Package ‘dSimer’

March 28, 2017

Type Package
Title Integration of Disease Similarity Methods
Version 1.0.0
Date 2015-12-10
Author Min Li <limin@mail.csu.edu.cn>, Peng Ni <nipeng@csu.edu.cn>
with contributions from Zhihui Fei and Ping Huang.
Maintainer Peng Ni <nipeng@csu.edu.cn>
Description dSimer is an R package which provides computation of nine
methods for measuring disease-disease similarity, including a
standard cosine similarity measure and eight function-based
methods. The disease similarity matrix obtained from these nine
methods can be visualized through heatmap and network. Biological
data widely used in disease-disease associations study are also
provided by dSimer.
Depends R (>= 3.3.0), igraph (>= 1.0.1)
Imports stats, Rcpp (>= 0.11.3), ggplot2, reshape2, GO.db,
org.Hs.eg.db, AnnotationDbi, graphics
Suggests knitr, rmarkdown, BiocStyle
LinkingTo Rcpp
License GPL (> = 2)
biocViews Software, Visualization, Network
VignetteBuilder knitr
RoxygenNote 5.0.1
NeedsCompilation yes

R topics documented:

dSimer-package .................................................. 2
BOG ...................................................................... 3
CosineDFV ............................................................ 4
d2go_sample ....................................................... 5
d2g_fundo_entrezid .............................................. 5
d2g_fundo_symbol ............................................... 6
d2g_separation ..................................................... 6
d2s_hsdn ............................................................... 7
dSimer-package

Integration of Disease Similarity Methods

Description
dSimer is an R package which provides computation of nine methods for measuring disease-disease similarity, including a standard cosine similarity measure and eight function-based methods. The disease similarity matrix obtained from these nine methods can be visualized through heatmap and network. Biological data widely used in disease-disease associations study are also provided by dSimer.

Details
Package: dSimer
Type: Package
Version: 0.99.6
Date: 12-10-2015
biocViews: Software, Visualization, Network
Depends: R (>= 3.3.0), igraph (>= 1.0.1)
calculate disease similarity by BOG

Description

given two vectors of diseases and a list of disease-gene associations, this function will calculate disease similarity by method BOG.

Usage

`BOG(D1, D2, d2g)`

Arguments

D1 a vector consists disease ids
D2 another vector consists disease ids
d2g a list of disease-gene associations

Value

a matrix of disease disease similarity which rownames is D1 and colnames is D2

Author(s)

Peng Ni, Min Li

References


See Also

Normalize

Examples

data(d2g_separation) #get disease-gene associations
ds<-sample(names(d2g_separation),5)
sim<-BOG(ds,ds,d2g_separation)
Normalize(sim) #normalize BOG sim scores
CosineDFV

*calculate disease similarity by using feature vectors*

**Description**

given two (lists of) disease names, this function will calculate cosine similarity between these diseases’ feature vectors.

**Usage**

```
CosineDFV(D1, D2, d2f, dcol = 2, fcol = 1, ccol = 3)
```

**Arguments**

- **D1**: a vector consists of disease ids/names
- **D2**: another vector consists of disease ids/names
- **d2f**: data.frame, contains term co-occurrences between features and diseases
- **dcol**: integer, disease column number in d2f
- **fcol**: integer, feature column number in d2f
- **ccol**: integer, co-occurrences column number in d2f

**Value**

a matrix of disease disease similarity which rownames and colnames are the disease names

**Author(s)**

Zhihui Fei, Peng Ni, Min Li

**References**


**Examples**

```r
### this is a disease-symptom-cooccurrence sample, if you want to use
### the complete data, please use "data(d2s_hsdn)" command
data(d2s_hsdn_sample)
ds <- sample(unique(d2s_hsdn_sample[,2]), 10)
simmat <- CosineDFV(ds, ds, d2s_hsdn_sample)
```
d2go_sample

Description

A sample list of disease-GO term associations.

Value

d2go_sample is a named list of length 3. The names are the DOIDs (DOIDs are ids of terms in Disease Ontology, e.g. "DOID:4") and list elements are vectors of GO term ids. The entire data of disease-GO term associations can be obtained by function HypergeometricTest.

