

Package ‘GOSemSim’

October 16, 2022

Type Package

Title GO-terms Semantic Similarity Measures

Version 2.22.0

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Description The semantic comparisons of Gene Ontology (GO) annotations provide quantitative ways to compute similarities between genes and gene groups, and have become important basis for many bioinformatics analysis approaches. GOSemSim is an R package for semantic similarity computation among GO terms, sets of GO terms, gene products and gene clusters. GOSemSim implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively.

Depends R (>= 3.5.0)

LinkingTo Rcpp

Imports AnnotationDbi, GO.db, methods, utils

Suggests AnnotationHub, BiocManager, clusterProfiler, DOSE, knitr, rmarkdown, org.Hs.eg.db, prettydoc, testthat, ROCR

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

Encoding UTF-8

URL <https://yulab-smu.top/biomedical-knowledge-mining-book/>

BugReports <https://github.com/YuLab-SMU/GOSemSim/issues>

biocViews Annotation, GO, Clustering, Pathways, Network, Software

RoxygenNote 7.1.2

git_url <https://git.bioconductor.org/packages/GOSemSim>

git_branch RELEASE_3_15

git_last_commit fd74aeb

git_last_commit_date 2022-04-26

Date/Publication 2022-10-16

Author Guangchuang Yu [aut, cre],
 Alexey Stukalov [ctb],
 Pingfan Guo [ctb],
 Chuanle Xiao [ctb],
 Lluís Revilla Sancho [ctb]

R topics documented:

GOSemSim-package	2
clusterSim	3
combineScores	4
geneSim	5
godata	6
GOSemSimDATA-class	7
goSim	7
go_term_table	8
infoContentMethod	8
load_OrgDb	9
mclusterSim	9
mgeneSim	10
mgoSim	12
tcss_cutoff	13
termSim	14
wangMethod_internal	15
Index	16

GOSemSim-package

Gene Ontology-based Sematic Similarity Measures

Description

Implementation of semantic similarity measures to estimate the functional similarities among Gene Ontology terms and gene products

Details

Quantitative measure of functional similarities among gene products is important for post-genomics study. and widely used in gene function prediction, cluster analysis and pathway modeling. This package is designed to estimate the GO terms' and genes' semantic similarities. Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively. Support many species, including Anopheles, Arabidopsis, Bovine, Canine, Chicken, Chimp, E coli strain K12 and strain Sakai, Fly, Human, Malaria, Mouse, Pig, Rhesus, Rat, Worm, Xenopus, Yeast, Zebrafish.

Package: GOSemSim
 Type: Package
 Version: 2.0.0

Date: 09-11-2012
biocViews: GO, Clustering, Pathways, Anopheles_gambiae, Arabidopsis_thaliana, Bos_taurus, Caenorhabditis_elegans, Ca
Depends:
Imports: methods, AnnotationDbi, GO.db
Suggests: clusterProfiler, DOSE
License: Artistic-2.0

Author(s)

Guangchuang Yu

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803
<http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

See Also

[goSim](#) [mgoSim](#) [geneSim](#) [mgeneSim](#) [clusterSim](#) [mclusterSim](#)

clusterSim

Semantic Similarity Between Two Gene Clusters

Description

Given two gene clusters, this function calculates semantic similarity between them.

Usage

```
clusterSim(  
  cluster1,  
  cluster2,  
  semData,  
  measure = "Wang",  
  drop = "IEA",  
  combine = "BMA"  
)
```

Arguments

cluster1 A set of gene IDs.
cluster2 Another set of gene IDs.
semData GOSemSimDATA object

measure	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
combine	One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins associated with protein cluster.

Value

similarity

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

See Also

[goSim](#) [mgoSim](#) [geneSim](#) [mgeneSim](#) [mclusterSim](#)

Examples

```
d <- godata('org.Hs.eg.db', ont="MF", computeIC=FALSE)
cluster1 <- c("835", "5261", "241", "994")
cluster2 <- c("307", "308", "317", "321", "506", "540", "378", "388", "396")
clusterSim(cluster1, cluster2, semData=d, measure="Wang")
```

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://guangchuangyu.github.io>

geneSim

Semantic Similarity Between two Genes

Description

Given two genes, this function will calculate the semantic similarity between them, and return their semantic similarity and the corresponding GO terms

Usage

```
geneSim(gene1, gene2, semData, measure = "Wang", drop = "IEA", combine = "BMA")
```

Arguments

gene1	Entrez gene id.
gene2	Another entrez gene id.
semData	GOSemSimDATA object
measure	One of "Resnik", "Lin", "Rel", "Jiang" "TCSS" and "Wang" methods.
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
combine	One of "max", "avg", "rmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins associated with protein cluster.

Value

list of similarity value and corresponding GO.

