Package ‘GoMiner’

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Title Automate the Mapping Between a List of Genes and Gene Ontology Categories

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Depends R (>= 4.2.0)

Imports minimalistGODB, HGNChelper, randomGODB, stats, gplots, grDevices, utils, vprint

LazyData true

LazyDataCompression xz

Description In gene-expression microarray studies, for example, one generally obtains a list of dozens or hundreds of genes that differ in expression between samples and then asks 'What does all of this mean biologically?' Alternatively, gene lists can be derived conceptually in addition to experimentally. For instance, one might want to analyze a group of genes known as housekeeping genes. The work of the Gene Ontology (GO) Consortium <geneontology.org> provides a way to address that question. GO organizes genes into hierarchical categories based on biological process, molecular function and subcellular localization. The role of 'GoMiner' is to automate the mapping between a list of genes and GO, and to provide a statistical summary of the results as well as a visualization.

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Encoding UTF-8

VignetteBuilder knitr

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

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Contents

`checkGeneListVsDB` *checkGeneListVsDB*

Description

determine if gene list and database contain compatible identifiers

Usage

```
checkGeneListVsDB(geneList, ontology, GOGOA3, thresh = 0.5, verbose = FALSE)
```

Arguments

`geneList`	character list of gene names
`ontology`	character string c("molecular_function", "cellular_component", "biological_process")
`GOGOA3`	return value of subsetGOGOA()
`thresh`	numeric acceptance threshold for fraction of gene list matching database identifiers
`verbose`	integer vector representing classes

Value

returns no value, but may have side effect of aborting the computation

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
checkGeneListVsDB(geneList=cluster52,ontology="biological_process",
 GOGOA3,thresh=0.5,verbose=TRUE)

# supposed to generate error message
load("/Users/barryzeeberg/personal/GODB_RDATA/sgd/GOGOA3_sgd.RData")
checkGeneListVsDB(geneList=xenopusGenes,ontology="biological_process",
 GOGOA3,thresh=0.5,verbose=TRUE)

## End(Not run)
```

`cluster52` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(cluster52)
```

`FDR` *FDR*

Description

compute the false discovery rate (FDR) of the hypergeometric p values of genes mapping to gene ontology (GO) categories

Usage

```
FDR(sampleList, tablePop3, hyper, GOGOA3, nrand, ontology, subd, opt = 0)
```

Arguments

`sampleList`	character vector of user-supplied genes of interest
`tablePop3`	return value of GOtable3()
`hyper`	return value of GOhypergeometric3()
`GOGOA3`	return value of subsetGOGOA()
`nrand`	integer number of randomizations
`ontology`	c("molecular_function","cellular_component","biological_process")
`subd`	character string pathname for directory containing sink.txt
`opt`	integer 0:1 parameter used to determine randomization method

Value

returns a list with FDR information

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
fdr<-FDR(x_sampleList1,x_tablePop31,x_hyper1,GOGOA3,3,"biological_process",tempdir(),0)

## End(Not run)
```

`GOenrich3` *GOenrich3*

Description

compute the gene enrichment in a GO category

Usage

```
GOenrich3(tableSample3, tablePop3)
```

Arguments

`tableSample3`	sample return value of GOtable3()
`tablePop3`	population return value of GOtable3()

Value

returns a matrix with columns c("SAMPLE","POP","ENRICHMENT")

Examples

```
m<-GOenrich3(x_tableSample3,x_tablePop3)
```

`GOGOA3small` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(GOGOA3small)
```

`GOheatmap` *GOheatmap*

Description

generate a matrix to be used as input to a heat map

Usage

```
GOheatmap(sampleList, x, thresh, fdrThresh = 0.105, verbose)
```

Arguments

`sampleList`	character list of gene names
`x`	DB component of return value of GOtable3()
`thresh`	output of GOthresh()
`fdrThresh`	numeric value of FDR acceptance threshold
`verbose`	integer vector representing classes

Value

returns a matrix to be used as input to a heat map

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
heatmap<-GOheatmap(cluster52,GOGOA3$ontologies[["biological_process"]],x_thresh,verbose=1)

## End(Not run)
```

`GOhypergeometric3` *GOhypergeometric*

Description

compute the hypergeometric p value for gene enrichment in a GO category

Usage

```
GOhypergeometric3(tableSample3, tablePop3)
```

Arguments

`tableSample3`	sample return value of GOtable3()
`tablePop3`	population return value of GOtable3()

Value

returns a matrix with columns c("x","m","n","k","p")

Examples

```
hyper<-GOhypergeometric3(x_tableSample3,x_tablePop3)
```

`GoMiner` *GoMiner*

Description

driver to generate heatmap

Usage

