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)

Guangchuang Yu, Li-Gen Wang

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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	*compute information content*

Description

compute information content

Usage

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

Arguments

ont	"DO"
organism	"human"

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   *enrich.internal*

Description

interal 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
minGSSize	minimal size of genes annotated by Ontology term for testing.
qvalueCutoff	cutoff of qvalue
readable	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

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)
```

---

enrichMap   *enrichMap*

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   *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

geneInCategory gene and category association

readable logical flag of gene ID in symbol or not.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichDO

EXTID2NAME	*EXTID2NAME*

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	*EXTID2TERMID*

Description

Mapping External ID to Ontology Term ID

Usage

```
EXTID2TERMID(gene, organism)
```

Arguments

gene	gene ID vector
organism	organism

EXTID2TERMID.DO   *EXTID2TERMID.DO*

Description

EXTID2TERMID.DO

Usage

```
## S3 method for class DO
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 *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 *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", "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   *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 *getGeneSet*

Description

preparing geneSets for gene set enrichment analysis

Usage

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

Arguments

setType   type of gene sets

organism   organism

---

getGeneSet.DO *getGeneSet.DO*

Description

getGeneSet.DO

Usage

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

Arguments

setType   setType

organism   organism

getGeneSet.DOLite *getGeneSet.DOLite*

Description

getGeneSet.DOLite

Usage

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

Arguments

setType   setType

organism   organism

gsea *gsea*

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

gseaResult	gseaResult object
geneSetID	geneSet ID
by	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

Slots

result GSEA anaysis

geneSets geneSets

geneList order rank geneList

permScores permutation scores

params parameters

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

gseaplot

---

list2graph   *convert gene IDs to igraph object*

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   *netplot*

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 enrichResult instance
type	one of bar, cnet or enrichMap
...	Additional argument list

Value

plot

plot

Author(s)

Guangchuang Yu <http://ygc.name>

Yu Guangchuang

---

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://ygc.name>

---

scaleNodeColor   *scaleNodeColor*

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

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   *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, 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   *summary method*

Description

summary method for `enrichResult` instance

summary method for `gseaResult` instance

Usage

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

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

Arguments

object   A `enrichResult` instance.

...   additional parameter

Value

A data frame

A data frame

Author(s)

Guangchuang Yu <http://ygc.name>

Guangchuang Yu <http://ygc.name>

TERM2NAME   *TERM2NAME*

Description

Mapping Ontology Term ID to Name Symbol or Description

Usage

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

Arguments

term   term ID vector

organism   organism

TERM2NAME.DO *TERM2NAME.DO*

Description

TERM2NAME.DO

Usage

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

Arguments

term   term id

organism   organism

TERM2NAME.DOLite *TERM2NAME.DOLite*

Description

TERM2NAME.DOLite

Usage

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

Arguments

term   term ID

organism   organism

TERMID2EXTID   *TERMID2EXTID*

Description

Mapping Ontology Term ID to External ID

Usage

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

Arguments

term   term ID vector

organism   organism

TERMID2EXTID.DO   *TERMID2EXTID.DO*

Description

TERMID2EXTID.DO

Usage

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

Arguments

term   term ID

organism   organism

TERMID2EXTID.DOLite	*TERMID2EXTID.DOLite*

Description

TERMID2EXTID.DOLite

Usage

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

Arguments

term	term ID
organism	organism

theme_dose	*theme_dose*

Description

ggplot theme of DOSE

Usage

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

Arguments

font.size	font size

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