

# Package ‘DOSE’

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**Type** Package

**Title** Disease Ontology Semantic and Enrichment analysis

**Version** 2.6.6

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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 (>= 3.1.0)

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

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

**VignetteBuilder** knitr

**License** Artistic-2.0

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

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

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

**NeedsCompilation** no

## 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

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

**See Also**

[enrichResult](#)

---

ALLEXTID

*ALLEXTID*

---

**Description**

Get all background External ID.

**Usage**

```
ALLEXTID(organism, ...)
```

**Arguments**

organism           organism  
...                 additional parameter

---

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

---

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", "average", "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, ont="MF", organism="human", measure="Wang")
```

---

`cnetplot`*cnetplot method*

---

**Description**

cnetplot method

**Usage**

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

```
## S4 method for signature 'enrichResult'
cnetplot(x, showCategory = 5,
         categorySize = "geneNum", foldChange = NULL, fixed = TRUE, ...)
```

**Arguments**

<code>x</code>	enrichResult object
<code>showCategory</code>	number of category plotted
<code>categorySize</code>	one of geneNum or pvalue
<code>foldChange</code>	fold change of expression value
<code>fixed</code>	logical
<code>...</code>	additional parameters

**Value**

plot

**Author(s)**Guangchuang Yu <http://ygc.name>

cnetplot\_internal      *cnetplot\_internal*

---

**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 parameters

**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*

---

**Description**

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>

---

dotplot

*dotplot method*

---

## Description

dotplot method

## Usage

```
dotplot(object, ...)
```

```
## S4 method for signature 'enrichResult'  
dotplot(object, x = "geneRatio",  
        colorBy = "p.adjust", showCategory = 10, font.size = 12, title = "")
```

## Arguments

object	an instance of <code>enrichResult</code>
...	additional parameter
x	variable for x axis
colorBy	one of 'pvalue', 'p.adjust' and 'qvalue'
showCategory	number of category
font.size	font size
title	plot title

## Value

plot

## Author(s)

Guangchuang Yu

Guangchuang Yu



---

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

**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
minGSSize	minimal size of genes annotated by Ontology term for testing.
qvalueCutoff	cutoff of qvalue
readable	whether mapping gene ID to gene Name
...	additional parameter

**Details**

using the hypergeometric model

**Value**

A enrichResult instance.

**Author(s)**

Guangchuang Yu <http://ygc.name>

---

`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 = 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`*enrichMap*

---

**Description**

enrichment map

**Usage**`enrichMap(x, n = 50, fixed = TRUE, ...)`**Arguments**

<code>x</code>	<code>gseaResult</code> or <code>enrichResult</code> object
<code>n</code>	maximum number of category to shown
<code>fixed</code>	if set to <code>FALSE</code> , will invoke <code>tkplot</code>
<code>...</code>	additional parameter

**Details**

enrichment map

**Value**

figure

**Author(s)**

G Yu

---

`enrichNCG`*enrichNCG*

---

**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 = 5, 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
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     *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  
 universe background gene  
 geneInCategory gene and category association  
 geneSets gene sets  
 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>
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---

**Description**

Mapping External ID to Ontology Term ID

**Usage**

EXTID2TERMID(gene, organism, ...)

**Arguments**

gene	gene ID vector
organism	organism
...	additional parameter

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>
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---

**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
...	additional parameter

---

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

---

**Description**

generic function for gene set enrichment analysis

**Usage**

```
gsea(geneList, geneSets, setType, organism, exponent, nPerm, minGSSize,
     pvalueCutoff, pAdjustMethod, verbose, seed = FALSE, ...)
```

**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
seed	set seed inside the function to make result reproducible. FALSE by default.
...	additional parameter

**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
...	additional parameters

**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>
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---

**Description**

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

**Slots**

result	GSEA analysis
setType	setType
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>

---

mclusterSim	<i>mclusterSim</i>
-------------	--------------------

---

**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", "average", "rmax", "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")
```

---

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**

<code>g</code>	igraph object
<code>vertex.label.font</code>	font size
<code>vertex.label.color</code>	font text color
<code>vertex.label.cex</code>	cex of vertex label
<code>layout</code>	layout
<code>foldChange</code>	fold change
<code>fixed</code>	logical
<code>col.bin</code>	number of legend color bin
<code>legend.x</code>	x-axis position of legend
<code>legend.y</code>	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>rebuilding annotation data</i>
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---

**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

*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 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 enrichResult 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
...	additional parameter

---

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

---

**Description**

Mapping Ontology Term ID to External ID

**Usage**

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

**Arguments**

term	term ID vector
organism	organism
...	additional parameter

---

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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