Package ‘HTGM3D’

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Title Three Dimensional High Throughput 'GoMiner'

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Depends R (>= 4.2.0)

Imports minimalistGODB, GoMiner, HTGM, HTGM2D, grDevices, stats, R2HTML, rgl, vprint, randomGODB, stringr

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>) can leverage GO to perform ontological analysis of microarray and proteomics studies, typically generating a list of significant functional categories. To capture the benefit of all three ontologies, I developed 'HTGM3D', a three-dimensional version of 'GoMiner'.

License GPL (>= 2)

Encoding UTF-8

VignetteBuilder knitr

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

RoxygenNote 7.3.2

Config/testthat/edition 3

NeedsCompilation no

Repository CRAN

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Contents

`blackBodyRadiationColors` *blackBodyRadiationColors*

Description

set up color scale for black body spectrum

Usage

```
blackBodyRadiationColors(x, max_value = 1)
```

Arguments

`x`	numeric should be between 0 (black) and 1 (white)
`max_value`	numeric maximum value to be used for scaling

Details

I obtained this by copy and paste from internet (reference unknown)

Value

returns no value, but has side effect of generating color map

Examples

```
colors.blackBody <- rev(blackBodyRadiationColors(seq(0.3,1,length.out=20)))
```

`catNum3` *catNum3*

Description

assign the axis coordinate number to be used for the plotting position for each category

Usage

```
catNum3(l)
```

Arguments

`l`	list each component corresponds to an ontology branch, and contains the decreasing sorted tabulation of output of the number of times that a category appears in a triplet

Details

a component of l is like: GO_0005515__protein_binding GO_0042802__identical_protein_binding GO_0005178__integrin_binding 38 4 3

#' a component of l1 is like: GO_0005515__protein_binding GO_0042802__identical_protein_binding GO_0005178__integrin_binding 1 2 3

Value

returns a list each component corresponds to an ontology branch, and contains a vector of category plotting positions

Examples

```
#load("data/x_l.RData")
catNum3(x_l)
```

`cluster52` *HTGM3D data set*

Description

HTGM3D data set

Usage

```
data(cluster52)
```

`graphIt` *graphIt*

Description

annotate a selected point in the 3d graphic

Usage

```
graphIt(mat3d, sp, w, r, verbose)
```

Arguments

`mat3d`	component of HTGM3Ddriver() output list
`sp`	integer vector containing c(x,y,z) coordinated of point
`w`	integer line number within mat3d
`r`	numeric max value of x,y,z ranges
`verbose`	integer vector representing vprint classes

Value

returns no value, but has side effect of annotating the 3D graph

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`Housekeeping_Genes` *HTGM3D data set*

Description

HTGM3D data set

Usage

```
data(Housekeeping_Genes)
```

`HTGM3D` *HTGM3D*

Description

compute matrix to use as input to plot3d()

Usage

```
HTGM3D(dir, geneList, GOGOA3, thresh1, thresh3, mn, mx, pcgMN, pcgMX, verbose)
```

Arguments

`dir`	character string full path name to the directory acting as result repository
`geneList`	character vector of user-supplied genes of interest
`GOGOA3`	return value of subsetGOGOA()
`thresh1`	numerical acceptance threshold for individual ontologies
`thresh3`	numerical acceptance threshold for joint ontology
`mn`	integer min category size threshold passed to trimGOGOA3()
`mx`	integer max category size threshold passed to trimGOGOA3()
`pcgMN`	integer param passed to pruneCatGenes
`pcgMX`	integer param passed to pruneCatGenes
`verbose`	integer vector representing vprint classes

Value

returns matrix containing information that provides the input needed for running plot3d()

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
dir<-tempdir()
mat3d<-HTGM3D(dir,geneList,GOGOA3,thresh1=3,thresh3=3,mn=2,
 mx=10000,pcgMN=2,pcgMX=200,verbose=1:5)

## End(Not run)
```

`HTGM3Ddriver` *HTGM3Ddriver*

Description

driver to invoke HTGM3D()

Usage

```
HTGM3Ddriver(
  dir,
  geneList,
  GOGOA3,
  thresh1,
  thresh3,
  mn,
  mx,
  pcgMN,
  pcgMX,
  verbose
)
```

Arguments

`dir`	character string full path name to the directory acting as result repository
`geneList`	character vector of user-supplied genes of interest
`GOGOA3`	return value of subsetGOGOA()
`thresh1`	numerical acceptance threshold for individual ontologies
`thresh3`	numerical acceptance threshold for joint ontology
`mn`	integer min category size threshold passed to trimGOGOA3()
`mx`	integer max category size threshold passed to trimGOGOA3()
`pcgMN`	integer param passed to pruneCatGenes
`pcgMX`	integer param passed to pruneCatGenes
`verbose`	integer vector representing vprint classes

Details

suggested standardized class codes for vprint() -1 = developer debugging only 0 = constitutively turned on 1 = help for new user 2 = follow progress of long computation 3 = primary results 4 = meta information (e.g. dims of a matrix before and after trimming) 5 = warnings 6 = errors

Value

returns matrix containing information that provides the input needed for running plot3d()

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")

#load("data/cluster52.RData")
geneList<-cluster52
dir<-tempdir()
l3<-HTGM3Ddriver(dir,geneList,GOGOA3,thresh1=3,thresh3=3,
 mn=2,mx=20000,pcgMN=2,pcgMX=200,verbose=1:5)

## End(Not run)
```

