Package 'DOSE'

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 1.2.1

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Description Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin
and Wang respectively for measuring DO semantic similarities, and
hypergeometric test for enrichment analysis.

Depends R (>= 2.10)

Imports methods, plyr, qvalue, stats4, AnnotationDbi, DO.db,org.Hs.eg.db, igraph0, scales, gg-
plot2, graphics

Suggests clusterProfiler, GOSemSim, ReactomePA

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biocViews Bioinformatics, Annotation

Collate 'AllGenerics.R' 'barplot.R' 'ClassDOParams.R' 'cnetplot.R''combineMethods.R' 'DOSE-
package.R' 'doSim.R''enrich.internal.R' 'enrichDO.R' 'geneSim.R' 'ICMethods.R''utilities.R' 'WangMethod.R' 'zzz

R topics documented:

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:	1.1.6
Date:	2-27-2012
biocViews:	Bioinformatics, Annotation
Depends:	
Imports:	methods, AnnotationDbi, DO.db
Suggests:	clusterProfiler, GOSemSim
License:	Artistic-2.0

Author(s)

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See Also

[DOParams, enrichResult](#)

ALLEXTID *Get all background External ID.*

Description

Get all background External ID.

Usage

```
ALLEXTID(organism)
```

Arguments

organism   organism

---

cnetplot *plot gene net by categories*

Description

plot function of gene Concept Net.

Usage

```
cnetplot(inputList, categorySize = "geneNum",
  showCategory = 5, pvalue = NULL, logFC = NULL,
  output = "fixed")
```

Arguments

inputList	a list of gene IDs
categorySize	setting category size
showCategory	number of categories to plot
pvalue	pvalue
logFC	log fold Change
output	output type

Value

plotted igraph0 object.

Author(s)

Guangchuang Yu http://ygc.name

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combineScores *combining similarity matrix to similarity score*

Description

Functions for combining similarity matrix to similarity score

Usage

```
combineScores(SimScores, combine)
```

Arguments

SimScores	similarity matrix
combine	combine method

Value

similarity value

Author(s)

Guangchuang Yu http://ygc.name

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computeIC *compute information content*

Description

compute information content

Usage

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

Arguments

ont	"DO"
organism	"human"

Value

NULL

Author(s)

Guangchuang Yu http://ygc.name

DataSet	*Datasets Information content and DO term to entrez gene IDs mapping*

Description

Datasets Information content and DO term to entrez gene IDs mapping

DOParams-class	*Class "DOParams" This class contains parameters for calculating DO semantic similarity among DO term or Gene list.*

Description

Class "DOParams" This class contains parameters for calculating DO semantic similarity among DO term or Gene list.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[sim](#)

doSim	*doSim*

Description

measuring similarities between two DO term vectors.

Usage

```
doSim(DOID1, DOID2, method = "Wang", organism = "human")
```

Arguments

DOID1	DO term vector
DOID2	DO term vector
method	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".
organism	only "human" supported

Details

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

Value

score matrix

Author(s)

Guangchuang Yu <http://ygc.name>

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enrich.internal	*enrich.internal*

Description

interal method for enrichment analysis

Usage

```
enrich.internal(gene, organism, pvalueCutoff,
  qvalueCutoff, ont, readable)
```

Arguments

gene	a vector of entrez gene id.
organism	supported organism.
pvalueCutoff	Cutoff value of pvalue.
qvalueCutoff	Cutoff value of qvalue.
ont	Ontology
readable	whether mapping gene ID to gene Name

Details

using the hypergeometric model

Value

A enrichResult instance.

Author(s)

Guangchuang Yu <http://ygc.name>

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enrichDO   *DO Enrichment Analysis of a gene set.*

Description

Given a vector of genes, this function will return the enrichment DO categories with FDR control.

Usage

```
enrichDO(gene, pvalueCutoff = 0.05, qvalueCutoff = 0.05,
  readable = F)
```

Arguments

gene   a vector of entrez gene id.

pvalueCutoff   Cutoff value of pvalue.

qvalueCutoff   Cutoff value of qvalue.

readable   whether mapping gene ID to gene Name

Value

A enrichResult instance.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichResult-class

Examples

```
set.seed(123)
data(EG2DO)
gene = sample(names(EG2DO), 30)
yy = enrichDO(gene, pvalueCutoff=0.05)
summary(yy)
```

enrichResult-class	*Class "enrichResult" This class represents the result of DO enrichment analysis.*

Description

Class "enrichResult" This class represents the result of DO enrichment analysis.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichDO

