

# Package ‘DOSE’

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**Type** Package

**Title** Disease Ontology Semantic and Enrichment analysis

**Version** 2.0.0

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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,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'

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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: 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**

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>

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computeIC	<i>compute information content</i>
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---

**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	<i>Datasets Information content and DO term to entrez gene IDs mapping</i>
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---

**Description**

Datasets Information content and DO term to entrez gene IDs mapping

---

doSim	<i>doSim</i>
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---

**Description**

measuring similarities between two DO term vectors.

**Usage**

```
doSim(DO1, DO2, 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>
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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
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>
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---

**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>
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---

**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
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