Package ‘DOSE’

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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.
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R topics documented:

DOSE-package ................................................................. 3
clusterSim ................................................................. 4
compareClusterResult-class .................................................. 5
computeIC ................................................................. 5
DataSet ................................................................. 6
doseSim ................................................................. 6
doSim ................................................................. 7
enrichDGN ............................................................... 7
enrichDGNv ............................................................ 8
enrichDO ............................................................... 10
enricher_internal ........................................................ 11
enrichHPO .............................................................. 12
enrichMPO .............................................................. 13
enrichNCG .............................................................. 14
enrichResult-class ........................................................ 15
EXTID2NAME ............................................................ 16
gene2DO ............................................................... 16
geneID ................................................................. 17
geneInCategory ........................................................ 17
geneSim ............................................................... 18
gseaResult-class ........................................................ 19
GSEA_internal ........................................................ 19
gseDGN ............................................................... 21
gseDO ............................................................... 22
gseHPO ............................................................... 23
gseMPO ............................................................... 24
gseNCG ............................................................... 25
gsfilter ............................................................... 26
hpoSim ............................................................... 26
mclusterSim .......................................................... 27
mpoSim .............................................................. 28
parse_ratio ............................................................. 28
rebuildAnnoData ......................................................... 29
reexports ............................................................... 29
setReadable ............................................................ 29
show ................................................................. 30
simplot ............................................................... 31
**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

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")
clusterSim(cluster1, cluster2)
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](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

Data Set

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

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

Description
Enrichment analysis based on the DisGeNET (http://www.disgenet.org/)
given a vector of genes, this function will return the enrichment NCG categories with FDR control
Usage

```r
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


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

enrichDO

**DO Enrichment Analysis**

**Description**

Given a vector of genes, this function will return the enrichment DO categories with FDR control.

**Usage**

```r
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](http://guangchuangyu.github.io)

**See Also**

- `enrichResult-class`
**enricher_internal**

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

**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](http://guangchuangyu.github.io)

---

**enrichHPO**


---

**Description**

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

**Usage**

```r
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

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


enrichNCG

Description

Enrichment analysis based on the Network of Cancer Genes database (http://ncg.kcl.ac.uk/)

Usage

enrichNCG(
  gene,   # a vector of entrez gene id
  pvalueCutoff = 0.05,   # pvalue cutoff
  pAdjustMethod = "BH",   # one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
  universe,   # background genes
  minGSSize = 10,   # minimal size of genes annotated by NCG category for testing
  maxGSSize = 500,   # maximal size of each geneSet for analyzing
  qvalueCutoff = 0.2,   # qvalue cutoff
  readable = FALSE   # whether mapping gene ID to gene Name
)

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  pvalue cutoff
pAdjustMethod  pvalue adjust method
qvalueCutoff  qvalue cutoff
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**

**Description**

mapping gene ID to gene Symbol

**Usage**

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

**Arguments**

- `OrgDb` : OrgDb
- `geneID` : entrez gene ID
- `keytype` : keytype

**Value**

gene symbol

**Author(s)**

Guangchuang Yu [https://yulab-smu.top](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**

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

**Arguments**

- `gene` : entrez gene ID
- `organism` : organism
- `ont` : ont

**Value**

DO Terms
geneID

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")
d <- names(geneList)[1:100]
x <- enrichDO(d)
geneID(x)

geneInCategory  geneInCategory generic

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)

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
**gseaResult-class**

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

---

**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
- `dr`: dimension reduction result

**Author(s)**

Guangchuang Yu [https://yulab-smu.top](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**

```r

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
DO Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

```r
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
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**

```r
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
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’
...

