

# Package ‘DOSE’

April 11, 2018

**Type** Package

**Title** Disease Ontology Semantic and Enrichment analysis

**Version** 3.4.0

**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

**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 (>= 3.3.1)

**Imports** AnnotationDbi, BiocParallel, DO.db, fgsea, ggplot2, GOSemSim (>= 2.0.0), graphics, grDevices, grid, igraph, methods, qvalue, reshape2, rvcheck, S4Vectors, scales, stats, stats4, utils

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

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**URL** <https://guangchuangyu.github.io/DOSE>

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

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

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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Giovanni Dall'Olio [ctb]

**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](#)

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barplot.enrichResult *barplot*

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## Description

barplot of enrichResult

## Usage

```
## S3 method for class 'enrichResult'  
barplot(height, x = "Count", colorBy = "pvalue",  
        showCategory = 5, font.size = 12, title = "", ...)
```

**Arguments**

height	enrichResult object
x	one of 'Count' and 'GeneRatio'
colorBy	one of 'pvalue', 'p.adjust', 'qvalue'
showCategory	number of categories to show
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", "avg", "rmax", "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)
```

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cnetplot	<i>cnetplot method</i>
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**Description**

cnetplot

**Usage**

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

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

## S4 method for signature 'gseaResult'
cnetplot(x, showCategory = 5,
         categorySize = "pvalue", 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://guangchuangyu.github.io>

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cnetplot_internal	<i>cnetplot_internal</i>
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**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>

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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"

**Author(s)**

Guangchuang Yu <http://guangchuangyu.github.io>

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DataSet	<i>Datasets</i>
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**Description**

Information content and DO term to entrez gene IDs mapping

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doSim	<i>doSim</i>
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**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 <https://guangchuangyu.github.io>

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dotplot	<i>dotplot method</i>
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---

**Description**

dotplot  
dotplot for enrichResult  
dotplot for gseaResult

**Usage**

```
dotplot(object, ...)  
  
## S4 method for signature 'enrichResult'  
dotplot(object, x = "geneRatio",  
        colorBy = "p.adjust", showCategory = 10, split = NULL, font.size = 12,  
        title = "")  
  
## S4 method for signature 'gseaResult'  
dotplot(object, x = "geneRatio",  
        colorBy = "p.adjust", showCategory = 10, split = NULL, 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
split	separate result by 'category' variable
font.size	font size
title	plot title

**Value**

plot

**Author(s)**

Guangchuang Yu  
 Guangchuang Yu  
 Guangchuang Yu

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enrichDGN	<i>Enrichment analysis based on the DisGeNET</i> ( <a href="http://www.disgenet.org/">http://www.disgenet.org/</a> )
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**Description**

given a vector of genes, this function will return the enrichment NCG categories with FDR control

**Usage**

```
enrichDGN(gene, pvalueCutoff = 0.05, pAdjustMethod = "BH", universe,
  minGSSize = 10, maxGSSize = 500, 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
maxGSSize	maximal size of each geneSet for analyzing
qvalueCutoff	qvalue cutoff
readable	whether mapping gene ID to gene Name

**Value**

A enrichResult instance



**Author(s)**

Guangchuang Yu

**References**

Janet et al. (2015) DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. *Database* bav028 <http://database.oxfordjournals.org/content/2015/bav028.long>

enrichDGNv

*enrichDGN***Description**

Enrichment analysis based on the DisGeNET (<http://www.disgenet.org/>)

**Usage**

```
enrichDGNv(snp, pvalueCutoff = 0.05, pAdjustMethod = "BH", universe,
            minGSSize = 10, maxGSSize = 500, qvalueCutoff = 0.2, readable = FALSE)
```

**Arguments**

snp	a vector of SNP
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
maxGSSize	maximal size of each geneSet for analyzing
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

**References**

Janet et al. (2015) DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. *Database* bav028 <http://database.oxfordjournals.org/content/2015/bav028.long>

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`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 = 10, maxGSSize = 500, 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>	pvalue cutoff
<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 NCG category for testing
<code>maxGSSize</code>	maximal size of each geneSet for analyzing
<code>qvalueCutoff</code>	qvalue cutoff
<code>readable</code>	whether mapping gene ID to gene Name

**Value**

A `enrichResult` instance.

**Author(s)**

Guangchuang Yu <http://guangchuangyu.github.io>

**See Also**

[enrichResult-class](#)

**Examples**

