Package ‘DOSE’
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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
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Suggests BiocStyle, clusterProfiler, knitr, org.Hs.eg.db, testthat,
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VignetteBuilder knitr
ByteCompile true
License Artistic-2.0
URL https://guangchuangyu.github.io/DOSE
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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.
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: methods, AnnotationDbi, DO.db
Imports: clusterProfiler, GOSemSim
License: Artistic-2.0

Author(s)

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

See Also

enrichResult

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

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

---

cnetplot_internal  cnetplot_internal

Description

plot function of gene Concept Net.

Usage

```r
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

- 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

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

enrichDGNv  enrichDGN

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  

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

**Usage**  
```r  
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)  
```
enricher_internal

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

enrichMap

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

Value
A enrichResult instance

Author(s)
Guangchuang Yu

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

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

fortify.enrichResult

Description
convert enrichResult object for ggplot2

Usage
## 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
### fortify.gseaResult

**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

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### gene2DO

**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

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

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](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

---

**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
convert gene IDs to igraph object

Description
convert a list of 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

---

**plot**

**plot method**

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)

**Description**
rebuilding entrez and DO mapping datasets

**Usage**
rebuildAnnoData(file)

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

**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

---

**setReadable**

**setReadable**

---

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**

**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
- `edge.width`: edge width
- `edge.color`: color of edge

**Details**

- setting size and color of node and edge

**Value**

igraph object

**Author(s)**

Yu Guangchuang

---

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

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

```r
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

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

## End(Not run)
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