Package ‘DOSE’

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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**

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

**Author(s)**

Guangchuang Yu, Li-Gen Wang

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

**See Also**

enrichResult
Description

semantic similarity between two gene clusters

Usage

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

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](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

DataSet

doseSim  doSim

Description

Information content and DO term to entrez gene IDs mapping

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)

**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

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
pAdjjustMethod 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

```r
data(geneList)
gene = names(geneList)[geneList > 1]
yy = enrichDO(gene, pvalueCutoff=0.05)
summary(yy)
```

Description

Internal method for enrichment analysis

Usage

```r
enricher_internal(
  gene,
  pvalueCutoff,
  pAdjustMethod = "BH",  
  universe = NULL,
  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.
enrichHPO

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

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)

Guangchuang Yu http://guangchuangyu.github.io

Erqiang Hu
enrichMPO

References

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

**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.

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.
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`: OrgDb
- `geneID`: entrez gene ID
- `keytype`: keytype

**Value**

gene symbol

**Author(s)**

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

---

### gene2DO

**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`: organism
- `ont`: 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")
d <- names(geneList)[1:100]
x <- enrichDO(d)
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")
d <- names(geneList)[1:100]
x <- enrichDO(d)
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

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
- dr: dimension reduction result

Author(s)

Guangchuang Yu http://ygc.name

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
**gseDGN**

*DisGeNET Gene Set Enrichment Analysis*

---

**Description**

perform gsea analysis

**Usage**

```r
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
DO Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

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
**Description**

perform gsea analysis

**Usage**

```r
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

mclusterSim  mclusterSim

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")
mpoSim

doSIm

Description

measuring similarities between two MPO term vectors.

Usage

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

Description

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

Usage

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](https://yulab-smu.top)

---

**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**

**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)**

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

Value
ggplot object

Author(s)
Yu Guangchuang
**summary**  
summary method

**Description**

summary method for gseaResult instance  
summary method for enrichResult instance

**Usage**

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

**Arguments**

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

**Value**

- A data frame
- A data frame

**Author(s)**

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

---

**theme_dose**  
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

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