Package 'GOSemSim'

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Type Package

Title GO-terms Semantic Similarity Measures

Version 1.26.0

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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, Coelicolor, E coli strain K12 and Sakai, Fly, Gondii, Human, Malaria, Mouse, Pig, Rhesus, Rat, Worm, Xenopus, Yeast, and Zebrafish.

Depends R (>= 3.1.0)

LinkingTo Rcpp

Imports Rcpp, AnnotationDbi, GO.db

Suggests DOSE, clusterProfiler, org.Hs.eg.db, knitr, BiocStyle, BiocInstaller

VignetteBuilder knitr

License Artistic-2.0

URL https://github.com/GuangchuangYu/GOSemSim

BugReports https://github.com/GuangchuangYu/GOSemSim/issues

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

NeedsCompilation yes

R topics documented:

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

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.

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Depends:	
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Suggests:	clusterProfiler
License:	Artistic-2.0

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

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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.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coelicolor", "ecolik12", "ecsakai", "fly", "gondii","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 assiciated 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*

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   *Semantic Similarity Between two Genes*

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", "gondii","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 assiciated 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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getDb	*getDb*

Description

mapping organism name to annotationDb package name

Usage

```
getDb(organism)
```

Arguments

organism	one of supported organism

Value

annotationDb name

Author(s)

Yu Guangchuang

---

getSupported_Org	*getSupported_Org*

Description

get supported organisms

Usage

```
getSupported_Org()
```

Value

supported organisms

Author(s)

Yu Guangchuang

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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", "coelicolor", "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")
```

IC   *Information content of GO terms*

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*

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>

`loadGOMap`	*loadGOMap*

Description

loading GOMap to GOSemSimEnv

Usage

```
loadGOMap(organism)
```

Arguments

`organism`	one of supported organisms

Value

envir

Author(s)

Yu Guangchuang

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loadICdata	*Load IC data*

Description

Load Information Content data to DOSEEnv environment

Usage

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

Arguments

organism	"human"
ont	"DO"

Author(s)

Guangchuang Yu <http://ygc.name>

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mclusterSim	*Pairwise Semantic Similarities for a List of Gene Clusters*

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.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coelicolor", "ecolik12", "ecsakai", "fly", "gondii","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 assiciated 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")
```

---

mgeneSim   *Pairwise Semantic Similarity for a List of Genes*

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.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coeli-color", "ecolik12", "ecsakai", "fly", "gondii","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 assiciated 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")
```

---

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, 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", "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.
combine	One of "max", "average", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple GO terms associated with protein or multiple proteins assiciated 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")
```

---

termSim   *termSim*

Description

measuring similarities between two term vectors.

Usage

```
termSim(t1, t2, method = c("Wang", "Resnik", "Rel", "Jiang", "Lin"),
  organism = "human", ont = "BP")
```

Arguments

t1	term vector
t2	term vector
method	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".
organism	about 20 species supported, please refer to the vignettes
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*

Description

Method Wang for semantic similarity measuring

Usage

```
wangMethod(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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