Package ‘DOSE’

September 24, 2012

Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 1.2.1

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)

Imports methods, plyr, qvalue, stats4, AnnotationDbi, DO.db.org.Hs egret.db, igraph0, scales, ggplot2, graphics

Suggests clusterProfiler, GOSemSim, ReactomePA

License Artistic-2.0

biocViews Bioinformatics, Annotation


R topics documented:

- DOSE-package ................................................................. 2
- ALLEXTID .................................................................. 3
- cnetplot ...................................................................... 3
- combineScores .............................................................. 4
- computeIC .......................................................... 4
- DataSet .................................................................... 5
- DOParams-class ......................................................... 5
- doSim ............................................................. 5
- enrich.internal .................................................. 6
- enrichDO .......................................................... 7
- enrichResult-class ................................................ 8
- EXTID2NAME .......................................................... 8
- EXTID2TERMID ....................................................... 9
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.

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 igraph0 object.

**Author(s)**

Guangchuang Yu http://ygc.name
**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](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](http://ygc.name)
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](http://ygc.name)

See Also

sim

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](http://ygc.name)

---

**Description**

internal method for enrichment analysis

**Usage**

```r
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](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, pvalueCutoff = 0.05, qvalueCutoff = 0.05,
         readable = F)

Arguments

gene a vector of entrez gene id.
pvalueCutoff Cutoff value of pvalue.
quvalueCutoff 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)
symbol(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

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](http://ygc.name)
Description

measuring similarities between 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 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)

Guangchuan 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")
**list2graph**

**Arguments**

<table>
<thead>
<tr>
<th>ID1</th>
<th>Ontology Term</th>
</tr>
</thead>
<tbody>
<tr>
<td>ID2</td>
<td>Ontology Term</td>
</tr>
<tr>
<td>ont</td>
<td>Ontology</td>
</tr>
<tr>
<td>method</td>
<td>one of &quot;Resnik&quot;, &quot;Jiang&quot;, &quot;Lin&quot; and &quot;Rel&quot;.</td>
</tr>
<tr>
<td>organism</td>
<td>one of supported species</td>
</tr>
</tbody>
</table>

**Details**

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

**Value**

semantic similarity score

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

---

**list2graph**  
*convert gene IDs to igraph0 object*

**Description**

convert a list of gene IDs to igraph0 object.

**Usage**

```r
list2graph(inputList)
```

**Arguments**

| inputList | a list of gene IDs |

**Value**

a igraph0 object.

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)
loadICdata  \hspace{1cm} \textit{Load IC data}

\textbf{Description}  
Load Information Content data to DOSEEnv environment

\textbf{Usage}  
loadICdata(organism, ont)

\textbf{Arguments}  
\begin{itemize}  
\item \textit{organism} \hspace{1cm} "human"  
\item \textit{ont} \hspace{1cm} "DO"  
\end{itemize}

\textbf{Value}  
NULL

\textbf{Author(s)}  
Guangchuang Yu \url{http://ygc.name}

\textbf{plot  \hspace{1cm} \textit{plot method}}

\textbf{Description}  
plot method generics

\textbf{Arguments}  
... Additional argument list

\textbf{Value}  
plot

\textbf{Author(s)}  
Guangchuang Yu \url{http://ygc.name}
rebuildAnnoData

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
**Description**

*show* method for *enrichResult* instance

**Arguments**

- **object**
  - A *enrichResult* instance.

**Value**

*message*

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

---

**Description**

*sim* method for *DOParams* instance

**Arguments**

- **params**
  - A *DOParams* instance.

**Value**

Semantic similarity value or matrix.

**Author(s)**

Guangchuang Yu [http://ygc.name](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](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 |
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
Index

*Topic classes
  DOParams-class, 5
  enrichResult-class, 8

*Topic datasets
  DataSet, 5

*Topic manip
  enrich.internal, 6
  enrichDO, 7

*Topic package
  DOSE-package, 2

ALLEXTID, 3

cnetplot, 3
combineScores, 4
computeIC, 4

DataSet, 5
DO2ALLEG (DataSet), 5
DO2EG (DataSet), 5
DOParams, 2
DOParams-class, 5
DOSE (DOSE-package), 2
DOSE-package, 2
doSim, 5

EG2ALLDO (DataSet), 5
EG2DO (DataSet), 5
enrich.internal, 6
enrichDO, 7, 8
enrichResult, 2
enrichResult-class, 8
EXTID2NAME, 8
EXTID2TERMID, 9
gene2DO, 9
geneSim, 10

IC (DataSet), 5
Info_Contents_human_DO (DataSet), 5
infoContentMethod, 10

list2graph, 11
loadICdata, 12

plot, 12
plot, enrichResult, ANY-method (plot), 12
plot, enrichResult-method
  (enrichResult-class), 8
rebuildAnnoData, 13
setReadable (setReadable<->), 13
setReadable-methods (setReadable<->), 13
setReadable<->, 13
setReadable<-, enrichResult, ANY-method
  (setReadable<->), 13
setReadable<-, enrichResult-method
  (enrichResult-class), 8
show, 14
show, enrichResult-method
  (enrichResult-class), 8
sim, 5, 14
sim, DOParams-method (DOParams-class), 5
summary, 15
summary, enrichResult-method
  (enrichResult-class), 8
TERM2NAME, 15
TERMID2EXTID, 15

wangMethod, 16

17