

# Package: GOSemSim (via r-universe)

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**Type** Package

**Title** GO-terms Semantic Similarity Measures

**Version** 2.38.0

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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.

**Depends** R (>= 4.2.0)

**LinkingTo** Rcpp

**Imports** AnnotationDbi, DBI, digest, GO.db, methods, rlang, stats, utils, yulab.utils (>= 0.2.3)

**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>

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buildGMap

*buildGMap*

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## Description

Adding indirect GO annotation

## Usage

```
buildGMap(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

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clusterSim

*Semantic similarity between two gene clusters*

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**Description**

Semantic similarity between two gene clusters

**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	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

**Author(s)**

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

**See Also**

[goSim\(\)](#) [mgoSim\(\)](#) [geneSim\(\)](#) [mgeneSim\(\)](#) [clusterSim\(\)](#) [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")
```

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combineScores	<i>combining similarity matrix to similarity score</i>
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**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 <https://yulab-smu.top>

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geneSim	<i>Semantic similarity between two genes</i>
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**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

**Author(s)**

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

**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")
```

---

get_organism	<i>Get organism name from OrgDb object</i>
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**Description**

Get organism name from OrgDb object

**Usage**

```
get_organism(object)
```

**Arguments**

object	OrgDb object or OrgDb package name
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**Value**

Organism name

**Author(s)**

Guangchuang Yu

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

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

### 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

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

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**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

**Author(s)**

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

**See Also**

[goSim\(\)](#) [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")
```

---

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://yulab-smu.top>

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

**Author(s)**

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

**See Also**

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

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

### Value

similarity matrix

### Author(s)

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

### See Also

[goSim\(\)](#) [mgoSim\(\)](#) [geneSim\(\)](#) [mgeneSim\(\)](#) [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 term sets*

---

**Description**

Given two sets of GO terms, calculate 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, used to combine multiple term scores.

**Value**

similarity

**Author(s)**

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

**See Also**

[goSim\(\)](#) [mgoSim\(\)](#) [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	<i>read.blast2go</i>
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---

**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'

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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

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    *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 <https://yulab-smu.top>

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