Package ‘DOSE’

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Type Package
Title Disease Ontology Semantic and Enrichment analysis
Version 3.28.2
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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.
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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

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Author(s)

Guangchuang Yu, Li-Gen Wang

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also

enrichResult
Description

semantic similarity between two gene clusters

Usage

```r
clusterSim(
  cluster1,
  cluster2,
  ont = "DO",
  organism = "hsa",
  measure = "Wang",
  combine = "BMA"
)
```

Arguments

- `cluster1` a vector of gene IDs
- `cluster2` another vector of gene IDs
- `ont` one of "DO" and "MPO"
- `organism` organism
- `measure` One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
- `combine` One of "max", "avg", "rcmax", "BMA" methods, for combining

Details

given two gene clusters, this function calculates semantic similarity between them.

Value

similarity

Author(s)

Yu Guangchuang

Examples

```r
cluster1 <- c("835", "5261", "241", "994")
clusterSim(cluster1, cluster2)
```
Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Slots

- compareClusterResult: cluster comparing result
- geneClusters: a list of genes
- fun: one of groupGO, enrichGO and enrichKEGG
- gene2Symbol: gene ID to Symbol
- keytype: Gene ID type
- readable: logical flag of gene ID in symbol or not.
- .call: function call
- termsim: Similarity between term
- method: method of calculating the similarity between nodes
- dr: dimension reduction result

Author(s)

Guangchuang Yu https://yulab-smu.top

See Also

enrichResult

computeIC

compute information content

Description

compute information content

Usage

computeIC(ont = "DO")
Arguments

ont one of "DO" and "MPO"

Author(s)

Guangchuang Yu [https://yulab-smu.top](https://yulab-smu.top)

---

**DataSet**

**Datasets**

---

**Description**

Information content and DO term to entrez gene IDs mapping

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**doseSim**

**doSim**

---

**Description**

measuring similarities between two DO term vectors.

**Usage**

doseSim(DOID1, DOID2, measure = "Wang", ont = "DO")

**Arguments**

**DOID1**

DO term, MPO term or HPO term vector

**DOID2**

DO term, MPO term or HPO term vector

**measure**

one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".

**ont**

one of "DO" and "MPO"

**Details**

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

**Value**

score matrix
**doSim**

Description

measuring similarities between two MPO term vectors.

Usage

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

Arguments

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

Details

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

Value

score matrix

Author(s)

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

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**enrichDGN**


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/)
enrichDGNv

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",  
organism = "hsa",  
pvalueCutoff = 0.05,  
pAdjustMethod = "BH",  
universe,  
minGSSize = 10,  
maxGSSize = 500,  
qvalueCutoff = 0.2,  
readable = FALSE
)

Arguments

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

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)

Description

Internal method for enrichment analysis

Usage

enricher_internal(
  gene,  # a vector of entrez gene id.
  pvalueCutoff,  # Cutoff value of pvalue.
  pAdjustMethod = "BH",  # one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
  universe = NULL,  # background genes
  minGSSize = 10,  # minimal size of genes annotated by Ontology term for testing.
  maxGSSize = 500,  # maximal size of each geneSet for analyzing
  qvalueCutoff = 0.2,  # cutoff of qvalue
  USER_DATA  # ontology information
)

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)

---

**enrichHPO**


---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A `enrichResult` instance

**Author(s)**

Erqiang Hu
References
Janet et al. (2015) DisGeNET: a discovery platform for the dynamical exploration of human
diseases and their genes. Database bav028 http://database.oxfordjournals.org/content/
2015/bav028.long

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

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

Value
A enrichResult instance

Author(s)
Erqiang Hu
References


enrichNCG

Description

Enrichment analysis based on the Network of Cancer Genes database (http://ncg.kcl.ac.uk/)

Usage

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

Arguments

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

Details

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

Value

A enrichResult instance

Author(s)

Guangchuang Yu
enrichResult-class

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

Description

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

Slots

result enrichment analysis
pvalueCutoff pvalue cutoff
pAdjustMethod pvalue adjust method
qvalueCutoff qvalue cutoff
organism only "human" supported
ontology biological ontology
gene Gene IDs
keytype Gene ID type
universe background gene
gene2Symbol mapping gene to Symbol
geneSets gene sets
readable logical flag of gene ID in symbol or not.
termsim Similarity between term
method method of calculating the similarity between nodes
dr dimension reduction result

Author(s)

Guangchuang Yu https://yulab-smu.top

See Also

enrichDO
**EXTID2NAME**

**Description**

mapping gene ID to gene Symbol

**Usage**

`EXTID2NAME(OrgDb, geneID, keytype)`

**Arguments**

- OrgDb
- geneID: entrez gene ID
- keytype

**Value**

gene symbol

**Author(s)**

Guangchuang Yu [https://yulab-smu.top](https://yulab-smu.top)

---

**gene2DO**

*convert Gene ID to DO Terms*

**Description**

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

**Usage**

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

**Arguments**

- gene: entrez gene ID
- organism
- ont

**Value**

DO Terms
geneID

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

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

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

### Description

measuring similarities between two gene vectors.

