

# Package ‘GOSemSim’

December 17, 2025

**Type** Package

**Title** GO-terms Semantic Similarity Measures

**Version** 2.37.1

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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)

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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

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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> |
|------------------|--------------------------------------------------------|

---

## 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.

## 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**

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**

|          |                                                                                    |
|----------|------------------------------------------------------------------------------------|
| 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

**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

*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>

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|         |                                              |
|---------|----------------------------------------------|
| 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

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

---

**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> |
|--------------------|-------------------------------------------------------------------------------------------------------------|

---

**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(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*, 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



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|                   |                                          |
|-------------------|------------------------------------------|
| 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

*Pairwise semantic similarities for a list of gene clusters***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**

|         |                                                                                    |
|---------|------------------------------------------------------------------------------------|
| genes   | A list of Entrez 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. |
| 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

*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**

|         |                                                                                    |
|---------|------------------------------------------------------------------------------------|
| 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 | <i>read.blast2go</i> |
|---------------|----------------------|

---

**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

*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 | <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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