See Also

HypergeometricTest

Examples

data(d2go_sample)

d2g_fundo_entrezid

Description

A list of disease-gene associations from FunDO.

Value

d2g_fundo_entrezid is a named list of length 1855 which stored disease-gene associations from FunDO. The names are the DOIDs (DOIDs are ids of terms in Disease Ontology, e.g. "DOID:4") and list elements are vectors of Entrez gene IDs.

References


Examples

data(d2g_fundo_entrezid)
**d2g_fundo_symbol**

**Description**

A list of disease-gene associations from FunDO.

**Value**

d2g_fundo_symbol is a named list of length 1855 which stored disease-gene associations from FunDO. The names are the DOIDs (DOIDs are ids of terms in Disease Ontology, e.g. "DOID:4") and list elements are vectors of gene symbols.

**References**


**Examples**

data(d2g_fundo_symbol)

---

**d2g_separation**

**Description**

A list of disease-gene associations from the reference paper (see below).

**Value**

d2g_separation is a named list of length 299 which stored disease-gene associations from the reference paper (see below). The names are diseases and list elements are vectors of gene entrez ids.

**References**


**Examples**

data(d2g_separation)
d2s_hsdn

Description
diseases, symptoms and their co-occurrences in PubMed

Value
d2s_hsdn is a data.frame of 73726 rows and 3 columns, contains PubMed co-occurrences of diseases and symptoms, will be used in method CosineDFV.

References

See Also
CosineDFV

Examples
data(d2s_hsdn)

d2s_hsdn_sample

Description
a sample of d2s_hsdn

Value
d2s_hsdn_sample is a data.frame of 1480 rows and 3 columns, contains PubMed co-occurrences of diseases and symptoms. It is a sample of d2s_hsdn.

References

See Also
d2s_hsdn, CosineDFV

Examples
data(d2s_hsdn_sample)
FunSim  

*calculate disease similarity by FunSim*

**Description**

Given two vectors of diseases, a list of disease-gene associations, and a list of gene-gene log-likelihood score from HumanNet, this function will calculate disease similarity by method FunSim.

**Usage**

`FunSim(D1, D2, d2g, LLSnList)`

**Arguments**

- `D1`: A vector consists of disease ids.
- `D2`: Another vector consists of disease ids.
- `d2g`: A list of disease-gene associations, where gene ids should be ENTREZ id.
- `LLSnList`: A list of gene-gene log-likelihood score from HumanNet.

**Value**

A matrix of disease disease similarity which rownames is `D1` and colnames is `D2`.

**Author(s)**

Peng Ni, Min Li

**References**


**See Also**

`LLSn2List`

**Examples**

```r
## in this method, we must use disease-gene associations
## which genes are represented by entrez ids because of
## HumanNet
data(d2g_fundo_entrezid)
data(HumanNet_sample)
## we specified 5 DOIDs to match Human_sample
llsnlist<-LLSn2List(HumanNet_sample)
FunSim(ds, ds, d2g_fundo_entrezid, llsnlist)
```
get.GOterm2GeneAssos

Description
get GO-gene associations from GO.db and org.Hs.eg.db

Usage
get.GOterm2GeneAssos(GOONTOLOGY = c("BP", "MF", "CC"),
geneid = c("ENTREZID", "SYMBOL"), rm.IEAs = TRUE,
rm.termlessthan3genes = TRUE)

Arguments
GOONTOLOGY "BP" or "MF" or "CC"
geneid gene id type, "ENTREZID" or "SYMBOL"
rm.IEAs logical value, remove GO terms with evidence "IEA" or not
rm.termlessthan3genes logical value, remove terms whose number of annotated genes are less than 3 or not

Value
a list which names are GO term IDs and elements are gene ids or symbols annotated with GO terms

Author(s)
Peng Ni, Min Li

References

See Also
PSB, Sun_function

Examples
go2g<-get.GOterm2GeneAssos(GOONTOLOGY="BP", geneid="SYMBOL")
go2g
### go2g_sample

**Description**

A sample list of GO term-gene associations.

