Package ‘DOSE’

April 1, 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

**VignetteBuilder**  knitr

**ByteCompile**  true

**License**  Artistic-2.0

**Encoding**  UTF-8

**URL**  https://yulab-smu.top/biomedical-knowledge-mining-book/

**BugReports**  https://github.com/GuangchuangYu/DOSE/issues

**biocViews**  Annotation, Visualization, MultipleComparison, GeneSetEnrichment, Pathways, Software

**RoxygenNote**  7.2.3

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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
```r
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

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

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

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](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

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)

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",
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 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](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**

**Author(s)**

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

---

<table>
<thead>
<tr>
<th>geneID</th>
<th>geneID generic</th>
</tr>
</thead>
</table>

**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)

---

<table>
<thead>
<tr>
<th>geneInCategory</th>
<th>geneInCategory generic</th>
</tr>
</thead>
</table>

**Description**

GeneInCategory generic

**Usage**

geneInCategory(x)

**Arguments**

x enrichResult
geneSim

Value

'geneInCategory' return a list of genes, by splitting the input gene vector to enriched functional categories

Examples

data(geneList, package="DOSE")
def <- 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
Author(s)

Guangchuang Yu [http://ygc.name](http://ygc.name)

---

**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 anaysis
- `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 [https://yulab-smu.top](https://yulab-smu.top)

---

**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
DisGeNET Gene Set Enrichment Analysis

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

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**

```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
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

Description

perform gsea analysis

Usage

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**

**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**

```r
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**

```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
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
**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)

---

**Description**

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

- [ggplot2](https://yulab-smu.top)
  - `facet_grid`

---

**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
```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
**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)**

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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

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