

Package ‘GOSemSim’

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Type Package

Title GO-terms Semantic Similarity Measures

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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.

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

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

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GOSemSim-package	<i>GOSemSim: GO-terms Semantic Similarity Measures</i>
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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.

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See Also

Useful links:

- <https://yulab-smu.top/biomedical-knowledge-mining-book/>
- Report bugs at <https://github.com/YuLab-SMU/GOSemSim/issues>

buildGOMap

buildGOMap

Description

Adding indirect GO annotation

Usage

```
buildGOMap(TERM2GENE)
```

Arguments

TERM2GENE	data.frame with two or three columns of GO TERM, GENE and ONTOLOGY (optional)
-----------	---

Details

provided by a data.frame of GO TERM (column 1), GENE (column 2) and ONTOLOGY (optional) that describes GO direct annotation, this function will add indirect GO annotation of genes.

Value

data.frame, GO annotation with direct and indirect annotation

Author(s)

Yu Guangchuang

`clusterSim`*Semantic similarity between two gene clusters*

Description

Given two gene clusters, calculate their semantic similarity.

Usage

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

Arguments

<code>cluster1</code>	A set of gene IDs
<code>cluster2</code>	Another set of gene IDs
<code>semData</code>	GOSemSimDATA object
<code>measure</code>	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.
<code>drop</code>	Evidence codes to drop; use NULL to keep all GO annotations
<code>combine</code>	One of "max", "avg", "rcmax", "BMA" methods, used to combine multiple term scores.

Value

similarity

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. *Bioinformatics*, 26(7): 976–978. <https://academic.oup.com/bioinformatics/article/26/7/976/211914>

See Also

[goSim\(\)](#), [mgoSim\(\)](#), [geneSim\(\)](#), [mgeneSim\(\)](#), [clusterSim\(\)](#), [mclusterSim\(\)](#), [termSim\(\)](#)

Other similarity: [geneSim\(\)](#), [goSim\(\)](#), [mclusterSim\(\)](#), [mgeneSim\(\)](#), [mgoSim\(\)](#)

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	<i>combining similarity matrix to similarity score</i>
---------------	--

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	<i>Semantic similarity between two genes</i>
---------	--

Description

Given two genes, calculate their semantic similarity and return the score with 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	Evidence codes to drop; use NULL to keep all GO annotations
combine	One of "max", "avg", "rcmax", "BMA" methods, used to combine multiple term scores.

Value

A list containing similarity value and corresponding GO terms

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. *Bioinformatics*, 26(7): 976–978. <https://academic.oup.com/bioinformatics/article/26/7/976/211914>

See Also

`goSim()`, `mgoSim()`, `geneSim()`, `mgeneSim()`, `clusterSim()`, `mclusterSim()`, `termSim()`

Other similarity: `clusterSim()`, `goSim()`, `mclusterSim()`, `mgeneSim()`, `mgoSim()`

Examples

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

get_organism	<i>Get organism name from OrgDb object</i>
--------------	--

Description

Get organism name from OrgDb object

Usage

```
get_organism(object)
```

Arguments

object	OrgDb object or OrgDb package name
--------	------------------------------------

Value

Organism name

Author(s)

Guangchuang Yu

godata*godata*

Description

prepare GO DATA for measuring semantic similarity

Usage

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

Arguments

OrgDb	OrgDb object (will be removed in future, please use annoDb instead)
annoDb	GO annotation database, can be OrgDb or a data.frame contains three columns of 'GENE', 'GO' and 'ONTOLOGY'.
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, calculate 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*, 26(7): 976–978. <https://academic.oup.com/bioinformatics/article/26/7/976/211914>

See Also

`goSim()`, `mgoSim()`, `geneSim()`, `mgeneSim()`, `clusterSim()`, `mclusterSim()`, `termSim()`
Other similarity: `clusterSim()`, `geneSim()`, `mclusterSim()`, `mgeneSim()`, `mgoSim()`

Examples

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

go_term_table	<i>Information content of GO terms</i>
---------------	--

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	<i>information content based methods</i>
-------------------	--

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_onto	<i>Load Ontology Database</i>
-----------	-------------------------------

Description

Load Ontology Database

Usage

```
load_onto(onto = "HDO")
```

Arguments

onto character. The ontology to load (e.g., "HDO").

