

# GOSemSim

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clusterSim	<i>Semantic Similarity Between Two Gene Clusters</i>
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### Description

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

### Usage

```
clusterSim(cluster1, cluster2, ont = "MF", organism="human", measure="Wang", dr
```

### 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 "human", "rat", "mouse", "fly" and "yeast".
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.

### Value

sim	Semantic Similarity.
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## References

Wang et al.(2007) A new method to measure the semantic similarity of go terms *Bioinformatics* (Oxford, England), 23:0 1274–81, May 2007. ISSN 1460-2059 <http://www.ncbi.nlm.nih.gov/pubmed/17344234> PMID: 17344234

P W Lord et al.(2003) Semantic similarity measures as tools for exploring the gene ontology *PacificSymposiumonBiocomputing* Pacific Symposium on Biocomputing, 2003:601-12, ISSN 1793-5091 <http://www.ncbi.nlm.nih.gov/pubmed/12603061> PMID: 12603061

## See Also

[goSim](#) [mgoSim](#) [geneSim](#) [mgeneSim](#) [\linke{mclusterSim}](#)

## Examples

```
cluster1 <- c("snR67", "snR40", "snR48", "snR17a", "snR8")
cluster2 <- c("YOR251C", "YPR137C-B", "YPR010C", "YPR072W")
clusterSim(cluster1, cluster2, ont="MF", organism="yeast", measure="Wang")
```

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geneSim

*Semantic Similarity Between two Genes*

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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
```

## Arguments

gene1	Entrez gene id.
gene2	Another entrez gene id.
ont	One of "MF", "BP", and "CC" subontologies.
organism	One of "human", "rat", "mouse", "fly" and "yeast".
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.

## Value

geneSim	Semantic similarity.
GO1	Corresponding GO terms for gene1.
GO2	Corresponding GO terms for gene2.

**References**

Wang et al.(2007) A new method to measure the semantic similarity of go terms *Bioinformatics* (Oxford, England), 23:0 1274–81, May 2007. ISSN 1460-2059 <http://www.ncbi.nlm.nih.gov/pubmed/17344234> PMID: 17344234

P W Lord et al.(2003) Semantic similarity measures as tools for exploring the gene ontology *PacificSymposiumonBiocomputing* Pacific Symposium on Biocomputing, 2003:601-12, ISSN 1793-5091 <http://www.ncbi.nlm.nih.gov/pubmed/12603061> PMID: 12603061

**See Also**

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

**Examples**

```
geneSim("241", "2561", ont="MF", organism="human", measure="Wang")
geneSim("snR18", "YPR062W", ont="MF", organism="yeast", measure="Wang")
```

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GOSemSim-package     *Gene Ontology-based Sematic Similarity Measures*

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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(Rel), Jiang, Lin and Wang respectively. Support five species: human, rat, mouse, fly, and yeast.

Package:	GOSemSim
Type:	Package
Version:	1.1.9
Date:	04-14-2009
biocViews:	GO, Clustering
Depends:	GO.db
Suggests:	Clustering, org.Hs.eg.db
License:	GPL Version 2

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**See Also**

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

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 goSim

*Semantic Similarity Between Two GO Terms*


---

**Description**

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

**Usage**

```
goSim(GO1D1, GO1D2, ont = "MF", organism="human", measure="Wang")
```

**Arguments**

GO1D1	GO ID 1.
GO1D2	GO ID 2.
ont	One of "MF", "BP", and "CC" subontologies.
organism	One of "human", "rat", "mouse", "fly" and "yeast".
measure	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.

**Value**

goSim            Semantic similarity.

**References**

Wang et al.(2007) A new method to measure the semantic similarity of go terms *Bioinformatics* (Oxford, England), 23:0 1274–81, May 2007. ISSN 1460-2059 <http://www.ncbi.nlm.nih.gov/pubmed/17344234> PMID: 17344234

P W Lord et al.(2003) Semantic similarity measures as tools for exploring the gene ontology *PacificSymposiumonBiocomputing* Pacific Symposium on Biocomputing, 2003:601-12, ISSN 1793-5091 <http://www.ncbi.nlm.nih.gov/pubmed/12603061> PMID: 12603061

**See Also**

[mgoSim](#) [geneSim](#) [genesim](#) [clusterSim](#) [mclusterSim](#)

**Examples**