Value

gseaResult object

Author(s)

Yu Guangchuang
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

----

**Description**

Pairwise semantic similarity for a list of gene clusters

**Usage**

```r
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**

```r
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")
```
**Description**

measuring similarities between two MPO term vectors.

**Usage**

```r
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**

**Description**

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

**Usage**

```r
parse_ratio(ratio)
```

**Arguments**

- **ratio**: character vector of ratio to parse

**Value**

A numeric vector (double) of parsed ratio

**Author(s)**

Guangchuang Yu
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
show

**Value**

enrichResult Object

**Author(s)**

Yu Guangchuang

---

**show**  
*show method*

---

**Description**

show method for gseaResult instance  
show method for enrichResult instance

**Usage**

```r
show(object)
show(object)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>A enrichResult instance.</td>
</tr>
</tbody>
</table>

**Value**

message
message

**Author(s)**

Guangchuang Yu [https://yulab-smu.top](https://yulab-smu.top)
Description
plotting similarity matrix

Usage

```r
simplot(
  sim,
  xlab = "",  # xlab
  ylab = "",  # ylab
  color.low = "white",  # color.low
  color.high = "red",  # color.high
  labs = TRUE,  # labs
  digits = 2,  # digits
  labs.size = 3,  # labs.size
  font.size = 14  # font.size
)
```

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

**Description**

Summary method for `gseaResult` instance

**Usage**

```r
summary(object, ...)
```

**Arguments**

- `object`: A `enrichResult` instance.
- `...`: Additional parameter

**Value**

A data frame

**Author(s)**

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

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**theme_dose**

**Description**

Ggplot theme of DOSE

**Usage**

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

**Arguments**

- `font.size`: Font size
theme_dose

Value

ggplot theme

Examples

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

* classes
  compareClusterResult-class, 5
enrichResult-class, 15
gseaResult-class, 19
* datasets
  DataSet, 6
* internal
  reexports, 29
* manip
  enrichDO, 10
  enricher_internal, 11
gseDGN, 21
gseDO, 22
gseHPO, 23
gseMPO, 24
gseNCG, 25
* package
  DOSE-package, 3
clustSim, 4
  compareClusterResult-class, 5
  computeIC, 5

DataSet, 6
  DGN_EXTID2PATHID (DataSet), 6
  DGN_PATHID2EXTID (DataSet), 6
  DGN_PATHID2NAME (DataSet), 6
  DO2ALLEG (DataSet), 6
  DO2EG (DataSet), 6
  DOIC (DataSet), 6
  DOLite2EG (DataSet), 6
  DOLiteTerm (DataSet), 6
  DOSE / DOSE-package, 3
  DOSE-package, 3
doseSim, 6
doSim, 7
dotbl (DataSet), 6
  EG2ALLLD0 (DataSet), 6
  EG2DO (DataSet), 6
  EG2DO (DataSet), 6

  EG2DOLite (DataSet), 6
  enrichDGN, 7
  enrichDO, 10, 15
  enricher_internal, 11
  enrichHPO, 12
  enrichMPO, 13
  enrichNCG, 14
  enrichResult, 3, 5
  enrichResult-class, 15
  EXTID2NAME, 16

  facet_grid, 29
  facet_grid (reexports), 29
gene2DO, 16
geneID, 17
geneInCategory, 17
geneList (DataSet), 6
geneSim, 18
  GSEA_internal, 19
  gseahResult-class (gseaResult-class), 19
  gseaResult-class, 19
  gseDGN, 21
  gseDO, 22
gseHPO, 23
  gseMPO, 24
gseNCG, 25
gsfilter, 26

  hpoSim, 26
  hpotbl (DataSet), 6
  mclusterSim, 27
  mpoSim, 28
  mpotbl (DataSet), 6
  NCG_EXTID2PATHID (DataSet), 6
  NCG_PATHID2EXTID (DataSet), 6
  NCG_PATHID2NAME (DataSet), 6
INDEX

parse_ratio, 28
plot, compareClusterResult-method
  (compareClusterResult-class), 5
rebuildAnnoData, 29
reexports, 29
setReadable, 29
show, 30
show, compareClusterResult-method
  (compareClusterResult-class), 5
show, enrichResult-method
  (enrichResult-class), 15
show, gseaResult-method
  (gseaResult-class), 19
simplot, 31
summary, 32
summary, compareClusterResult-method
  (compareClusterResult-class), 5
summary, enrichResult-method
  (enrichResult-class), 15
summary, gseaResult-method
  (gseaResult-class), 19
theme_dose, 32
VDGN_EXTID2PATHID (DataSet), 6
VDGN_PATHID2EXTID (DataSet), 6
VDGN_PATHID2NAME (DataSet), 6