

Package ‘DOSE’

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Type Package

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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.

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DOSE-package	<i>DOSE: Disease Ontology Semantic and Enrichment analysis</i>
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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.

Author(s)

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See Also

Useful links:

- <https://yulab-smu.top/biomedical-knowledge-mining-book/>
- Report bugs at <https://github.com/GuangchuangYu/DOSE/issues>

clusterSim	<i>clusterSim</i>
------------	-------------------

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

Description

compute information content

Usage

```
computeIC(ont = "DO")
```

Arguments

ont one of "DO" and "MPO"

Author(s)

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

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

Description

Information content and DO term to entrez gene IDs mapping

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

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

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	<i>Enrichment analysis based on the DisGeNET</i> (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	<i>enrichDGN</i>
------------	------------------

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	<i>enrich.internal</i>
-------------------	------------------------

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, default is the intersection of the 'universe' with genes that have annotations. Users can set 'options(enrichment_force_universe = TRUE)' to force the 'universe' untouched.

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 <https://yulab-smu.top>

enrichHPO	<i>Enrichment analysis based on the DisGeNET</i> (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	<i>Enrichment analysis based on the DisGeNET</i> (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	<i>enrichNCG</i>
-----------	------------------

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

<code>enrichResult-class</code>	<i>Class "enrichResult" This class represents the result of enrichment analysis.</i>
---------------------------------	--

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

gene2DO	<i>convert Gene ID to DO Terms</i>
---------	------------------------------------

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	<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

*geneSim***Description**

measuring similarities between 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	<i>Class "gseaResult" This class represents the result of GSEA analysis</i>
------------------	---

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

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

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

<code>geneList</code>	order ranked geneList
<code>organism</code>	one of "hsa" and "mmu"
<code>exponent</code>	weight of each step
<code>minGSSize</code>	minimal size of each geneSet for analyzing
<code>maxGSSize</code>	maximal size of each geneSet for analyzing
<code>pvalueCutoff</code>	pvalue Cutoff
<code>pAdjustMethod</code>	p value adjustment method
<code>verbose</code>	print message or not
<code>seed</code>	logical
<code>by</code>	one of 'fgsea' or 'DOSE'
<code>...</code>	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

<code>geneList</code>	order ranked geneList
<code>exponent</code>	weight of each step
<code>minGSSize</code>	minimal size of each geneSet for analyzing
<code>maxGSSize</code>	maximal size of each geneSet for analyzing
<code>pvalueCutoff</code>	pvalue Cutoff
<code>pAdjustMethod</code>	p value adjustment method
<code>verbose</code>	print message or not
<code>seed</code>	logical
<code>by</code>	one of 'fgsea' or 'DOSE'
<code>...</code>	other parameter

Value

`gseaResult` object

Author(s)

Erqiang Hu

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

<code>geneList</code>	order ranked geneList
<code>exponent</code>	weight of each step
<code>minGSSize</code>	minimal size of each geneSet for analyzing
<code>maxGSSize</code>	maximal size of each geneSet for analyzing
<code>pvalueCutoff</code>	pvalue Cutoff
<code>pAdjustMethod</code>	p value adjustment method
<code>verbose</code>	print message or not
<code>seed</code>	logical
<code>by</code>	one of 'fgsea' or 'DOSE'
<code>...</code>	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 <code>enrichResult</code> or <code>compareClusterResult</code>
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(D0ID1, D0ID2, measure = "Wang")
```

Arguments

D0ID1	HPO term vector
D0ID2	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	<i>mclusterSim</i>
-------------	--------------------

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

Description

measuring similarities between two MPO term vectors.

Usage

```
mpoSim(D0ID1, D0ID2, measure = "Wang")
```

Arguments

D0ID1	MPO term vector
D0ID2	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	<i>parse_ratio</i>
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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	<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 <https://yulab-smu.top>

reexports	<i>Objects exported from other packages</i>
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Description

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

ggplot2 [facet_grid](#)

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

show	<i>show method</i>
------	--------------------

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

<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	<i>summary method</i>
---------	-----------------------

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

Author(s)

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

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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Value

ggplot theme

Examples

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


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