Package ‘DOSE’

January 31, 2017

Type Package
Title Disease Ontology Semantic and Enrichment analysis
Version 3.0.10
Author Guangchuang Yu <guangchuangyu@gmail.com> with contributions from Li-Gen Wang, Vladislav Petyuk and Giovanni Dall’Olio.
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 (>= 3.3.1)
Imports AnnotationDbi, BiocParallel, DO.db, fgsea, ggplot2, GOSemSim (>= 2.0.0), graphics, grDevices, grid, igraph, methods, qvalue, reshape2, S4Vectors, scales, stats, stats4, utils
Suggests BiocStyle, clusterProfiler, knitr, org.Hs.eg.db, testthat, UpSetR
VignetteBuilder knitr
ByteCompile true
License Artistic-2.0
URL https://guangchuangyu.github.io/DOSE
BugReports https://github.com/GuangchuangYu/DOSE/issues
biocViews Annotation, Visualization, MultipleComparison, GeneSetEnrichment, Pathways, Software
RoxygenNote 5.0.1
NeedsCompilation no

R topics documented:

  DOSE-package ................................................................. 2
  barplot.enrichResult ..................................................... 3
  clusterSim ................................................................. 4
<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>cnetplot</td>
<td>4</td>
</tr>
<tr>
<td>cnetplot_internal</td>
<td>5</td>
</tr>
<tr>
<td>computeIC</td>
<td>6</td>
</tr>
<tr>
<td>DataSet</td>
<td>6</td>
</tr>
<tr>
<td>doSim</td>
<td>7</td>
</tr>
<tr>
<td>dotplot</td>
<td>7</td>
</tr>
<tr>
<td>enrichDGN</td>
<td>8</td>
</tr>
<tr>
<td>enrichDGNv</td>
<td>9</td>
</tr>
<tr>
<td>enrichDO</td>
<td>10</td>
</tr>
<tr>
<td>enricher_internal</td>
<td>11</td>
</tr>
<tr>
<td>enrichMap</td>
<td>11</td>
</tr>
<tr>
<td>enrichNCG</td>
<td>12</td>
</tr>
<tr>
<td>enrichResult-class</td>
<td>13</td>
</tr>
<tr>
<td>EXTID2NAME</td>
<td>14</td>
</tr>
<tr>
<td>fortify.enrichResult</td>
<td>14</td>
</tr>
<tr>
<td>fortify.gseaResult</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>gseaplot</td>
<td>17</td>
</tr>
<tr>
<td>gseaResult-class</td>
<td>18</td>
</tr>
<tr>
<td>GSEA_internal</td>
<td>19</td>
</tr>
<tr>
<td>gseDGN</td>
<td>19</td>
</tr>
<tr>
<td>gseDO</td>
<td>20</td>
</tr>
<tr>
<td>gseNCG</td>
<td>21</td>
</tr>
<tr>
<td>gsfilter</td>
<td>22</td>
</tr>
<tr>
<td>list2graph</td>
<td>22</td>
</tr>
<tr>
<td>mclusterSim</td>
<td>23</td>
</tr>
<tr>
<td>netplot</td>
<td>23</td>
</tr>
<tr>
<td>plot</td>
<td>24</td>
</tr>
<tr>
<td>rebuildAnnoData</td>
<td>25</td>
</tr>
<tr>
<td>scaleNodeColor</td>
<td>25</td>
</tr>
<tr>
<td>setReadable</td>
<td>26</td>
</tr>
<tr>
<td>setting.graph.attributes</td>
<td>26</td>
</tr>
<tr>
<td>show</td>
<td>27</td>
</tr>
<tr>
<td>simplot</td>
<td>28</td>
</tr>
<tr>
<td>summary</td>
<td>28</td>
</tr>
<tr>
<td>theme_dose</td>
<td>29</td>
</tr>
<tr>
<td>upsetplot</td>
<td>29</td>
</tr>
</tbody>
</table>

**Index**

**DOSE-package**

*Disease Ontology Semantic and Enrichment analysis Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring DO semantic similarities, and hypergeometric test for enrichment analysis.*
Description

This package is designed to estimate DO-based semantic similarity measurement and enrichment analysis.

Details

Package: DOSE
Type: Package
Version: 2.3.5
Date: 2-27-2012
biocViews: Bioinformatics, Annotation
Depends:
Imports: methods, AnnotationDbi, DO.db
Suggests: clusterProfiler, GOSemSim
License: Artistic-2.0

Author(s)

Guangchuang Yu, Li-Gen Wang
Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also

enrichResult

barplot.enrichResult  barplot

Description

barplot of enrichResult

Usage

## S3 method for class 'enrichResult'
barplot(height, x = "Count", colorBy = "pvalue",
showCategory = 5, font.size = 12, title = "", ...)