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

See Also

[goSim](#) [mgoSim](#) [mgeneSim](#) [clusterSim](#) [mclusterSim](#)

Examples

```
d <- godata('org.Hs.eg.db', ont="MF", computeIC=FALSE)
geneSim("241", "251", semData=d, measure="Wang")
```

godata	<i>godata</i>
--------	---------------

Description

prepare GO DATA for measuring semantic similarity

Usage

```
godata(  
  OrgDb = NULL,  
  keytype = "ENTREZID",  
  ont,  
  computeIC = TRUE,  
  processTCSS = FALSE,  
  cutoff = NULL  
)
```

Arguments

OrgDb	OrgDb object
keytype	keytype
ont	one of 'BP', 'MF', 'CC'
computeIC	logical, whether computer IC
processTCSS	logical, whether to process TCSS
cutoff	cutoff of TCSS

Value

GOSemSimDATA object

Author(s)

Guangchuang Yu

GOSemSimDATA-class	<i>Class "GOSemSimDATA" This class stores IC and gene to go mapping for semantic similarity measurement</i>
--------------------	---

Description

Class "GOSemSimDATA" This class stores IC and gene to go mapping for semantic similarity measurement

Slots

keys gene ID
 ont ontology
 IC IC data
 geneAnno gene to GO mapping
 tcssdata tcssdata
 metadata metadata

goSim	<i>Semantic Similarity Between Two GO Terms</i>
-------	---

Description

Given two GO IDs, this function calculates their semantic similarity.

Usage

```
goSim(GO1D1, GO1D2, semData, measure = "Wang")
```

Arguments

GO1D1	GO ID 1.
GO1D2	GO ID 2.
semData	GOSemSimDATA object
measure	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.

Value

similarity

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

See Also

[mgoSim](#) [geneSim](#) [mgeneSim](#) [clusterSim](#) [mclusterSim](#)

Examples

```
d <- godata('org.Hs.eg.db', ont="MF", computeIC=FALSE)
goSim("GO:0004022", "GO:0005515", semData=d, measure="Wang")
```

go_term_table

Information content of GO terms

Description

These datasets are the information contents of GOterms.

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

infoContentMethod

information content based methods

Description

Information Content Based Methods for semantic similarity measuring

Usage

```
infoContentMethod(ID1, ID2, method, godata)
```

Arguments

ID1	Ontology Term
ID2	Ontology Term
method	one of "Resnik", "Jiang", "Lin" and "Rel", "TCSS".
godata	GOSemSimDATA object

Details

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

Value

semantic similarity score

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

load_OrgDb

load_OrgDb

Description

load OrgDb

Usage

```
load_OrgDb(OrgDb)
```

Arguments

OrgDb OrgDb object or OrgDb name

Value

OrgDb object

Author(s)

Guangchuang Yu

mclusterSim

Pairwise Semantic Similarities for a List of Gene Clusters

Description

Given a list of gene clusters, this function calculates pairwise semantic similarities.

Usage

```
mclusterSim(clusters, semData, measure = "Wang", drop = "IEA", combine = "BMA")
```

Arguments

clusters	A list of gene clusters.
semData	GOSemSimDATA object
measure	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
combine	One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins associated with protein cluster.

Value

similarity matrix

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

See Also

[goSim](#) [mgoSim](#) [geneSim](#) [mgeneSim](#) [clusterSim](#)

Examples

```
d <- godata('org.Hs.eg.db', ont="MF", computeIC=FALSE)
cluster1 <- c("835", "5261", "241")
cluster2 <- c("578", "582")
cluster3 <- c("307", "308", "317")
clusters <- list(a=cluster1, b=cluster2, c=cluster3)
mclusterSim(clusters, semData=d, measure="Wang")
```

mgeneSim

Pairwise Semantic Similarity for a List of Genes

Description

Given a list of genes, this function calculates pairwise semantic similarities.

Usage

```
mGeneSim(  
  genes,  
  semData,  
  measure = "Wang",  
  drop = "IEA",  
  combine = "BMA",  
  verbose = TRUE  
)
```

Arguments

genes	A list of entrez gene IDs.
semData	GOSemSimDATA object
measure	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
combine	One of "max", "avg", "rmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins associated with protein cluster.
verbose	show progress bar or not.

Value

similarity matrix

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

See Also

[goSim](#) [mgoSim](#) [geneSim](#) [clusterSim](#) [mclusterSim](#)

Examples

```
d <- godata('org.Hs.eg.db', ont="MF", computeIC=FALSE)  
mGeneSim(c("835", "5261", "241"), semData=d, measure="Wang")
```

`mgoSim`*Semantic Similarity Between two GO terms lists*

Description

Given two GO term sets, this function will calculate the semantic similarity between them, and return their semantic similarity

Usage

```
mgoSim(GO1, GO2, semData, measure = "Wang", combine = "BMA")
```

Arguments

<code>GO1</code>	A set of go terms.
<code>GO2</code>	Another set of go terms.
<code>semData</code>	GOSemSimDATA object
<code>measure</code>	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.
<code>combine</code>	One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins associated with protein cluster.

