Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 1.4.0

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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), ggplot2

Imports methods, plyr, qvalue, stats4, AnnotationDbi, DO.db,org.Hs.eg.db, igraph, scales, reshape2, graphics, GOSemSim

Suggests clusterProfiler, ReactomePA

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biocViews Bioinformatics, Annotation

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

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 igraph object.

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

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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

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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

---

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, ont = "DOLite", pvalueCutoff = 0.05,
  qvalueCutoff = 1, readable = F)
```

Arguments

gene	a vector of entrez gene id.
ont	one of DO or DOLite.
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)
```

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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 = "BMA")
```

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", "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

list2graph *convert gene IDs to igraph object*

Description

convert a list of gene IDs to igraph object.

Usage

```
list2graph(inputList)
```

Arguments

inputList	a list of gene IDs

Value

a igraph object.

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

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simplot *simplot*

Description

plotting similarity matrix

Usage

```
simplot(sim, xlab = "", ylab = "")
```

Arguments

sim	similarity matrix
xlab	xlab
ylab	ylab

Value

ggplot object

Author(s)

Yu Guangchuang

---

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

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