Package ‘DOSE’
March 27, 2024

Type Package
Title Disease Ontology Semantic and Enrichment analysis
Version 3.28.2
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>
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 (>= 3.5.0)
Imports AnnotationDbi, HDO.db, BiocParallel, fgsea, ggplot2, GOSemSim (>= 2.27.1), methods, qvalue, reshape2, stats, utils, yulab.utils
Suggests prettydoc, clusterProfiler, gson (>= 0.0.5), knitr, rmarkdown, org.Hs.eg.db, MPO.db, HPO.db, testthat
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License Artistic-2.0
Encoding UTF-8
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       Giovanni Dall'Olio [ctb],
       Erqiang Hu [ctb]

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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
clusterSim

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

Description

Information content and DO term to entrez gene IDs mapping

doseSim doSim

Description

measuring similarities between two DO term vectors.

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOI1</td>
<td>DO term, MPO term or HPO term vector</td>
</tr>
<tr>
<td>DOI2</td>
<td>DO term, MPO term or HPO term vector</td>
</tr>
<tr>
<td>measure</td>
<td>one of &quot;Wang&quot;, &quot;Resnik&quot;, &quot;Rel&quot;, &quot;Jiang&quot;, &quot;Lin&quot;, and &quot;TCSS&quot;.</td>
</tr>
<tr>
<td>ont</td>
<td>one of &quot;DO&quot; and &quot;MPO&quot;</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOID1</td>
<td>DO term vector</td>
</tr>
<tr>
<td>DOID2</td>
<td>DO term vector</td>
</tr>
<tr>
<td>measure</td>
<td>one of &quot;Wang&quot;, &quot;Resnik&quot;, &quot;Rel&quot;, &quot;Jiang&quot;, &quot;Lin&quot;, and &quot;TCSS&quot;.</td>
</tr>
</tbody>
</table>

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

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 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

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
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,
  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


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)

Erqiang Hu
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",
umiverse,
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"
umiverse 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.
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

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  organism
ont  ont

Value
DO Terms
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**

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

geneInCategory

**Description**
geneInCategory generic

**Usage**
geneInCategory(x)

**Arguments**

- **x**  
enrichResult object
geneSim

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
geneSim

Description

measuring similarities between two gene vectors.

Usage

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://yulab-smu.top](http://yulab-smu.top)
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'

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
**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**
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 Guangchuan
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

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

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

**Description**

measuring similarities between two MPO term vectors.

**Usage**

```r
doisim <- 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**

A score matrix

### parse_ratio

**Description**

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

**Usage**

```r
doisim <- 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 method

Description

show method for gseaResult instance
show method for enrichResult instance

Usage

show(object)

Arguments

object A enrichResult instance.

Value

message
message

Author(s)

Guangchuang Yu https://yulab-smu.top
**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` label size
- `font.size` font size

**Value**

`ggplot` object

**Author(s)**

Yu Guangchuang
**theme_dose**

**Description**

ggplot theme of DOSE

**Usage**

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

**Arguments**

- `font.size` font size

---

**summary**

**summary method**

**Description**

summary method for `gseaResult` instance

summary method for `enrichResult` instance

**Usage**

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

**Arguments**

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

**Value**

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

Value

ggplot theme

Examples

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