

Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 2.4.0

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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 (>= 3.0.0)

Imports methods, plyr, qvalue, stats4, AnnotationDbi, DO.db, igraph, scales, reshape2, graphics, GOSemSim, grid, ggplot2

Suggests org.Hs.eg.db, clusterProfiler, ReactomePA, ChIPseeker, knitr

VignetteBuilder knitr

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URL <https://github.com/GuangchuangYu/DOSE>

biocViews Annotation, Visualization, MultipleComparison, GeneSetEnrichment

R topics documented:

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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)

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See Also

[enrichResult](#)

ALLEXTID

ALLEXTID

Description

Get all background External ID.

Usage

ALLEXTID(organism)

Arguments

organism organism

ALLEXTID.DO

ALLEXTID.DO

Description

ALLEXTID.DO

Usage

```
## S3 method for class DO
ALLEXTID(organism)
```

Arguments

organism organism

ALLEXTID.DOLite

ALLEXTID.DOLite

Description

ALLEXTID.DOLite

Usage

```
## S3 method for class DOLite
ALLEXTID(organism)
```

Arguments

organism organism

barplot.enrichResult *barplot*

Description

barplot

Usage

```
## S3 method for class enrichResult
barplot(height, font.size = 12, title = "", ...)
```

Arguments

height	enrichResult object
font.size	font size
title	plot title
...	other parameter, ignored

cnetplot *cnetplot method*

Description

cnetplot method generics
cnetplot method generics

Usage

```
cnetplot(x, showCategory = 5, categorySize = "geneNum", foldChange = NULL,
         fixed = TRUE, ...)
```

```
cnetplot(x, showCategory=5, categorySize="geneNum", foldChange=NULL, fixed=TRUE, ...)
```

Arguments

x	enrichResult object
showCategory	number of category plotted
categorySize	one of geneNum or pvalue
foldChange	fold change of expression value
fixed	logical
...	additional parameter

Value

plot
plot

Author(s)

Guangchuang Yu <http://ygc.name>

Guangchuang Yu <http://ygc.name>

cnetplot.internal *plot gene net by categories*

Description

plot function of gene Concept Net.

Usage

```
cnetplot.internal(inputList, categorySize = "geneNum", showCategory = 5,  
  pvalue = NULL, foldChange = NULL, fixed = TRUE, DE.foldChange = NULL,  
  ...)
```

Arguments

inputList	a list of gene IDs
categorySize	setting category size
showCategory	number of categories to plot
pvalue	pvalue
foldChange	fold Change
fixed	logical
DE.foldChange	logical
...	additional parameter

Value

plotted igraph object.

Author(s)

Guangchuang Yu <http://ygc.name>

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://ygc.name>

DataSet	<i>Datasets Information content and DO term to entrez gene IDs mapping</i>
---------	--

Description

Datasets 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

DROID1	DO term vector
DROID2	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 <http://ygc.name>

<code>enrich.internal</code>	<i>enrich.internal</i>
------------------------------	------------------------

Description

interal method for enrichment analysis

Usage

```
enrich.internal(gene, organism, pvalueCutoff, pAdjustMethod = "BH", ont,
  universe, minGSSize = 5, qvalueCutoff = 0.2, readable = FALSE)
```

Arguments

<code>gene</code>	a vector of entrez gene id.
<code>organism</code>	supported organism.
<code>pvalueCutoff</code>	Cutoff value of pvalue.
<code>pAdjustMethod</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
<code>ont</code>	Ontology
<code>universe</code>	background genes
<code>minGSSize</code>	minimal size of genes annotated by Ontology term for testing.
<code>qvalueCutoff</code>	cutoff of qvalue
<code>readable</code>	whether mapping gene ID to gene Name

Details

using the hypergeometric model

Value

A `enrichResult` instance.

Author(s)

Guangchuang Yu <http://ygc.name>

`enrichDO`*DO Enrichment Analysis of a gene set.*

Description

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

Usage

```
enrichDO(gene, ont = "DOLite", pvalueCutoff = 0.05, pAdjustMethod = "BH",  
         universe, minGSSize = 5, qvalueCutoff = 0.2, readable = FALSE)
```

Arguments

<code>gene</code>	a vector of entrez gene id.
<code>ont</code>	one of DO or DOLite.
<code>pvalueCutoff</code>	Cutoff value of pvalue.
<code>pAdjustMethod</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
<code>universe</code>	background genes
<code>minGSSize</code>	minimal size of genes annotated by Ontology term for testing.
<code>qvalueCutoff</code>	qvalue Cutoff
<code>readable</code>	whether mapping gene ID to gene Name

Value

A `enrichResult` instance.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[enrichResult-class](#)

Examples

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

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

Description

enrichment map

Usage

```
enrichMap(x, fixed = TRUE)
```

Arguments

x	gseaResult or enrichResult object
fixed	if set to FALSE, will invoke tkplot

Details

enrichment map

Value

figure

Author(s)