EXTID2NAME	*EXTID2NAME*

Description

mapping gene ID to gene Symbol

Usage

```
EXTID2NAME(geneID, organism)
```

Arguments

geneID	entrez gene ID
organism	one of "human", "mouse" and "yeast"

Value

gene symbol

Author(s)

Guangchuang Yu http://ygc.name

EXTID2TERMID *Mapping External ID to Ontology Term ID*

Description

Mapping External ID to Ontology Term ID

Usage

```
EXTID2TERMID(gene, organism)
```

Arguments

gene   gene ID vector

organism   organism

---

gene2DO *convert Gene ID to DO Terms*

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://ygc.name>

geneSim   *geneSim*

Description

measuring similarities bewteen two gene vectors.

Usage

```
geneSim(geneID1, geneID2, method = "Wang",
  organism = "human", combine = "rcmax.avg")
```

Arguments

geneID1   entrez gene vector

geneID2   entrez gene vector

method   one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".

organism   only "human" supported

combine   One of "max", "average", "rcmax", "rcmax.avg" methods, for combining seman-
                 tic 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>

infoContentMethod   *information content based methods*

Description

Information Content Based Methods for semantic similarity measuring

Usage

```
infoContentMethod(ID1, ID2, ont = "DO", method,
  organism = "human")
```

Arguments

ID1	Ontology Term
ID2	Ontology Term
ont	Ontology
method	one of "Resnik", "Jiang", "Lin" and "Rel".
organism	one of supported species

Details

implemented for methods proposed by Resnik, Jiang, Lin and Schlicker.

Value

semantic similarity score

Author(s)

Guangchuang Yu http://ygc.name

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list2graph	*convert gene IDs to igraph0 object*

Description

convert a list of gene IDs to igraph0 object.

Usage

```
list2graph(inputList)
```

Arguments

inputList	a list of gene IDs

Value

a igraph0 object.

Author(s)

Guangchuang Yu http://ygc.name

`loadICdata` *Load IC data*

Description

Load Information Content data to DOSEEnv environment

Usage

```
loadICdata(organism, ont)
```

Arguments

organism   "human"

ont   "DO"

Value

NULL

Author(s)

Guangchuang Yu http://ygc.name

`plot` *plot method*

Description

plot method generics

Arguments

...   Additional argument list

Value

plot

Author(s)

Guangchuang Yu http://ygc.name

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rebuildAnnoData *rebuiding annotation data*

Description

rebuilding entrez and DO mapping datasets

Usage

```
rebuildAnnoData(file)
```

Arguments

file   do_rif.human.txt

Value

NULL

Author(s)

Guangchuang Yu <http://ygc.name>

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setReadable<- *Methods mapping gene ID to gene symbol for* enrichResult *instance*

Description

setReadable method for enrichResult instance

Arguments

x   A enrichResult instance.

value   readable flag.

Value

A enrichResult instance.

Author(s)

Guangchuang Yu <http://ygc.name>

---

show *show method*

Description

show method for enrichResult instance

Arguments

object   A enrichResult instance.

Value

message

Author(s)

Guangchuang Yu <http://ygc.name>

---

sim *Methods for calculating semantic similarity*

Description

sim method for DOParams instance

Arguments

params   A DOParams instance.

Value

Semantic similarity value or matrix.

Author(s)

Guangchuang Yu <http://ygc.name>

summary   *summary method*

Description

summary method for enrichResult instance

Arguments

object   A enrichResult instance.

Value

A data frame

Author(s)

Guangchuang Yu <http://ygc.name>

TERM2NAME   *Mapping Ontology Term ID to Name Symbol or Description*

Description

Mapping Ontology Term ID to Name Symbol or Description

Usage

```
TERM2NAME(term)
```

Arguments

term   term ID vector

TERMID2EXTID   *Mapping Ontology Term ID to External ID*

Description

Mapping Ontology Term ID to External ID

Usage

```
TERMID2EXTID(term, organism)
```

Arguments

term   term ID vector
organism   organism

wangMethod　　　　　　　　　　*wangMethod*

Description

Method Wang for semantic similarity measuring

Usage

```
wangMethod(ID1, ID2, ont = "DO", weight.isa = 0.8,
    weight.partof = 0.6, weight.do = 0.7)
```

Arguments

`ID1`	Ontology Term
`ID2`	Ontology Term
`ont`	Ontology
`weight.isa`	weight of isa relationship
`weight.partof`	weight of partof relationship
`weight.do`	weight of DO

Value

semantic similarity score

Author(s)

Guangchuang Yu http://ygc.name

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