```
data(geneList)
gene = names(geneList)[geneList > 1]
yy = enrichDO(gene, pvalueCutoff=0.05)
summary(yy)
```

---

enricher\_internal      *enrich.internal*

---

**Description**

internal method for enrichment analysis

**Usage**

```
enricher_internal(gene, pvalueCutoff, pAdjustMethod = "BH", universe = NULL,
  minGSSize = 10, maxGSSize = 500, qvalueCutoff = 0.2, USER_DATA)
```

**Arguments**

gene	a vector of entrez gene id.
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.
maxGSSize	maximal size of each geneSet for analyzing
qvalueCutoff	cutoff of qvalue
USER_DATA	ontology information

**Details**

using the hypergeometric model

**Value**

A enrichResult instance.

**Author(s)**

Guangchuang Yu <http://guangchuangyu.github.io>

---

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 = 10, maxGSSize = 500, 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
maxGSSize	maximal size of each geneSet for analyzing
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  
keytype Gene ID type  
universe background gene  
gene2Symbol mapping gene to Symbol  
geneSets gene sets  
readable logical flag of gene ID in symbol or not.

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

**See Also**

[enrichDO](#)

---

EXTID2NAME	<i>EXTID2NAME</i>
------------	-------------------

---

**Description**

mapping gene ID to gene Symbol

**Usage**

```
EXTID2NAME(OrgDb, geneID, keytype)
```

**Arguments**

OrgDb	OrgDb
geneID	entrez gene ID
keytype	keytype

**Value**

gene symbol

**Author(s)**

Guangchuang Yu <http://guangchuangyu.github.io>

---

fortify.enrichResult	<i>fortify</i>
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---

**Description**

convert enrichResult object for ggplot2

**Usage**

```
## S3 method for class 'enrichResult'
fortify(model, data, showCategory = 5, by = "Count",
        order = FALSE, drop = FALSE, split = NULL, ...)
```

**Arguments**

model	enrichResult object
data	not use here
showCategory	Category numbers to show
by	one of Count and GeneRatio
order	logical
drop	logical
split	separate result by 'split' variable
...	additional parameter

---

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://guangchuangyu.github.io>

---

geneID	<i>geneID generic</i>
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---

**Description**

geneID generic

**Usage**

```
geneID(x)
```

**Arguments**

x                        enrichResult object

**Value**

'geneID' return the 'geneID' column of the enriched result which can be converted to data.frame via 'as.data.frame'

**Examples**

```
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichDO(de)
geneID(x)
```

---

geneInCategory	<i>geneInCategory generic</i>
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---

**Description**

geneInCategory generic

**Usage**

```
geneInCategory(x)
```

**Arguments**

x	enrichResult
---	--------------

**Value**

'geneInCategory' return a list of genes, by splitting the input gene vector to enriched functional categories

**Examples**

```
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichDO(de)
geneInCategory(x)
```

---

geneSim	<i>geneSim</i>
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---

**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", "avg", "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>

---

gseaplot

*visualize analyzing result of GSEA*

---

**Description**

plotting function for gseaResult

**Usage**

```
gseaplot(gseaResult, geneSetID, by = "all", title = "", color = "black",  
         color.line = "green", color.vline = "#FA5860")
```

**Arguments**

gseaResult	gseaResult object
geneSetID	geneSet ID
by	one of "runningScore" or "position"
title	plot title
color	color of line segments
color.line	color of running enrichment score line
color.vline	color of vertical line which indicating the maximum/minimal running enrichment score

**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  
 organism organism  
 setType setType  
 geneSets geneSets  
 geneList order rank geneList  
 keytype ID type of gene  
 permScores permutation scores  
 params parameters  
 gene2Symbol gene ID to Symbol  
 readable whether convert gene ID to symbol

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

**See Also**

[gseaplot](#)

---

GSEA_internal	<i>GSEA_internal</i>
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---

**Description**

generic function for gene set enrichment analysis

**Usage**

