Package ‘DOSE’

May 29, 2024

Type Package
Title Disease Ontology Semantic and Enrichment analysis
Version 3.30.1
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>
Description This package implements five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring semantic similarities among DO terms and gene products. Enrichment analyses including hypergeometric model and gene set enrichment analysis are also implemented for discovering disease associations of high-throughput biological data.
Depends R (>= 3.5.0)
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, HPO.db, MPO.db, testthat
VignetteBuilder knitr
ByteCompile true
License Artistic-2.0
Encoding UTF-8

BugReports https://github.com/GuangchuangYu/DOSE/issues
biocViews Annotation, Visualization, MultipleComparison, GeneSetEnrichment, Pathways, Software
RoxygenNote 7.3.1

git_url https://git.bioconductor.org/packages/DOSE
git_branch RELEASE_3_19
git_last_commit 651ad4c
git_last_commit_date 2024-05-16
Repository Bioconductor 3.19
Date/Publication 2024-05-29
Author Guangchuang Yu [aut, cre], Li-Gen Wang [ctb], Vladislav Petyuk [ctb], Giovanni Dall'Olio [ctb], Erqiang Hu [ctb]

Contents

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOSE-package</td>
<td>3</td>
</tr>
<tr>
<td>clusterSim</td>
<td>3</td>
</tr>
<tr>
<td>compareClusterResult-class</td>
<td>4</td>
</tr>
<tr>
<td>computeIC</td>
<td>5</td>
</tr>
<tr>
<td>DataSet</td>
<td>5</td>
</tr>
<tr>
<td>doseSim</td>
<td>6</td>
</tr>
<tr>
<td>doSim</td>
<td>6</td>
</tr>
<tr>
<td>enrichDGN</td>
<td>7</td>
</tr>
<tr>
<td>enrichDGNv</td>
<td>8</td>
</tr>
<tr>
<td>enrichDO</td>
<td>9</td>
</tr>
<tr>
<td>enricher_internal</td>
<td>10</td>
</tr>
<tr>
<td>enrichHPO</td>
<td>11</td>
</tr>
<tr>
<td>enrichMPO</td>
<td>12</td>
</tr>
<tr>
<td>enrichNCG</td>
<td>13</td>
</tr>
<tr>
<td>enrichResult-class</td>
<td>14</td>
</tr>
<tr>
<td>EXTID2NAME</td>
<td>15</td>
</tr>
<tr>
<td>gene2DO</td>
<td>15</td>
</tr>
<tr>
<td>geneID</td>
<td>16</td>
</tr>
<tr>
<td>geneInCategory</td>
<td>16</td>
</tr>
<tr>
<td>geneSim</td>
<td>17</td>
</tr>
<tr>
<td>gseaResult-class</td>
<td>18</td>
</tr>
<tr>
<td>GSEA_internal</td>
<td>18</td>
</tr>
<tr>
<td>gseDGN</td>
<td>20</td>
</tr>
<tr>
<td>gseDO</td>
<td>21</td>
</tr>
<tr>
<td>gseHPO</td>
<td>22</td>
</tr>
<tr>
<td>gseMPO</td>
<td>23</td>
</tr>
<tr>
<td>gseNCG</td>
<td>24</td>
</tr>
<tr>
<td>gsfilter</td>
<td>25</td>
</tr>
<tr>
<td>hpoSim</td>
<td>25</td>
</tr>
<tr>
<td>mclusterSim</td>
<td>26</td>
</tr>
<tr>
<td>mpoSim</td>
<td>27</td>
</tr>
<tr>
<td>parse_ratio</td>
<td>27</td>
</tr>
<tr>
<td>rebuildAnnoData</td>
<td>28</td>
</tr>
<tr>
<td>reexports</td>
<td>28</td>
</tr>
<tr>
<td>setReadable</td>
<td>28</td>
</tr>
<tr>
<td>show</td>
<td>29</td>
</tr>
<tr>
<td>simplot</td>
<td>30</td>
</tr>
</tbody>
</table>
DOSE-package

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)

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

Other contributors:

- Li-Gen Wang <reeganwang020@gmail.com> [contributor]
- Vladislav Petyuk <petyuk@gmail.com> [contributor]
- Giovanni Dall’Olio <giovanni.dallolio@upf.edu> [contributor]
- Erqiang Hu <13766876214@163.com> [contributor]

See Also

Useful links:

- Report bugs at https://github.com/GuangchuangYu/DOSE/issues

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

```r
cluster1 <- c("835", "5261","241", "994")
clusterSim(cluster1, cluster2)
```

compareClusterResult-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
computeIC

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

Description
Information content and DO term to entrez gene IDs mapping
**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

---

**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.
enrichDGN

Value
    score matrix

Author(s)
    Guangchuang Yu https://guangchuangyu.github.io

---


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

enrichDGNv

description

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>snp</td>
<td>a vector of SNP</td>
</tr>
<tr>
<td>pvalueCutoff</td>
<td>pvalue cutoff</td>
</tr>
<tr>
<td>pAdjustMethod</td>
<td>one of &quot;holm&quot;, &quot;hochberg&quot;, &quot;hommel&quot;, &quot;bonferroni&quot;, &quot;BH&quot;, &quot;BY&quot;, &quot;fdr&quot;, &quot;none&quot;</td>
</tr>
<tr>
<td>universe</td>
<td>background genes</td>
</tr>
<tr>
<td>minGSSize</td>
<td>minimal size of genes annotated by NCG category for testing</td>
</tr>
<tr>
<td>maxGSSize</td>
<td>maximal size of each geneSet for analyzing</td>
</tr>
<tr>
<td>qvalueCutoff</td>
<td>qvalue cutoff</td>
</tr>
<tr>
<td>readable</td>
<td>whether mapping gene ID to gene Name</td>
</tr>
</tbody>
</table>

