Package ‘rrvgo’

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Type Package
Title Reduce + Visualize GO
Version 1.16.0
Description Reduce and visualize lists of Gene Ontology terms by identifying redundancy based on semantic similarity.
URL https://www.bioconductor.org/packages/rrvgo,
License GPL-3
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, orig.Pt.eg.db,
org.Rn.eg.db, org.Sc.sgd.db, org.Ss.eg.db, org.Xl.eg.db
VignetteBuilder knitr
RoxygenNote 7.2.3
biocViews Annotation, Clustering, GO, Network, Pathways, Software
NeedsCompilation no
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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(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/release/bioc/html/GOSemSim.html), 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#semantic-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="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

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

Description
gTermDisp 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
gTermDisp(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**

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

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**gg_color_hue**

Emulate ggplot2 color palette.

**Description**

**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

Description
loadOrgdb Load an orgdb object

Usage
loadOrgdb(orgdb)

Arguments
orgdb one of org.* Bioconductor packages

Value
the loaded orgdb

reduceSimMatrix

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)")
scatterPlot 

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(simMatrix, reducedTerms, algorithm = c("pca", "umap"), onlyParents = FALSE)

Description

scatterPlot Plot GO terms as scattered points.

Usage

scatterPlot(simMatrix, reducedTerms, algorithm = c("pca", "umap"), onlyParents = FALSE)
```r
scatterPlot

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


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)
```
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

```r
# 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 **Plot GO reduced terms as a wordcloud.**

Description

wordcloudPlot Plot GO reduced terms as a wordcloud.

Usage

```r
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

```r
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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