Value

similarity

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products *Bioinformatics* (Oxford, England), 26:7 976–978, April 2010. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/26/7/976> PMID: 20179076

See Also

[goSim](#) [geneSim](#) [geneSim](#) [clusterSim](#) [mclusterSim](#)

Examples

```
d <- godata('org.Hs.eg.db', ont="MF", computeIC=FALSE)
go1 <- c("GO:0004022", "GO:0004024", "GO:0004023")
go2 <- c("GO:0009055", "GO:0020037")
mgoSim("GO:0003824", go2, semData=d, measure="Wang")
mgoSim(go1, go2, semData=d, measure="Wang")
```

tcss_cutoff	<i>determine the topological cutoff for TCSS method</i>
-------------	---

Description

determine the topological cutoff for TCSS method

Usage

```
tcss_cutoff(
  OrgDb = NULL,
  keytype = "ENTREZID",
  ont,
  combine_method = "max",
  ppidata
)
```

Arguments

OrgDb	OrgDb object
keytype	keytype
ont	ontology : "BP", "MF", "CC"
combine_method	"max", "BMA", "avg", "rcmax", "rcmax.avg"
ppidata	A data.frame contains positive set and negative set. Positive set is PPI pairs that already verified. ppidata has three columns, column 1 and 2 are character, column 3 must be logical value:TRUE/FALSE.

Value

numeric, topological cutoff for given parameters

Examples

```
## Not run:
library(org.Hs.eg.db)
library(STRINGdb)

string_db <- STRINGdb$new(version = "11.0", species = 9606,
  score_threshold = 700)
string_proteins <- string_db$get_proteins()

#get relationship
ppi <- string_db$get_interactions(string_proteins$protein_external_id)

ppi$from <- vapply(ppi$from, function(e)
  strsplit(e, "9606.")[[1]][2], character(1))
ppi$to <- vapply(ppi$to, function(e)
```

```

                                strsplit(e, "9606.")[[1]][2], character(1))
len <- nrow(ppi)

#select length
s_len <- 100
pos_1 <- sample(len, s_len, replace = T)
#negative set
pos_2 <- sample(len, s_len, replace = T)
pos_3 <- sample(len, s_len, replace = T)
#union as ppidata
ppidata <- data.frame(pro1 = c(ppi$from[pos_1], ppi$from[pos_2]),
  pro2 = c(ppi$to[pos_1], ppi$to[pos_3]),
  label = c(rep(TRUE, s_len), rep(FALSE, s_len)),
  stringsAsFactors = FALSE)

cutoff <- tcss_cutoff(OrgDb = org.Hs.eg.db, keytype = "ENSEMBLPROT",
  ont = "BP", combine_method = "max", ppidata)

## End(Not run)

```

termSim

termSim

Description

measuring similarities between two term vectors.

Usage

```

termSim(
  t1,
  t2,
  semData,
  method = c("Wang", "Resnik", "Rel", "Jiang", "Lin", "TCSS")
)

```

Arguments

t1	term vector
t2	term vector
semData	GOSemSimDATA object
method	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin", "TCSS".

Details

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

Value

score matrix

Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

wangMethod_internal *wangMethod*

Description

Method Wang for semantic similarity measuring

Usage

wangMethod_internal(ID1, ID2, ont = "BP")

Arguments

ID1	Ontology Term
ID2	Ontology Term
ont	Ontology

Value

semantic similarity score

Author(s)

Guangchuang Yu <http://ygc.name>

Index

- * **classes**
 - GOSemSimDATA-class, 7
- * **datasets**
 - go_term_table, 8
- * **manip**
 - clusterSim, 3
 - geneSim, 5
 - goSim, 7
 - mclusterSim, 9
 - mgeneSim, 10
 - mgoSim, 12
- * **package**
 - GOSemSim-package, 2

clusterSim, 3, 3, 5, 8, 10–12

combineScores, 4

geneSim, 3, 4, 5, 8, 10–12

GO (go_term_table), 8

go_term_table, 8

godata, 6

GOSemSim (GOSemSim-package), 2

GOSemSim-package, 2

GOSemSimDATA-class, 7

goSim, 3–5, 7, 10–12

gotbl (go_term_table), 8

infoContentMethod, 8

load_OrgDb, 9

mclusterSim, 3–5, 8, 9, 11, 12

mgeneSim, 3–5, 8, 10, 10, 12

mgoSim, 3–5, 8, 10, 11, 12

show, GOSemSimDATA-method
(GOSemSimDATA-class), 7

tcss_cutoff, 13

termSim, 14

wangMethod_internal, 15