Package ‘DOSE’

October 9, 2013

Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 1.6.0

Author Guangchuang Yu, Li-Gen Wang

Maintainer Guangchuang Yu <`guangchuangyu@gmail.com`>

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)

Guangchuang Yu, Li-Gen Wang

Maintainer: Guangchuang Yu `<guangchuangyu@gmail.com>`

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`

`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`

`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`

`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)
```

`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`

`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`

`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

`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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