**Value**

go2g_sample is a named list of length 465. The names are GO term ids (GOIDs) and list elements are vectors of gene symbols. The entire data of GO term-gene assos can be obtained by function get_GOterm2GeneAssos.

**See Also**

get_GOterm2GeneAssos

**Examples**

data(go2g_sample)

### graphlet_sig_hprd

**Description**

Graphlet signature of nodes in HPRD PPI network.

**Value**

graphlet_sig_hprd is a matrix of 9270 rows and 73 rows. The rownames of graphlet_sig_hprd are gene symbols of nodes from HPRD. Each row indicates a graphlet signature of one node. Graphlet signatures of nodes in HPRD PPI network were calculated by ORCA tool, will be used in method Sun_topology.

**References**


**See Also**

Sun_topology

**Examples**

data(graphlet_sig_hprd)
Description

a sample of HumanNet likelihood score data which will be used in method FunSim.

Value

HumanNet_sample is a data.frame has 22708 rows and 3 columns. Each row indicates a pair of
genes and their normalized likelihood score in HumanNet. HumanNet_sample will be used in
method FunSim after being converted to list by method LLSn2List. The entire data of HumanNet
can be downloaded from the website http://www.functionalnet.org/humannet/.

References


See Also

FunSim, LLSn2List

Examples

data(HumanNet_sample)

HypergeometricTest

Hypergeometric test and multiple testing

Description

given disease-gene associations and go-gene associations, return disease-go associations by using
hypergeometric test and fdr multiple testing

Usage

HypergeometricTest(d2g, go2g, method = "BH", cutoff = 0.05)

Arguments

d2g a list of disease-gene associations

go2g a list of GOterm-gene associations

method multiple testing method, the same as parameter in method p.adjust

cutoff multiple testing cut off value

Value

a list of disease-GO term associations
ICod

Author(s)
Peng Ni, Min Li

See Also
PSB, Sun_function, get_GOterm2GeneAssos

Examples
```r
# see more examples in function PSB or Sun_function
data(d2go_sample)
data(go2g_sample)
data(d2g_fundo_symbol)
HypergeometricTest(d2g_fundo_symbol[names(d2go_sample)], go2g_sample)
```

__Description__

given two vectors of diseases, a list of disease-gene associations and a PPI network, this function will calculate disease similarity by method ICod

__Usage__

```r
ICod(D1, D2, d2g, graph, A = 0.9, b = 1, C = 0)
```

__Arguments__

- **D1**
  a vector consists disease ids

- **D2**
  another vector consists disease ids

- **d2g**
  a list of disease-gene associations

- **graph**
  an igraph graph object of PPI network

- **A**
  a parameter used in ICod to calculate transformed distance of node pair, default 0.9

- **b**
  a parameter used in ICod to calculate transformed distance of node pair, default 1

- **C**
  a parameter used in ICod to calculate disease similarity, default 0

__Value__
a matrix of disease disease similarity which rownames is D1 and colnames is D2

__Author(s)__
Peng Ni, Min Li
References


Examples

data(d2g_fundo_symbol)
data(PPI_HPRD)

graph_hprd<-graph.data.frame(PPI_HPRD,directed=FALSE) #get a igraph object based on HPRD data
ds<-sample(names(d2g_fundo_symbol),5)
ICod(ds,ds,d2g_fundo_symbol,graph_hprd)

InformationContent  calculating information content

Description

calculate information content of all term ids in a term list

Usage

InformationContent(T2G)

Arguments

T2G  a list of Term-Gene associations which names are term ids

Value

a list of IC values of inputted term ids

Author(s)

Peng Ni, Min Li

Examples

data(d2g_fundo_symbol)
InformationContent(d2g_fundo_symbol[1:5])
Description
interactome data

Value
interactome is a data.frame of 141296 rows and 2 columns. Each row indicates an interaction of two gene entrez ids. It was obtained from the reference below.

