Package ‘categoryCompare’

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Version 1.48.0

Title Meta-analysis of high-throughput experiments using feature annotations

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URL https://github.com/rmflight/categoryCompare

BugReports https://github.com/rmflight/categoryCompare/issues

License GPL-2

Depends R (>= 2.10), Biobase, BiocGenerics (>= 0.13.8),

Suggests knitr, GO.db, KEGGREST, estrogen, org.Hs.eg.db, hgu95av2.db,
limma, affy, genefilter, rmarkdown

Imports AnnotationDbi, hwriter, GSEABase, Category (>= 2.33.1),
GOstats, annotate, colorspace, graph, RCy3 (>= 1.99.29),
methods, grDevices, utils

LazyLoad yes

Description Calculates significant annotations (categories) in each of two (or more) feature (i.e. gene) lists, determines the overlap between the annotations, and returns graphical and tabular data about the significant annotations and which combinations of feature lists the annotations were found to be significant.
Interactive exploration is facilitated through the use of RCytoscape (heavily suggested).

SystemRequirements Cytoscape (>= 3.6.1) (if used for visualization of results, heavily suggested)

TODO Text and HTML output without graphs.

biocViews Annotation, GO, MultipleComparison, Pathways, GeneExpression

VignetteBuilder knitr

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Description

Calculates significant annotations (categories) in each of two (or more) feature (i.e. gene) lists, determines the overlap between the annotations, and returns graphical and tabular data about the significant annotations and which combinations of feature lists the annotations were found to be significant. Interactive exploration is facilitated through the use of RCytoscape (heavily suggested).

Details

Package: categoryCompare
Version: 1.21.2
License: GPL-2
Depends: Biobase (>= 1.15.29), AnnotationDbi (>= 0.1.15), Category
Suggests: methods, GSEABase, hwriter, colorspace, graph, GO.db, KEGG.db, estrogen, org.Hs.eg.db, hgu95av2.db
Imports: Biobase (>= 1.15.29), AnnotationDbi (>= 0.1.15), hwriter, GSEABase, Category (>= 2.21.2), GOSTats
LazyLoad: yes
biocViews: Bioinformatics, Annotation, GO, MultipleComparisons, Pathways, GeneExpression
SystemRequirements: Cytoscape (>= 2.8.0) (if used for visualization of results, heavily suggested), CytoscapeRPC plugin (>= 1.8)
TODO: Text and HTML output without graphs.
Built: R 2.15.0; ; 2012-03-15 18:42:40 UTC; windows

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Further information is available in the following vignettes:

categoryCompare_vignette categoryCompare: High-throughput data meta-analysis using gene annotations (source)

Author(s)

Robert M. Flight <rflight79@gmail.com>
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Description

Methods for function breakEdges in package categoryCompare

Methods

signature(cwObject = "ccCompareResult", cutoff = "numeric") Allows one to remove edges in the ccCompareResult mainGraph slot prior to passing it into Cytoscape for visualization. Given that the number of edges can be rather large (especially for Gene Ontology) this can easily speed up the transfer, without actually losing any information.

signature(cwObject = "numeric", cutoff = "numeric") Once an annotation graph is in Cytoscape, remove edges above or below the cutoff. Note that this does not affect the original graph in the ccCompareResult object.

Author(s)

Robert M Flight

See Also

breakEdges ccCompareResult ccOutCyt

Examples

data(ccData)

# breaking the edges in a ccCompareResult
ccResults$BP <- breakEdges(ccResults$BP, 0.8)
## Not run:
hasCy <- (if (.Platform$OS.type %in% "windows") {
(length(grep("Cytoscape", system("tasklist", intern=TRUE))) > 0))

if hasCy {

cwObj <- ccOutCyt(ccResults$BP, ccOpts)
# now breaking them in the CytoscapeWindow object
breakEdges(cwObj, 0.85)
Sys.sleep(10)
RCy3::deleteWindow(cwObj)
}
## End(Not run)
Usage

cCompare(ccEnrichResult, ccOptions)

Arguments

ccEnrichResult  The enriched annotations collection returned from ccEnrich. This can be the ccEnrichCollection, GOccEnrichResult, or KEGGccEnrichResult
ccOptions       A ccOptions object that will determine which lists to actually compare against each other. See details below.

Details

Based on the enrichments found for each gene list, we now want to compare the annotations between lists. ccCompare accesses the annotations for each enrichment performed for each list, and makes the comparisons defined in ccOptions.

Value

ccCompare generates both a graph of the comparisons (to show how the categories are linked to each list and each other) and tabular output. The tabular output is a data frame, with ID for each term that was considered as a candidate annotation for each list, as well as a long description (Desc) of what the term is, and then membership and statistics from each gene list.

For each type of comparison (GO, KEGG, etc) a ccCompareResult is generated, with the following slots:

mainGraph       Annotations arranged as a graph
mainTable       The tabular results from all enrichment calculations combined into one
allAnnotation    A list of lists, where each entry is the annotation identifier, then a list for each comparison, with the genes that are annotated to that term that also belong to each list

The default is to generate an overlap graph for GO and KEGG, where the overlap is a measure of the similarity of the features (genes) annotated to each annotation term (based on a formula from EnrichmentMap). Optionally for GO, one can generate a hierarchical layout where the parent GO terms of the significant terms will also be included in the graph, with term origin saved in the node annotation (see example below to do this).

