Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.0.9

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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

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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.
**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

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**Description**

barplot of enrichResult

**Usage**

```r
## 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
clusterSim

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, ont="MF", organism="human", measure="Wang")

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

---

cnetplot_internal  cnetplot_internal

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
- 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

enrichDGN: Enrichment analysis based on the DisGeNET (http://www.disgenet.org/)

Description

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

Usage

enrichDGN(gene, pvalueCutoff = 0.05, pAdjustMethod = "BH", universe,
          minGSSize = 10, maxGSSize = 500, qvalueCutoff = 0.2, readable = FALSE)

Arguments

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

Value

A enrichResult instance
Author(s)

Guangchuang Yu

References


Description

Enrichment analysis based on the DisGeNET (http://www.disgenet.org/)

Usage

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

Arguments

snp a vector of SNP
pvalueCutoff p-value 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 q-value 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

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
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, ...)
enrichNCG

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

---

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

---

**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

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

---

**gseNCG**

*NCG Gene Set Enrichment Analysis*

**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
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

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

Description

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, ...)
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", ...)
```

```r
## 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
Yu Guangchuang

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

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**

**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

---

**setting.graph.attributes**

**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

- `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)`

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

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

---

**theme_dose**

**Description**

`ggplot` theme of DOSE

**Usage**

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

**Arguments**

- font.size: font size

---

**upsetplot**

**upsetplot method**

**Description**

upsetplot method generics

upsetplot

**Usage**

```r
upsetplot(x, ...)
```

### S4 method for signature 'enrichResult'

```r
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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