Package 'DOSE'

April 15, 2024

Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.28.2

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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 (>= 3.5.0)

Imports AnnotationDbi, HDO.db, BiocParallel, fgsea, ggplot2, GOSemSim
(>= 2.27.1), methods, qvalue, reshape2, stats, utils,
yulab.utils

Suggests prettydoc, clusterProfiler, gson (>= 0.0.5), knitr,
rmarkdown, org.Hs.eg.db, MPO.db, HPO.db, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

Encoding UTF-8

URL https://yulab-smu.top/biomedical-knowledge-mining-book/

BugReports https://github.com/GuangchuangYu/DOSE/issues

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

RoxygenNote 7.2.3

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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, HDO.dbb
Suggests:	clusterProfiler, GOSemSim
License:	Artistic-2.0

Author(s)

Guangchuang Yu, Li-Gen Wang

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also

[enrichResult](#)

clusterSim	*clusterSim*

Description

semantic similarity between two gene clusters

Usage

```
clusterSim(
  cluster1,
  cluster2,
  ont = "DO",
  organism = "hsa",
  measure = "Wang",
  combine = "BMA"
)
```

Arguments

cluster1	a vector of gene IDs
cluster2	another vector of gene IDs
ont	one of "DO" and "MPO"
organism	organism
measure	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
combine	One of "max", "avg", "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)
```

---

compareClusterResult-class

> *Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.*

Description

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Slots

compareClusterResult cluster comparing result

geneClusters a list of genes

fun one of groupGO, enrichGO and enrichKEGG

gene2Symbol gene ID to Symbol

keytype Gene ID type

readable logical flag of gene ID in symbol or not.

.call function call

termsim Similarity between term

method method of calculating the similarity between nodes

dr dimension reduction result

Author(s)

Guangchuang Yu https://yulab-smu.top

See Also

enrichResult

---

computeIC   *compute information content*

Description

compute information content

Usage

computeIC(ont = "DO")

Arguments

ont   one of "DO" and "MPO"

Author(s)

Guangchuang Yu <https://yulab-smu.top>

DataSet   *Datasets*

Description

Information content and DO term to entrez gene IDs mapping

---

doseSim   *doSim*

Description

measuring similarities between two DO term vectors.

Usage

```
doseSim(DOID1, DOID2, measure = "Wang", ont = "DO")
```

Arguments

DOID1   DO term, MPO term or HPO term vector

DOID2   DO term, MPO term or HPO term vector

measure   one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".

ont   one of "DO" and "MPO"

Details

provide two term vectors, this function will calculate their similarities.

Value

score matrix

---

doSim   *doSim*

Description

measuring similarities between two MPO term vectors.

Usage

```
doSim(DOID1, DOID2, measure = "Wang")
```

Arguments

DOID1	DO term vector
DOID2	DO term vector
measure	one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".

Details

provide two DO term vectors, this function will calculate their similarities.

Value

score matrix

Author(s)

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

---

enrichDGN   *Enrichment analysis based on the DisGeNET (*[http://www.](http://www.disgenet.org/)
                       [disgenet.org/)](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",
  organism = "hsa",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  readable = FALSE
)
```

Arguments

gene	a vector of entrez gene id
ont	one of DO and DOLite.
organism	one of "hsa" and "mmu"
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 <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

interal 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>

---

enrichHPO	*Enrichment analysis based on the DisGeNET (*[http://www.](http://www.disgenet.org/)[disgenet.org/](http://www.disgenet.org/)*)*

Description

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

Usage

```
enrichHPO(
  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)

Erqiang Hu

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

---

enrichMPO	*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

```
enrichMPO(
  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)

Erqiang Hu

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

---

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.

termsim Similarity between term

method method of calculating the similarity between nodes

dr dimension reduction result

Author(s)

Guangchuang Yu https://yulab-smu.top

See Also

enrichDO

EXTID2NAME   *EXTID2NAME*

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 <https://yulab-smu.top>

---

gene2DO   *convert Gene ID to DO Terms*

Description

provide gene ID, this function will convert to the corresponding DO Terms

Usage

```
gene2DO(gene, organism = "hsa", ont = "DO")
```

Arguments

gene	entrez gene ID
organism	organism
ont	ont

Value

DO Terms

Author(s)

Guangchuang Yu <https://yulab-smu.top>

---

geneID *geneID generic*

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 *geneInCategory generic*

Description

geneInCategory generic

Usage

```
geneInCategory(x)
```

Arguments

x   enrichResult

Value

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

Examples

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

---

geneSim   *geneSim*

Description

measuring similarities bewteen two gene vectors.