Arguments

height  enrichResult object
x  one of 'Count' and 'GeneRatio'
colorBy  one of 'pvalue', 'p.adjust', 'qvalue'
showCategory  number of categories to show
font.size  font size
title  plot title
...  other parameter, ignored
Description

semantic similarity between two gene clusters

Usage

clusterSim(cluster1, cluster2, measure = "Wang", combine = "BMA")

Arguments

cluster1          a vector of gene IDs
cluster2          another vector of gene IDs
measure           One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
combine           One of "max", "average", "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)

---

cnetplot

cnetplot method

Description

cnetplot
Usage

cnetplot(x, showCategory = 5, categorySize = "geneNum", foldChange = NULL, fixed = TRUE, ...)

## S4 method for signature 'enrichResult'

cnetplot(x, showCategory = 5, categorySize = "pvalue", foldChange = NULL, fixed = TRUE, ...)

## S4 method for signature 'gseaResult'

cnetplot(x, showCategory = 5, categorySize = "pvalue", foldChange = NULL, fixed = TRUE, ...)

Arguments

x enrichResult object
showCategory number of category plotted
categorySize one of geneNum or pvalue
foldChange fold change of expression value
fixed logical
...
additional parameters

Value

plot

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

description

plot function of gene Concept Net.

Usage

cnetplot_internal(inputList, categorySize = "geneNum", showCategory = 5, pvalue = NULL, foldChange = NULL, fixed = TRUE, DE.foldChange = NULL, ...)

Arguments

inputList a list of gene IDs
categorySize setting category size
showCategory number of categories to plot
pvalue pvalue
foldChange  fold Change
fixed      logical
DE.foldChange logical
...       additional parameters

Value

plotted igraph object.

Author(s)

Guangchuang Yu http://ygc.name

computeIC  compute information content

Description

compute information content

Usage

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

Arguments

ont        "DO"
organism   "human"

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

DataSet  Datasets

Description

Information content and DO term to entrez gene IDs mapping
doSim

Description
measuring similarities between two DO term vectors.

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOID1</td>
<td>DO term vector</td>
</tr>
<tr>
<td>DOID2</td>
<td>DO term vector</td>
</tr>
<tr>
<td>measure</td>
<td>one of &quot;Wang&quot;, &quot;Resnik&quot;, &quot;Rel&quot;, &quot;Jiang&quot;, and &quot;Lin&quot;.</td>
</tr>
</tbody>
</table>

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

Value
score matrix

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

dotplot

Description
dotplot
dotplot method

Usage
dotplot(object, ...)

## S4 method for signature 'enrichResult'
dotplot(object, x = "geneRatio", colorBy = "p.adjust", showCategory = 10, category = NULL, font.size = 12, title = "")
enrichDGN

Arguments

- object: an instance of enrichResult
- ...: additional parameter
- x: variable for x axis
- colorBy: one of 'pvalue', 'p.adjust' and 'qvalue'
- showCategory: number of category
- category: separate result by 'category' variable
- font.size: font size
- title: plot title

Value

- plot

Author(s)

Guangchuang Yu
Guangchuang Yu

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

enrichDGNv

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

enrichDO(gene, ont = "DO", 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 or DOLite.
pvalueCutoff  pvalue cutoff
pAdjustMethod  one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
uuniverse  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

**Description**

Internal method for enrichment analysis

**Usage**

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

**Arguments**

- `gene`: a vector of entrez gene id.
- `pvalueCutoff`: Cutoff value of pvalue.
- `pAdjustMethod`: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
- `universe`: background genes
- `minGSSize`: minimal size of genes annotated by Ontology term for testing.
- `maxGSSize`: maximal size of each geneSet for analyzing
- `qvalueCutoff`: cutoff of qvalue
- `USER_DATA`: ontology information

**Details**

Using the hypergeometric model

**Value**

A enrichResult instance.

**Author(s)**

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

---

enrichMap

**Description**

Enrichment map

**Usage**

```r
enrichMap(x, n = 50, fixed = TRUE, vertex.label.font = 1, ...)
```
Arguments

- **x**: gseaResult or enrichResult object
- **n**: maximum number of category to shown
- **fixed**: if set to FALSE, will invoke tkplot
- **vertex.label.font**: font size of vertex label
- **...**: additional parameter

Details

enrichment map

Value

figure

Author(s)

G Yu

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**

This class represents the result of enrichment analysis.