```
GSEA_internal(geneList, exponent, nPerm, minGSSize, maxGSSize, pvalueCutoff,
  pAdjustMethod, verbose, seed = FALSE, USER_DATA, by = "fgsea")
```

**Arguments**

geneList	order ranked geneList
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal 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.
USER_DATA	annotation data
by	one of 'fgsea' or 'DOSE'

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseDGN

*DisGeNET Gene Set Enrichment Analysis*

---

**Description**

perform gsea analysis

**Usage**

```
gseDGN(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
       maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH",
       verbose = TRUE, seed = FALSE, by = "fgsea")
```

**Arguments**

geneList	order ranked geneList
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseDO

*DO Gene Set Enrichment Analysis*

---

**Description**

perform gsea analysis

**Usage**

```
gseDO(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,  
      maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH",  
      verbose = TRUE, seed = FALSE, by = "fgsea")
```

**Arguments**

geneList	order ranked geneList
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseNCG *NCG Gene Set Enrichment Analysis*

---

**Description**

perform gsea analysis

**Usage**

```
gseNCG(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
       maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH",
       verbose = TRUE, seed = FALSE, by = "fgsea")
```

**Arguments**

geneList	order ranked geneList
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gsfilter *gsfilter*

---

**Description**

filter enriched result by gene set size or gene count

**Usage**

```
gsfilter(x, by = "GSSize", min = NA, max = NA)
```

**Arguments**

x	instance of enrichResult or compareClusterResult
by	one of 'GSSize' or 'Count'
min	minimal size
max	maximal size

**Value**

update object

**Author(s)**

Guangchuang Yu

---

gsInfo

*gsInfo*

---

**Description**

extract gsea result of selected geneSet

**Usage**

```
gsInfo(object, geneSetID)
```

**Arguments**

object	gseaResult object
geneSetID	gene set ID

**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

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>

---

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", "avg", "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
<code>...</code>	additional parameters

**Details**

plot network of igraph object

**Value**

plot

**Author(s)**

Yu Guangchuang



---

plot	<i>plot method</i>
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---

**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://guangchuangyu.github.io>  
Yu Guangchuang

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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
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**Author(s)**

Guangchuang Yu <http://guangchuangyu.github.io>

---

ridgeplot	<i>ridgeplot</i>
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**Description**

ridgeplot for GSEA result

**Usage**

```
ridgeplot(x, showCategory = 30, fill = "p.adjust", core_enrichment = TRUE)
```

**Arguments**

x	gseaResult object
showCategory	number of categories for plotting
fill	one of "pvalue", "p.adjust", "qvalue"
core_enrichment	whether only using core_enriched genes

**Value**

ggplot object

**Author(s)**

guangchuang yu

---

scaleNodeColor	<i>scaleNodeColor</i>
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**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>
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**Description**

mapping geneID to gene Symbol

**Usage**

```
setReadable(x, OrgDb, keytype = "auto")
```

**Arguments**

x	enrichResult Object
OrgDb	OrgDb
keytype	keytype of gene

**Value**

enrichResult Object

**Author(s)**

Yu Guangchuang

---

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

<code>g</code>	igraph object
<code>node.size</code>	size of node
<code>node.color</code>	color of node
<code>edge.width</code>	edge width
<code>edge.color</code>	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 <https://guangchuangyu.github.io>

Guangchuang Yu <https://guangchuangyu.github.io>

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simplot	<i>simplot</i>
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---

**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>
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**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://guangchuangyu.github.io>  
 Guangchuang Yu <https://guangchuangyu.github.io>

---

theme_dose	<i>theme_dose</i>
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---

**Description**

ggplot theme of DOSE

**Usage**

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

**Arguments**

font.size        font size

---

upsetplot	<i>upsetplot method</i>
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---

**Description**

upsetplot method generics  
 upsetplot

**Usage**

```
upsetplot(x, ...)  
  
## S4 method for signature 'enrichResult'  
upsetplot(x, n = 10, ...)
```

**Arguments**

x                object  
 ...              additional parameters  
 n                number of categories to be plotted

**Value**

plot

**Author(s)**

Guangchuang Yu

**Examples**

```
## Not run:  
require(DOSE)  
data(geneList)  
de=names(geneList)[1:100]  
x <- enrichDO(de)  
upsetplot(x, 8)  
  
## End(Not run)
```

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