Only those terms with more than 10 and less than 500 annotated genes (according to the GO annotation file) are included.

When using weighted overlap graphs and RCy3 for viewing, it is recommended to use breakEdges and minNodes to remove edges with low weights and nodes with only a few genes from the dataset annotated to them.

Author(s)

Robert M Flight
See Also

ccCompareResult ccCompareCollection ccOutCyt breakEdges outType ccEnrich

Examples

```r
## Not run:
require(GO.db)
require(KEGG.db)
require(org.Hs.eg.db)

## End(Not run)
data(ccData)

# note that enrichLists is generated from ccEnrich
# ccResults <- ccCompare(enrichLists,ccOpts)
ccResults

# use the GO hierarchy tree
graphType(enrichLists$BP) <- "hierarchical"
# ccResultsBPHier <- ccCompare(enrichLists$BP,ccOpts)
ccResultsBPHier
```

ccCompareCollection-class

Class "ccCompareCollection"

Description

Holds multiple ccCompareResult objects.

Objects from the Class

Objects can be created by calls of the form new("ccCompareCollection", ...).
These are not normally created by the user, but rather by ccCompare while performing the categorical comparisons for each type of category

Slots

.Data: Object of class "list"

names: Object of class "character"

Extends

Methods

No methods defined with class "ccCompareCollection" in the signature.

Author(s)

Robert M Flight

See Also

cCompareResult ccCompare

Examples

showClass("ccCompareCollection")
**Slots**

- `mainGraph`: Object of class "graph". Holds the graph describing the relationships between the annotations.
- `subGraph`: Object of class "list". Not currently used.
- `mainTable`: Object of class "data.frame". Table of results, with all the various statistics for each annotation in the category.
- `allAnnotation`: Object of class "list". For each annotation, which genes from which comparison are annotated to that particular annotation.
- `categoryName`: Object of class "character". Which category (e.g. GO, KEGG, etc) was used.
- `ontology`: Object of class "character". If GO, which ontology was used.

**Methods**

- `allAnnotation` signature(object = "ccCompareResult"): ...
- `mainGraph` signature(object = "ccCompareResult"): ...
- `mainTable<-` signature(object = "ccCompareResult"): ...

**Author(s)**

Robert M Flight

**See Also**

`ccCompare` `ccCompareCollection`

**Examples**

```r
showClass("ccCompareResult")
```

---

**ccData**

Test data for `categoryCompare`

**Description**

Processed data from the estrogen example data set

**Usage**

```r
data(ccData)
```
Format

table10: Log-ratio output from limma for the comparison of presence-absence of estrogen at 10 hours
table48: Log-ratio output from limma for the comparison of presence-absence of estrogen at 48 hours
gUniverse: All of the genes measured on the chip
gseaRes: Toy results of GSEA analysis of 3 different tissues
enrichLists: Apply ccEnrich to a ccGeneList from table10 and table48
ccResults: Apply ccCompare to enrichLists
ccResultsBPHier: Modify enrichLists$BP to use a "hierarchical" layout
geneLists: a ccGeneList generated from genes in table10 and table48
ccOpts: a ccOptions object describing what we are going to do as far as feature list comparisons

Author(s)

Robert M Flight

Source

Taken from the estrogen package in Bioconductor, and then processed using the normal affy and limma tools.

See Also

ccGeneList ccEnrichCollection ccCompareCollection ccEnrich ccCompare

Examples

data(ccData)

ccEnrich-method

Perform annotation enrichment for multiple gene lists

Description

Takes a ccGeneList object containing all the information needed to perform enrichment calculations for Gene Ontology.

Usage

ccEnrich(ccGeneList)
Arguments

- **ccGeneList**: A `ccGeneList` object, which is really just a list of lists, with some extra slots to tell us how to examine results. Each entry in the list should be named to allow identification later on. Each sub list should contain a vector `genes` denoting the genes of interest, a vector `universe` denoting the gene background (i.e. all genes on the chip), and an entry `annotation` denoting an organism database package (such as `org.Hs.eg.db`). See `ccGeneList` for more details regarding this object.

Details

This function is essentially a wrapper for `hyperGTestCC` that performs all of the calculations for the many gene lists in one go, returning a list of `HyperGResultCC` objects, one for each of the ccTypes and each gene list. These various `HyperGResultCC` objects can then be accessed and results compared among the lists for each of the ontologies.

Value

A list of `HyperGResultCC` objects, one for each ccType and gene list, returned as `ccEnrichResult` objects for each ccType. This can be passed with a `ccOptions` object to `ccCompare` to generate actual annotation comparisons.