**Description**

Class "enrichResult" This class represents the result of enrichment analysis.

**Slots**

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>result</td>
<td>enrichment analysis</td>
</tr>
<tr>
<td>pvalueCutoff</td>
<td></td>
</tr>
<tr>
<td>pAdjustMethod</td>
<td>pvalue adjust method</td>
</tr>
<tr>
<td>qvalueCutoff</td>
<td>qvalueCutoff</td>
</tr>
<tr>
<td>organism</td>
<td>only &quot;human&quot; supported</td>
</tr>
<tr>
<td>ontology</td>
<td>biological ontology</td>
</tr>
<tr>
<td>gene</td>
<td>Gene IDs</td>
</tr>
<tr>
<td>keytype</td>
<td>Gene ID type</td>
</tr>
<tr>
<td>universe</td>
<td>background gene</td>
</tr>
<tr>
<td>gene2Symbol</td>
<td>mapping gene to Symbol</td>
</tr>
<tr>
<td>geneSets</td>
<td>gene sets</td>
</tr>
<tr>
<td>readable</td>
<td>logical flag of gene ID in symbol or not.</td>
</tr>
</tbody>
</table>

Author(s)

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

See Also

enrichDO
### 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 [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

---

### fortify.enrichResult

**Description**

convert enrichResult object for ggplot2

**Usage**

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

**Arguments**

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

convert gsea result for ggplot2

**Usage**

```r
## S3 method for class 'gseaResult'
fortify(model, data, geneSetID, ...)
```

**Arguments**

- `model`: gseaResult object
- `data`: not used.
- `geneSetID`: gene set ID
- `...`: additional parameter

**Value**

figure

**Author(s)**

G Yu

---

**gene2DO**

**convert Gene ID to DO Terms**

**Description**

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

**Usage**

```r
gene2DO(gene)
```

**Arguments**

- `gene`: entrez gene ID

**Value**

DO Terms

**Author(s)**

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

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

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")
d <- names(geneList)[1:100]
x <- enrichDO(d)
geneInCategory(x)
**geneSim**

description

measuring similarities between two gene vectors.

Usage

geneSim(geneID1, geneID2 = NULL, measure = "Wang", combine = "BMA")

Arguments

- geneID1: entrez gene vector
- geneID2: entrez gene vector
- measure: one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".
- combine: One of "max", "average", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.

Details

provide two entrez gene vectors, this function will calculate their similarity.

Value

score matrix

Author(s)

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

**gseaplot**

visualize analyzing result of GSEA

Description

plotting function for gseaResult

Usage

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

Arguments

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

ggplot2 object

Author(s)

Yu Guangchuang

---

Class “gseaResult” This class represents the result of GSEA analysis

Description

Class "gseaResult" This class represents the result of GSEA analysis

Slots

result  GSEA analysis
organism  organism
setType  setType
geneSets  geneSets
geneList  order rank geneList
keytype  ID type of gene
permScores  permutation scores
params  parameters
gene2Symbol  gene ID to Symbol
readable  whether convert gene ID to symbol

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

See Also

gseaplot
GSEA_internal

Description

generic function for gene set enrichment analysis

Usage

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

Arguments

geneList order ranked geneList
exponent weight of each step
nPerm permutation numbers
minGSSize minimal size of each geneSet for analyzing
maxGSSize maximal size of each geneSet for analyzing
pvalueCutoff p value Cutoff
pAdjustMethod p value adjustment method
verbose print message or not
seed set seed inside the function to make result reproducible. FALSE by default.
USER_DATA annotation data
by one of ’fgsea’ or ’DOSE’

Value

gseaResult object

Author(s)

Yu Guangchuang

gseDGN

DisGeNET Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

gseDGN(geneList, exponent = 1, nPerm = 1000, minGSSize = 10, 
maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = “BH”, 
verbose = TRUE, seed = FALSE, by = ”fgsea”)
Arguments

geneList  order ranked geneList
exponent  weight of each step
nPerm  permutation numbers
minGSSize  minimal size of each geneSet for analyzing
maxGSSize  maximal size of each geneSet for analyzing
pvalueCutoff  pvalue Cutoff
pAdjustMethod  p value adjustment method
verbose  print message or not
seed  logical
by  one of ‘fgsea’ or ‘DOSE’

Value

gseaResult object

Author(s)

Yu Guangchuang

Description

perform gsea analysis

Usage

gseDO(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH",
verbose = TRUE, seed = FALSE, by = "fgsea")

