

# Package ‘GOSemSim’

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**Type** Package

**Title** GO-terms Semantic Similarity Measures

**Version** 1.18.0

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**Description** Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for estimating GO semantic similarities. Support many species, including Anopheles, Arabidopsis, Bovine, Canine, Chicken, Chimp, Coelocolor, E coli strain K12 and Sakai, Fly, Human, Malaria, Mouse, Pig, Rhesus, Rat, Worm, Xenopus, Yeast, and Zebrafish.

**Depends** R (>= 2.10), Rcpp

**LinkingTo** Rcpp

**Imports** methods, AnnotationDbi, GO.db, org.Hs.eg.db

**Suggests** DOSE, clusterProfiler, BiocInstaller

**biocViews** GO, Clustering, Pathways, NetworkAnalysis

**Collate**

'clusterSim.R' 'combineMethods.R' 'computeIC.R' 'ICMethods.R' 'gene2GO.R' 'geneSim.R' 'goSim.R' 'termSim.R' 'WangSim.R' 'package.R' 'mGeneSim.R' 'mgoSim.R' 'mclusterSim.R'

**License** GPL-2

**URL** <http://bioinformatics.oxfordjournals.org/content/26/7/976.full>

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GOSemSim-package	<i>Gene Ontology-based Sematic 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  
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biocViews: GO, Clustering, Pathways, Anopheles\_gambiae, Arabidopsis\_thaliana, Bos\_taurus, Caenorhabditis\_elegans, Canine, Chicken, Chimp, E\_coli, Human, Malaria, Mouse, Pig, Rhesus, Rat, Worm, Xenopus, Yeast, Zebrafish  
Depends:  
Imports: methods, AnnotationDbi, GO.db, org.Hs.eg.db, org.Ag.eg.db, org.At.tair.db, org.Bt.eg.db, org.Ce.eg.db, org.Cf.eg.db, org.Dr.eg.db, org.Ec.eg.db, org.Gg.eg.db, org.Mm.eg.db, org.Rn.eg.db, org.Sc.eg.db, org.Xl.eg.db  
Suggests: clusterProfiler  
License: GPL Version 2

**Author(s)**

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**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](#)

clusterSim

*Semantic Similarity Between Two Gene Clusters***Description**

Given two gene clusters, this function calculates semantic similarity between them.

**Usage**

```
clusterSim(cluster1, cluster2, ont = "MF",
  organism = "human", measure = "Wang", drop = "IEA",
  combine = "BMA")
```

**Arguments**

cluster1	A set of gene IDs.
cluster2	Another set of gene IDs.
ont	One of "MF", "BP", and "CC" subontologies.
measure	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coeli-color", "ecolik12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
combine	One of "max", "average", "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](#) [mgoSim](#) [geneSim](#) [mgeneSim](#) [mclusterSim](#)

## Examples

```
## cluster1 <- c("835", "5261", "241", "994")
## cluster2 <- c("307", "308", "317", "321", "506", "540", "378", "388", "396")
## clusterSim(cluster1, cluster2, ont="MF", organism="human", measure="Wang")
```

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combineScores

*combining similarity matrix to similarity score*

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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://ygc.name>

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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, ont = "MF", organism = "human",
        measure = "Wang", drop = "IEA", combine = "BMA")
```

**Arguments**

gene1	Entrez gene id.
gene2	Another entrez gene id.
ont	One of "MF", "BP", and "CC" subontologies.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coeli-color", "ecolik12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
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", "average", "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**

```
geneSim("241", "251", ont="MF", organism="human", measure="Wang")
```

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goSim*Semantic Similarity Between Two GO Terms*

---

**Description**

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

**Usage**

```
goSim(GOID1, GOID2, ont = "MF", organism = "human",  
      measure = "Wang")
```

**Arguments**

GOID1	GO ID 1.
GOID2	GO ID 2.
ont	One of "MF", "BP", and "CC" subontologies.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coeli-color", "ecolik12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
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**

```
goSim("GO:0004022", "GO:0005515", ont="MF", measure="Wang")
```

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IC	<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, ont = "DO", method,
  organism = "human")
```

**Arguments**

ID1	Ontology Term
ID2	Ontology Term
ont	Ontology
method	one of "Resnik", "Jiang", "Lin" and "Rel".
organism	one of supported species

**Details**

implemented for methods proposed by Resnik, Jiang, Lin and Schlicker.

**Value**

semantic similarity score

**Author(s)**

Guangchuang Yu <http://ygc.name>

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loadICdata	<i>Load IC data</i>
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**Description**

Load Information Content data to DOSEnv environment

**Usage**

```
loadICdata(organism, ont)
```

**Arguments**

organism	"human"
ont	"DO"

**Value**

NULL

**Author(s)**

Guangchuang Yu <http://ygc.name>

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

Given a list of gene clusters, this function calculates pairwise semantic similarities.

**Usage**

```
mclusterSim(clusters, ont = "MF", organism = "human",
  measure = "Wang", drop = "IEA", combine = "BMA")
```

**Arguments**

clusters	A list of gene clusters.
ont	One of "MF", "BP", and "CC" subontologies.
measure	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coeliorcolor", "ecolik12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".



drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
combine	One of "max", "average", "rmax", "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

```
## cluster1 <- c("835", "5261", "241")
## cluster2 <- c("578", "582")
## cluster3 <- c("307", "308", "317")
## clusters <- list(a=cluster1, b=cluster2, c=cluster3)
## mclusterSim(clusters, ont="MF", organism="human", measure="Wang")
```

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mgeneSim

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*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, ont = "MF", organism = "human",
         measure = "Wang", drop = "IEA", combine = "BMA",
         verbose = TRUE)
```

## Arguments

genes	A list of entrez gene IDs.
ont	One of "MF", "BP", and "CC" subontologies.
measure	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.

organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coeli-color", "ecoli12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.
combine	One of "max", "average", "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

```
mgeneSim(c("835", "5261", "241"), ont="MF", organism="human", measure="Wang")
```

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mgoSim

*Semantic Similarity Between two GO terms lists*

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### Description

Given two GO term sets, this function will calculate the semantic similarity between them, and return their semantic similarity

### Usage

```
mgoSim(GO1, GO2, ont = "MF", organism = "human",
       measure = "Wang", combine = "BMA")
```

**Arguments**

GO1	A set of go terms.
GO2	Another set of go terms.
ont	One of "MF", "BP", and "CC" subontologies.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coel-color", "ecolik12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
measure	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
combine	One of "max", "average", "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**

```
go1 <- c("GO:0004022", "GO:0004024", "GO:0004023")
go2 <- c("GO:0009055", "GO:0020037")
mgoSim("GO:0003824", go2, measure="Wang")
mgoSim(go1, go2, ont="MF", organism="human", measure="Wang")
```

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termSim

termSim

---

**Description**

measuring similarities between two term vectors.

**Usage**

```
termSim(t1, t2, method = "Wang", organism = "human", ont)
```

**Arguments**

t1	term vector
t2	term vector
method	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".
organism	only "human" supported
ont	ontology

**Details**

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

**Value**

score matrix

**Author(s)**

Guangchuang Yu <http://ygc.name>

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wangMethod

*wangMethod*

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**Description**

Method Wang for semantic similarity measuring

**Usage**

```
wangMethod(ID1, ID2, ont)
```

**Arguments**

ID1	Ontology Term
ID2	Ontology Term
ont	Ontology

**Value**

semantic similarity score

**Author(s)**

Guangchuang Yu <http://ygc.name>

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