Author(s)

Robert M Flight

See Also

`ccGeneList, hyperGTestCC, ccEnrichResult`

Examples

```r
## Not run:
require(GO.db)
require(KEGG.db)
require(org.Hs.eg.db)

## End(Not run)
data(ccData)

g10 <- (unique(table10$Entrez[1:100]))
g48 <- (unique(table48$Entrez[1:100]))

list10 <- list(genes=g10, universe=gUniverse, annotation="org.Hs.eg.db")
list48 <- list(genes=g48, universe=gUniverse, annotation="org.Hs.eg.db")

geneLists <- list(T10=list10, T48=list48)
geneLists <- new("ccGeneList", geneLists, ccType=c("BP","KEGG"))
geneLists <- new("ccGeneList", geneLists, ccType=c("CC","KEGG"))

# set number of fdr runs to 0 to speed up runtime, not generally recommended.
```
genelists <- new("ccGeneList", geneLists, ccType = c('BP', 'KEGG'), pvalueCutoff=0.01, fdr=0)
# enrichLists <- ccEnrich(genelists)

**ccEnrichCollection-class**

*Class* "ccEnrichCollection"

**Description**

Holds multiple classes of *ccEnrichResult* in one object to allow *ccCompare* to work on only the one object and generate all of the results of a comparison.

**Objects from the Class**

Objects can be created by calls of the form new("ccEnrichCollection", ...).

**Slots**

.Data: Object of class "list"

names: Object of class "character" The names (generally GO ontologies or KEGG, but can be changed) of each set of results

**Extends**


**Methods**

pvalueCutoff<- signature(r = "ccEnrichCollection"): Changes the pvalueCutoff to be used to decide significant annotations for all of the contained ccEnrichResult objects

pvalueType<- signature(object = "ccEnrichCollection"): Changes whether to use p-values or fdr values to determine those annotations that are significant in all of the contained ccEnrichResult objects

minCount<- signature(object = "ccEnrichCollection"): how many features have to be annotated to a term to be reported as significant

graphType signature(object = "ccEnrichCollection"): Gets the type of graph that should be output for this collection

**Author(s)**

Robert M Flight

**See Also**

ccEnrich hyperGTestCC ccCompare ccEnrichResult
Description

Acts as a container object for multiple HyperGResultCC objects.

Objects from the Class

Objects can be created by calls of the form new("ccEnrichResult", ...).

Extends


Methods

fdr signature(object = "ccEnrichResult"): get the number of runs using random feature lists were performed

pvalueCutoff signature(r = "ccEnrichResult"): what is the pvalueCutoff to determine significant annotations

pvalueCutoff<- signature(r = "ccEnrichResult"): change the pvalueCutoff for an annotation to be considered significant

pvalueType<- signature(object = "ccEnrichResult"): change whether p-values used are from "FDR" or raw p-values

minCount signature(object = "ccEnrichResult"): how many features need to belong to an annotation to be reported

minCount<- signature(object = "ccEnrichResult"): adjust the minCount

graphType signature(object = "ccEnrichResult"): what type of graph should be generated (generally set by the class of object)

graphType<- signature(object = "ccEnrichResult"): change the type of graph to generate by ccCompare

Author(s)

Robert M Flight
Examples

```r
data(ccData)
enrichRes <- enrichLists[[1]]
fdr(enrichRes)
pvalueType(enrichRes)
enrichRes
pvalueType(enrichRes) <- 'pval'
enrichRes

pvalueCutoff(enrichRes)
pvalueCutoff(enrichRes) <- 0.01
enrichRes
```

### ccGeneList-class

**Class** "ccGeneList"

**Description**

This stores the actual gene lists and related information that will be used in categoryCompare.

**Objects from the Class**

Objects can be created by calls of the form `new("ccGeneList", list)`. ccGeneList is actually just an extension of R list objects. The input list should be a list of lists. See Details for more information.

**Slots**

- **fdr**: Object of class "numeric" The number of fdr runs to perform to account for different list sizes and term dependence
- **pvalueCutoff**: Object of class "numeric" Value used to determine whether or not a particular term is significant or not
- **ccType**: Object of class "character" What types of annotations to use. Currently supported ones include "BP", "MF", "CC" (from Gene Ontology) and "KEGG"
- **testDirection**: Object of class "character" Are you interested in "over" or "under" represented annotations

**Methods**

- **fdr** signature(object = "ccGeneList"): how many random runs to perform
- **fdr<-** signature(object = "ccGeneList"): change the number of random runs
- **pvalueCutoff** signature(object = "ccGeneList"): what is the pvalue to consider significant
- **pvalueCutoff<-** signature(object = "ccGeneList"): change the cutoff for significance
- **ccType** signature(object = "ccGeneList"): what type of annotations are going to be examined
- **ccType<-** signature(object = "ccGeneList"): change the type of annotations to examine
**Details**

The input list should be a list of lists, with at least three sub-lists.

testList <- list(list1=list(genes='...',universe='...',annotation='...'), list2=list(...))

genes : These are the gene identifiers of the genes that are of interest (differentially expressed genes)

universe : All of the genes that were measured in this particular experiments (i.e. all the genes on the chip)

annotation : What organism or chip do these ID’s come from (e.g. "org.Hs.eg.db" for Human Entrez gene ID’s, "hgu133a.db" for probe ID’s from the Affymetrix U133A chip)

data : A data-frame that contains extra information about the genes of interest. At the very least, the data-frame must have a column ID that matches the ID’s contained in genes

What actually happens when running ccEnrich is that the appropriate HyperGParamsCC objects are generated for each geneList and each type of annotation (e.g. BP, CC, KEGG), and then the calculations performed on each one.

