

Package ‘rrvgo’

August 5, 2022

Type Package

Title Reduce + Visualize GO

Version 1.9.1

Description Reduce and visualize lists of Gene Ontology terms by identifying redundancy based on semantic similarity.

URL <https://www.bioconductor.org/packages/rrvgo>,
<https://ssayols.github.io/rrvgo/index.html>

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Encoding UTF-8

Imports GOSemSim, AnnotationDbi, GO.db, pheatmap, ggplot2, ggrepel,
treemap, tm, wordcloud, shiny, grDevices, grid, stats, methods,
umap

Suggests knitr, rmarkdown, BiocStyle, testthat (>= 2.1.0),
shinydashboard, DT, plotly, heatmaply, magrittr, utils,
clusterProfiler, DOSE, slam, org.Ag.eg.db, org.At.tair.db,
org.Bt.eg.db, org.Ce.eg.db, org.Cf.eg.db, org.Dm.eg.db,
org.Dr.eg.db, org.EcK12.eg.db, org.EcSakai.eg.db, org.Gg.eg.db,
org.Hs.eg.db, org.Mm.eg.db, org.Mmu.eg.db, org.Pt.eg.db,
org.Rn.eg.db, org.Sc.sgd.db, org.Ss.eg.db, org.Xl.eg.db

VignetteBuilder knitr

RoxygenNote 7.2.0

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

NeedsCompilation no

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| | |
|--------------------|---|
| calculateSimMatrix | <i>calculateSimMatrix Calculate the score similarity matrix between terms</i> |
|--------------------|---|

Description

calculateSimMatrix Calculate the score similarity matrix between terms

Usage

```
calculateSimMatrix(
  x,
  orgdb,
  keytype = "ENTREZID",
  semdata = GOSemSim::godata(orgdb, ont = ont, keytype = keytype),
  ont = c("BP", "MF", "CC"),
  method = c("Resnik", "Lin", "Rel", "Jiang", "Wang")
)
```

Arguments

| | |
|---------|---|
| x | vector of GO terms |
| orgdb | one of org.* Bioconductor packages (the package name, or the package itself) |
| keytype | keytype passed to AnnotationDbi::keys to retrieve GO terms associated to gene ids in your orgdb |
| semdata | object with prepared GO DATA for measuring semantic similarity |
| ont | ontology. One of c("BP", "MF", "CC") |
| method | distance method. One of the supported methods by GOSemSim: c("Resnik", "Lin", "Rel", "Jiang", "Wang") |

Details

All similarity measures available are those implemented in the [GOSemSim package](https://www.bioconductor.org/packages/namely the Resnik, Lin, Relevance, Jiang and Wang methods. See the [Semantic Similarity Measurement Based on GO](https://www.bioconductor.org/packages/release/bioc/vignettes/GOSemSim/inst/doc/GOSemSim.html#similarity-measurement-based-on-go) section from the GOSemSim documentation for more details.

Value

a square matrix with similarity scores between terms

Examples

```
go_analysis <- read.delim(system.file("extdata/example.txt", package="rrvgo"))
simMatrix <- calculateSimMatrix(go_analysis$ID, orgdb="org.Hs.eg.db", ont="BP", method="Re1")
```

| | |
|-----------|--|
| getGoSize | <i>getGoSize</i> Get GO term size (# of genes) |
|-----------|--|

Description

getGoSize Get GO term size (# of genes)

Usage

```
getGoSize(terms, orgdb, keytype)
```

Arguments

| | |
|---------|---|
| terms | GO terms |
| orgdb | one of org.* Bioconductor packages (the package name, or the package itself) |
| keytype | keytype passed to AnnotationDbi::keys to retrieve GO terms associated to gene ids in your orgdb |

Value

number of genes associated with each term

| | |
|-----------|---|
| getGoTerm | <i>getGoTerm</i> Get the description of a GO term |
|-----------|---|

Description

getGoTerm Get the description of a GO term

Usage

```
getGoTerm(x)
```

Arguments

x GO terms

Value

the Term slot in GO.db::GOTERM[[x]]

| | |
|--------------|--|
| gg_color_hue | <i>gg_color_hue</i> Emulate ggplot2 color palette. |
|--------------|--|

Description

gg_color_hue Emulate ggplot2 color palette.