`insertCatSize` *insertCatSize*

Description

compute fraction of total genes in the entire ontology that map to each category, and insert column into matrix mat

Usage

```
insertCatSize(mat, GOGOA3)
```

Arguments

`mat`	return value of Jaccard3()
`GOGOA3`	return value of subsetGOGOA()

Value

returns augmented version of matrix mat

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")

mat2<-insertCatSize(x_mat,GOGOA3)

## End(Not run)
```

`interactWithGraph3D` *interactWithGraph3D*

Description

rotate the 3d graph and/or select a point within the 3D graph, and annotate that point

Usage

```
interactWithGraph3D(mat3d, maxfract = 1, newWindow = TRUE, verbose = TRUE)
```

Arguments

`mat3d`	component of HTGM3Ddriver() output list
`maxfract`	numeric upper threshold for category size to display
`newWindow`	Boolean if TRUE open new window to avoid over writing current window
`verbose`	integer vector representing vprint classes

Value

returns no value, but has side effect of annotating the 3D graph

Examples

```
if(interactive()){
#load("data/x_mat3d.RData")
interactWithGraph3D(x_mat3d)
}
```

`Jaccard3` *Jaccard3*

Description

compute the number of genes in the intersection of categories from 3 ontology branches

Usage

```
Jaccard3(dir, m, thresh1 = 3, thresh3 = 3, verbose = 2)
```

Arguments

`dir`	character string full path name to the directory acting as result repository
`m`	return value of pruneCatGenes()
`thresh1`	parameter passed to Jaccard3()
`thresh3`	parameter passed to Jaccard3()
`verbose`	integer vector representing vprint classes

Value

returns matrix tabulating genes in the intersection of categories from 3 ontology branches also has side effect of saving files containing those genes

Examples

```
#load("data/x_m11.RData")
Jaccard3(tempdir(),x_m11,thresh1=3,thresh3=3,verbose=1:5)
```

`plot3Dmat` *plot3Dmat*

Description

compute x,y,z coordinates for each triplet

Usage

```
plot3Dmat(mat, l)
```

Arguments

`mat`	return value of HTGM3D()
`l`	return value of catNum3()

Value

augmented version of matrix containing x,y,z coordinates for each triplet

Examples

```
#load("data/x_mat.RData")
#load("data/x_l.RData")
p3<-plot3Dmat(x_mat,x_l)
```

`pruneCatGenes` *pruneCatGenes*

Description

eliminate those categories to which no genes map

Usage

```
pruneCatGenes(m, mn = 2, mx = 200)
```

Arguments

`m`	the return value of catGenes()
`mn`	integer min category size threshold passed to trimGOGOA3()
`mx`	integer max category size threshold passed to trimGOGOA3()

Value

returns pruned version of matrix m

Examples

```
#load("data/x_cg.RData")
m<-pruneCatGenes(x_cg,2,200)
```

`showGenes` *showGenes*

Description

open gene list in a textEdit window

Usage

```
showGenes(mat3d, w, range, npad)
```

Arguments

`mat3d`	component of HTGM3Ddriver() output list
`w`	integer line number within mat3d
`range`	list of ranges
`npad`	integer number of blanks for padding

Value

returns no value, but has side effect of opening textEdit

`subMatDiffs` *subMatDiffs*

Description

retrieve submatrices of common rownames and colnames, and report differences

Usage

```
subMatDiffs(m1, m2, verbose = 3)
```

Arguments

`m1`	matrix
`m2`	matrix
`verbose`	integer vector representing vprint classes

Details

compare submatrices of m1 and m2 that have common rownames and colnames

Value

returns no values

Examples

```
rn<-c("a","b","c")
cn<-c("a","b","c","d")
m1<-matrix(1:12,nrow=length(rn),ncol=length(cn))
rownames(m1)<-rn
colnames(m1)<-cn
m2<-m1
subMatDiffs(m1,m2)

m3<-m1
m3[1,1]<-0
m3[1,2]<-0
subMatDiffs(m1,m3)

m4<-m3
colnames(m4)<-c("aa","b","c","d")
subMatDiffs(m1,m4)
```

`x_cg` *HTGM3D data set*

Description

HTGM3D data set

Usage

```
data(x_cg)
```

`x_l` *HTGM3D data set*

Description

HTGM3D data set

Usage

```
data(x_l)
```

`x_m11` *HTGM3D data set*

Description

HTGM3D data set

Usage

```
data(x_m11)
```

`x_mat` *HTGM3D data set*

Description

HTGM3D

Usage

```
data(x_mat)
```

`x_mat3d` *HTGM3D data set*

Description

HTGM3D

Usage

```
data(x_mat3d)
```

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