**Note**

The ccGeneList object is what will undergo all of the enrichment calculations. When the results are combined with the ccOptions object, we can get our results of actual comparisons between experiments.

**Author(s)**

Robert M Flight

**See Also**

ccOptions

**Examples**

data(ccData)
g10 <- (unique(table10$Entrez[1:100]))
g48 <- (unique(table48$Entrez[1:100]))

list10 <- list(genes=g10, universe=gUniverse, annotation="org.Hs.eg.db")
list48 <- list(genes=g48, universe=gUniverse, annotation="org.Hs.eg.db")

geneLists <- list(T10=list10, T48=list48)
geneLists <- new("ccGeneList", geneLists, ccType=c("BP","KEGG"))
geneLists
**ccOptions-class**

**Class "ccOptions"**

**Description**

These objects store the various options required by categoryCompare for actually making comparisons and generating output.

**Objects from the Class**

Objects can be created by calls of the form `new("ccOptions", listNames=c('list1','list2',etc)).` This is the minimum call required, and will generate a ccOptions object where comparisons are assumed between all the lists supplied. See the examples section for more examples of how to initialize new objects.

**Slots**

- `listNames`: Object of class "character" The actual names of the various datasets defined in the `ccData` object
- `compareNames`: Object of class "character" Which lists to compare, each entry should be a comma separated list
- `compareIndx`: Object of class "list" List indices for each of the comparison, not usually set by the user. Generated automatically.
- `compareColors`: Object of class "character" For graphical and tabular output each comparison can be colored. Should be one color for each comparison. Can be either an n by 3 matrix of rgb triples, or a character vector of hexadecimal color codes, or character vector of color names ('red','green','blue', etc)
- `cssClass`: Object of class "character" Classnames used when generating HTML tables to color entries. Generated automatically upon initialization, or modifying `compareNames`
- `outType`: Object of class "character" Sets the type of output generated by `ccTables`. Valid types are "html", "text", "rcy3" or "none", default is "text" when the `ccOptions` object is initialized without an `outType` specified.

**Methods**

- `compareColors` signature(object = "ccOptions"): ...
- `compareColors<-` signature(object = "ccOptions"): ...
- `compareIndx` signature(object = "ccOptions"): ...
- `compareNames` signature(object = "ccOptions"): ...
- `compareNames<-` signature(object = "ccOptions"): ...
- `cssClass` signature(object = "ccOptions"): ...
- `listNames` signature(object = "ccOptions"): ...
- `listNames<-` signature(object = "ccOptions"): ...
- `outType` signature(object = "ccOptions"): ...
- `outType<-` signature(object = "ccOptions"): ...
Examples

showClass("ccOptions")
## A very basic "ccOptions" for a comparison of two sets of data, "list1" and "list2"
c1 <- new("ccOptions", listNames=c('list1','list2'))
c1

## Now lets get a little more complicated
c1 <- new("ccOptions", listNames=c('list1','list2'),
compareNames=c('list1,list2','list1,list3'), compareColors=c('red','blue'))
c1

# set the type of output you want to eventually produce
c1 <- new("ccOptions", listNames=c('list1','list2'), outType='html')
c1
c1 <- new("ccOptions", listNames=c('list1','list2'), outType=c('html','text','none'))
c1

## Using RGB colors
cCols <- matrix(c(255,0,0, 0,0,255), nrow=2, ncol=3)
cCols <- rgb(cCols, maxColorValue=255)
c1 <- new("ccOptions", listNames=c('list1','list2','list3'),
compareNames=c('list1,list2','list1,list3'), compareColors=cCols)

## Using Hex colors
c1 <- new("ccOptions", listNames=c('list1','list2','list3'),
compareNames=c('list1,list2','list1,list3'), compareColors=c('#FF0000','#0000FF'))
c1

## or even using a color palette from R.
## Note that you need at least enough colors to cover all of individual and
## possible permutations (n!) if you use compareNames='all'
c1 <- new("ccOptions", listNames=c('list1','list2','list3'),
compareNames=c('list1,list2','list1,list3'), compareColors=rainbow(4))
c1

Description

Passes a ccCompareResult object to Cytoscape for interactive visualization of ccCompare results.
Details

Note that only some basic, required methods have been imported from RCy3 for use with categoryCompare, and these are hidden in the functions within categoryCompare and are not visible to the user. If access to all the functionality of RCytoscape is desired (and trust me, there is a lot of useful stuff in there), then the user should use library(RCy3) directly.

It should also be noted that deletion of edges via RCy3 is slow, so some edge filtering should be done by breakEdges prior to using ccOutCyt.