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

Value
A `enrichResult` instance
**enrichDO**

**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
enricher_internal

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)

---

tenricher_internal

Description
internal method for enrichment analysis

Usage

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

Arguments
gene a vector of entrez gene id.
pvalueCutoff Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes, 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.
enrichHPO

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](https://yulab-smu.top)


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


---

enrichMPO


Description

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

Usage

```r
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


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**

**Description**

mapping gene ID to gene Symbol

**Usage**

`EXTID2NAME(OrgDb, geneID, keytype)`

**Arguments**

- **OrgDb**
- **geneID**
- **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**

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

**Arguments**

- **gene**
- **organism**
- **ont**

**Value**

DO Terms
Author(s)
Guangchuang Yu https://yulab-smu.top

<table>
<thead>
<tr>
<th>geneID</th>
<th>geneID generic</th>
</tr>
</thead>
</table>

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)

<table>
<thead>
<tr>
<th>geneInCategory</th>
<th>geneInCategory generic</th>
</tr>
</thead>
</table>

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

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

Value

gseaResult object

Author(s)

Yu Guangchuang
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
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,
iminGSSize = 10,
imaxGSSize = 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

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'
...             other parameter

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**

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

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**

**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**

**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
Description
rebuilding entrez and DO mapping datasets

Usage
rebuildAnnoData(file)

Arguments
file
do_rif.human.txt

Author(s)
Guangchuang Yu https://yulab-smu.top

Description
Objects exported from other packages

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

ggplot2 facet_grid

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

Description

show method for gseaResult instance
show method for enrichResult instance

Usage

show(object)

Arguments

object A enrichResult instance.

Value

message
message

Author(s)

Guangchuang Yu https://yulab-smu.top
Description
plotting similarity matrix

Usage

```r
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**: label size
- **font.size**: font size

Value

ggplot object

Author(s)

Yu Guangchuang
# summary

**Description**

summary method for gseaResult instance
summary method for enrichResult 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)
Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

---

# theme_dose

**Description**

ggplot theme of DOSE

**Usage**

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

**Arguments**

- `font.size` font size
Value

ggplot theme

Examples

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

* classes
  compareClusterResult-class, 4
  enrichResult-class, 14
  gseaResult-class, 18
* datasets
  DataSet, 5
* internal
  DOSE-package, 3
  reexports, 28
* manip
  enrichDO, 9
  enricher_internal, 10
  gseDGN, 20
  gseDO, 21
  gseHPO, 22
  gseMPO, 23
  gseNCG, 24
clusterSim, 3
compareClusterResult-class, 4
computeIC, 5

DataSet, 5
DGN_EXTID2PATHID (DataSet), 5
DGN_PATHID2EXTID (DataSet), 5
DGN_PATHID2NAME (DataSet), 5
DO2ALLEG (DataSet), 5
DO2EG (DataSet), 5
DOIC (DataSet), 5
DOLite2EG (DataSet), 5
DOLiteTerm (DataSet), 5
DOSE (DOSE-package), 3
DOSE-package, 3
doseSim, 6
doSim, 6
dotbl (DataSet), 5

EG2ALLDO (DataSet), 5
EG2DO (DataSet), 5
EG2DOLite (DataSet), 5

enrichDGN, 7
enrichDGNv, 8
enrichDO, 9, 14
enricher_internal, 10
enrichHPO, 11
enrichMPO, 12
enrichNCG, 13
enrichResult, 5
enrichResult-class, 14
EXTID2NAME, 15

facet_grid, 28
facet_grid(reexports), 28

gene2DO, 15
geneID, 16
geneInCategory, 16
geneList (DataSet), 5
geneSim, 17
GSEA_internal, 18
gseaahResult-class (gseaResult-class), 18
gseaResult-class, 18
gseDGN, 20
gseDO, 21
gseHPO, 22
gseMPO, 23
gseNCG, 24
gsfilter, 25

hpoSim, 25
hpotbl (DataSet), 5

mclusterSim, 26
mpoSim, 27
mpotbl (DataSet), 5

NCG_EXTID2PATHID (DataSet), 5
NCG_PATHID2EXTID (DataSet), 5
NCG_PATHID2NAME (DataSet), 5

parse_ratio, 27
plot,compareClusterResult-method  
  (compareClusterResult-class), 4
rebuildAnnoData, 28
reexports, 28
setReadable, 28
show, 29
show,compareClusterResult-method  
  (compareClusterResult-class), 4
show,enrichResult-method  
  (enrichResult-class), 14
show,gseaResult-method  
  (gseaResult-class), 18
simplot, 30
summary, 31
summary,compareClusterResult-method  
  (compareClusterResult-class), 4
summary,enrichResult-method  
  (enrichResult-class), 14
summary,gseaResult-method  
  (gseaResult-class), 18
theme_dose, 31
VDGN EXTID2PATHID (DataSet), 5
VDGN PATHID2EXTID (DataSet), 5
VDGN PATHID2NAME (DataSet), 5