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Description topGO package provides tools for testing GO terms while accounting for the topology of the GO graph. Different test statistics and different methods for eliminating local similarities and dependencies between GO terms can be implemented and applied.

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Contents

topGO-package . . . 2
annFUN . . . 3
classicCount-class . . . 6
classicExpr-class . . . 7
classicScore-class . . . 8
Determines the levels of a Directed Acyclic Graph (DAG) . . . 9
dignostic-methods . . . 11
elimCount-class . . . 13
elimExpr-class . . . 14
elimScore-class . . . 16
Gene set tests statistics . . . 17
geneList . . . 18
getPvalues . . . 18
getSigGroups . . . 19
GOdata . . . 21
groupGOTerms . . . 22
groupStats-class . . . 22
inducedGraph . . . 23
parentChild-class . . . 24
printGraph-methods . . . 26
topGOdata-class . . . 27
topGOresult-class . . . 31
weightCount-class . . . 32

Index **34**

`topGO-package` *Enrichment analysis for Gene Ontology*

Description

topGO package provides tools for testing GO terms while accounting for the topology of the GO graph. Different test statistics and different methods for eliminating local similarities and dependencies between GO terms can be implemented and applied.

Details

Package:	topGO
Type:	Package
Version:	1.0
Date:	2006-10-02

License: What license is it under?

TODO: An overview of how to use the package, including the most important functions

Author(s)

Adrian Alexa, J\"org Rahnenf\"uhrer

Maintainer: Adrian Alexa

References

Alexa A., Rahnenf\"uhrer J., Lengauer T., Improved scoring of functional groups from gene expression data by decorrelating GO graph structure, Bioinformatics 22(13): 1600-1607, 2006

See Also

topGOdata-class, groupStats-class, getSigGroups-methods

---

annFUN *Functions which map gene identifiers to GO terms*

Description

These functions are used to compile a list of GO terms such that each element in the list is a character vector containing all the gene identifiers that are mapped to the respective GO term.

Usage

```
annFUN.db(whichOnto, feasibleGenes = NULL, affyLib)
annFUN.org(whichOnto, feasibleGenes = NULL, mapping, ID = "entrez")
annFUN(whichOnto, feasibleGenes = NULL, affyLib)
annFUN.gene2GO(whichOnto, feasibleGenes = NULL, gene2GO)
annFUN.GO2genes(whichOnto, feasibleGenes = NULL, GO2genes)
annFUN.file(whichOnto, feasibleGenes = NULL, file, ...)

readMappings(file, sep = "\t", IDsep = ",")
inverseList(l)
```

Arguments

whichOnto	character string specifying one of the three GO ontologies, namely: "BP", "MF", "CC"
feasibleGenes	character vector containing a subset of gene identifiers. Only these genes will be used to annotate GO terms. Default value is NULL which means that there are no genes filtered.

affyLib	character string containing the name of the Bioconductor annotation package for a specific microarray chip.
gene2GO	named list of character vectors. The list names are genes identifiers. For each gene the character vector contains the GO identifiers it maps to. Only the most specific annotations are required.
GO2genes	named list of character vectors. The list names are GO identifiers. For each GO the character vector contains the genes identifiers which are mapped to it. Only the most specific annotations are required.
mapping	character string specifying the name of the Bioconductor package containing the gene mappings for a specific organism. For example: `mapping = "org.Hs.eg.db"`.
ID	character string specifying the gene identifier to use. Currently only the following identifiers can be used: `c("entrez", "genbank", "alias", "ensembl", "symbol", "genename", "unigene")`
file	character string specifying the file containing the annotations.
...	other parameters
sep	the character used to separate the columns in the CSV file
IDsep	the character used to separate the annotated entities
l	a list containing mappings

Details

All these function restrict the GO terms to the ones belonging to the specified ontology and to the genes listed in the `feasibleGenes` attribute (if not empty).

The function `annFUN.db` uses the mappings provided in the Bioconductor annotation data packages. For example, if the Affymetrix `hgu133a` chip it is used, then the user should set `affyLib = "hgu133a.db"`.

The functions `annFUN.gene2GO` and `annFUN.GO2genes` are used when the user provide his own annotations either as a gene-to-GOs mapping, either as a GO-to-genes mapping.

The `annFUN.org` function is using the mappings from the "org.XX.XX" annotation packages. The function supports different gene identifiers.

The `annFUN.file` function will read the annotationsof the type gene2GO or GO2genes from a text file.

Value

A named(GO identifiers) list of character vectors.