Methods

signature(ccCompRes = "ccCompareResult", ccOpts = "ccOptions", ...) At a minimum, this method requires a ccCompareResult and a ccOptions to work.

... may include:

layout = "character" to override the default layout set by ccCompare, as well as options
postText = "character" to add a user set string to the Cytoscape window

In addition, any of the arguments to CytoscapeWindow may also be set, such as host or port.

See Also

ccCompareResult ccOptions ccCompare CytoscapeWindowClass

Examples

## Not run:
hasCy <- (if (.Platform$OS.type %in% "windows") {
  (length(grep("Cytoscape", system("tasklist", intern=TRUE))) > 0))

if hasCy {
  ccResults$BP <- breakEdges(ccResults$BP, 0.8)
  cwObj <- ccOutCyt(ccResults$BP, ccOpts)
  Sys.sleep(10)
  RCy3::deleteWindow(cwObj)
}

## End(Not run)

ccSigList-class

Class "ccSigList"

Description

Holds a generic list of significant annotations. Allows one to use Bioconductor annotation packages, or when combined into a GENccEnrichResult, use custom annotation / gene mappings.

Objects from the Class

Objects can be created by calls of the form new("ccSigList", ...).
Slots

- **sigID**: Object of class "character"
- **categoryName**: Object of class "character"
- **ontology**: Object of class "character"
- **annotation**: Object of class "character"

Methods

- **annotation** signature(object = "ccSigList"): ...
- **category** signature(object = "ccSigList"): ...
- **ontology** signature(object = "ccSigList"): ...
- **sigID** signature(object = "ccSigList"): ...

Author(s)

Robert M Flight

See Also

- **GENccEnrichResult ccCompareGeneric**

Examples

- `showClass("ccSigList")`

---

**cwReload-methods**

Methods for Function `cwReload` in Package `categoryCompare`

Description

Methods for function `cwReload` in package `categoryCompare`

Methods

```
signature(oldCW = "numeric", windowName = "character", ccOpts = "ccOptions")
```

This method is now deprecated as the cwObj doesn’t store anything, but is merely the network SUID pointing to the network in Cytoscape. See RCy3::getNetworkSuid.
Methods for Function cytOutData

Description
Takes the saveObj generated by cytOutNodes and writes the data to a file

Value
A text file with the annotations previously saved using cytOutNodes

Methods
signature(saveObj = "list", compareResult = "ccCompareResult", mergedData = "mergedData")
saveObj is the list object generated by cytOutNodes, compareResult is the object from
ccCompare, and mergedData is created using mergeLists, but is optional.

... : optional arguments also include: orgType, default is "header" where each group is separate, "annotate" pushes all the data into one table with a new column that designates which groups the annotation was found in; fileName, the name of a text file to output the results to; displayFile, whether or not to display the file (default is "FALSE")

Examples

## Not run:
hasCy <- (if (.Platform$OS.type %in% "windows") {
  (length(grep("Cytoscape", system("tasklist", intern=TRUE))) > 0))}
if hasCy {
data(ccData)
ccResults$BP <- breakEdges(ccResults$BP, 0.8)
cwObj <- ccOutCyt(ccResults$BP, ccOpts)
# user selects some nodes in Cytoscape
RCy3::selectNodes(cwObj, c("GO:0007017", "GO:0000226", "GO:0007051", "GO:0007052"))
savedNodes <- cytOutNodes("random1", cwObj) # save them
# and selects some other nodes
RCy3::selectNodes(cwObj,
c("GO:0071103", "GO:0034728", "GO:0006323", "GO:0030261", "GO:0006334"),
preserve.current.selection=FALSE)
savedNodes <- cytOutNodes("random2", cwObj, savedNodes)

# now spit results out to a file
cytOutData(savedNodes, ccResults$BP)
}
## End(Not run)
Methods for Function `cytOutNodes`

### Description

Allows export of currently selected nodes in the Cytoscape window for data export.

### Methods

```r
signature(descStr = "character", cwObj = "numeric", saveObj = "list")
```

- `descStr` is a string describing the nodes that are currently selected.
- `cwObj` is the `CytoscapeWindow` that the nodes are in, and then `saveObj` is a previously generated `cytOutNodes` list, and is optional.

### Examples

```r
## Not run:
hasCy <- (if (.Platform$OS.type %in% "windows") {
  (length(grep("Cytoscape", system("tasklist", intern=TRUE))) > 0))
if hasCy {
  ccResults$BP <- breakEdges(ccResults$BP, 0.8)
  cwObj <- ccOutCyt(ccResults$BP, ccOpts)
  # user selects some nodes in Cytoscape
  RCy3::selectNodes(cwObj, c("GO:0007017", "GO:0000226", "GO:0007051", "GO:0007052"))
  savedNodes <- cytOutNodes("random1", cwObj) # save them
  # and selects some other nodes
  RCy3::selectNodes(cwObj, c("GO:0071103", "GO:0034728", "GO:0006323", "GO:0030261", "GO:0006334"),
  preserve.current.selection=FALSE)
  savedNodes <- cytOutNodes("random2", cwObj, savedNodes)
}
## End(Not run)
```

### fdr

#### Description

Queries or sets the number of random runs to perform to generate an estimate of the false discovery rate. Defaults to 50.

