

Package: HTGM4D (via r-universe)

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Title Four Dimensional High Throughput 'GoMiner'

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Depends R (>= 4.2.0)

Imports minimalistGODB, GoMiner, HTGM, HTGM2D, grDevices, stats,
gplots, vprint, randomGODB, HGNC helper, png, magick, svglite,
utils, graphics

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 now present an enhancement of the existing two-dimensional
version of 'High-Throughput GoMiner' ('HTGM2D'), which is
called 'HTGM4D'. The original 'HTGM2D' is augmented by adding
two instances of the original 'GoMiner' genes versus categories
heatmaps, aligned with the categories axes of the 'HTGM2D'
heatmap.

License GPL (>= 2)

Encoding UTF-8

VignetteBuilder knitr

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

RoxygenNote 7.3.3

Config/testthat/edition 3

NeedsCompilation no

Config/pak/sysreqs cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev make libharfbuzz-dev libmagick++-dev gsfonts libicu-dev libpng-dev libuv1-dev libssl-dev zlib1g-dev

Repository <https://barryzee.r-universe.dev>

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buildSubdirs	<i>buildSubdirs</i>
--------------	---------------------

Description

create the directory structure for the output file

Usage

```
buildSubdirs(dir)
```

Arguments

dir character string path name for the top level output directory

Value

returns no values, but has side effect of creating some subdirectories

Examples

```
stamp<-gsub(":", "_", format(Sys.time(), "%a_%b_%d_%Y_%X"))
dir<-sprintf("%s/%s/", tempdir(), stamp)
dir.create(dir)
print(c("dir: ", dir))
buildSubdirs(dir)
```

cluster52	<i>HTGM4D data set</i>
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Description

HTGM4D data set

Usage

```
data(cluster52)
```

combine3SVG

combine3SVG

Description

combine 3 svg objects into a single svg object

Usage

```
combine3SVG(svg1, svg2, svg3, browser = "Safari")
```

Arguments

svg1	an svg object, presumably the result of HTGM2D()
svg2	an svg object, presumably the result of GoMiner()
svg3	an svg object, presumably the result of GoMiner()
browser	character string c("Safari","Google Chrome","Firefox","Brave Browser")

Details

sort of works, but rendering of axis labels are distorted for the "below" GoMiner heatmap

Value

returns the composite svg object

Examples

```
## Not run:  
# must be run in the R Console, NOT from RStudio Console  
# because the window for edit() is not rendered properly  
# in RStudio Console  
  
svg9<-combine3SVG(x_svg1,x_svg2,x_svg3)  
  
## End(Not run)
```

editor	<i>editor</i>
--------	---------------

Description

iteratively invoke `edit()` to allow user to adjust relative positions of `svg`'s

Usage

```
editor(svg, lines, m, browser)
```

Arguments

<code>svg</code>	an <code>svg</code> object
<code>lines</code>	integer vector of <code>svg</code> line numbers
<code>m</code>	numerical matrix of parameter values for <code>svg</code> "transform" tag
<code>browser</code>	character string <code>c("Safari", "Google Chrome", "Firefox", "Brave Browser")</code>

Value

returns an `svg` object

Examples

```
## Not run:  
# must be run in the R Console, NOT from RStudio Console  
# because the window for edit() is not rendered properly  
# in RStudio Console  
  
m<-matrix(nrow=2,ncol=4)  
colnames(m)<-c("x","y","scale","rotate")  
m[1,]<-c(300,0,.5,0)  
m[2,]<-c(150,200,.5,90)  
svg9<-editor(x_svg3,x_lines,m,browser="Safari")  
  
## End(Not run)
```

fillLines	<i>fillLines</i>
-----------	------------------

Description

insert <g transform line into svg

Usage

```
fillLines(svg, lines, m)
```

Arguments

svg	an svg object
lines	integer vector of svg line numbers
m	numerical matrix of parameter values for svg "transform" tag

