Package 'DOSE'

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 2.2.1

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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, igraph,scales, reshape2, graphics, GOSemSim, grid

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

VignetteBuilder knitr

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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'

biocViews Annotation

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:	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)

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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

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"

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 *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
`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   *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 *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 *geneSim*

Description

measuring similarities bewteen 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 *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   *preparing geneSets for gene set enrichment analysis*

Description

preparing geneSets for gene set enrichment analysis

Usage

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

Arguments

setType   type of gene sets
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

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

Arguments

...	Additional argument list
...	ignored.

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

Value

NULL

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

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	*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 `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	*Mapping Ontology Term ID to Name Symbol or Description*

Description

Mapping Ontology Term ID to Name Symbol or Description

Usage

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

Arguments

term	term ID vector
organism	organism

TERMID2EXTID   *Mapping Ontology Term ID to External ID*

Description

Mapping Ontology Term ID to External ID

Usage

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

Arguments

term	term ID vector
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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