#### Usage

```r
defr(object)
```
**GENccEnrichResult-class**

**Arguments**

object Can be ccGeneList, HyperGParamsCC, HyperGResultCC, ccEnrichResult. See Details for more information.

**Details**

fdr(object) gets the number of fdr runs for ccGeneList, HyperGParamsCC, HyperGResultCC, ccEnrichResult.

fdr(object)<- will set the number of fdr runs to be used by ccEnrich and HyperGTestCC when performing calculations on either a ccGeneList or HyperGParamsCC, respectively.

**Author(s)**

Robert M Flight

**See Also**

HyperGResultCC ccEnrichResult ccGeneList HyperGParamsCC

**Description**

Holds generic ccEnrich type results

**Objects from the Class**

Objects can be created by calls of the form new("GENccEnrichResult", ...).

**Slots**

.Data: Object of class "list" The actual list containing the ccEnrichResults

categoryName: Object of class "character"

ontology: Object of class "character"

geneAnnMapping: Object of class "namedList"

graphType: Object of class "character"

names: Object of class "character"

**Extends**

getGeneSymbol

Methods

[ signature(x = "GENccEnrichResult", i = "ANY", j = "ANY")]: Subsets the object to just those lists that are desired

categoryName signature(object = "GENccEnrichResult"): ...

collapseGeneric signature(gccResult = "GENccEnrichResult", ccOptions = "ccOptions"): ...

geneAnnMapping signature(object = "GENccEnrichResult"): ...

graphType signature(object = "GENccEnrichResult"): ...

graphType<- signature(object = "GENccEnrichResult"): ...

ontology signature(object = "GENccEnrichResult"): ...

Author(s)

Robert M Flight

See Also

collapseGeneric ccSigList

Examples

data(ccData)
locA <- grep("A", gseaRes$Tissues)
locL <- grep("L", gseaRes$Tissues)
locM <- grep("M", gseaRes$Tissues)

A <- new("ccSigList", sigID=gseaRes$KEGGID[locA], categoryName="KEGG", annotation="org.Mm.eg")
L <- new("ccSigList", sigID=gseaRes$KEGGID[locL], categoryName="KEGG", annotation="org.Mm.eg")
M <- new("ccSigList", sigID=gseaRes$KEGGID[locM], categoryName="KEGG", annotation="org.Mm.eg")
ccEnrichCol <- list(A=A, L=L, M=M)
ccEnrichCol <- new("GENccEnrichResult", ccEnrichCol, categoryName="KEGG")

getGeneSymbol

Entrez to name, symbol, GO and path conversion, as well as general ID to ID conversion.

Description

Get different attributes for the Entrez gene Ids

Usage

getGeneSymbol(id, annPackage)
geName(id, annPackage)
getGO2ALLEGS(id, annPackage)
getPATH2EG(id, annPackage)
geAnnotation(id, annPackage, mapID, doUnlist=TRUE)
Arguments

- id: The IDs one wants to get information for.
- annPackage: Which annotation package to use.
- mapID: Which mapping to use.
- doUnlist: Should the results be unlisted or not?

Details

The type of ID will change depending on the function. For `getGene`... the ID should be Entrez IDs. For `getGO2ALLEGS` Gene Ontology IDs should be used, and for `getPATH2EG` KEGG pathways IDs should be used. For `getAnnotation`, any ID can be used.

Value

Returns the requested information.

Note

These functions are generally called internally for mapping between genes and various objects.

Author(s)

Robert M Flight

Description

Gets and sets the `graphType` for a couple of different `ccEnrichResult` objects.

Methods

- `signature(object = "ccEnrichResult")`
- `signature(object = "GENccEnrichResult")`

See Also

`ccEnrichResult` `GENccEnrichResult`
Description

This class extends the HyperGParams class in Category by providing options for multiple testing and the storing of extra data in addition to the gene list of interest (not currently used, but might be in the future).

Objects from the Class

Objects can be created by calls of the form `new("HyperGParamsCC", ...)`. In general the user will not create these directly, but they are created and used by to carry out the enrichment calculations.

Slots

- `fdr`: Object of class "numeric" The number of FDR runs to perform
- `data`: Object of class "data.frame" Extra data stored in the object
- `geneIds`: Object of class "ANY" The genes of interest
- `universeGeneIds`: Object of class "ANY" The gene universe or background used (all the genes on the chip)
- `annotation`: Object of class "character" The annotation package used to get information about the geneIds
- `datPkg`: Object of class "DatPkg" Generated automatically from the annotation slot
- `categorySubsetIds`: Object of class "ANY" A specific set of category IDs that one wants to restrict the testing to
- `categoryName`: Object of class "character" What type of category to use, currently either "GO" or "KEGG"
- `pvalueCutoff`: Object of class "numeric" What should be the p-value to decide significance
- `testDirection`: Object of class "character" "over" or "under" represented annotation terms

Extends

Class "GOHyperGParams", directly.

