

# Package ‘GOSemSim’

October 16, 2019

**Type** Package

**Title** GO-terms Semantic Similarity Measures

**Version** 2.10.0

**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

**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 (>= 3.4.0)

**LinkingTo** Rcpp

**Imports** AnnotationDbi, GO.db, methods, utils

**Suggests** AnnotationHub, BiocManager, clusterProfiler, DOSE, knitr, org.Hs.eg.db, prettydoc, testthat

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**Encoding** UTF-8

**URL** <https://guangchuangyu.github.io/software/GOSemSim>

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

**biocViews** Annotation, GO, Clustering, Pathways, Network, Software

**RoxygenNote** 6.1.1

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GOSemSim-package	<i>Gene Ontology-based Semantic Similarity Measures</i>
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**Description**

Implementation of semantic similarity measures to estimate the functional similarities among Gene Ontology terms and gene products

**Details**

Quantitative measure of functional similarities among gene products is important for post-genomics study. and widely used in gene function prediction, cluster analysis and pathway modeling. This package is designed to estimate the GO terms' and genes' semantic similarities. Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively. Support many species, including Anopheles, Arabidopsis, Bovine, Canine, Chicken, Chimp, E coli strain K12 and strain Sakai, Fly, Human, Malaria, Mouse, Pig, Rhesus, Rat, Worm, Xenopus, Yeast, Zebrafish.

Package: GOSemSim  
 Type: Package  
 Version: 2.0.0  
 Date: 09-11-2012  
 biocViews: GO, Clustering, Pathways, Anopheles\_gambiae, Arabidopsis\_thaliana, Bos\_taurus, Caenorhabditis\_elegans  
 Depends:  
 Imports: methods, AnnotationDbi, GO.db  
 Suggests: clusterProfiler, DOSE  
 License: Artistic-2.0

**Author(s)**

Guangchuang Yu

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

**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](#) [mclusterSim](#)

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clusterSim

*Semantic Similarity Between Two Gene Clusters*

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**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" 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**

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")
```

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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 <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" 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**

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")
```

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godata

*godata*

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**Description**

prepare GO DATA for measuring semantic similarity

**Usage**

```
godata(OrgDb = NULL, keytype = "ENTREZID", ont, computeIC = TRUE)
```

**Arguments**

OrgDb	OrgDb object
keytype	keytype
ont	one of 'BP', 'MF', 'CC'
computeIC	logical, whether computer IC

**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  
 metadata metadata

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goSim	<i>Semantic Similarity Between Two GO Terms</i>
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**Description**

Given two GO IDs, this function calculates 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" 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")
```

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go\_term\_table

*Information content of GO terms*

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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

*information content based methods*

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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".
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>

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load\_OrgDb

*load\_OrgDb*

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**Description**

load OrgDb

**Usage**

```
load_OrgDb(OrgDb)
```

**Arguments**

OrgDb                      OrgDb object or OrgDb name

**Value**

OrgDb object

**Author(s)**

Guangchuang Yu

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mclusterSim

*Pairwise Semantic Similarities for a List of Gene Clusters*

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**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" 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*


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**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" 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" and "Wang" methods.
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

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")
```

---

termSim

*termSim*

---

## Description

measuring similarities between two term vectors.

## Usage

```
termSim(t1, t2, semData, method = c("Wang", "Resnik", "Rel", "Jiang",
  "Lin"))
```

## Arguments

t1	term vector
t2	term vector
semData	GOSemSimDATA object
method	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".

## Details

provide two term vectors, this function will calculate their similarities.

## Value

score matrix

## Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

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wangMethod\_internal    *wangMethod*

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**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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