Usage

```
gg_color_hue(n)
```

Arguments

n number of colors

Details

It is just equally spaced hues around the color wheel, starting from 15:

Value

a vector with colors (alphanumeric)

Examples

```
## Not run:  
plot(1:10, pch=16, cex=2, col=gg_color_hue(10))  
  
## End(Not run)
```

| | |
|-------------|--|
| heatmapPlot | <i>heatmapPlot Plot similarity matrix as a heatmap</i> |
|-------------|--|

Description

heatmapPlot Plot similarity matrix as a heatmap

Usage

```
heatmapPlot(  
  simMatrix,  
  reducedTerms = NULL,  
  annotateParent = TRUE,  
  annotationLabel = "parentTerm",  
  ...  
)
```

Arguments

| | |
|-----------------|--|
| simMatrix | a (square) similarity matrix. |
| reducedTerms | a data.frame with the reduced terms from reduceSimMatrix() |
| annotateParent | whether to add annotation of the parent |
| annotationLabel | display "parent" ids or "parentTerm" string |
| ... | other parameters sent to pheatmap::pheatmap() |

Details

Matrix with similarity scores between terms is represented as a heatmap.

Value

Invisibly a pheatmap object that is a list with components

Examples

```
go_analysis <- read.delim(system.file("extdata/example.txt", package="rrvgo"))  
simMatrix <- calculateSimMatrix(go_analysis$ID, orgdb="org.Hs.eg.db", ont="BP", method="Rel")  
scores <- setNames(-log10(go_analysis$qvalue), go_analysis$ID)  
reducedTerms <- reduceSimMatrix(simMatrix, scores, threshold=0.7, orgdb="org.Hs.eg.db")  
heatmapPlot(simMatrix, reducedTerms, annotateParent=TRUE, annotationLabel="parentTerm", fontsize=6)
```

| | |
|-----------|---------------------------------------|
| loadOrgdb | <i>loadOrgdb Load an orgdb object</i> |
|-----------|---------------------------------------|

Description

loadOrgdb Load an orgdb object

Usage

```
loadOrgdb(orgdb)
```

Arguments

orgdb one of org.* Bioconductor packages

Value

the loaded orgdb

| | |
|-----------------|--|
| reduceSimMatrix | <i>reduceSimMatrix Reduce a set of GO terms based on their semantic similarity and scores.</i> |
|-----------------|--|

Description

reduceSimMatrix Reduce a set of GO terms based on their semantic similarity and scores.

Usage

```
reduceSimMatrix(
  simMatrix,
  scores = NULL,
  threshold = 0.7,
  orgdb,
  keytype = "ENTREZID"
)
```

Arguments

simMatrix a (square) similarity matrix

scores *named* vector with scores (weights) assigned to each term. Higher is better. Can be NULL (default, means no scores. In this case, a default score based on set size is assigned, thus favoring larger sets). Note: if you have p-values as scores, consider $-1 \cdot \log$ -transforming them ($-\log(p)$)

| | |
|-----------|---|
| threshold | similarity threshold (0-1). Some guidance: Large (allowed similarity=0.9), Medium (0.7), Small (0.5), Tiny (0.4) Defaults to Medium (0.7) |
| orgdb | one of org.* Bioconductor packages (the package name, or the orgdb object itself) |
| keytype | keytype passed to AnnotationDbi::keys to retrieve GO terms associated to gene ids in your orgdb |

Details

Currently, rrvgo uses the similarity between pairs of terms to compute a distance matrix, defined as $(1 - \text{simMatrix})$. The terms are then hierarchically clustered using complete linkage, and the tree is cut at the desired threshold, picking the term with the highest score as the representative of each group.

Therefore, higher thresholds lead to fewer groups, and the threshold should be read as the expected similarity of terms within a group (though this is not entirely correct, and you'll see similarities below this threshold being put in the same group).

Value

a data.frame with all terms and it's "reducer" (NA if the term was not reduced)

Examples

```
go_analysis <- read.delim(system.file("extdata/example.txt", package="rrvgo"))
simMatrix <- calculateSimMatrix(go_analysis$ID, orgdb="org.Hs.eg.db", ont="BP", method="Rel")
scores <- setNames(-log10(go_analysis$qvalue), go_analysis$ID)
reducedTerms <- reduceSimMatrix(simMatrix, scores, threshold=0.7, orgdb="org.Hs.eg.db")
```

| | |
|-------------|---|
| scatterPlot | <i>scatterPlot Plot GO terms as scattered points.</i> |
|-------------|---|

Description

scatterPlot Plot GO terms as scattered points.