References

Examples
data(interactome)

jaccardindex

Description
calculating Jaccard Index

Usage
jaccardindex(x1, x2, x2y)

Arguments
x1 a disease id
x2 another disease id
x2y a list of disease-gene associations which consists x1 and x2

Value
numeric value of a jaccard index of x1 and x2

Author(s)
Peng Ni, Min Li

Examples
## this function is not just for disease-gene associations
data(d2go_sample)
d1<-names(d2go_sample)[1]
d2<-names(d2go_sample)[2]
jaccardindex(d1,d2,d2go_sample)
**LLSn2List**

convert data.frame of HumanNet log-likelihood Score to list

---

**Description**

convert HumanNet normalized log-likelihood score from data.frame to list, which will be used in FunSim method

**Usage**

```r
LLSn2List(LLSn)
```

**Arguments**

- `LLSn`: data.frame of gene-gene normalized log-likelihood score in HumanNet

**Value**

- a list of normalized log-likelihood score

**Author(s)**

Peng Ni, Min Li

**References**


**See Also**

- `FunSim`

**Examples**

```r
## see examples in function FunSim
data(HumanNet_sample)
llsnlist<-LLSn2List(HumanNet_sample[1:100,])
llsnlist
```
Normalize

Description

normalize a vector or a matrix based on the formula from SemFunSim

Usage

Normalize(data)

Arguments

data: a numeric/integer vector or matrix

Value

normalized vector or matrix

Author(s)

Peng Ni, Min Li

References


Examples

sim<-matrix(1:9,3,3)
Normalize(sim)

orbit_dependency_count

Description

orbit dependency count

Value

orbit_dependency_count is a 73-dim vector, indicating 73 orbits’ dependency count in graphlet theory, used to calculate weight factor in method setWeight.

References

plot_bipartite

See Also

setWeight

Examples

```r
data(orbit_dependency_count)
```

Description

plot a bipartite graph which visualizes associations between diseases and genes (or GO terms etc.)

Usage

```r
plot_bipartite(xylist, vertex.size = 12, vertex.shape1 = "circle",
vertex.shape2 = "square", vertex.color1 = "darkseagreen",
vertex.color2 = "turquoise1", vertex.label.font = 2,
vertex.label.dist = 0, vertex.label.color = "black",
vertex.label.cex = 0.8, edge.color = "black",
layout = layout.kamada.kawai)
```

Arguments

- `xylist`: a named list object which names are diseases and each element of the list is a gene set with respect to each disease.
- `vertex.size`: vertex size
- `vertex.shape1`: shape for one kind of vertex
- `vertex.shape2`: shape for another kind of vertex
- `vertex.color1`: color for one kind of vertex
- `vertex.color2`: color for another kind of vertex
- `vertex.label.font`: label text font
- `vertex.label.dist`: label text dist
- `vertex.label.color`: label text color
- `vertex.label.cex`: label text cex
- `edge.color`: edge color
- `layout`: layout

Value

an igraph plot object

Author(s)

Peng Ni, Min Li
Examples

```r
data(d2g_fundo_symbol)
d2g_sample<-sample(d2g_fundo_symbol, 3)
plot_bipartite(d2g_sample)
```

**Description**

plot heatmap of a disease similarity matrix

**Usage**

```r
plot_heatmap(simmat, xlab = "", ylab = "", color.low = "white", color.high = "red", labs = TRUE, digits = 2, labs.size = 3, font.size = 14)
```

**Arguments**

- `simmat`: a 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`: label size
- `font.size`: font size

**Value**

a ggplot object

**Author(s)**

Peng Ni, Min Li

**References**

Examples

data(d2g_separation)
data(interactome)

graph_interactome<-graph.data.frame(interactome,directed=FALSE)
ds<-c("myocardial ischemia","myocardial infarction","coronary artery disease",
"cerebrovascular disorders","arthritis, rheumatoid","diabetes mellitus, type 1",
"autoimmune diseases of the nervous system","demyelinating autoimmune diseases, cns",
"respiratory hypersensitivity","asthma","retinitis pigmentosa",
"retinal degeneration","macular degeneration")

sep<-Separation(ds,ds,d2g_separation,graph_interactome)
sim<-Separation2Similarity(sep)
plot_heatmap(sim)

plot_net

plot a network based on a symmetric disease similarity matrix

Description

plot a network/graph of a symmetric disease similarity matrix, note that a unsymmetric matrix can’t be visualized into a network by this method.

