

Package ‘HTGM2D’

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Title Two Dimensional High Throughput 'GoMiner'

Maintainer Barry Zeeberg <barryz2013@gmail.com>

Author Barry Zeeberg [aut, cre]

Depends R (>= 4.2.0)

Imports minimalistGODB, GoMiner, HTGM, grDevices, stats, gplots,
jaccard, vprint, randomGODB, HGNCHELPER

LazyData true

LazyDataCompression xz

Description The Gene Ontology (GO) Consortium <<https://geneontology.org/>> organizes genes into hierarchical categories based on biological process (BP), molecular function (MF) and cellular component (CC, i.e., subcellular localization). Tools such as 'GoMiner' (see Zeeberg, B.R., Feng, W., Wang, G. et al. (2003) <[doi:10.1186/gb-2003-4-4-r28](https://doi.org/10.1186/gb-2003-4-4-r28)>) can leverage GO to perform ontological analysis of microarray and proteomics studies, typically generating a list of significant functional categories. Microarray studies are usually analyzed with BP, whereas proteomics researchers often prefer CC. To capture the benefit of both of those ontologies, I developed a two-dimensional version of 'High-Throughput GoMiner' ('HTGM2D'). I generate a 2D heat map whose axes are any two of BP, MF, or CC, and the value within a picture element of the heat map reflects the Jaccard metric p-value for the number of genes in common for the corresponding pair.

License GPL (>= 2)

Encoding UTF-8

VignetteBuilder knitr

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

RoxygenNote 7.3.2

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catGenes	<i>catGenes</i>
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Description

match up genes in gene list with categories in GOGOA3 database

Usage

catGenes(geneList, GOGOA3, ontology)

Arguments

- | | |
|----------|---|
| geneList | character vector of user-supplied genes of interest |
| GOGOA3 | return value of subsetGOGOA() |
| ontology | c("molecular_function","cellular_component","biological_process") |

Value

returns a matrix of 1's and 0's indicating the presence or absence of gene-category pairs

Examples

```
#load("data/GOGOA3small.RData")
geneList<-cluster52
m1<-catGenes(geneList,GOGOA3small,"biological_process")
```

cluster52

HTGM2D data set

Description

HTGM2D data set

Usage

```
data(cluster52)
```

```
compareGoMinerHTGM2D  compareGoMinerHTGM2D
```

Description

compare the results of GoMiner and HTGM2D

Usage

```
compareGoMinerHTGM2D(subd, mat, l, ontologies)
```

Arguments

subd	character string full path name to the output subdirectory
mat	return value of Jaccard()
l	of return values of GoMiner()
ontologies	character vector of 2 ontologies e.g. c("biological_process","cellular_component")

Value

returns no value, but saves files that list category difference between GoMiner and HTG2D

Examples

```
ontologies<-c("biological_process","cellular_component")
#load("data/x_l.Rdata")
#load("data/x_mat.Rdata")
subd<-tempdir()
compareGoMinerHTGM2D(subd,x_mat,x_l,ontologies)
```

GOGO3small

HTGM2D data set

Description

HTGM2D data set

Usage

```
data(GOGO3small)
```

Housekeeping_Genes

HTGM2D data set

Description

HTGM2D data set

Usage

```
data(Housekeeping_Genes)
```

HTGM2D

HTGM2D

Description

run 2D version of GoMiner

Usage

```
HTGM2D(dir, geneList, ontologies, GOGO3)
```

Arguments

dir	character string full path name to the directory acting as result repository
geneList	character vector of user-supplied genes of interest
ontologies	character vector of 2 ontologies e.g. c("biological_process","cellular_component")
GOGO3	return value of subsetGOGOA()

Value

returns the return value of Jaccard()

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")
subd<-tempdir()
geneList<-cluster52
ontologies<-c("biological_process","cellular_component")
mat<-HTGM2D(subd,geneList,ontologies,GOGOA3)

## End(Not run)
```

HTGM2Ddriver

HTGM2Ddriver

Description

driver to invoke GoMiner and HTGM2D, and compare the results

Usage

```
HTGM2Ddriver(
  dir,
  geneList,
  ontologies,
  GOGOA3,
  enrichThresh = 2,
  countThresh = 5,
  pvalThresh = 0.1,
  fdrThresh = 0.1,
  nrand = 100,
  mn,
  mx,
  opt = 0,
  verbose = 1
)
```

Arguments

<code>dir</code>	character string full path name to the directory acting as result repository
<code>geneList</code>	character vector of user-supplied genes of interest
<code>ontologies</code>	character vector of 2 ontologies e.g. <code>c("biological_process","cellular_component")</code>

GOGOA3	return value of subsetGOGOA()
enrichThresh	numerical acceptance threshold for enrichment passed to GoMiner
countThresh	numerical acceptance threshold for gene count passed to GoMiner
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

Value

returns no value, but saves hyperlinked SVG heatmap files to a results directory

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")
geneList<-cluster52
ontologies<-c("biological_process","cellular_component")
dir<-tempdir()
HTGM2Ddriver(dir,geneList,ontologies,GOGOA3,enrichThresh=2,
  countThresh=5,pvalThresh=0.10,fdrThresh=0.10,nrand=100,mn=2,mx=2000)

## End(Not run)
```

Jaccard	<i>Jaccard</i>
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Description

create the heat map data that is needed as input to JaccardHeatMap()

Usage

```
Jaccard(dir, m1, m2, thresh1 = 2, thresh2 = 3, B = 100)
```

Arguments

dir	character string full pathname to the directory acting as result repository
m1	return value of catGenes
m2	return value of catGenes
thresh1	integer acceptance threshold for the number of genes in a cat
thresh2	integer acceptance threshold for the number of common genes in 2 cats
B	integer a total bootstrap iteration

Value

returns a numerical matrix containing number of genes and associated p value in the intersection of 2 categories

Examples

```
#load("data/x_m1.RData")
#load("data/x_m2.RData")
mat<-Jaccard(dir=tempdir(),x_m1,x_m2)
```

JaccardHeatMap

JaccardHeatMap

Description

use the Jaccard metric to construct 2D heat map

Usage

```
JaccardHeatMap(dir, mat)
```

Arguments

dir	character string containing path name of output directory
mat	return value of Jaccard()

Value

returns a Jaccard matrix of cat1 vs cat2 FDR, and also saves hyperlinked SVG heatmap files to a results directory

Examples

```
#load("data/x_jmat.RData")
dir<-tempdir()
jHeatMap<-JaccardHeatMap(dir,x_jmat)
```

x_jmat	<i>HTGM2D data set</i>
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Description

HTGM2D data set

Usage

data(x_jmat)

x_l	<i>HTGM2D data set</i>
-----	------------------------

Description

HTGM2D data set

Usage

data(x_l)

x_m1	<i>HTGM2D data set</i>
------	------------------------

Description

HTGM2D data set

Usage

data(x_m1)

x_m2	<i>HTGM2D data set</i>
------	------------------------

Description

HTGM2D

Usage

data(x_m2)

x_mat

HTGM2D data set

Description

HTGM2D

Usage

`data(x_mat)`

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