Arguments

geneList  order ranked geneList
exponent  weight of each step
nPerm  permutation numbers
minGSSize  minimal size of each geneSet for analyzing
maxGSSize  maximal size of each geneSet for analyzing
pvalueCutoff  pvalue Cutoff
pAdjustMethod  p value adjustment method
verbose  print message or not
seed  logical
by  one of ‘fgsea’ or ‘DOSE’
**gseNCG**

**Value**

`gseaResult` object

**Author(s)**

Yu Guangchuang

---

**gseNCG**

*NCG Gene Set Enrichment Analysis*

**Description**

perform gsea analysis

**Usage**

```r
gseNCG(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH",
verbose = TRUE, seed = FALSE, by = "fgsea")
```

**Arguments**

- `geneList`: order ranked geneList
- `exponent`: weight of each step
- `nPerm`: permutation numbers
- `minGSSize`: minimal size of each geneSet for analyzing
- `maxGSSize`: maximal size of each geneSet for analyzing
- `pvalueCutoff`: pvalue Cutoff
- `pAdjustMethod`: p value adjustment method
- `verbose`: print message or not
- `seed`: logical
- `by`: one of `fgsea` or `DOSE`

**Value**

`gseaResult` object

**Author(s)**

Yu Guangchuang
Description
filter enriched result by gene set size or gene count

Usage
\texttt{gsfilter}(x, by = "GSSize", min = NA, max = NA)

Arguments
- \texttt{x}: instance of \texttt{enrichResult} or \texttt{compareClusterResult}
- \texttt{by}: one of 'GSSize' or 'Count'
- \texttt{min}: minimal size
- \texttt{max}: maximal size

Value
update object

Author(s)
Guangchuang Yu

Description
convert a list of gene IDs to igraph object.

Usage
\texttt{list2graph}(inputList)

Arguments
- \texttt{inputList}: a list of gene IDs

Value
a igraph object.

Author(s)
Guangchuang Yu \url{http://ygc.name}
mclusterSim

Description
Pairwise semantic similarity for a list of gene clusters

Usage
mclusterSim(clusters, measure = "Wang", combine = "BMA")

Arguments
- clusters: A list of gene clusters
- measure: one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".
- combine: One of "max", "average", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.

Value
similarity matrix

Author(s)
Yu Guangchuang

Examples
cluster1 <- c("835", "5261","241")
cluster2 <- c("578","582")
cluster3 <- c("307", "308", "317")
clusters <- list(a=cluster1, b=cluster2, c=cluster3)
mclusterSim(clusters, measure="Wang")

netplot

Description
plot network

Usage
netplot(g, vertex.label.font = 2, vertex.label.color = "#666666",
vertex.label.cex = 1.5, layout = layout.fruchterman.reingold,
foldChange = NULL, fixed = TRUE, col.bin = 10, legend.x = 1,
legend.y = 1, ...)
plot

Arguments

- `g`: igraph object
- `vertex.label.font`: font size
- `vertex.label.color`: font text color
- `vertex.label.cex`: cex of vertex label
- `layout`: layout
- `foldChange`: fold change
- `fixed`: logical
- `col.bin`: number of legend color bin
- `legend.x`: x-axis position of legend
- `legend.y`: y-axis position of legend
- `...`: additional parameters

Details

- plot network of igraph object

Value

- plot

Author(s)

- Yu Guangchuang

Description

- plot method generics
- plot method for gseaResult

Usage

```r
## S4 method for signature 'enrichResult,ANY'
plot(x, type = "bar", ...)

## S4 method for signature 'gseaResult,ANY'
plot(x, type = "gseaplot", ...)
```

Arguments

- `x`: A enrichResult instance
- `type`: one of bar, cnet or enrichMap
- `...`: Additional argument list
**rebuildAnnoData**

**Value**
- plot
- plot

**Author(s)**
Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)
Yu Guangchuang

---

**Description**
rebuilding entrez and DO mapping datasets

**Usage**
```r
rebuildAnnoData(file)
```

**Arguments**
- `file`  do_rif.human.txt

**Author(s)**
Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

---

**scaleNodeColor**

**Description**
scale color nodes

**Usage**
```r
scaleNodeColor(g, foldChange, node.idx = NULL, DE.foldChange)
```

**Arguments**
- `g`  igraph object
- `foldChange`  fold Change
- `node.idx`  index of node to color
- `DE.foldChange`  logical