Methods

No methods defined with class "HyperGParamsCC" in the signature.

Author(s)

Robert M Flight

See Also

HyperGResultCC ccEnrich Category-package
Examples

showClass("HyperGParamsCC")

HyperGResultCC-class  Class "HyperGResultCC"

Description

Contains the results of performing a hypergeometric test on a HyperGParams object.

Objects from the Class

Objects can be created by calls of the form new("HyperGResultCC", ...).

Slots

- `fdr`: Object of class "numeric" The number of FDR runs performed
- `fdrValues`: Object of class "numeric" The FDR values generated
- `pvalueType`: Object of class "character" Whether to use p-values or FDR values in determining the significant terms returned
- `data`: Object of class "data.frame" Extra data
- `pValues`: Object of class "numeric" P-values calculated for each term
- `oddsRatios`: Object of class "numeric"
- `expectedCounts`: Object of class "numeric"
- `catToGeneId`: Object of class "list"
- `organism`: Object of class "character"
- `annotation`: Object of class "character"
- `geneIds`: Object of class "ANY"
- `testName`: Object of class "character"
- `pvalueCutoff`: Object of class "numeric"
- `testDirection`: Object of class "character"

Extends

Class "HyperGResult", directly. Class "HyperGResultBase", by class "HyperGResult", distance 2.
Methods

- `fdr` signature(object = "HyperGResultCC"): ...  
- `fdrvalues` signature(object = "HyperGResultCC"): ...  
- `pCC` signature(object = "HyperGResultCC"): ...  
- `pvalueCutoff<-` signature(r = "HyperGResultCC"): ...  
- `pvalueType` signature(object = "HyperGResultCC"): ...  
- `pvalueType<-` signature(object = "HyperGResultCC"): ...  
- `minCount` signature(object = "HyperGResultCC"): ...  
- `minCount<-` signature(object = "HyperGResultCC"): ...

Author(s)

Robert M Flight

See Also

- `hyperGTestCC`

Examples

```r
showClass("HyperGResultCC")
```

---

Description

Performs the hypergeometric testing for `HyperGParamsCC` objects.

Usage

```r
hyperGTestCC(p)
```

Arguments

- `p` A `HyperGParamsCC` object

Details

This is the heart of `categoryCompare`, the function that calculates the HyperGeometric statistics for the given categories of annotation for each gene list.

Value

Returns a `HyperGResultCC` object
listNames

Author(s)
Robert M Flight

See Also
HyperGParamsCC HyperGResultCC GOHyperGParamsCC KEGGHyperGParamsCC GOHyperGResultCC KEGGHyperGResultCC

Examples
require(GO.db)
require(org.Hs.eg.db)
data(ccData)
g10 <- unique(table10$Entrez)
testGO <- new("GOHyperGParamsCC", geneIds=g10, universeGeneIds=gUniverse, annotation="org.Hs.eg.db", ontology="CC", conditional=FALSE, testDirection="over", fdr=0, pvalueCutoff = 0.01)
# ccHypRes <- hyperGTestCC(testGO)
# summary(ccHypRes)

listNames

Description
Extracts the listNames from ccGeneList or ccOptions objects.

Usage
listNames(object)

Arguments
object This will be either a ccGeneList or ccOptions object

Author(s)
Robert M Flight

See Also
ccGeneList ccOptions
Description

Stores merged data tables from the "data" entry in a ccGeneList. This is useful for output later.

Objects from the Class

Objects can be created by calls of the form `new("mergedData", ...)`.

Slots

- `.Data`: Object of class "list"
- `useIDName`: Object of class "character"
- `names`: Object of class "character"
- `row.names`: Object of class "data.frameRowLabels"
- `.S3Class`: Object of class "character"

Extends

Class "data.frame", directly. Class "list", by class "data.frame", distance 2. Class "oldClass", by class "data.frame", distance 2. Class "data.frameOrNULL", by class "data.frame", distance 2. Class "vector", by class "data.frame", distance 3.

Methods

signature(saveObj = "list", compareResult = "ccCompareResult", mergedData = "mergedData")

Author(s)

Robert M. Flight

See Also

mergeLists cytOutData

Examples

showClass("mergedData")

data(ccData)
mergeDat <- mergeLists(geneLists, ccOpts)
Function `mergeLists` in Package `categoryCompare`

Description

Merges the gene lists or the data tables from a `ccGeneList` object, providing a single table with all the input data, that can then be queried later, using `cytTableOut`

Usage

`mergeLists(ccGeneList, ccOptions, isGene=TRUE)`

Arguments

- `ccGeneList` a `ccGeneList` object
- `ccOptions` a `ccOptions` object
- `isGene` are the identifiers genes, or something else (metabolites, etc)

Value

A `mergedData` object which is really just a glorified data frame. If the `ccGeneList` input had a data list, then these are all merged into a single table. Otherwise, it contains just the gene names and which list they were present in.