Value

returns an svg object

Examples

```
m<-matrix(nrow=2,ncol=4)
colnames(m)<-c("x","y","scale","rotate")
m[1,]<-c(300,0,.5,0)
m[2,]<-c(150,200,.5,90)
svg9<-fillLines(x_svg3,x_lines,m)
```

findSVGtags	<i>findSVGtags</i>
-------------	--------------------

Description

locate <svg and </svg tags

Usage

```
findSVGtags(svg)
```

Arguments

svg	svg object
-----	------------

Value

returns a vector containing the line numbers of the tags

Examples

```
findSVGtags(x_svg1)
```

GoMiner4

GoMiner4

Description

version of GoMiner() to use with HTGM4D

Usage

```
GoMiner4(
  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

see full details in the original GoMiner() this version differs from the original GoMiner in returning "heatmap" now. I should make the original GoMiner, but I am afraid of breaking several programs that invoke the original GoMiner.

Value

returns a list whose elements are an svg object and 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")

stamp<-gsub(":", "_", format(Sys.time(), "%a_%b_%d_%Y_%X"))
dir<-sprintf("%s/%s/", tempdir(), stamp)
dir.create(dir)
print(c("dir: ", dir))
buildSubdirs(dir)

l<-GoMiner4("Cluster52", dir, 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)

## End(Not run)
```

HTGM4D

HTGM4D

Description

run 4D version of GoMiner

Usage

```
HTGM4D(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 a list containing the return value of Jaccard() and JaccardHeatMap4()

Examples

```
## Not run:
# GOGO3.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/GOGO3_goa_human.RData")

stamp<-gsub(":", "_", format(Sys.time(), "%a_%b_%d_%Y_%X"))
dir<-sprintf("%s/%s/", tempdir(), stamp)
dir.create(dir)
print(c("dir: ", dir))
buildSubdirs(dir)

geneList<-cluster52
ontologies<-c("biological_process", "cellular_component")
mat<-HTGM4D(dir, geneList, ontologies, GOGO3)

## End(Not run)
```

HTGM4Ddriver

HTGM4Ddriver

Description

driver to invoke GoMiner and HTGM4D, and compare the results

Usage

```

HTGM4Ddriver(
  dir,
  geneList,
  ontologies,
  GOGO3,
  enrichThresh = 2,
  countThresh = 5,
  pvalThresh = 0.1,
  fdrThresh = 0.1,
  nrand = 100,
  mn,
  mx,
  opt = 0,
  SVG3 = FALSE,
  browser = "Safari",
  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>
<code>GOGO3</code>	return value of <code>subsetGOGO3()</code>
<code>enrichThresh</code>	numerical acceptance threshold for enrichment passed to <code>GoMiner</code>
<code>countThresh</code>	numerical acceptance threshold for gene count passed to <code>GoMiner</code>
<code>pvalThresh</code>	numerical acceptance threshold for <code>pval</code>
<code>fdrThresh</code>	numerical acceptance threshold for <code>fdr</code>
<code>nrand</code>	numeric number of randomizations to compute FDR
<code>mn</code>	integer param passed to <code>trimGOGO3</code> , min size threshold for a category
<code>mx</code>	integer param passed to <code>trimGOGO3</code> , max size threshold for a category
<code>opt</code>	integer 0:1 parameter used to select randomization method
<code>SVG3</code>	Boolean if TRUE invoke <code>combine3SVG()</code>
<code>browser</code>	character string <code>c("Safari","Google Chrome","Firefox","Brave Browser")</code>
<code>verbose</code>	integer vector representing classes

Value

returns the path name of the output subdirectory

Examples

```
## Not run:
# must be run in the R Console, NOT from RStudio Console
# because the window for edit() is not rendered properly
# in RStudio Console

# GOGO3.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/GOGO3_goa_human.RData")
geneList<-cluster52
ontologies<-c("biological_process","cellular_component")
dir<-tempdir()
odir<-HTGM4Driver(dir,geneList,ontologies,GOGO3,enrichThresh=2,
  countThresh=5,pvalThresh=0.10,fdrThresh=0.10,nrand=100,mn=2,mx=2000)

## End(Not run)
```

JaccardHeatMap4

JaccardHeatMap4

Description

use the Jaccard metric to construct HTGM2D heat map

Usage

```
JaccardHeatMap4(dir, mat)
```

Arguments

<code>dir</code>	character string containing path name of output directory
<code>mat</code>	return value of Jaccard()

Details

computes heatmap twice, once with and once without axis labels. for the composite svg, the axis labels generate too much screen clutter. the version with axis labels is used only for quality assurance checking.

