

Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.20.1

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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, BiocParallel, DO.db, fgsea, ggplot2, GOSemSim (>= 2.0.0), methods, qvalue, reshape2, stats, utils

Suggests prettydoc, clusterProfiler, knitr, rmarkdown, org.Hs.eg.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

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DOSE-package *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, DO.db
Suggests: clusterProfiler, GOSemSim
License: Artistic-2.0

Author(s)

Guangchuang Yu, Li-Gen Wang

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also

[enrichResult](#)

clusterSim

clusterSim

Description

semantic similarity between two gene clusters

Usage

```
clusterSim(cluster1, cluster2, measure = "Wang", combine = "BMA")
```

Arguments

| | |
|----------|--|
| cluster1 | a vector of gene IDs |
| cluster2 | another vector of gene IDs |
| 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")
cluster2 <- c("307", "308", "317", "321", "506", "540", "378", "388", "396")
clusterSim(cluster1, cluster2)
```

compareClusterResult-class

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Description

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://guangchuangyu.github.io>

See Also

[enrichResult](#)

| | |
|-----------|------------------------------------|
| computeIC | <i>compute information content</i> |
|-----------|------------------------------------|

Description

compute information content

Usage

```
computeIC(ont = "DO", organism = "human")
```

Arguments

| | |
|----------|---------|
| ont | "DO" |
| organism | "human" |

Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

| | |
|---------|-----------------|
| DataSet | <i>Datasets</i> |
|---------|-----------------|

Description

Information content and DO term to entrez gene IDs mapping

| | |
|-------|--------------|
| doSim | <i>doSim</i> |
|-------|--------------|

Description

measuring similarities between two DO term vectors.

Usage

```
doSim(DO1D1, DO1D2, measure = "Wang")
```

Arguments

| | |
|---------|---|
| DO1D1 | DO term vector |
| DO1D2 | DO term vector |
| measure | one of "Wang", "Resnik", "Rel", "Jiang", and "Lin". |

Details

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

Value

score matrix

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

| | |
|-----------|--|
| enrichDGN | <i>Enrichment analysis based on the DisGeNET</i> (http://www.disgenet.org/) |
|-----------|--|

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

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>

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

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

Arguments

| | |
|----------------------------|--|
| <code>gene</code> | a vector of entrez gene id |
| <code>ont</code> | one of DO or DOLite. |
| <code>pvalueCutoff</code> | pvalue cutoff |
| <code>pAdjustMethod</code> | one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none" |
| <code>universe</code> | background genes |
| <code>minGSSize</code> | minimal size of genes annotated by NCG category for testing |
| <code>maxGSSize</code> | maximal size of each geneSet for analyzing |
| <code>qvalueCutoff</code> | qvalue cutoff |
| <code>readable</code> | 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)
```

| | |
|-------------------|------------------------|
| enricher_internal | <i>enrich.internal</i> |
|-------------------|------------------------|

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.

Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

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 | <i>Class "enrichResult" This class represents the result of enrichment analysis.</i> |
|--------------------|--|

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://guangchuangyu.github.io>

See Also

[enrichDO](#)

| | |
|------------|-------------------|
| EXTID2NAME | <i>EXTID2NAME</i> |
|------------|-------------------|

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 <http://guangchuangyu.github.io>

| | |
|---------|------------------------------------|
| gene2DO | <i>convert Gene ID to DO Terms</i> |
|---------|------------------------------------|

Description

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

Usage

```
gene2DO(gene)
```

Arguments

| | |
|------|----------------|
| gene | entrez gene ID |
|------|----------------|

Value

DO Terms

Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

| | |
|--------|-----------------------|
| geneID | <i>geneID generic</i> |
|--------|-----------------------|

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 | <i>geneInCategory generic</i> |
|----------------|-------------------------------|

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

```
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, measure = "Wang", combine = "BMA")
```

Arguments

| | |
|---------|---|
| geneID1 | entrez gene vector |
| geneID2 | entrez gene vector |
| measure | one of "Wang", "Resnik", "Rel", "Jiang", and "Lin". |
| combine | One of "max", "avg", "rmax", "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 | <i>Class "gseaResult" This class represents the result of GSEA analysis</i> |
|------------------|---|

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://guangchuangyu.github.io>

| | |
|---------------|----------------------|
| GSEA_internal | <i>GSEA_internal</i> |
|---------------|----------------------|

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

```

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

```

gseD0(
  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

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

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

mclusterSim

mclusterSim

Description

Pairwise semantic similarity for a list of gene clusters

Usage

```
mclusterSim(clusters, measure = "Wang", combine = "BMA")
```

Arguments

| | |
|----------|--|
| clusters | A list of gene clusters |
| 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

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

rebuilding annotation data

Description

rebuilding entrez and DO mapping datasets

Usage

```
rebuildAnnoData(file)
```

Arguments

file do_rif.human.txt

Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

| | |
|-------------|--------------------|
| setReadable | <i>setReadable</i> |
|-------------|--------------------|

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 | <i>show method</i> |
|------|--------------------|

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://guangchuangyu.github.io>

Guangchuang Yu <https://guangchuangyu.github.io>

simplot

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 | lable size |
| font.size | font size |

Value

ggplot object

Author(s)

Yu Guangchuang

| | |
|---------|-----------------------|
| summary | <i>summary method</i> |
|---------|-----------------------|

Description

summary method for gseaResult instance
summary method for enrichResult instance

Usage

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>Guangchuang Yu <http://guangchuangyu.github.io>

| | |
|------------|-------------------|
| theme_dose | <i>theme_dose</i> |
|------------|-------------------|

Description

ggplot theme of DOSE

Usage

theme_dose(font.size = 14)

Arguments

`font.size` font size

Value

ggplot theme

Examples

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

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