```
GoMiner(
  title = NULL,
  dir,
  sampleList,
  GOGOA3,
  ontology,
  enrichThresh = 2,
  countThresh = 5,
  pvalThresh = 0.1,
  fdrThresh = 0.1,
  nrand = 100,
  mn = 2,
```

```
  mx = 200,
  opt,
  verbose = 1
)
```

Arguments

`title`	character string descriptive title
`dir`	character string full pathname to the directory acting result repository
`sampleList`	character list of gene names
`GOGOA3`	return value of subsetGOGOA()
`ontology`	character string c("molecular_function", "cellular_component", "biological_process")
`enrichThresh`	numerical acceptance threshold for enrichment
`countThresh`	numerical acceptance threshold for gene count
`pvalThresh`	numerical acceptance threshold for pval
`fdrThresh`	numerical acceptance threshold for fdr
`nrand`	numeric number of randomizations to compute FDR
`mn`	integer param passed to trimGOGOA3, min size threshold for a category
`mx`	integer param passed to trimGOGOA3, max size threshold for a category
`opt`	integer 0:1 parameter used to select randomization method
`verbose`	integer vector representing classes

Details

modes of FDR estimation: opt=0 use original database with randomized geneLists opt=1 use original geneList with internally scrambled genes databases (uses randomGODB())

databases that can be used with the real geneList: these are explicitly passed as parameter to GoMiner() (1) original GOGOA3 (2) randomized version of GOGOSA GOGOA3R<-randomGODB(GOGOA3) (3) database containing a subset of the big hitters genes (randomGODB2driver()) attempts to compensate for the over-annotation of some genes, that might lead to false positive if gene G has a lot of mappings to categories, randomly sample G/category pairs to retain a reasonable number of them. e.g., reduce G from 100 category mappings to 7 category mappings, by omitting 93 of the mappings G/category mappings

Value

returns a matrix suitable to generate a heatmap

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
```

```
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
l<-GoMiner("Cluster52",tempdir(),cluster52,
 GOGOA3=GOGOA3,ontology="biological_process",enrichThresh=2,
 countThresh=5,pvalThresh=0.10,fdrThresh=0.10,nrand=2,mn=2,mx=200,opt=0,verbose=1)

 # try out yeast database!
 load("/Users/barryzeeberg/personal/GODB_RDATA/sgd/GOGOA3_sgd.RData")
 # make sure this is in fact the database for the desired species
 GOGOA3$species
 # use database to find genes mapping to an interesting category
 cat<-"GO_0042149__cellular_response_to_glucose_starvation"
 w<-which(GOGOA3$ontologies[["biological_process"]][,"GO_NAME"]==cat)
 geneList<-GOGOA3$ontologies[["biological_process"]][w,"HGNC"]
 l<-GoMiner("YEAST",tempdir(),geneList,
  GOGOA3,ontology="biological_process",enrichThresh=2,
  countThresh=3,pvalThresh=0.10,fdrThresh=0.10,nrand=2,mn=2,mx=200,opt=0)

## End(Not run)
```

`GOtable3` *GOtable3*

Description

tabulate number of geneList mappings to GO categories

Usage

```
GOtable3(hgncList, DB)
```

Arguments

`hgncList`	character list of gene names
`DB`	selected ontology branch of return value of subsetGOGOA

Value

returns a list whose components are c("DB","table","ngenes") where 'DB' is the GO DB subsetted to the desired ONTOLOGY, and 'table' is tabulation of number of occurrences of each GO category name within the desired ONTOLOGY, and ngenes is the total number of hgncList genes mapping to GOGOA

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
x<-GOtable3(cluster52,GOGOA3$ontologies[["biological_process"]])

## End(Not run)
```

`GOthresh` *GOthresh*

Description

retrieve lines of m that meet both enrichThresh and countThresh

Usage

```
GOthresh(m, sampleFDR, enrichThresh, countThresh, pvalThresh, fdrThresh)
```

Arguments

`m`	return value of GOenrich3()
`sampleFDR`	component of return value of RCPD()
`enrichThresh`	numerical acceptance threshold for enrichment
`countThresh`	numerical acceptance threshold for gene count
`pvalThresh`	numerical acceptance threshold for pval
`fdrThresh`	numerical acceptance threshold for fdr

Value

returns a subset of matrix (m joined with fdr$sampleFDR) with entries meeting all thresholds

Examples

```
thresh<-GOthresh(x_m,x_fdr$sampleFDR,enrichThresh=2,countThresh=2,pvalThresh=0.1,fdrThresh=0.100)
```

`HCCS66` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(HCCS66)
```