Usage

plot_net(simmat, cutoff = 1, vertex.label.font = 2,
vertex.label.dist = 0.5, vertex.label.color = "black",
vertex.label.cex = 0.8, vertex.shape = "circle",
vertex.color = "paleturquoise", vertex.size = 20, edge.color = "red",
layout = layout.fruchterman.reingold)

Arguments

simmat a symmetric similarity matrix
cutoff a cutoff value, only disease pairs have similarity scores no less than cutoff will be visualized in the network
vertex.label.font label text font
vertex.label.dist label text dist
vertex.label.color label text color
vertex.label.cex label text cex
vertex.shape vertex shape
vertex.color vertex color
vertex.size vertex size
edge.color edge color
layout layout
plot_topo

Value
an igraph plot object

Author(s)
Peng Ni, Min Li

Examples

data(d2g_separation)
data(interactome)

d$s<-$graph.data.frame(interactome, directed=FALSE)
d$s<-$c("myocardial ischemia","myocardial infarction","coronary artery disease",
"cerebrovascular disorders","arthritis, rheumatoid","diabetes mellitus, type 1",
"autoimmune diseases of the nervous system","demyelinating autoimmune diseases, cns",
"respiratory hypersensitivity","asthma","retinitis pigmentosa",
"retinal degeneration","macular degeneration")

sep<-Separation(d$s,d$s,d2g_separation,graph_interactome)
sim<-Separation2Similarity(sep)
plot_net(sim,cutoff=0.2)

plot_topo

plot topological relationship of two gene sets

Description
plot topological relationship of two gene sets (which are associated with two diseases respectively).

Usage
plot_topo(geneset1, geneset2, graph, vertexcolor = c("tomato", "orange",
"lightsteelblue"), vertex.shape = "circle", vertex.size = 14,
vertex.label.font = 1, vertex.label.dist = 0,
vertex.label.color = "black", vertex.label.cex = 0.5,
edge.color = "black", layout = layout.auto)

Arguments

geneset1 a character vector contains gene ids
geneset2 another character vector contains gene ids
graph an igraph graph object which represents a gene network
vertexcolor a character vector contains 3 colors for vertexs
vertex.shape vertex shape
vertex.size vertex size
vertex.label.font label text font
vertex.label.dist label text dist
PPI_HPRD

vertex.label.color
  label text color
vertex.label.cex
  label text cex
edge.color
  edge color
layout
  layout

Value

an igraph plot object

Author(s)

Peng Ni, Min Li

Examples

data("PPI_HPRD")
g<-graph.data.frame(PPI_HPRD,directed = FALSE) #get an igraph graph
data(d2g_fundo_symbol)
a<-d2g_fundo_symbol[["DOID:8242"]]
  # get gene set a
b<-d2g_fundo_symbol[["DOID:4914"]]
  # get gene set b
plot_topo(a,b,g)

Description

PPI data from HPRD

Value

PPI_HPRD is a data.frame of 36867 rows and 2 columns. Each rows indicates an interaction of two
gene symbols. It was fetched from HPRD.

References


Examples

data(PPI_HPRD)
Description

given two vectors of diseases, a list of disease-GO term associations and a list of GO term-gene associations, this function will calculate disease similarity by method PSB

Usage

PSB(D1, D2, d2go, go2g)

Arguments

D1  a vector consists disease ids
D2  another vector consists disease ids
d2go a list of disease-go associations
go2g a list of go-gene associations

Value

a matrix of disease disease similarity which rownames is D1 and colnames is D2

Author(s)

Peng Ni, Min Li

References


See Also

get_GOterm2GeneAssos, HypergeometricTest, Normalize

Examples

## these are samples of GO-gene associations and disease-GO associations
data(go2g_sample)
data(d2go_sample)

##### the entire associations can be obtained by follows:
## go2g<get_GOterm2GeneAssos(GOONTOLOGY = "BP", geneid="SYMBOL") #get go-gene associations
## data(d2g_fundo_symbol)
## d2go<HypergeometricTest(d2g = d2g_fundo_symbol,go2g = go2g)
##### ###################################################################
dsc<names(d2go_sample)
sim<PSB(ds,ds,d2go_sample,go2g_sample)
Normalize(sim)
Separation

calculating network-based separation of disease pairs

Description
given two vectors of diseases, a list of disease-gene associations and a PPI network, this function will calculate network-based separation by method Separation.