### Usage

```r
geneSim(
geneID1,
geneID2 = NULL,
ont = "DO",
organism = "hsa",
measure = "Wang",
combine = "BMA"
)
```

### Arguments

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

### Details

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

### Value

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

Slots

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

Author(s)

Guangchuang Yu http://ygc.name

GSEA_internal  GSEA_internal

Description

generic function for gene set enrichment analysis
Usage

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

Arguments

geneList          order ranked geneList
exponent          weight of each step
minGSSize         minimal size of each geneSet for analyzing
maxGSSize         maximal size of each geneSet for analyzing
eps               This parameter sets the boundary for calculating the p value.
pvalueCutoff      p value Cutoff
pAdjustMethod     p value adjustment method
verbose           print message or not
seed              set seed inside the function to make result reproducible. FALSE by default.
USER_DATA         annotation data
by                one of 'fgsea' or 'DOSE'
...               other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang
Description

perform gsea analysis

Usage

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

Arguments

geneList order ranked geneList
exponent weight of each step
minGSSize minimal size of each geneSet for analyzing
maxGSSize maximal size of each geneSet for analyzing
pvalueCutoff pvalue Cutoff
pAdjustMethod p value adjustment method
verbose print message or not
seed logical
by one of 'fgsea' or 'DOSE'
... other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang
**gseDO**

**DO Gene Set Enrichment Analysis**

**Description**

perform gsea analysis

**Usage**

```r
gseDO(
geneList, 
organism = "hsa", 
exponent = 1, 
minGSSize = 10, 
maxGSSize = 500, 
pvalueCutoff = 0.05, 
pAdjustMethod = "BH", 
verbose = TRUE, 
seed = FALSE, 
by = "fgsea", 
...
)
```

**Arguments**

- `geneList` order ranked geneList
- `organism` one of "hsa" and "mmu"
- `exponent` weight of each step
- `minGSSize` minimal size of each geneSet for analyzing
- `maxGSSize` maximal size of each geneSet for analyzing
- `pvalueCutoff` pvalue Cutoff
- `pAdjustMethod` p value adjustment method
- `verbose` print message or not
- `seed` logical
- `by` one of 'fgsea' or 'DOSE'
- `...` other parameter

**Value**

`gseaResult` object

**Author(s)**

Yu Guangchuang
gseHPO

MPO Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

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

Arguments

geneList       order ranked geneList
exponent       weight of each step
minGSSize      minimal size of each geneSet for analyzing
maxGSSize      maximal size of each geneSet for analyzing
pvalueCutoff   pvalue Cutoff
pAdjustMethod  p value adjustment method
verbose        print message or not
seed           logical
by             one of 'fgsea' or 'DOSE'
...             other parameter

Value

gseaResult object

Author(s)

Erqiang Hu
gseMPO  

*MPO Gene Set Enrichment Analysis*

**Description**
perform gsea analysis

**Usage**

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

**Arguments**

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

**Value**
gseaResult object

**Author(s)**

Erqiang Hu
gseNCG  

**NCG Gene Set Enrichment Analysis**

**Description**

perform gsea analysis

**Usage**

```r

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

**Arguments**

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

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang
gsfilter

Description
filter enriched result by gene set size or gene count

Usage
gsfilter(x, by = "GSSize", min = NA, max = NA)

Arguments
x instance of enrichResult or compareClusterResult
by one of `GSSize` or `Count`
min minimal size
max maximal size

Value
update object

Author(s)
Guangchuang Yu

hpoSim
doSim

Description
measuring similarities between two MPO term vectors.

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

Arguments
DOID1 HPO term vector
DOID2 HPO term vector
measure one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".
Details

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

Value

score matrix

Description

Pairwise semantic similarity for a list of gene clusters

Usage

mclusterSim(
  clusters,
  ont = "DO",
  organism = "hsa",
  measure = "Wang",
  combine = "BMA"
)

Arguments

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

Value

similarity matrix

Author(s)

Yu Guangchuang

Examples

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

---

**mpoSim**  
*doSim*

**Description**  
measuring similarities between two MPO term vectors.

**Usage**  
```r  
mpoSim(DOID1, DOID2, measure = "Wang")  
```  

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

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

**Value**  
score matrix

---

**parse_ratio**  
*parse_ratio*

**Description**  
parse character ratio to double value, such as 1/5 to 0.2

**Usage**  
```r  
parse_ratio(ratio)  
```  

**Arguments**  
- **ratio**: character vector of ratio to parse

**Value**  
A numeric vector (double) of parsed ratio

**Author(s)**  
Guangchuang Yu
rebuildAnnoData

Description

rebuilding entrez and DO mapping datasets

Usage

rebuildAnnoData(file)

Arguments

file  do_rif.human.txt

Author(s)

Guangchuang Yu https://yulab-smu.top

reexports

Objects exported from other packages

Description

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

ggplot2 facet_grid

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

---

**show method**

**Description**

show method for gseaResult instance
show method for enrichResult instance

**Usage**

show(object)
show(object)

**Arguments**

object A enrichResult instance.

**Value**

message
message

**Author(s)**

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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
**theme_dose**

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**summary**

**Summary method**

**Description**

summary method for gseaResult instance  
summary method for enrichResult instance

**Usage**

```r
summary(object, ...)  
```  

**Arguments**

- `object` A enrichResult instance.  
- `...` additional parameter  

**Value**

A data frame  
A data frame

**Author(s)**

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**theme_dose**

**Description**

ggplot theme of DOSE

**Usage**

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

**Arguments**

- `font.size` font size
theme_dose

Value

ggplot theme

Examples

library(ggplot2)
qplot(1:10) + theme_dose()
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