Value

returns the return value of heatmap.2, and also saves hyperlinked SVG heatmap files to a results directory

Examples

```
# takes too long to run in CRAN check
stamp<-gsub(":", "_", format(Sys.time(), "%a_%b_%d_%Y_%X"))
dir<-sprintf("%s/%s/", tempdir(), stamp)
dir.create(dir)
print(c("dir: ", dir))
buildSubdirs(dir)

jHeatMap<-JaccardHeatMap4(dir, x_jmat)
```

```
mergeGoMinerHTGM2D      mergeGoMinerHTGM2D
```

Description

match the categories in the results of GoMiner and HTGM2D

Usage

```
mergeGoMinerHTGM2D(
  dir,
  htgm4d,
  l,
  ontologies,
  fdrThresh,
  doRow = FALSE,
  SVG3 = FALSE,
  browser = "Safari",
  verbose = 4
)
```

Arguments

dir	character string path name of output directory
htgm4d	return value of HTGM4D()
l	return value of GoMiner4()
ontologies	character vector of 2 ontologies e.g. c("biological_process", "cellular_component")
fdrThresh	numeric background value to initialize matrix m
doRow	Boolean param passed to heatmap.2
SVG3	Boolean if TRUE invoke combine3SVG()
browser	character string c("Safari", "Google Chrome", "Firefox", "Brave Browser")
verbose	param passed to vprint()

Value

returns no values but has side effect of saving some .png and .svg images

parseSVGline	<i>parseSVGline</i>
--------------	---------------------

Description

scale the width and height parameters of <svg line in svg object

Usage

```
parseSVGline(svg)
```

Arguments

svg an svg object

Value

returns modified svg object

Examples

```
s<-parseSVGline(x_svg1)
```

pngBorder	<i>pngBorder</i>
-----------	------------------

Description

manual adjustment of border in composite png

Usage

```
pngBorder(dir, border = "500", bcol = "white")
```

Arguments

dir character string path name for main output directory
border character string containing border width
bcol character string containing border color

Value

returns path name of ofile

`pngDims`*pngDims*

Description

carefully compute the parameters for heatmap.2()

Usage

```
pngDims(  
  mat,  
  margins = c(50, 50),  
  cex = 4,  
  inchPerDendro = 0.25,  
  inchPerChar = 0.05,  
  verbose = 4  
)
```

Arguments

<code>mat</code>	numerical matrix input for heatmap.2()
<code>margins</code>	param passed to heatmap.2()
<code>cex</code>	param passed to heatmap.2()
<code>inchPerDendro</code>	numerical value how many inches to allocate to dendrogram
<code>inchPerChar</code>	empirically determined value for character size, that results in square heatmap elements
<code>verbose</code>	integer param passed to vprint()

Details

the goal here is to compute the parameters that result in square, rather than rectangular, heatmap elements

Value

returns a list of parameter values to be used by heatmap.2()

Examples

```
m<-matrix(1:28,nrow=4,ncol=7)  
pngDims(m)
```

`pngDisplay3`*pngDisplay3*

Description

use magick package to display arrangement of aligned 3 pngs

Usage

```
pngDisplay3(HTGM2D.png, side.png, below.png, border = "500", bcol = "white")
```

Arguments

HTGM2D.png	character string path name for HTGM2D .png
side.png	character string path name for side .png
below.png	character string path name for below .png
border	character string border size like "500"
bcol	character string border color like "white"