Usage
Separation(D1, D2, d2g, graph)

Arguments
- D1: a vector consists disease ids
- D2: another vector consists disease ids
- d2g: a list of disease-gene associations
- graph: an igraph graph object of PPI network

Value
a matrix of disease disease network-based separation which rownames is D1 and colnames is D2

Author(s)
Peng Ni, Min Li

References

See Also
Separation2Similarity

Examples
data(d2g_separation)
data(interactome)

graph_interactome<-graph.data.frame(interactome,directed=FALSE)
ds<-sample(names(d2g_separation),5)
sep<-Separation(ds,ds,d2g_separation,graph_interactome)
sim<-Separation2Similarity(sep)
sim
### Separation2Similarity

**Description**

convert a separation matrix to a similarity matrix

**Usage**

Separation2Similarity(data)

**Arguments**

- data: a numeric/integer matrix calculated by method Separation

**Value**

a similarity matrix

**Author(s)**

Peng Ni

**See Also**

Separation

**Examples**

```r
a <- matrix(c(-4:4), 3, 3)
Separation2Similarity(a)
```

### setWeight

**Description**

set weight factor of 73-orbits in graphlet theory

**Usage**

setWeight(orbit_dependency_count)

**Arguments**

- orbit_dependency_count: a vector which each element are the dependency count of each orbit

**Value**

a vector which contains weight factors to each orbit

**Examples**

```r
a <- matrix(c(-4:4), 3, 3)
setWeight(a)
```
**Sun_annotation**

**Author(s)**

Peng Ni

**References**


**Examples**

```r
data(orbit_dependency_count)
setWeight(orbit_dependency_count)
```

---

**Sun_annotation**

*Sun’s annotation measure of disease similarity calculating*

**Description**

given two vectors of diseases and a list of disease-gene associations, this function will calculate disease similarity by method Sun_annotation

**Usage**

```r
Sun_annotation(D1, D2, d2g)
```

**Arguments**

- `D1`: a vector consists disease ids
- `D2`: another vector consists disease ids
- `d2g`: a list of disease-gene associations

**Value**

a matrix of disease disease simialrity which rownames is D1 and colnames is D2

**Author(s)**

Peng Ni, Min Li

**References**


**Examples**

```r
data(d2g_separation)
ds<-sample(names(d2g_separation),5)
Sun_annotation(ds,ds,d2g_separation)
```
Sun_function

Sun's function measure of disease similarity calculating

Description

given two vectors of diseases and a list of disease-go term associations, this function will calculate
disease similarity by method Sun_function

Usage

Sun_function(D1, D2, d2go)

Arguments

D1 a vector consists disease ids
D2 another vector consists disease ids
d2go a list of disease-go term associations

Value

a matrix of disease disease simialrity which rownames is D1 and colnames is D2

Author(s)

Peng Ni, Min Li

References


See Also

get_GOterm2GeneAssos, HypergeometricTest

Examples

```r
## get a sample of disease-GO associations
data(d2go_sample)

##### the entire disease-GO associations can be obtained by follows:
## go2g<-get_GOterm2GeneAssos(GOONTOLOGY = "BP", geneid="SYMBOL") #get go-gene associations
## data(d2g_fundo_symbol)
## d2go<-HypergeometricTest(d2g = d2g_fundo_symbol,go2g = go2g)
##### ###################################################
ds<-names(d2go_sample)
Sun_function(ds ,ds, d2go_sample)
```
**Sun_topology**

Sun’s topology measure of disease similarity calculating

**Description**

given two vectors of diseases, a list of disease-gene associations, a matrix of genes’ graphlet signature in a PPI network and a weight vector of 73 orbits in graphlet theory, this function will calculate disease similarity by method Sun_function

**Usage**

Sun_topology(D1, D2, d2g, graphlet_sig_mat, weight)

