

# Package ‘DOSE’

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**Type** Package

**Title** Disease Ontology Semantic and Enrichment analysis

**Version** 2.8.0

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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 (>= 3.1.0)

**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	<i>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.</i>
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## 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**

x	enrichResult object
showCategory	number of category plotted
categorySize	one of geneNum or pvalue
foldChange	fold change of expression value
fixed	logical
...	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(DO1D1, DO1D2, measure = "Wang")
```

### Arguments

DO1D1	DO term vector
DO1D2	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 enrichResult
...	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 *enrich.internal*

---

### 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**

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 = enrichD0(gene, pvalueCutoff=0.05)
summary(yy)
```

---

enrichMap

*enrichMap*

---

**Description**

enrichment map

**Usage**

```
enrichMap(x, n = 50, fixed = TRUE, vertex.label.font = 1, ...)
```

**Arguments**

x	gseaResult or enrichResult object
n	maximum number of category to shown
fixed	if set to FALSE, will invoke tkplot
vertex.label.font	font size of vertex label
...	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

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

---

**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     *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 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	<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`*getGeneSet*

---

**Description**

preparing geneSets for gene set enrichment analysis

**Usage**`getGeneSet(setType, organism, ...)`**Arguments**

<code>setType</code>	type of gene sets
<code>organism</code>	organism
<code>...</code>	additional parameter

---

`gsea`*gsea*

---

**Description**

generic function for gene set enrichment analysis

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

<code>geneList</code>	order ranked geneList
<code>geneSets</code>	gene sets
<code>setType</code>	Type of geneSet
<code>organism</code>	organism
<code>exponent</code>	weight of each step
<code>nPerm</code>	permutation numbers
<code>minGSSize</code>	minimal size of each geneSet for analyzing
<code>pvalueCutoff</code>	p value Cutoff
<code>pAdjustMethod</code>	p value adjustment method
<code>verbose</code>	print message or not
<code>seed</code>	set seed inside the function to make result reproducible. FALSE by default.
<code>...</code>	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", "rcmax", "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	<i>plot method</i>
------	--------------------

---

**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	<i>rebuilding 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  
*setting.graph.attributes*

---

**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**

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

*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	<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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