G 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
 geneInCategory gene and category association
 readable logical flag of gene ID in symbol or not.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[enrichD0](#)

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

Description

mapping gene ID to gene Symbol

Usage

EXTID2NAME(geneID, organism)

Arguments

geneID	entrez gene ID
organism	one of "human", "mouse" and "yeast"

Value

gene symbol

Author(s)

Guangchuang Yu <http://ygc.name>

EXTID2TERMID	<i>EXTID2TERMID</i>
--------------	---------------------

Description

Mapping External ID to Ontology Term ID

Usage

EXTID2TERMID(gene, organism)

Arguments

gene	gene ID vector
organism	organism

EXTID2TERMID.D0 *EXTID2TERMID.DO*

Description

EXTID2TERMID.DO

Usage

```
## S3 method for class D0
EXTID2TERMID(gene, organism)
```

Arguments

gene	gene ID
organism	organism

EXTID2TERMID.DOLite *EXTID2TERMID.DOLite*

Description

EXTID2TERMID.DOLite

Usage

```
## S3 method for class DOLite
EXTID2TERMID(gene, organism)
```

Arguments

gene	gene ID
organism	organism

fortify.enrichResult *fortify*

Description

fortify

Usage

```
## S3 method for class enrichResult
fortify(model, data, showCategory = 5, order = FALSE,
        drop = FALSE, ...)
```

Arguments

model	enrichResult object
data	not use here
showCategory	Category numbers to show
order	logical
drop	logical
...	additional parameter

fortify.gseaResult *fortify.gseaResult*

Description

fortify.gseaResult

Usage

```
## S3 method for class gseaResult
fortify(model, data, geneSetID, ...)
```

Arguments

model	gseaResult object
data	not used.
geneSetID	gene set ID
...	additional parameter

Value

figure

Author(s)

G Yu

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://ygc.name>

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", "average", "rmax", "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>

getALLEG

getALLEG

Description

get all entrezgene ID of a specific organism

Usage

getALLEG(organism)

Arguments

organism species

Value

entrez gene ID vector

Author(s)

Yu Guangchuang

getGeneSet	<i>getGeneSet</i>
------------	-------------------

Description

preparing geneSets for gene set enrichment analysis

Usage

```
getGeneSet(setType, organism)
```

Arguments

setType	type of gene sets
organism	organism

getGeneSet.DO	<i>getGeneSet.DO</i>
---------------	----------------------

Description

getGeneSet.DO

Usage

```
## S3 method for class DO  
getGeneSet(setType = "DO", organism)
```

Arguments

setType	setType
organism	organism

getGeneSet.DOLite	<i>getGeneSet.DOLite</i>
-------------------	--------------------------

Description

getGeneSet.DOLite

Usage

```
## S3 method for class DOLite
getGeneSet(setType = "DOLite", organism)
```

Arguments

setType	setType
organism	organism

gsea	<i>gsea</i>
------	-------------

Description

generic function for gene set enrichment analysis

Usage

```
gsea(geneList, geneSets, setType, organism, exponent, nPerm, minGSSize,
     pvalueCutoff, pAdjustMethod, verbose)
```

Arguments

geneList	order ranked geneList
geneSets	gene sets
setType	Type of geneSet
organism	organism
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
pvalueCutoff	p value Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not

Value

gseaResult object

Author(s)

Yu Guangchuang

gseAnalyzer

Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

```
gseAnalyzer(geneList, setType, organism = "human", exponent = 1,  
            nPerm = 1000, minGSSize = 10, pvalueCutoff = 0.05,  
            pAdjustMethod = "BH", verbose = TRUE)
```

Arguments

geneList	order ranked geneList
setType	Type of geneSet
organism	organism
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not

Value

gseaResult object

Author(s)

Yu Guangchuang

gseaplot	<i>visualize analyzing result of GSEA</i>
----------	---

Description

plotting function for gseaResult

Usage

```
gseaplot(gseaResult, geneSetID, by = "all")
```

Arguments

gseaResult	gseaResult object
geneSetID	geneSet ID
by	one of "runningScore" or "position"

Value

ggplot2 object

Author(s)

Yu Guangchuang

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

Description

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

Slots

result	GSEA analysis
geneSets	geneSets
geneList	order rank geneList
permScores	permutation scores
params	parameters

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[gseaplot](#)

list2graph	<i>convert gene IDs to igraph object</i>
------------	--

Description

convert a list of gene IDs to igraph object.

Usage

```
list2graph(inputList)
```

Arguments

inputList a list of gene IDs

Value

a igraph object.