Methods

signature(ccGeneList = "ccGeneList", ccOptions = "ccOptions")

See Also

`ccGeneList` `ccOptions` `mergedData`

Examples

data(ccData)
g10 <- unique(table10$Entrez[1:100])
g48 <- unique(table48$Entrez[1:100])

list10 <- list(genes=g10, universe=gUniverse, annotation="org.Hs.eg.db", data=table10[1:100,])
list48 <- list(genes=g48, universe=gUniverse, annotation="org.Hs.eg.db", data=table48[1:100,])

geneLists <- list(T10=list10, T48=list48)
geneLists <- new("ccGeneList", geneLists, ccType=c("BP","KEGG"))
ccOpts <- new("ccOptions", listNames = names(geneLists))
mergedDat <- mergeLists(geneLists, ccOpts)

list10 <- list(genes=g10, universe=gUniverse, annotation="org.Hs.eg.db")
list48 <- list(genes=g48, universe=gUniverse, annotation="org.Hs.eg.db")
```r
geneLists <- list(T10=list10, T48=list48)
geneLists <- new("ccGeneList", geneLists, ccType=c("BP","KEGG"))
ccOpts <- new("ccOptions", listNames = names(geneLists))
mergedDat <- mergeLists(geneLists, ccOpts)
```

---

### minCount

#### Description

Extracts and sets the minimum number of genes that an annotation must have to be considered in subsequent steps.

#### Usage

```r
minCount(object)
```

#### Arguments

- `object` This will be either a `HyperGResultCC`, `ccEnrichResult`, or `ccEnrichCollection` object. See Details for more information.

#### Details

- `minCount(object)` fetches the set `minCount` for `HyperGResultCC` and `ccEnrichResult` objects
- `minCount(object) <-` will set the `minCount` for `HyperGResultCC` objects, and when applied to `ccEnrichResult` and `ccEnrichCollection` sets the `minCount` for all of the contained objects, so be careful if you want to use different `minCounts` for different results

#### Author(s)

Robert M Flight

#### See Also

- `HyperGResultCC`
- `ccEnrichResult`
- `ccEnrichCollection`

#### Examples

```r
data(ccData)
enrichLists
minCount(enrichLists) <- 5
enrichLists
```
minNodes

Delete nodes with less than a certain number of genes annotated

Description

Deletes from the graph those annotations with less than a certain number of genes

Usage

minNodes(cwObj, cutoff)

Arguments

cwObj a CytoscapeWindowClass object returned from ccOutCyt
cutoff the minimum number of genes that an annotation must have

Author(s)

Robert M Flight

See Also

CytoscapeWindowClass ccOutCyt

Examples

```r
## Not run:
hasCy <- (if (.Platform$OS.type %in% "windows") {
  (length(grep("Cytoscape", system("tasklist", intern=TRUE))) > 0))}
if hasCy {
data(ccData)
ccResults$BP <- breakEdges(ccResults$BP, 0.8)
cwObj <- ccOutCyt(ccResults$BP, ccOpts)
minNodes(cwObj, 5)
}
## End(Not run)
```
pvalueType

| pvalueType | Type of p-values to return from object |

**Description**

Queries or sets the type of p-values to return from objects, either base calculated (pvals) or from fdr calculations (fdr)

**Usage**

pvalueType(object)

**Arguments**

object Can be HyperGResultCC, ccEnrichResult, ccEnrichCollection. See Details for more information

**Details**

pvalueType(object) gets the type of p-values to be returned from HyperGResultCC and ccEnrichResult objects

pvalueType(object)<- will set the type of p-values to be returned from HyperGResultCC, ccEnrichResult, ccEnrichCollection. Note that for a ccEnrichCollection, the type is changed for all contained ccEnrichResults

**Author(s)**

Robert M Flight

**See Also**

HyperGResultCC ccEnrichResult ccEnrichCollection

**Examples**

# pvalueType-Methods
data(ccData)

## Not run: pvalueType(enrichLists) # this returns an error
pvalueType(enrichLists[[1]])
pvalueType(enrichLists[[1]][[1]])

# change the type for one of the results
pvalueType(enrichLists[[1]]) <- 'pval' # Not recommended practice
enrichLists

# change for all of the results
pvalueType(enrichLists) <- 'pval'
enrichLists
**Description**

If the color of particular nodes have been modified from the original color scheme in `ccOptions`, this will reset them.

**Methods**

`signature(cwObj = "numeric", ccOpts = "ccOptions")` What CytoscapeWindow to apply this to, and what `ccOptions` to use for the color scheme.

**Optional Arguments:** Note that optional arguments include `node.attribute.name` (default is 'fillcolor') and `mode` (default is 'lookup')

**Author(s)**

Robert M Flight

**See Also**

`ccOptions` `setNodeColorMapping`

---

**Description**

The show and summary methods for `HyperGResultCC` objects generated using `hyperGTestCC`.

**Methods**

`show, signature(object = "HyperGResultCC")`

`summary, signature(object = "HyperGResultCC")`

**Author(s)**

Robert M Flight

**Examples**

```r
## Not run:
data(ccData)
show(enrichLists)
summary(enrichLists[[1]][[1]])
```

## End(Not run)
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