```
goSim("GO:0043121", "GO:0019838", measure="Wang")
goSim("GO:0043121", "GO:0019838", ont="MF", organism="human", measure="Wang")
```

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 IC

*Information content of GO terms*


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**Description**

These datasets are the information contents of GOterms.

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

## 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 "human", "rat", "mouse", "fly" and "yeast".
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.

## Value

simmat A Matrix of Pairwise Semantic Similarities

## References

Wang et al.(2007) A new method to measure the semantic similarity of go terms *Bioinformatics* (Oxford, England), 23:0 1274–81, May 2007. ISSN 1460-2059 <http://www.ncbi.nlm.nih.gov/pubmed/17344234> PMID: 17344234

P W Lord et al.(2003) Semantic similarity measures as tools for exploring the gene ontology *PacificSymposiumonBiocomputing* Pacific Symposium on Biocomputing, 2003:601-12, ISSN 1793-5091 <http://www.ncbi.nlm.nih.gov/pubmed/12603061> PMID: 12603061

## See Also

[goSim](#) [mgoSim](#) [geneSim](#) [mgeneSim](#) [\linke{clusterSim}](#)

## Examples

```
cluster1 <- c("snR67", "snR40", "snR48", "snR17a", "snR8")
cluster2 <- c("YOR251C", "YPR137C-B", "YPR010C", "YPR072W")
cluster3 <- c("YNL133C", "YOL041C", "YOL018C", "YOR236W", "YOR179C", "YOR230W")
clusters <- list(a=cluster1, b=cluster2, c=cluster3)
mclusterSim(clusters, ont="MF", organism="yeast", measure="Wang")
```

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

### 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 "human", "rat", "mouse", "fly" and "yeast".
drop	A set of evidence codes based on which certain annotations are dropped. Use NULL to keep all GO annotations.

### Value

simMatrix A Matrix of Pairwise Semantic Similarities

### References

Wang et al.(2007) A new method to measure the semantic similarity of go terms *Bioinformatics* (Oxford, England), 23:0 1274–81, May 2007. ISSN 1460-2059 <http://www.ncbi.nlm.nih.gov/pubmed/17344234> PMID: 17344234

P W Lord et al.(2003) Semantic similarity measures as tools for exploring the gene ontology *PacificSymposiumonBiocomputing* Pacific Symposium on Biocomputing, 2003:601-12, ISSN 1793-5091 <http://www.ncbi.nlm.nih.gov/pubmed/12603061> PMID: 12603061

### See Also

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

### Examples

```
mgeneSim(c("835", "5261", "241", "994"), 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")
```

**Arguments**

<code>GO1</code>	A set of go terms.
<code>GO2</code>	Another set of go terms.
<code>ont</code>	One of "MF", "BP", and "CC" subontologies.
<code>organism</code>	One of "human", "rat", "mouse", "fly" and "yeast".
<code>measure</code>	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.

**Value**

`mgoSim` Semantic similarity.

**References**

Wang et al.(2007) A new method to measure the semantic similarity of go terms *Bioinformatics* (Oxford, England), 23:0 1274–81, May 2007. ISSN 1460-2059 <http://www.ncbi.nlm.nih.gov/pubmed/17344234> PMID: 17344234

P W Lord et al.(2003) Semantic similarity measures as tools for exploring the gene ontology *PacificSymposiumonBiocomputing* Pacific Symposium on Biocomputing, 2003:601-12, ISSN 1793-5091 <http://www.ncbi.nlm.nih.gov/pubmed/12603061> PMID: 12603061

**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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