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 became 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)

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Suggests AnnotationHub, BiocManager, clusterProfiler, DOSE, knitr, org.Hs.eg.db, prettydoc, readr, rmarkdown, testthat, tidyr, tidyselect, 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

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Contents

`GOSemSim-package` *GOSemSim: GO-terms Semantic Similarity Measures*

Description

The semantic comparisons of Gene Ontology (GO) annotations provide quantitative ways to compute similarities between genes and gene groups, and have became 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.

Author(s)

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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

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`buildGOmap` *buildGOmap*

Description

Addding 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, 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 assiciated 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", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins assiciated 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 *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 *Class "GOSemSimDATA" This class stores IC and gene to go mapping for semantic similarity measurement*

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 *Semantic Similarity Between Two GO Terms*

Description

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

Usage

```
goSim(GOID1, GOID2, semData, measure = "Wang")
```

Arguments

GOID1	GO ID 1.
GOID2	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 assiciated 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", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins assiciated 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

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, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins assiciated 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 mgeneSim 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")
```

---

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 *read.gaf*

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 conlumns of 'GENE', 'GO' and 'ONTOLOGY'

tcss_cutoff *determine the topological cutoff for TCSS method*

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

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