Author(s)

Adrian Alexa

See Also

topGOdata-class

Examples

```
library(hgu133a.db)
set.seed(111)

## generate a gene list and the GO annotations
selGenes <- sample(ls(hgu133aGO), 50)
gene2GO <- lapply(mget(selGenes, envir = hgu133aGO), names)
gene2GO[sapply(gene2GO, is.null)] <- NA

## the annotation for the first three genes
gene2GO[1:3]

## inverting the annotations
G2g <- inverseList(gene2GO)

## inverting the annotations and selecting an ontology
go2genes <- annFUN.gene2GO(whichOnto = "CC", gene2GO = gene2GO)


## generate a GO list with the genes annotations
selGO <- sample(ls(hgu133aGO2PROBE), 30)
GO2gene <- lapply(mget(selGO, envir = hgu133aGO2PROBE), as.character)

GO2gene[1:3]

## select only the GO terms for a specific ontology
go2gene <- annFUN.GO2genes(whichOnto = "CC", GO2gene = GO2gene)


##################################################
## Using the org.XX.xx.db annotations
##################################################

## GO to Symbol mappings (only the BP ontology is used)
xx <- annFUN.org("BP", mapping = "org.Hs.eg.db", ID = "symbol")
head(xx)

## Not run:

allGenes <- unique(unlist(xx))
myInterestedGenes <- sample(allGenes, 500)
geneList <- factor(as.integer(allGenes
names(geneList) <- allGenes

GOdata <- new("topGOdata",
              ontology = "BP",
              allGenes = geneList,
              nodeSize = 5,
              annot = annFUN.org,
              mapping = "org.Hs.eg.db",
              ID = "symbol")
```

```
## End(Not run)
```

`classicCount-class` *Class "classicCount"*

Description

This class that extends the virtual class "groupStats" by adding a slot representing the significant members.

Details

This class is used for test statistic based on counts, like Fisher's exact test

Objects from the Class

Objects can be created by calls of the form `new("classicCount", testStatistic = "function", name = "character", allMembers = "character", groupMembers = "character", sigMembers = "character")`.

Slots

`significant`**:** Object of class `"integer"` ~~

`name`**:** Object of class `"character"` ~~

`allMembers`**:** Object of class `"character"` ~~

`members`**:** Object of class `"character"` ~~

`testStatistic`**:** Object of class `"function"` ~~

Extends

Class `"groupStats"`, directly.

Methods

contTable `signature(object = "classicCount")`: ...

initialize `signature(.Object = "classicCount")`: ...

numSigAll `signature(object = "classicCount")`: ...

numSigMembers `signature(object = "classicCount")`: ...

sigAllMembers `signature(object = "classicCount")`: ...

sigMembers<- `signature(object = "classicCount")`: ...

sigMembers `signature(object = "classicCount")`: ...

Author(s)

Adrian Alexa

See Also

classicScore-class, groupStats-class, getSigGroups-methods

Examples

```
##---- Should be DIRECTLY executable !! ----
```

---

classicExpr-class *Class "classicExpr"*

Description

This class that extends the virtual class "groupStats" by adding two slots for accommodating gene expression data.

Objects from the Class

Objects can be created by calls of the form `new("classicExpr", testStatistic, name, groupMembers, exprDat, pType, ...)`.

Slots

eData: Object of class `"environment"` ~~

pType: Object of class `"factor"` ~~

name: Object of class `"character"` ~~

allMembers: Object of class `"character"` ~~

members: Object of class `"character"` ~~

testStatistic: Object of class `"function"` ~~

testStatPar: Object of class `"list"` ~~

Extends

Class "groupStats", directly.

Methods

allMembers<- `signature(object = "classicExpr")`: ...

emptyExpr `signature(object = "classicExpr")`: ...

getSigGroups `signature(object = "topGOdata", test.stat = "classicExpr")`: ...

GOglobalTest `signature(object = "classicExpr")`: ...

initialize `signature(.Object = "classicExpr")`: ...

membersExpr `signature(object = "classicExpr")`: ...

pType<- `signature(object = "classicExpr")`: ...

pType `signature(object = "classicExpr")`: ...

Author(s)

Adrian Alexa

See Also

classicScore-class, groupStats-class, getSigGroups-methods

Examples

```
showClass("classicExpr")
```

---

classicScore-class *Class "classicScore"*

Description

A class that extends the virtual class "groupStats" by adding a slot representing the score of each gene. It is used for tests like Kolmogorov-Smirnov test.

Objects from the Class

Objects can be created by calls of the form `new("classicScore", testStatistic, name, allMembers, groupMembers, score, decreasing)`.

