

# Package ‘GOSemSim’

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**Type** Package

**Title** GO-terms Semantic Similarity Measures

**Version** 2.30.0

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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 (>= 3.5.0)

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

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## Contents

GOSemSim-package . . . . .	2
buildGOMap . . . . .	3
clusterSim . . . . .	4
combineScores . . . . .	5
geneSim . . . . .	5
godata . . . . .	6
GOSemSimDATA-class . . . . .	7
goSim . . . . .	8
go_term_table . . . . .	9
infoContentMethod . . . . .	9
load_OrgDb . . . . .	10
mclusterSim . . . . .	10
mgeneSim . . . . .	11
mgoSim . . . . .	12
read.blast2go . . . . .	13
read.gaf . . . . .	14
tcss_cutoff . . . . .	14
termSim . . . . .	16
wangMethod_internal . . . . .	16
<b>Index</b>	<b>18</b>

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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 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>

---

buildGMap

*buildGMap*

---

**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

---

`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

<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>	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
<code>combine</code>	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

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	<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>

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geneSim	<i>Semantic Similarity Between two Genes</i>
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**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

*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

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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`*Semantic Similarity Between Two GO Terms*

---

**Description**

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

**Usage**

```
goSim(GO1, GO2, semData, measure = "Wang")
```

**Arguments**

GO1	GO ID 1.
GO2	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	<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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infoContentMethod	<i>information content based methods</i>
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---

**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	<i>load_OrgDb</i>
------------	-------------------

---

**Description**

load OrgDb

**Usage**

```
load_OrgDb(OrgDb)
```

**Arguments**

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

**Value**

OrgDb object

**Author(s)**

Guangchuang Yu

---

mclusterSim	<i>Pairwise Semantic Similarities for a List of Gene Clusters</i>
-------------	---

---

**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", "rcmax", "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**

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 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](#) [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	<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**

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, [9](#)
- \* **internal**
  - GOSemSim-package, [2](#)
- \* **manip**
  - clusterSim, [4](#)
  - geneSim, [5](#)
  - goSim, [8](#)
  - mclusterSim, [10](#)
  - mgeneSim, [11](#)
  - mgoSim, [12](#)

[buildGOMap](#), [3](#)

[clusterSim](#), [4](#), [6](#), [8](#), [11–13](#)

[combineScores](#), [5](#)

[geneSim](#), [4](#), [5](#), [8](#), [11–13](#)

[GO](#) ([go\\_term\\_table](#)), [9](#)

[go\\_term\\_table](#), [9](#)

[godata](#), [6](#)

[GOSemSim](#) ([GOSemSim-package](#)), [2](#)

[GOSemSim-package](#), [2](#)

[GOSemSimDATA-class](#), [7](#)

[goSim](#), [4](#), [6](#), [8](#), [11–13](#)

[gotbl](#) ([go\\_term\\_table](#)), [9](#)

[infoContentMethod](#), [9](#)

[load\\_OrgDb](#), [10](#)

[mclusterSim](#), [4](#), [6](#), [8](#), [10](#), [12](#), [13](#)

[mgeneSim](#), [4](#), [6](#), [8](#), [11](#), [11](#), [13](#)

[mgoSim](#), [4](#), [6](#), [8](#), [11](#), [12](#), [12](#)

[parse\\_gff](#) ([read.gaf](#)), [14](#)

[read.blast2go](#), [13](#)

[read.gaf](#), [14](#)

[show](#), [GOSemSimDATA-method](#)  
([GOSemSimDATA-class](#)), [7](#)

[tcss\\_cutoff](#), [14](#)

[termSim](#), [16](#)

[wangMethod\\_internal](#), [16](#)