Usage

```
scatterPlot(
  simMatrix,
  reducedTerms,
  algorithm = c("pca", "umap"),
  onlyParents = FALSE,
  size = "score",
  addLabel = TRUE,
  labelSize = 3
)
```

Arguments

| | |
|---------------------------|--|
| <code>simMatrix</code> | a (square) similarity matrix. |
| <code>reducedTerms</code> | a data.frame with the reduced terms from <code>reduceSimMatrix()</code> |
| <code>algorithm</code> | algorithm for dimensionality reduction. Either <code>pca</code> or <code>umap</code> . |
| <code>onlyParents</code> | plot only parent terms. Point size is the number of aggregated terms under the parent. |
| <code>size</code> | what to use as point size. Can be either GO term's "size" or "score". |
| <code>addLabel</code> | add labels with the most representative term of the group. |
| <code>labelSize</code> | text size in the label. |

Details

Distances between points represent the similarity between terms. Axes are the first 2 components of applying one of this dimensionality reduction algorithms: - a PCoA to the (di)similarity matrix. - a UMAP (Uniform Manifold Approximation and Projection,[1]) Size of the point represents the provided scores or, in its absence, the number of genes the GO term contains.

Value

ggplot2 object ready to be printed (or manipulated)

References

[1] Konopka T (2022). `_umap: Uniform Manifold Approximation and Projection_`. R package version 0.2.8.0, <https://CRAN.R-project.org/package=umap>.

Examples

```
go_analysis <- read.delim(system.file("extdata/example.txt", package="rrvgo"))
simMatrix <- calculateSimMatrix(go_analysis$ID, orgdb="org.Hs.eg.db", ont="BP", method="Rel")
scores <- setNames(-log10(go_analysis$qvalue), go_analysis$ID)
reducedTerms <- reduceSimMatrix(simMatrix, scores, threshold=0.7, orgdb="org.Hs.eg.db")
scatterPlot(simMatrix, reducedTerms)
```

shiny_rrvgo

shiny_rrvgo Launch an interactive web interface.

Description

shiny_rrvgo Launch an interactive web interface.

Usage

```
shiny_rrvgo(...)
```

Arguments

... other params sent to shiny::runApp().

Value

Nothing

treemapPlot *treemapPlot* Plot GO terms as a treemap.

Description

treemapPlot Plot GO terms as a treemap.

Usage

```
treemapPlot(reducedTerms, size = "score", title = "", ...)
```

Arguments

reducedTerms a data.frame with the reduced terms from reduceSimMatrix()
size what to use as point size. Can be either GO term's "size" or "score"
title title of the plot. Defaults to nothing
... other parameters sent to treemap::treemap()

Value

A list from the call to the 'treemap()' function is silently returned

Examples

```
## Not run:  
go_analysis <- read.delim(system.file("extdata/example.txt", package="rrvgo"))  
simMatrix <- calculateSimMatrix(go_analysis$ID, orgdb="org.Hs.eg.db", ont="BP", method="Rel")  
scores <- setNames(-log10(go_analysis$qvalue), go_analysis$ID)  
reducedTerms <- reduceSimMatrix(simMatrix, scores, threshold=0.7, orgdb="org.Hs.eg.db")  
treemapPlot(reducedTerms)  
  
## End(Not run)
```

| | |
|---------------|--|
| wordcloudPlot | <i>wordcloudPlot Plot GO reduced terms as a wordcloud.</i> |
|---------------|--|

Description

wordcloudPlot Plot GO reduced terms as a wordcloud.

Usage

```
wordcloudPlot(reducedTerms, onlyParents = TRUE, ...)
```

Arguments

| | |
|--------------|---|
| reducedTerms | a data.frame with the reduced terms from reduceSimMatrix(). |
| onlyParents | use only parent terms to calculate frequencies. |
| ... | other parameters sent to wordcloud::wordcloud() |

Value

Nothing

Examples

```
go_analysis <- read.delim(system.file("extdata/example.txt", package="rrvgo"))
simMatrix <- calculateSimMatrix(go_analysis$ID, orgdb="org.Hs.eg.db", ont="BP", method="Re1")
scores <- setNames(-log10(go_analysis$qvalue), go_analysis$ID)
reducedTerms <- reduceSimMatrix(simMatrix, scores, threshold=0.7, orgdb="org.Hs.eg.db")
wordcloudPlot(reducedTerms, min.freq=1, colors="black")
```

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