`hitterBeforeAfterDriver` *hitterBeforeAfterDriver*

Description

driver to invoke hitters2() and trimGOGOA3()

Usage

```
hitterBeforeAfterDriver(GOGOA3, mn = 20, mx = 200, verbose)
```

Arguments

`GOGOA3`	return value of minimalistGODB::buildGODatabase()
`mn`	integer minimum category size
`mx`	integer maximum category size
`verbose`	integer vector representing classes

Value

returns the return value of trimGOGOA3()

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# This example is given in full detail in the package vignette.
# You can generate GOGOA3.RData using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO
dir<-"/Users/barryzeeberg/personal/GODB_RDATA/goa_human/"
load(sprintf("%s/%s",dir,"GOGOA3_goa_human.RData"))
```

```
geneList<-GOGOA3$ontologies[["biological_process"]][1:10,"HGNC"]
GOGOA3tr<-hitterBeforeAfterDriver(GOGOA3,mn=20,mx=200,1)

## End(Not run)
```

`hitters2` *hitters2*

Description

determine the number of mappings for the top several genes

Usage

```
hitters2(GOGOA3, verbose = 1)
```

Arguments

`GOGOA3`	return value of minimalistGODB::buildGODatabase()
`verbose`	integer vector representing classes

Value

returns no value, but has side effect of printing information

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# This example is given in full detail in the package vignette.
# You can generate GOGOA3.RData using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO
dir<-"/Users/barryzeeberg/personal/GODB_RDATA/goa_human/"
load(sprintf("%s/%s",dir,"GOGOA3_goa_human.RData"))
geneList<-GOGOA3$ontologies[["biological_process"]][1:10,"HGNC"]
hitters2(GOGOA3,1)

## End(Not run)
```

`Housekeeping_Genes` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(Housekeeping_Genes)
```

`human` *human*

Description

determine if database represents human species

Usage

```
human(GOGOA3, verbose = TRUE)
```

Arguments

`GOGOA3`	return value of subsetGOGOA()
`verbose`	integer vector representing classes

Value

returns Boolean TRUE if species is human

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
hum<-human(GOGOA3)

load("/Users/barryzeeberg/personal/GODB_RDATA/sgd/GOGOA3_sgd.RData")
hum<-human(XENOPUS,1)

## End(Not run)
```

`preprocessDB` *preprocessDB*

Description

driver to perform several preprocessing steps: quick peek trim small and large categories is the database for human species validate validated HGNC symbols in sampleList determine up to date (ie, contains GOGOA3$species) or legacy version of human database

Usage

```
preprocessDB(sampleList, GOGOA3, ontology, mn, mx, thresh, verbose)
```

Arguments

`sampleList`	character list of gene names
`GOGOA3`	return value of subsetGOGOA()
`ontology`	character string c("molecular_function", "cellular_component", "biological_process")
`mn`	integer param passed to trimGOGOA3, min size threshold for a category
`mx`	integer param passed to trimGOGOA3, max size threshold for a category
`thresh`	numerical paramter passed to checkGeneListVsDB()
`verbose`	integer vector representing classes

Value

returns a list whose components are a trimmed version of GOGOA3 and (for human) a sampleList with validated HGNC symbols

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
pp<-preprocessDB(cluster52,GOGOA3,"biological_process",20,200,0.5,3)

## End(Not run)
```

`randSubsetGeneList` *randSubsetGeneList*

Description

retrieve n unique random genes

Usage

```
randSubsetGeneList(geneList, ngenes)
```

Arguments

`geneList`	character vector geneList
`ngenes`	integer desired number of random genes

Value

returns a character vector of genes

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
genes<-randSubsetGeneList(GOGOA3$genes[["biological_process"]],20)

## End(Not run)
```

`RCPD` *RCPD*

Description

prepare a cpd of p values from randomized gene sets

Usage

```
RCPD(GOGOA3, tablePop, geneList, nrand, ontology, hyper, subd, opt)
```

Arguments

`GOGOA3`	return value of subsetGOGOA()
`tablePop`	return value of GOtable3()
`geneList`	character vector lisgt of genes to randomize
`nrand`	integer number of randomizations
`ontology`	c("molecular_function","cellular_component","biological_process")
`hyper`	return value of GOhypergeometric3() from real (nonrandom) data
`subd`	character string pathname for directory containing sink.txt
`opt`	integer 0:1 parameter used to select randomization method

Details

the cpd of the randomizations is to be used for estimating the false discovery rate (FDR) of the real sampled genes

Value

returns a histogram of log10(p)