Usage

```
geneSim(
  geneID1,
  geneID2 = NULL,
  ont = "DO",
  organism = "hsa",
  measure = "Wang",
  combine = "BMA"
)
```

Arguments

geneID1	entrez gene vector
geneID2	entrez gene vector
ont	one of "DO" and "MPO"
organism	organism
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>

---

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 anaysis

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

dr dimension reduction result

Author(s)

Guangchuang Yu <https://yulab-smu.top>

GSEA_internal   *GSEA_internal*

Description

generic function for gene set enrichment analysis

Usage

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

Arguments

geneList	order ranked geneList
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
eps	This parameter sets the boundary for calculating the p value.
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'
...	other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

---

gseDGN   *DisGeNET Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseDGN(
  geneList,
  exponent = 1,
  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
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'
...	other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

---

gseDO   *DO Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

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

Arguments

geneList	order ranked geneList
organism	one of "hsa" and "mmu"
exponent	weight of each step
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'
...	other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

---

gseHPO *MPO Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseHPO(
  geneList,
  exponent = 1,
  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
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'
...	other parameter

Value

gseaResult object

Author(s)

Erqiang Hu

gseMPO   *MPO Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseMPO(
  geneList,
  exponent = 1,
  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
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'
...	other parameter

Value

gseaResult object

Author(s)

Erqiang Hu

---

gseNCG   *NCG Gene Set Enrichment Analysis*

Description

perform gsea analysis

Usage

```
gseNCG(
  geneList,
  exponent = 1,
  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
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'
...	other parameter

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

---

hpoSim *doSim*

Description

measuring similarities between two MPO term vectors.

Usage

```
hpoSim(DOID1, DOID2, measure = "Wang")
```

Arguments

DOID1	HPO term vector
DOID2	HPO term vector
measure	one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".

Details

provide two HPO term vectors, this function will calculate their similarities.

Value

score matrix

---

mclusterSim	*mclusterSim*

Description

Pairwise semantic similarity for a list of gene clusters

Usage

```
mclusterSim(
  clusters,
  ont = "DO",
  organism = "hsa",
  measure = "Wang",
  combine = "BMA"
)
```

Arguments

clusters	A list of gene clusters
ont	one of "DO" and "MPO"
organism	organism
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")
```

---

mpoSim   *doSim*

Description

measuring similarities between two MPO term vectors.

Usage

```
mpoSim(DOID1, DOID2, measure = "Wang")
```

Arguments

DOID1	MPO term vector
DOID2	MPO term vector
measure	one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".

Details

provide two MPO term vectors, this function will calculate their similarities.

Value

score matrix

---

parse_ratio   *parse_ratio*

Description

parse character ratio to double value, such as 1/5 to 0.2

Usage

```
parse_ratio(ratio)
```

Arguments

ratio	character vector of ratio to parse

Value

A numeric vector (double) of parsed ratio

Author(s)

Guangchuang Yu

---

rebuildAnnoData *rebuiding annotation data*

Description

rebuilding entrez and DO mapping datasets

Usage

```
rebuildAnnoData(file)
```

Arguments

file   do_rif.human.txt

Author(s)

Guangchuang Yu <https://yulab-smu.top>

---

reexports *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

ggplot2 `facet_grid`

---

setReadable *setReadable*

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

---

show   *show method*

Description

show method for `gseaResult` instance

show method for `enrichResult` instance

Usage

```
show(object)

show(object)
```

Arguments

`object`   A `enrichResult` instance.

Value

message

message

Author(s)

Guangchuang Yu <https://yulab-smu.top>

---

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

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   *summary method*

Description

summary method for `gseaResult` instance

summary method for `enrichResult` instance

Usage

```
summary(object, ...)

summary(object, ...)
```

Arguments

object   A `enrichResult` instance.

...   additional parameter

Value

A data frame

A data frame

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theme_dose   *theme_dose*

Description

ggplot theme of DOSE

Usage

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

Arguments

font.size   font size

Value

ggplot theme

Examples

```
library(ggplot2)
qplot(1:10) + theme_dose()
```

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