Author(s)

Guangchuang Yu <http://ygc.name>

netplot	<i>netplot</i>
---------	----------------

Description

plot network

Usage

```
netplot(g, vertex.label.font = 2, vertex.label.color = "#666666",  
        vertex.label.cex = 1.5, layout = layout.fruchterman.reingold,  
        foldChange = NULL, fixed = TRUE, col.bin = 10, legend.x = 1,  
        legend.y = 1)
```

Arguments

g igraph object
vertex.label.font font size
vertex.label.color font text color
vertex.label.cex cex of vertex label

layout	layout
foldChange	fold change
fixed	logical
col.bin	number of legend color bin
legend.x	x-axis position of legend
legend.y	y-axis position of legend

Details

plot network of igraph object

Value

plot

Author(s)

Yu Guangchuang

plot *plot method*

Description

plot method generics

plot method for gseaResult

Usage

```
## S4 method for signature enrichResult,ANY
plot(x, type = "bar", ...)
```

```
## S4 method for signature gseaResult,ANY
plot(x, type = "gseaplot", ...)
```

Arguments

x	A <code>enrichResult</code> instance
type	one of <code>bar</code> , <code>cnet</code> or <code>enrichMap</code>
...	Additional argument list

Value

plot

plot

Author(s)

Guangchuang Yu <http://ygc.name>
 Yu Guangchuang

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://ygc.name>

scaleNodeColor	<i>scaleNodeColor</i>
----------------	-----------------------

Description

scale color nodes

Usage

```
scaleNodeColor(g, foldChange, node.idx = NULL, DE.foldChange)
```

Arguments

g	igraph object
foldChange	fold Change
node.idx	index of node to color
DE.foldChange	logical

Details

color nodes based on fold change of expression

Value

igraph object

Author(s)

Yu Guangchuang

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

Description

mapping geneID to gene Symbol

Usage

setReadable(x)

Arguments

x enrichResult Object

Value

enrichResult Object

Author(s)

Yu Guangchuang

setting.graph.attributes	<i>setting.graph.attributes</i>
--------------------------	---------------------------------

Description

setting basic attributes of a graph

Usage

```
setting.graph.attributes(g, node.size = 8, node.color = "#B3B3B3",  
                          edge.width = 2, edge.color = "#8DA0CB")
```

Arguments

<code>g</code>	igraph object
<code>node.size</code>	size of node
<code>node.color</code>	color of node
<code>edge.width</code>	edge width
<code>edge.color</code>	color of edge

Details

setting size and color of node and edge

Value

igraph object

Author(s)

Yu Guangchuang

show

show method

Description

show method for enrichResult instance

show method for gseaResult instance

Usage

```
show(object)
```

```
show(object)
```

Arguments

`object` A enrichResult instance.

Value

message

message

Author(s)

Guangchuang Yu <http://ygc.name>

Guangchuang Yu <http://ygc.name>

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, readable = FALSE)
```

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
readable	TRUE or FALSE

Value

ggplot object

Author(s)

Yu Guangchuang

summary	<i>summary method</i>
---------	-----------------------

Description

summary method for `enrichResult` instance
summary method for `gseaResult` instance

Usage

```
summary(object, ...)
```

```
summary(object, ...)
```

Arguments

object	A <code>enrichResult</code> instance.
...	additional parameter

Value

A data frame
A data frame

Author(s)

Guangchuang Yu <http://ygc.name>
Guangchuang Yu <http://ygc.name>

TERM2NAME	<i>TERM2NAME</i>
-----------	------------------

Description

Mapping Ontology Term ID to Name Symbol or Description

Usage

```
TERM2NAME(term, organism)
```

Arguments

term	term ID vector
organism	organism

TERM2NAME.DO	<i>TERM2NAME.DO</i>
--------------	---------------------

Description

TERM2NAME.DO

Usage

```
## S3 method for class DO
TERM2NAME(term, organism)
```

Arguments

term	term id
organism	organism

TERM2NAME.DOLite	<i>TERM2NAME.DOLite</i>
------------------	-------------------------

Description

TERM2NAME.DOLite

Usage

```
## S3 method for class DOLite
TERM2NAME(term, organism)
```

Arguments

term	term ID
organism	organism

TERMID2EXTID	<i>TERMID2EXTID</i>
--------------	---------------------

Description

Mapping Ontology Term ID to External ID

Usage

```
TERMID2EXTID(term, organism)
```

Arguments

term	term ID vector
organism	organism

TERMID2EXTID.DO	<i>TERMID2EXTID.DO</i>
-----------------	------------------------

Description

TERMID2EXTID.DO

Usage

```
## S3 method for class DO  
TERMID2EXTID(term, organism)
```

Arguments

term	term ID
organism	organism

TERMID2EXTID.DOLite	<i>TERMID2EXTID.DOLite</i>
---------------------	----------------------------

Description

TERMID2EXTID.DOLite

Usage

```
## S3 method for class DOLite
TERMID2EXTID(term, organism)
```

Arguments

term	term ID
organism	organism

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

Description

ggplot theme of DOSE

Usage

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

Arguments

font.size	font size
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