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
rcpd<-RCPD(GOGOA3,x_tablePop31,10,3,"biological_process",x_hyper1,tempdir(),0)

## End(Not run)
```

`runGoMinerExamples` *runGoMinerExamples*

Description

driver to run GoMiner under several randomization procedures

Usage

```
runGoMinerExamples(
  title = NULL,
  dir,
  sampleList,
  GOGOA3,
  ontology,
  enrichThresh = 2,
  countThresh = 5,
  pvalThresh = 0.1,
  fdrThresh = 0.1,
  nrand = 2,
  mn = 2,
  mx = 200,
  verbose = 1
)
```

Arguments

`title`	character string descriptive title
`dir`	character string full pathname to the directory acting result repository
`sampleList`	character list of gene names
`GOGOA3`	return value of subsetGOGOA()
`ontology`	character string c("molecular_function", "cellular_component", "biological_process")
`enrichThresh`	numerical acceptance threshold for enrichment
`countThresh`	numerical acceptance threshold for gene count
`pvalThresh`	numerical acceptance threshold for pval
`fdrThresh`	numerical acceptance threshold for fdr
`nrand`	numeric number of randomizations to compute FDR
`mn`	integer param passed to trimGOGOA3, min size threshold for a category
`mx`	integer param passed to trimGOGOA3, max size threshold for a category
`verbose`	integer vector representing classes

Value

returns a list containing the return value of GoMiner()

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# you can generate it using the package 'minimalistGODB'
```

```
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases
load("/Users/barryzeeberg/personal/GODB_RDATA/goa_human/GOGOA3_goa_human.RData")
ontology<-"biological_process"
t<-sort(table(GOGOA3$ontologies[[ontology]][,"HGNC"]),decreasing=TRUE)
dir<-tempdir()

sampleList<-names(t)[1:50]
title<-"hi_hitters"
hh<-runGoMinerExamples(title,dir,sampleList,GOGOA3,ontology,nrand=5)

sampleList<-names(t)[1001:1050]
title<-"hi_hitters5"
hh<-runGoMinerExamples(title,dir,sampleList,GOGOA3,ontology,nrand=5)

sampleList<-cluster52
title<-"cluster52"
hh<-runGoMinerExamples(title,dir,sampleList,GOGOA3,ontology,nrand=5)

## End(Not run)
```

`trimGOGOA3` *trimGOGOA3*

Description

remove categories from GOGOA3 that are too small or too large

Usage

```
trimGOGOA3(GOGOA3, mn, mx, verbose)
```

Arguments

`GOGOA3`	return value of subsetGOGOA()
`mn`	integer min size threshold for a category
`mx`	integer max size threshold for a category
`verbose`	integer vector representing classes

Details

If a category is too small, it is unreliable for statistical evaluation Also, in the extreme case of size = 1, then that category is essentially equivalent to a gene rather than a category. Same is partially true for size = 2. If a category is too large, it is too generic to be useful for categorization. Finally, by trimming the database, analyses will run faster.

Value

returns trimmed version of GOGOA3

Examples

```
## Not run:
# GOGOA3.RData is too large to include in the R package
# so I need to load it from a file that is not in the package.
# Since this is in a file in my own file system, I could not
# include this as a regular example in the package.
# This example is given in full detail in the package vignette.
# You can generate GOGOA3.RData using the package 'minimalistGODB'
# or you can retrieve it from https://github.com/barryzee/GO/tree/main/databases

GOGO3tr<-trimGOGOA3(GOGOA3,mn=2,mx=200,1)

## End(Not run)
```

`validHGNCSymbols` *validHGNCSymbols*

Description

convert outdated HGNC symbols to current HGNC symbols

Usage

```
validHGNCSymbols(geneList)
```

Arguments

`geneList`	character vector of HGNC symbols

Details

removes NA and /// from output of checkGeneSymbols()

Value

returns list of mapping table and vector of current HGNC symbols

Examples

```
geneList<-c("FN1", "tp53", "UNKNOWNGENE","7-Sep",
 "9/7", "1-Mar", "Oct4", "4-Oct","OCT4-PG4", "C19ORF71",
  "C19orf71")
l<-validHGNCSymbols(geneList)
```

`x_fdr` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_fdr)
```

`x_hyper1` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_hyper1)
```

`x_m` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_m)
```

`x_sampleList1` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_sampleList1)
```

`x_tablePop3` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_tablePop3)
```

`x_tablePop31` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_tablePop31)
```

`x_tableSample3` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_tableSample3)
```

`x_thresh` *GoMiner data set*

Description

GoMiner data set

Usage

```
data(x_thresh)
```

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