Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.30.1

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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 (>= 3.5.0)

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, markdown, org.Hs.eg.db, HPO.db, MPO.db, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

Encoding UTF-8


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

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

RoxygenNote 7.3.1

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**DOSE-package**

**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.

**Author(s)**

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**See Also**

Useful links:
- [https://yulab-smu.top/biomedical-knowledge-mining-book/](https://yulab-smu.top/biomedical-knowledge-mining-book/)
- Report bugs at [https://github.com/GuangchuangYu/DOSE/issues](https://github.com/GuangchuangYu/DOSE/issues)

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**clusterSim**

**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

cluster1 <- c("835", "5261", "241", "994")
clusterSim(cluster1, cluster2)
computeIC

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 (ont = "DO")

Arguments

ont one of "DO" and "MPO"

Author(s)

Guangchuang Yu https://yulab-smu.top

DataSet

Description

Information content and DO term to entrez gene IDs mapping
doSim

doseSim

dosSim

doSim

doseSim

dosSim

doSim

doseSim

dosSim

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

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,  # a vector of entrez gene id
  pvalueCutoff = 0.05,  # pvalue cutoff
  pAdjustMethod = "BH",  # one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
  universe,  # background genes
  minGSSSize = 10,  # minimal size of genes annotated by NCG category for testing
  maxGSSize = 500,  # maximal size of each geneSet for analyzing
  qvalueCutoff = 0.2,  # qvalue cutoff
  readable = FALSE)  # whether mapping gene ID to gene Name
```

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


enrichDGNv enrichDGN

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
enrichDO

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
enricher_internal

Description

ternal 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, default is the intersection of the 'universe' with genes that have annotations. Users can set 'options(enrichment_force_universe = TRUE)' to force the 'universe' untouched.
enrichHPO

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 https://yulab-smu.top

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
enrichNCG

Value
A enrichResult instance

Author(s)
Erqiang Hu

References

enrichNCG 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 pvalueCutoff
pAdjustMethod pvalue adjust method
qvalueCutoff qvalueCutoff
organism only "human" supported
ontology biological ontology
gene Gene IDs
drug type 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**

*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
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

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)

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

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
dr dimension reduction result

Author(s)

Guangchuang Yu https://yulab-smu.top

GSEA_internal  
GSEA_internal

Description

generic function for gene set enrichment analysis
GSEA_internal

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
**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
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

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**

```r
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**

```r
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")
**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

---

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

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setReadable  

**Description**

mapping geneID to gene Symbol

**Usage**

setReadable(x, OrgDb, keyType = "auto")

**Arguments**

- **x**
  - enrichResult Object
- **OrgDb**
  - OrgDb
- **keyType**
  - keyType of gene

---

reexports  

**Description**

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

- ggplot2  
  - facet_grid

---

setReadable  

**Description**

setReadable
show

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
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    lable size
font.size    font size

Value

ggplot object

Author(s)

Yu Guangchuang
Summary

Summary method for gseaResult instance
Summary method for enrichResult instance

Usage

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

Arguments

object
A enrichResult instance.
...
a additional parameter

Value

A data frame
A data frame

Author(s)

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Guangchuang Yu http://guangchuangyu.github.io

Theme_dose

Description

ggplot theme of DOSE

Usage

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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