

Package ‘DOSE’

April 5, 2014

Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 2.0.0

Author Guangchuang Yu, Li-Gen Wang

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Description Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring DO semantic similarities, and hypergeometric test for enrichment analysis.

Depends R (>= 2.10), ggplot2

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

Suggests clusterProfiler, ReactomePA, knitr

VignetteBuilder knitr

License Artistic-2.0

biocViews Bioinformatics, Annotation

Collate 'AllGenerics.R' 'barplot.R' 'cnetplot.R' 'DOSE-package.R'
'doSim.R' 'enrich.internal.R' 'enrichDO.R' 'geneSim.R' 'gsea.R'
'simplot.R' 'utilities.R' 'zzz.R' 'gseAnalyzer.R'

R topics documented:

DOSE-package	2
ALLEXTID	3
barplot.enrichResult	4
cnetplot	4
cnetplot.internal	5
computeIC	6

DataSet	6
doSim	6
enrich.internal	7
enrichDO	8
enrichResult-class	9
EXTID2NAME	9
EXTID2TERMID	10
gene2DO	10
geneSim	11
getALLEG	11
getGeneSet	12
gsea	12
gseaAnalyzer	13
gseaplot	14
gseaResult-class	14
list2graph	15
netplot	15
plot	16
rebuildAnnoData	17
scaleNodeColor	17
setReadable	18
setting.graph.attributes	19
show	19
simplot	20
summary	21
TERM2NAME	21
TERMID2EXTID	22
theme_dose	22

Index**23**

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: 1.1.6
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](#)

ALLEXTID

Get all background External ID.

Description

Get all background External ID.

Usage

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

Arguments

...	Additional argument list
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 = FALSE, ...)
```

Arguments

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

Value

plotted igraph object.

Author(s)

Guangchuang Yu <http://ygc.name>

computeIC *compute information content*

Description

compute information content

Usage

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

Arguments

ont	"DO"
organism	"human"

Value

NULL

Author(s)

Guangchuang Yu <http://ygc.name>

DataSet *Datasets Information content and DO term to entrez gene IDs mapping*

Description

Datasets 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 <http://ygc.name>

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

Description

internal method for enrichment analysis

Usage

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

Arguments

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

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

gene	a vector of entrez gene id.
ont	one of DO or DOLite.
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.
qvalueCutoff	qvalue Cutoff
readable	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)
```

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

Description

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

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[enrichDO](#)

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

Mapping External ID to Ontology Term ID

Description

Mapping External ID to Ontology Term ID

Usage

EXTID2TERMID(gene, organism)

Arguments

gene	gene ID vector
organism	organism

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://ygc.name>

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

Description

measuring similarities between two gene vectors.

Usage

```
geneSim(geneID1, geneID2, 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", "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>

getALLEG	<i>getALLEG</i>
----------	-----------------

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>preparing geneSets for gene set enrichment analysis</i>
------------	--

Description

preparing geneSets for gene set enrichment analysis

Usage

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

Arguments

setType	type of gene sets
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` *visualize analyzing result of GSEA*

Description

plotting function for gseaResult

Usage

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

Arguments

<code>gseaResult</code>	gseaResult object
<code>geneSetID</code>	geneSet ID
<code>by</code>	one of "runningScore" or "position"

Value

ggplot2 object

Author(s)

Yu Guangchuang

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

Description

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

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

Arguments

... Additional argument list
 ... ignored.

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
------	------------------

Value

NULL

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

setReadable

Description

mapping geneID to gene Symbol

Usage

```
setReadable(x)
```

Arguments

x enrichResult Object

Value

enrichResult Object

Author(s)

Yu Guangchuang

setting.graph.attributes
setting.graph.attributes

Description

setting basic attributes of a graph

Usage

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

Arguments

g	igraph object
node.size	size of node
node.color	color of node
edege.width	edege width
edege.color	color of edege

Details

setting size and color of node and edege

Value

igraph object

Author(s)

Yu Guangchuang

show *show method*

Description

show method for enrichResult instance

show method for gseaResult instance

Arguments

object A enrichResult instance.
 object A gseaResult 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)
```

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

Description

summary method for `enrichResult` instance

summary method for `gseaResult` instance

Arguments

object A `enrichResult` instance.

object A `gseaResult` instance.

Value

A data frame

A data frame

Author(s)

Guangchuang Yu <http://ygc.name>

Guangchuang Yu <http://ygc.name>

TERM2NAME	<i>Mapping Ontology Term ID to Name Symbol or Description</i>
-----------	---

Description

Mapping Ontology Term ID to Name Symbol or Description

Usage

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

Arguments

term term ID vector

organism organism

TERMID2EXTID	<i>Mapping Ontology Term ID to External ID</i>
--------------	--

Description

Mapping Ontology Term ID to External ID

Usage

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

Arguments

term	term ID vector
organism	organism

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

Description

ggplot theme of DOSE

Usage

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

Arguments

font.size	font size
-----------	-----------

Index

- *Topic **classes**
 - enrichResult-class, 9
 - gseaResult-class, 14
- *Topic **datasets**
 - DataSet, 6
- *Topic **manip**
 - enrich.internal, 7
 - enrichDO, 8
 - gseAnalyzer, 13
- *Topic **package**
 - DOSE-package, 2
- ALLEXTID, 3
- barplot.enrichResult, 4
- cnetplot, 4
- cnetplot, enrichResult, ANY-method (cnetplot), 4
- cnetplot, enrichResult-method (enrichResult-class), 9
- cnetplot.internal, 5
- computeIC, 6
- DataSet, 6
- DO2ALLEG (DataSet), 6
- DO2EG (DataSet), 6
- DOLite2EG (DataSet), 6
- DOLiteTerm (DataSet), 6
- DOSE (DOSE-package), 2
- DOSE-package, 2
- DOSEEnv (DataSet), 6
- doSim, 6
- EG2ALLDO (DataSet), 6
- EG2DO (DataSet), 6
- EG2DOLite (DataSet), 6
- enrich.internal, 7
- enrichDO, 8, 9
- enrichResult, 3
- enrichResult-class, 9
- EXTID2NAME, 9
- EXTID2TERMID, 10
- gene2DO, 10
- geneList (DataSet), 6
- geneSim, 11
- getALLEG, 11
- getGeneSet, 12
- gsea, 12
- gseahResult-class (gseaResult-class), 14
- gseAnalyzer, 13
- gseaplot, 14, 14
- gseaResult-class, 14
- IC (DataSet), 6
- Info_Contents_human_DO (DataSet), 6
- list2graph, 15
- netplot, 15
- plot, 16
- plot, enrichResult, ANY-method (plot), 16
- plot, enrichResult-method (enrichResult-class), 9
- plot, gseaResult, ANY-method (plot), 16
- plot, gseaResult-method (gseaResult-class), 14
- rebuildAnnoData, 17
- scaleNodeColor, 17
- setReadable, 18
- setting.graph.attributes, 19
- show, 19
- show, enrichResult-method (enrichResult-class), 9
- show, gseaResult-method (gseaResult-class), 14
- simplot, 20
- summary, 21

summary, enrichResult-method
(enrichResult-class), [9](#)

summary, gseaResult-method
(gseaResult-class), [14](#)

TERM2NAME, [21](#)

TERMID2EXTID, [22](#)

theme_dose, [22](#)