Value

returns the path name of the output file .png

Examples

```
# takes too long to run in CRAN check
HTGM2D.png <- system.file("extdata/files", "HTGM2D.png", package = "HTGM4D")
side.png <- system.file("extdata/files", "side.png", package = "HTGM4D")
below.png <- system.file("extdata/files", "below.png", package = "HTGM4D")
png<-pngDisplay3(HTGM2D.png,side.png,below.png)
```

`pngHeat`*pngHeat*

Description

generate .png heatmap using parameters carefully computed by pngDims()

Usage

```
pngHeat(  
  filename,  
  mat,  
  labs = FALSE,  
  Rowv = TRUE,  
  Colv = TRUE,  
  res = 300,  
  border = FALSE,  
  verbose = 4  
)
```

Arguments

filename	character string path name for .png output file
mat	numerical matrix input for heatmap.2()
labs	Boolean if TRUE display row and col labels
Rowv	parameter for heatmap.2()
Colv	parameter for heatmap.2()
res	numeric screen resolution
border	Boolean if TRUE add red border to periphery of png
verbose	integer param passed to vprint()

Value

returns the path name for the output heatmap .png file

Examples

```
# takes too long to run in CRAN check  
stamp<-gsub(":", "_", format(Sys.time(), "%a_%b_%d_%Y_%X"))  
dir<-sprintf("%s/%s/", tempdir(), stamp)  
dir.create(dir)  
print(c("dir: ", dir))  
buildSubdirs(dir)  
  
m<-matrix(1:28, nrow=4, ncol=7)  
pngHeat(filename=sprintf("%s/%s/%s", dir, "standards", "xpng.png"), mat=m)
```

renderSVG	<i>renderSVG</i>
-----------	------------------

Description

cluster a GoMiner (but not HTGM2D) heatmap and save it as an SVG file

Usage

```
renderSVG(dir, heatmap, identifier, doRow = TRUE, verbose)
```

Arguments

dir	character string containing path name of output directory
heatmap	matrix to be clustered
identifier	character string "side" or "below"
doRow	Boolean if TRUE cluster row
verbose	input param for vprint()

Value

returns a list containing the SVG file and the SVG also has side effect of saving the svg file

Examples

```
# takes too long to run in CRAN check
stamp<-gsub(":", "_", format(Sys.time(), "%a_%b_%d_%Y_%X"))
dir<-sprintf("%s/%s/", tempdir(), stamp)
dir.create(dir)
print(c("dir: ", dir))
buildSubdirs(dir)

m<-matrix(data=1:16, nrow=4, ncol=4)
rownames(m)<-c("a", "b", "c", "d")
colnames(m)<-c("a", "b", "c", "d")
svg<-renderSVG(sprintf("%s/%s/", dir, "standards"), m, "example", verbose=-1)
```

setSVGtransparency *setSVGtransparency*

Description

modify svg code so that background opacity is set to 0

Usage

```
setSVGtransparency(svg)
```

Arguments

svg svg object

Details

this prevents the background of one svg from overlaying the content of a second svg in combine3SVG()

Value

returns modified version of svg object

Examples

```
svgt<-setSVGtransparency(x_svg1)
```

whoRanMe

whoRanMe

Description

wrapper for commandArgs()

Usage

```
whoRanMe()
```

Value

Returns a character string containing the identity of who ran the program in which this is called.

Examples

```
whoRanMe()
```

x_jmat	<i>HTGM4D data set</i>
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Description

HTGM4D data set

Usage

data(x_jmat)

x_l	<i>HTGM4D data set</i>
-----	------------------------

Description

HTGM4D data set

Usage

data(x_l)

x_lines	<i>HTGM4D data set</i>
---------	------------------------

Description

HTGM4D data set

Usage

data(x_lines)

x_svg1	<i>HTGM4D data set</i>
--------	------------------------

Description

HTGM4D data set

Usage

data(x_svg1)

x_svg2

HTGM4D data set

Description

HTGM4D data set

Usage

data(x_svg2)

x_svg3

HTGM4D data set

Description

HTGM4D data set

Usage

data(x_svg3)

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