Package ‘DOSE’

March 22, 2017

Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.0.10

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Description This package implements five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring semantic similarities among DO terms and gene products. Enrichment analyses including hypergeometric model and gene set enrichment analysis are also implemented for discovering disease associations of high-throughput biological data.

Depends R (>= 3.3.1)

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:

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DOSE-package

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

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
sematic 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

description

cnetplot method

description
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
computeIC  

**Usage**

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

**Arguments**

- **ont**  
  "DO"

- **organism**  
  "human"

**Author(s)**

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

**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

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

Details

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

Value

score matrix

Author(s)

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

dotplot

dotplot method

Description

dotplot
dotplot for enrichResult

Usage

dotplot(object, ...)

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

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**enrichDGN**


Description

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
**enrichDGNv**

**Author(s)**

Guangchuang Yu

**References**


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**Description**


**Usage**

```r
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"
- 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

Examples
```r
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,
  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

Description

enrichment map

Usage

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

---

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.

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>OrgDb</td>
<td>OrgDb</td>
</tr>
<tr>
<td>geneID</td>
<td>entrez gene ID</td>
</tr>
<tr>
<td>keytype</td>
<td>keytype</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>model</td>
<td>enrichResult object</td>
</tr>
<tr>
<td>data</td>
<td>not use here</td>
</tr>
<tr>
<td>showCategory</td>
<td>Category numbers to show</td>
</tr>
<tr>
<td>by</td>
<td>one of Count and GeneRatio</td>
</tr>
<tr>
<td>order</td>
<td>logical</td>
</tr>
<tr>
<td>drop</td>
<td>logical</td>
</tr>
<tr>
<td>category</td>
<td>separate result by 'category' variable</td>
</tr>
<tr>
<td>...</td>
<td>additional parameter</td>
</tr>
</tbody>
</table>
**fortify.gseaResult**

**Description**
convert gsea result for ggplot2

**Usage**
```
## 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**
gene2DO(gene)

**Arguments**
- `gene`: entrez gene ID

**Value**
DO Terms

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

Description
geneID generic

Usage
geneID(x)

Arguments
x  enrichResult object

Value
'geneID' return the 'geneID' column of the enriched result which can be converted to data.frame via 'as.data.frame'

Examples

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

geneInCategory
geneInCategory generic

Description
geneInCategory generic

Usage
geneInCategory(x)

Arguments
x  enrichResult

Value
'geneInCategory' return a list of genes, by 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

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

gseaplot

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

---

**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

Author(s)

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

---

**Description**

perform gsea analysis

**Usage**

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
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

list2graph

Description
convert gene IDs to igraph object.

Usage
list2graph(inputList)

Arguments
inputList  a list of gene IDs

Value
a igraph object.

Author(s)
Guangchuang Yu http://ygc.name
**mclusterSim**

**Description**
Pairwise semantic similarity for a list of gene clusters

**Usage**

```r
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**

```r
ccluster1 <- c("835", "5261","241")
ccluster2 <- c("578","582")
ccluster3 <- c("307", "308", "317")
cclusters <- list(a=cluster1, b=cluster2, c=cluster3)
mclusterSim(clusters, measure="Wang")
```

---

**netplot**

**Description**

plot network

**Usage**

```r
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, ...)
```
**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
Value
plot
plot

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

rebuildAnnoData rebuilding annotation data

Description
rebuilding entrez and DO mapping datasets

Usage
rebuildAnnoData(file)

Arguments
file do_rif.human.txt

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

scaleNodeColor scaleNodeColor

Description
scale color nodes

Usage
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

---

**setDescription**

**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

---

**setting.graph.attributes**

**Description**

setting basic attributes of a graph

**Usage**

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

Arguments

g igraph object
node.size size of node
node.color color of node
dege.width edge width
dege.color color of edge

Details

setting size and color of node and edge

Value

igraph object

Author(s)

Yu Guangchuang

show

Description

show method for enrichResult instance
show method for gseaResult instance

Usage

show(object)
show(object)

Arguments

object A enrichResult instance.

Value

message
message

Author(s)

Guangchuang Yu https://guangchuangyu.github.io
Guangchuang Yu https://guangchuangyu.github.io
**simplot**

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`: 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

```r
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

theme_dose

Description

ggplot theme of DOSE

Usage

theme_dose(font.size = 14)

Arguments

font.size  font size

upsetplot

upsetplot method

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)
de=names(geneList)[1:100]
x <- enrichDO(de)
upsetplot(x, 8)

## End(Not run)
```
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