,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  verbose = TRUE,
  seed = FALSE,
  by = "fgsea",
  ...
)
```

Arguments

`geneList`	order ranked geneList
`exponent`	weight of each step
`minGSSize`	minimal size of each geneSet for analyzing
`maxGSSize`	maximal size of each geneSet for analyzing
`pvalueCutoff`	pvalue Cutoff
`pAdjustMethod`	p value adjustment method
`verbose`	print message or not
`seed`	logical
`by`	one of 'fgsea' or 'DOSE'
`...`	other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

`gsfilter` *gsfilter*

Description

filter enriched result by gene set size or gene count

Usage

```
gsfilter(x, by = "GSSize", min = NA, max = NA)
```

Arguments

`x`	instance of enrichResult or compareClusterResult
`by`	one of 'GSSize' or 'Count'
`min`	minimal size
`max`	maximal size

Value

update object

Author(s)

Guangchuang Yu

`mclusterSim` *mclusterSim*

Description

Pairwise semantic similarity for a list of gene clusters

Usage

```
mclusterSim(clusters, measure = "Wang", combine = "BMA")
```

Arguments

`clusters`	A list of gene clusters
`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.

Value

similarity matrix

Author(s)

Yu Guangchuang

Examples

```
cluster1 <- c("835", "5261","241")
cluster2 <- c("578","582")
cluster3 <- c("307", "308", "317")
clusters <- list(a=cluster1, b=cluster2, c=cluster3)
mclusterSim(clusters, measure="Wang")
```

`parse_ratio` *parse_ratio*

Description

parse character ratio to double value, such as 1/5 to 0.2

Usage

```
parse_ratio(ratio)
```

Arguments

`ratio`	character vector of ratio to parse

Value

A numeric vector (double) of parsed ratio

Author(s)

Guangchuang Yu

`rebuildAnnoData` *rebuiding annotation data*

Description

rebuilding entrez and DO mapping datasets

Usage

```
rebuildAnnoData(file)
```

Arguments

`file`	do_rif.human.txt

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

`setReadable` *setReadable*

Description

mapping geneID to gene Symbol

Usage

```
setReadable(x, OrgDb, keyType = "auto")
```

Arguments

`x`	enrichResult Object
`OrgDb`	OrgDb
`keyType`	keyType of gene

Value

enrichResult Object

Author(s)

Yu Guangchuang

`show` *show method*

Description

show method for `gseaResult` instance

show method for `enrichResult` instance

Usage

```
show(object)

show(object)
```

Arguments

`object`	A `enrichResult` instance.

Value

message

message

Author(s)

Guangchuang Yu `https://guangchuangyu.github.io`

Guangchuang Yu `https://guangchuangyu.github.io`

`simplot` *simplot*

Description

plotting similarity matrix

Usage

```
simplot(
  sim,
  xlab = "",
  ylab = "",
  color.low = "white",
  color.high = "red",
  labs = TRUE,
  digits = 2,
  labs.size = 3,
  font.size = 14
)
```

Arguments

`sim`	similarity matrix
`xlab`	xlab
`ylab`	ylab
`color.low`	color of low value
`color.high`	color of high value
`labs`	logical, add text label or not
`digits`	round digit numbers
`labs.size`	lable size
`font.size`	font size

Value

ggplot object

Author(s)

Yu Guangchuang

`summary` *summary method*

Description

summary method for `gseaResult` instance

summary method for `enrichResult` instance

Usage

```
summary(object, ...)

summary(object, ...)
```

Arguments

`object`	A `enrichResult` instance.
`...`	additional parameter

Value

A data frame

A data frame

Author(s)

Guangchuang Yu `https://guangchuangyu.github.io`

Guangchuang Yu `http://guangchuangyu.github.io`

`theme_dose` *theme_dose*

Description

ggplot theme of DOSE

Usage

```
theme_dose(font.size = 14)
```

Arguments

`font.size`	font size

Value

ggplot theme

Examples

```
library(ggplot2)
qplot(1:10) + theme_dose()
```

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