

Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

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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 (>= 3.3.1)

Imports AnnotationDbi, BiocParallel, DO.db, fgsea, ggplot2, GOSemSim (>= 2.0.0), graphics, grDevices, grid, igraph, methods, qvalue, reshape2, 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 5.0.1

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](#)

barplot.enrichResult *barplot*

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", "average", "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)
```

cnetplot*cnetplot method*

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>

cnetplot_internal	<i>cnetplot_internal</i>
-------------------	--------------------------

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

Description

compute information content

Usage

```
computeIC(ont = "DO", organism = "human")
```

Arguments

ont	"DO"
organism	"human"

Author(s)

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

DataSet	<i>Datasets</i>
---------	-----------------

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 <https://guangchuangyu.github.io>

`dotplot`*dotplot method*

Description

dotplot
dotplot for enrichResult

Usage

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

Value

plot

Author(s)

Guangchuang Yu
Guangchuang Yu

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

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>

`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,
  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>
----------------------	----------------

Description

convert enrichResult object for ggplot2

Usage

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

Arguments

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

fortify.gseaResult *fortify.gseaResult*

Description

convert gsea result for ggplot2

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://guangchuangyu.github.io>

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

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>
----------------	-------------------------------

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>
---------	----------------

Description

measuring similarities between 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)

Guangchuan Yu <http://ygc.name>

gseaplot	<i>visualize analyzing result of GSEA</i>
----------	---

Description

plotting function for gseaResult

Usage

```
gseaplot(gseaResult, geneSetID, by = "all", title = "")
```

Arguments

gseaResult	gseaResult object
geneSetID	geneSet ID
by	one of "runningScore" or "position"
title	plot title

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

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>
---------------	----------------------

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	<i>DisGeNET Gene Set Enrichment Analysis</i>
--------	--

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

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>

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	<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
...	additional parameters

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://guangchuangyu.github.io>
Yu Guangchuang

rebuildAnnoData	<i>rebuiding annotation data</i>
-----------------	----------------------------------

Description

rebuilding entrez and DO mapping datasets

Usage

```
rebuildAnnoData(file)
```

Arguments

file	do_rif.human.txt
------	------------------

Author(s)

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

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, 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>
--------------------------	---------------------------------

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>

`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

<code>sim</code>	similarity matrix
<code>xlab</code>	xlab
<code>ylab</code>	ylab
<code>color.low</code>	color of low value
<code>color.high</code>	color of high value
<code>labs</code>	logical, add text label or not
<code>digits</code>	round digit numbers
<code>labs.size</code>	lable size
<code>font.size</code>	font size

Value

ggplot object

Author(s)

Yu Guangchuang

`summary`*summary method*

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)

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 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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