Value

An AnnotationDb object.

mclusterSim	<i>Pairwise semantic similarities for a list of gene clusters</i>
-------------	---

Description

Calculate pairwise semantic similarities for a list of gene clusters.

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	Evidence codes to drop; use NULL to keep all GO annotations
combine	One of "max", "avg", "rcmax", "BMA" methods, used to combine multiple term scores.

Value

similarity matrix

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. *Bioinformatics*, 26(7): 976–978. <https://academic.oup.com/bioinformatics/article/26/7/976/211914>

See Also

`goSim()`, `mgoSim()`, `geneSim()`, `mgeneSim()`, `clusterSim()`, `mclusterSim()`, `termSim()`

Other similarity: `clusterSim()`, `geneSim()`, `goSim()`, `mgeneSim()`, `mgoSim()`

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

Calculate pairwise semantic similarities for a given list of genes.

Usage

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

Arguments

<code>genes</code>	A list of Entrez gene IDs
<code>semData</code>	GOSemSimDATA object
<code>measure</code>	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.
<code>drop</code>	Evidence codes to drop; use NULL to keep all GO annotations

combine	One of "max", "avg", "rcmax", "BMA" methods, used to combine multiple term scores.
verbose	Whether to show a progress bar

Value

similarity matrix

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. Bioinformatics, 26(7): 976–978. <https://academic.oup.com/bioinformatics/article/26/7/976/211914>

See Also

[goSim\(\)](#), [mgoSim\(\)](#), [geneSim\(\)](#), [mgeneSim\(\)](#), [clusterSim\(\)](#), [mclusterSim\(\)](#), [termSim\(\)](#)
Other similarity: [clusterSim\(\)](#), [geneSim\(\)](#), [goSim\(\)](#), [mclusterSim\(\)](#), [mgoSim\(\)](#)

Examples

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

mgoSim	<i>Semantic similarity between two GO term sets</i>
--------	---

Description

Given two sets of GO terms, calculate their semantic similarity.

Usage

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

Arguments

GO1	A set of GO terms
GO2	Another set of GO terms
semData	GOSemSimDATA object
measure	One of "Resnik", "Lin", "Rel", "Jiang", "TCSS" and "Wang" methods.
combine	One of "max", "avg", "rcmax", "BMA" methods, used to combine multiple term scores.

Value

similarity

References

Yu et al. (2010) GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. Bioinformatics, 26(7): 976–978. <https://academic.oup.com/bioinformatics/article/26/7/976/211914>

See Also

`goSim()`, `mgoSim()`, `geneSim()`, `mgeneSim()`, `clusterSim()`, `mclusterSim()`, `termSim()`

Other similarity: `clusterSim()`, `geneSim()`, `goSim()`, `mclusterSim()`, `mgeneSim()`

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")
```

read.blast2go

read.blast2go

Description

given a BLAST2GO file, this function extracts the information from it and make it use for TERM2GENE.

Usage

```
read.blast2go(file, add_indirect_GO = FALSE)
```

Arguments

file	BLAST2GO file
add_indirect_GO	whether add indirect GO annotation

Value

a data frame with three columns: GENE, GO and ONTOLOGY

read.gaf	<i>read.gaf</i>
----------	-----------------

Description

parse GAF files

Usage

```
read.gaf(file, asis = FALSE, add_indirect_GO = FALSE)
```

```
parse_gff(file, asis = FALSE, add_indirect_GO = FALSE)
```

Arguments

file	GAF file
asis	logical, whether output the original contains of the file and only works if 'add_indirect_GO = FALSE'
add_indirect_GO	whether to add indirect GO annotation

Details

given a GAF file, this function extracts the information from it

Value

A data.frame. Original table if 'asis' works, otherwise contains 3 columns of 'GENE', 'GO' and 'ONTOLOGY'

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	<i>termSim</i>
---------	----------------

Description

Measure 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", "Lin", "TCSS"

Details

Provide two term vectors, this function calculates their similarities.

Value

score matrix

Author(s)

Guangchuang Yu <https://yulab-smu.top>

wangMethod_internal	<i>wangMethod</i>
---------------------	-------------------

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 <https://yulab-smu.top>

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