

Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.6.1

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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 (>= 3.4.0)

Imports AnnotationDbi, BiocParallel, DO.db, fgsea, ggplot2, GOSemSim (>= 2.0.0), methods, qvalue, reshape2, S4Vectors, stats, utils

Suggests BiocStyle, clusterProfiler, knitr, org.Hs.eg.db, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

URL <https://guangchuangyu.github.io/software/DOSE>

BugReports <https://github.com/GuangchuangYu/DOSE/issues>

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

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DOSE-package	<i>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.</i>
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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

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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)
```

computeIC	<i>compute information content</i>
-----------	------------------------------------

Description

compute information content

Usage

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

Arguments

ont	"DO"
organism	"human"

Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

DataSet	<i>Datasets</i>
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Description

Information content and DO term to entrez gene IDs mapping

doSim	<i>doSim</i>
-------	--------------

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	<i>Enrichment analysis based on the DisGeNET</i> (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>

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

internal 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>

enrichMap	<i>enrichMap</i>
-----------	------------------

Description

enrichment map

Usage

```
enrichMap(x, n = 50, ...)
```

Arguments

x	gseaResult or enrichResult object
n	maximum number of category to shown
...	additional parameter

Details

enrichment map

Value

figure

Author(s)

G Yu

enrichNCG	<i>enrichNCG</i>
-----------	------------------

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	<i>Class "enrichResult" This class represents the result of enrichment analysis.</i>
--------------------	--

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.

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

See Also

[enrichDO](#)

EXTID2NAME	<i>EXTID2NAME</i>
------------	-------------------

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>

fortify.enrichResult	<i>fortify</i>
----------------------	----------------

Description

convert enrichResult object for ggplot2

Usage

```
## S3 method for class 'enrichResult'
fortify(model, data, showCategory = 5, by = "Count",
        order = FALSE, drop = FALSE, split = NULL, ...)
```

Arguments

model	enrichResult object
data	not use here
showCategory	Category numbers to show
by	one of Count and GeneRatio
order	logical
drop	logical
split	separate result by 'split' variable
...	additional parameter

gene2DO	<i>convert Gene ID to DO Terms</i>
---------	------------------------------------

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	<i>geneID generic</i>
--------	-----------------------

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	<i>geneInCategory generic</i>
----------------	-------------------------------

Description

geneInCategory generic

Usage

```
geneInCategory(x)
```

Arguments

x	enrichResult
---	--------------

Value

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

Examples

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

geneSim	<i>geneSim</i>
---------	----------------

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	<i>Class "gseaResult" This class represents the result of GSEA analysis</i>
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Description

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

Slots

result GSEA analysis
 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	<i>GSEA_internal</i>
---------------	----------------------

Description

generic function for gene set enrichment analysis

Usage

```
GSEA_internal(geneList, exponent, nPerm, minGSSize, maxGSSize, pvalueCutoff,
  pAdjustMethod, verbose, seed = FALSE, USER_DATA, by = "fgsea")
```

Arguments

geneList	order ranked geneList
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
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'

Value

gseaResult object

Author(s)

Yu Guangchuang

gseDGN

DisGeNET Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

```
gseDGN(geneList, exponent = 1, nPerm = 1000, 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
nPerm	permutation numbers
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'

Value

gseaResult object

Author(s)

Yu Guangchuang

gseDO

DO Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

```
gseDO(geneList, exponent = 1, nPerm = 1000, 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
nPerm	permutation numbers
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'

Value

gseaResult object

Author(s)

Yu Guangchuang

gseNCG *NCG Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseNCG(geneList, exponent = 1, nPerm = 1000, 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
nPerm	permutation numbers
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'

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")
```

rebuildAnnoData	<i>rebuiding annotation data</i>
-----------------	----------------------------------

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	<i>setReadable</i>
-------------	--------------------

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	<i>show method</i>
------	--------------------

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	<i>simplot</i>
---------	----------------

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	<i>theme_dose</i>
------------	-------------------

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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