**Arguments**

- **D1** a vector consists disease ids
- **D2** another vector consists disease ids
- **d2g** a list of disease-gene associations
- **graphlet_sig_mat** matrix of graphlet signature of nodes in a ppi network calculated by orca, see examples below.
- **weight** a vector which elements are weight factors to each orbit in graphlet theory

**Value**

a disease disease similarity matrix

**Author(s)**

Peng Ni, Min Li

**References**


**Examples**

data(d2g_fundo_symbol)
data(graphlet_sig_hprd) #get graphlet signatures of genes in HPRD PPI network
data(weight)
dsc<-sample(names(d2g_fundo_symbol),5)
Sun_topology(ds,ds,d2g_fundo_symbol,graphlet_sig_hprd,weight)
weight

Description
weight factor

Value
weight is a 73-dim vector, indicating 73 orbits’ weight factor, will be used in method Sun_topology.

References

See Also
setWeight, Sun_topology

Examples
data(weight)

x2y_conv2_y2x

Description
convert list of x-y associations to list of y-x associations

Usage
x2y_conv2_y2x(x2ylist)

Arguments
x2ylist a list which the names are xs and the elements are ys of each x

Value
a list of y2x

Author(s)
Peng Ni, Min Li

Examples
data(go2g_sample)
g2go_sample<-x2y_conv2_y2x(go2g_sample[1:100])
Description
convert x-y associations (e.g. disease-gene associations) from data.frame to list

Usage
x2y_df2list(x2ydf, xcol = 1, ycol = 2)

Arguments
- x2ydf: data.frame of x-y associations
- xcol: col of x in x2ydf
- ycol: col of y in x2ydf

Value
a list of x-y associations

Author(s)
Peng Ni, Min Li

Examples
options(stringsAsFactors = FALSE)
d2g_fundo_sample<-read.table(text = "DOID:5218  IL6
DOID:8649  EGFR
DOID:8649  PTGS2
DOID:8649  VHL
DOID:8649  ERBB2
DOID:8649  PDCD1
DOID:8649  KLRC1
DOID:5214  MPZ
DOID:5214  EGR2
DOID:5210  AMH")
d2g_fundo_list<-x2y_df2list(d2g_fundo_sample)
Index

*Topic dataset
  - d2g_fundo_entrezid, 5
  - d2g_fundo_symbol, 6
  - d2g_separation, 6
  - d2go_sample, 5
  - d2s_hsdn, 7
  - d2s_hsdn_sample, 7
  - go2g_sample, 10
  - graphlet_sig_hprd, 10
  - HumanNet_sample, 11
  - interactome, 14
  - orbit_dependency_count, 16
  - PPI_HPRD, 21
  - weight, 28

*Topic package
  - dSimer-package, 2
  - BOG, 3
  - CosineDFV, 4, 7
  - d2g_fundo_entrezid, 5
  - d2g_fundo_symbol, 6
  - d2g_separation, 6
  - d2go_sample, 5
  - d2s_hsdn, 7, 7
  - d2s_hsdn_sample, 7
  - dSimer (dSimer-package), 2
  - dSimer-package, 2
  - FunSim, 8, 11, 15
  - get_GOterm2GeneAssos, 9, 10, 12, 22, 26
  - go2g_sample, 10
  - graphlet_sig_hprd, 10
  - HumanNet_sample, 11
  - HypergeometricTest, 5, 11, 22, 26
  - ICod, 12
  - InformationContent, 13
  - interactome, 14
  - jaccardindex, 14
  - LLSn2List, 8, 11, 15
  - Normalize, 3, 16, 22
  - orbit_dependency_count, 16
  - plot_bipartite, 17
  - plot_heatmap, 18
  - plot_net, 19
  - plot_topo, 20
  - PPI_HPRD, 21
  - PSB, 9, 12, 22
  - Separation, 23, 24
  - Separation2Similarity, 23, 24
  - setWeight, 17, 24, 28
  - Sun_annotation, 25
  - Sun_function, 9, 12, 26
  - Sun_topology, 10, 27, 28
  - weight, 28
  - x2y_conv2_y2x, 28
  - x2y_df2list, 29