Package 'rrvgo'

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Type Package

Title Reduce + Visualize GO

Version 1.24.0

Description Reduce and visualize lists of Gene Ontology terms by identifying redudance 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

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`calculateSimMatrix` *calculateSimMatrix Calculate the score similarity matrix between terms*

Description

calculateSimMatrix Calculate the score similarity matrix between terms

Usage

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

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")
include_terms_without_IC	whether to include terms for which there's no Information Content in OrgDb. NOTE: Including them can mess up with the algorithm that aggregates the distances. Default: FALSE.

Details

All similarity measures available are those implemented in the [GOSemSim package](https://www.bioconductor.org/package
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.htm
similarity-measurement-based-on-go) section from the GOSeSim 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="Rel")
```

---

getGoSize *getGoSize Get GO term size (# of genes)*

Description

getGoSize Get GO term size (# of genes)

Usage

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

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
children	include genes in children terms (based on relationships in the GO DAG hierarchy)

Value

number of genes associated with each term

---

getGoTerm *getGoTerm 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]]

---

getTermDisp *getTermDisp Calculate the term dispensability score, defined as the semantic similarity threshold a term was assigned to a cluster (namely, the similarity of a term to the cluster representative term).*

Description

getTermDisp Calculate the term dispensability score, defined as the semantic similarity threshold a term was assigned to a cluster (namely, the similarity of a term to the cluster representative term).

Usage

```
getTermDisp(simMatrix, cluster, clusterRep)
```

Arguments

simMatrix	a (square) similarity matrix
cluster	the cluster assignment for each term
clusterRep	the cluster representative term

Value

a vector of term dispensability scores

---

getTermUniq *getTermUniq Calculate the term uniqueness score, defined as 1 minus the average semantic similarity of a term to all other terms.*

Description

getTermUniq Calculate the term uniqueness score, defined as 1 minus the average semantic similarity of a term to all other terms.

Usage

```
getTermUniq(simMatrix, cluster = NULL)
```

Arguments

simMatrix	a (square) similarity matrix
cluster	vector with the cluster each entry in the simMatrix belongs to. If NULL, a

Value

a vector of term uniqueness scores

---

gg_color_hue *gg_color_hue 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` *heatmapPlot Plot similarity matrix as a heatmap*

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` *loadOrgdb Load an orgdb object*

Description

loadOrgdb Load an orgdb object

Usage

```
loadOrgdb(orgdb)
```

Arguments

`orgdb`	one of org.* Bioconductor packages

Value

the loaded orgdb

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

Description

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

Usage

```
reduceSimMatrix(
  simMatrix,
  scores = c("uniqueness", "size"),
  threshold = 0.7,
  orgdb,
  keytype = "ENTREZID",
  children = TRUE
)
```

Arguments

simMatrix	a (square) similarity matrix
scores	one of c("uniqueness", "size"), or a *named* vector with scores provided for each term, where higher values favor choosing the term as the cluster representative. The default "uniqueness" uses a score reflecting how unique the term is. Note: if you like to use p-values as scores, consider -1*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
children	when retrieving GO term size, include genes in children terms. (based on relationships in the GO DAG hierarchy). Defaults to TRUE

Details

Group terms which are at least within a similarity below ‘threshold‘. Decide which term remains based on a score. If no score is provided, then decide based on the "uniqueness" or the term "size".

Currently, rrvgo uses the similarity between pairs of terms to compute a distance matrix, defined as (1-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 minimum similarity between group representatives.

Value

a data.frame identifying the different clusters of terms, the parent term representing the cluster, and some metrics of importance describing how unique and dispensable a term is.

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 *scatterPlot Plot GO terms as scattered points.*

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

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

Description

wordlcoudPlot 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$ID, orgdb="org.Hs.eg.db", ont="BP", method="Rel")
scores <- setNames(-log10(go_analysis$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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