**Details**
color nodes based on fold change of expression
### Value

igraph object

### Author(s)

Yu Guangchuang

---

#### Description

mapping geneID to gene Symbol

#### Usage

```r
setReadable(x, OrgDb, keytype = "auto")
```

#### Arguments

- `x`: enrichResult Object
- `OrgDb`: OrgDb
- `keytype`: keytype of gene

#### Value

enrichResult Object

### Author(s)

Yu Guangchuang

---

#### Description

setting basic attributes of a graph

#### Usage

```r
setting.graph.attributes(g, node.size = 8, node.color = "#B3B3B3",
                         edge.width = 2, edge.color = "#8DA0CB")
```
**show**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>g</td>
<td>igraph object</td>
</tr>
<tr>
<td>node.size</td>
<td>size of node</td>
</tr>
<tr>
<td>node.color</td>
<td>color of node</td>
</tr>
<tr>
<td>edge.width</td>
<td>edge width</td>
</tr>
<tr>
<td>edge.color</td>
<td>color of edge</td>
</tr>
</tbody>
</table>

**Details**

setting size and color of node and edge

**Value**

igraph object

**Author(s)**

Yu Guangchuang

**show**

**show method**

**Description**

show method for enrichResult instance
show method for gseaResult instance

**Usage**

show(object)

show(object)

**Arguments**

<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

**Author(s)**

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

Description
summary method for enrichResult instance
summary method for gseaResult instance

Usage
summary(object, ...)
summary(object, ...)
theme_dose

Arguments

object A enrichResult instance.
...
additional parameter

Value

A data frame
A data frame

Author(s)

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

upsetplot

Description

upsetplot method generics
upsetplot

Usage

upsetplot(x, ...)

## S4 method for signature 'enrichResult'
upsetplot(x, n = 10, ...)

Arguments

x object
...
additional parameters
n number of categories to be plotted
Value

plot

Author(s)

Guangchuang Yu

Examples

```r
## Not run:
require(DOSE)
data(geneList)
d <- names(geneList)[1:100]
x <- enrichDO(d)
upsetplot(x, 8)

## End(Not run)
```
Index

*Topic **classes**
  enrichResult-class, 13
  gseaResult-class, 18
*Topic **datasets**
  DataSet, 6
*Topic **manip**
  enrichDO, 10
  enricher_internal, 11
  gseDGN, 19
  gseDO, 20
  gseNCG, 21
*Topic **package**
  DOSE-package, 2

barplot.enrichResult, 3
clusterSim, 4
cnetplot, 4
cnetplot,enrichResult-method
  (cnetplot), 4
cnetplot,gseaResult-method(cnetplot), 4
cnetplot.internal, 5
computeIC, 6

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), 2
DOSE-package, 2
doSim, 7
dotbl (DataSet), 6
dotplot, 7
dotplot,enrichResult,ANY-method
  (dotplot), 7
dotplot,enrichResult-method(dotplot), 7
EG2ALLDO (DataSet), 6
EG2DO (DataSet), 6
EG2DOLite (DataSet), 6
enrichDGN, 8
enrichDGNv, 9
enrichDO, 10, 13
enricher_internal, 11
enrichMap, 11
enrichNCG, 12
enrichResult, 3
enrichResult-class, 13
EXTID2NAME, 14

fortify.enrichResult, 14
fortify.gseaResult, 15

geneDO, 15
geneID, 16
geneInCategory, 16
genelist (DataSet), 6
genSim, 17
GSEA_internal, 19
gseahResult-class (gseaResult-class), 18
gseaPlot, 17, 18
gseaResult-class, 18
gseDGN, 19
gseDO, 20
gseNCG, 21
gsfilter, 22

list2graph, 22

mclusterSim, 23

NCG_EXTID2PATHID (DataSet), 6
NCG_PATHID2EXTID (DataSet), 6
NCG_PATHID2NAME (DataSet), 6

netplot, 23

plot, 24
plot,enrichResult,ANY-method(plot), 24
plot,enrichResult-method
  (enrichResult-class), 13
plot,gseaResult,ANY-method(plot), 24
plot,gseaResult-method
  (gseaResult-class), 18
rebuildAnnoData, 25
scaleNodeColor, 25
setReadable, 26
setting.graph.attributes, 26
show, 27
show, enrichResult-method
  (enrichResult-class), 13
show, gseaResult-method
  (gseaResult-class), 18
simplot, 28
summary, 28
summary, enrichResult-method
  (enrichResult-class), 13
summary, gseaResult-method
  (gseaResult-class), 18

theme_dose, 29
upsetplot, 29
upsetplot, enrichResult, ANY-method
  (upsetplot), 29
upsetplot, enrichResult-method
  (upsetplot), 29

VDGN_EXTID2PATHID (DataSet), 6
VDGN_PATHID2EXTID (DataSet), 6
VDGN_PATHID2NAME (DataSet), 6