Slots

score: Object of class "numeric" ~~

name: Object of class "character" ~~

allMembers: Object of class "character" ~~

members: Object of class "character" ~~

testStatistic: Object of class "function" ~~

scoreOrder: Object of class "character" ~~

testStatPar: Object of class "ANY" ~~

Extends

Class "groupStats", directly.

Methods

allScore Method to obtain the score of all members.

scoreOrder Returns TRUE if the score should be ordered increasing, FALSE otherwise.

membersScore `signature(object = "classicScore")`: ...

rankMembers `signature(object = "classicScore")`: ...

score<- `signature(object = "classicScore")`: ...

Author(s)

Adrian Alexa

See Also

classicCount-class, groupStats-class, getSigGroups-methods

Examples

```
## define the type of test you want to use
test.stat <- new("classicScore", testStatistic = GOKSTest, name = "KS tests")
```

Determines the levels of a Directed Acyclic Graph (DAG)

Utility functions to work with Directed Acyclic Graphs (DAG)

Description

Basic functions to work with DAGs

Usage

```
buildLevels(dag, root = NULL, leafs2root = TRUE)
getNoOfLevels(graphLevels)
getGraphRoot(dag, leafs2root = TRUE)
reverseArch(dirGraph, useAlgo = "sparse", useWeights = TRUE)
```

Arguments

dag	A graphNEL object.
root	A character vector specifying the root(s) of the DAG. If not specified the root node is automatically computed.
leafs2root	The leafs2root parameter tell if the graph has edges directed from the leaves to the root, or vice-versa
graphLevels	An object of type list, returned by the buildLevels function.
dirGraph	A graphNEL object containing a directed graph.
useAlgo	A character string specifying one of the following options c("sparse", "normal"). By default, useAlgo = "sparse", a sparse matrix object is used to transpose the adjacency matrix. Otherwise a standard R martix is used.
useWeights	If weights should be used (if useAlgo = "normal" then the weights are used anyway)

Details

`buildLevels` function determines the levels of a Directed Acyclic Graph (DAG). The level of a node is defined as the longest path from the node to the root. The function take constructs a named list containing various information about each nodes level. The root has level 1.

`getNoOfLevels` - a convenient function to extract the number of levels from the object returned by `buildLevels`

`getGraphRoot` finds the root(s) of the DAG

`reverseArch` - simple function to invert the direction of edges in a DAG. The returned graph is of class graphNEL. It can use either simple matrices or sparse matrices (SparseM library)

Value

`buildLevels` returns a list containing:

`level2nodes`	Environment where the key is the level number with the value being the nodes on that level.
`nodes2level`	Environment where the key is the node label (the GO ID) and the value is the level on which that node lies.
`noOfLevels`	The number of levels
`noOfNodes`	The number of nodes

An object of class `graphNEL-class` is returned.

Author(s)

Adrian Alexa

See Also

`topGOdata-class`, `inducedGraph`

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##-- or do  help(data=index)  for the standard data sets.
```

dignostic-methods *Diagnostic functions for topGOdata and topGOresult objects.*

Description

The GenTable function generates a summary of the results of the enrichment analysis.

The showGroupDensity function plots the distributions of the gene' scores/ranks inside a GO term.

The printGenes function shows a short summary of the top genes annotated to the specified GO terms.

Usage

```
GenTable(object, ...)

showGroupDensity(object, whichGO, ranks = FALSE, rm.one = TRUE)

printGenes(object, whichTerms, file, ...)
```

Arguments

object	an object of class topGOdata.
whichGO	the GO terms for which the plot should be generated.
ranks	if ranks should be used instead of scores.
rm.one	the p-values which are 1 are removed.
whichTerms	character vector listing the GO terms for which the summary should be printed.
file	character string specifying the file in which the results should be printed.
...	Extra arguments for GenTable can be: ... one or more objects of class topGOresult. orderBy if more than one topGOresult object is given then orderBy gives the index of which scores will be used to order the resulting table. Can be an integer index or a character vector given the name of the topGOresult object. ranksOf same as orderBy argument except that this parameter shows the relative ranks of the specified result. topNodes the number of top GO terms to be included in the table. numChar the GO term definition will be truncated such that only the first numChar characters are shown. Extra arguments for printGenes can be: chip character string containing the name of the Bioconductor annotation package for a microarray chip. numChar the gene description is trimmed such that it has numChar characters. simplify logical variable affecting how the results are returned. geneCutOff the maximal number of genes shown for each term. pvalCutOff only the genes with a p-value less than pvalCutOff are shown. oneFile if TRUE then a file for each GO term is generated.

Details

GenTable is an easy to use function for summarising the most significant GO terms and the corresponding p-values. The function dispatches for topGOdata and topGOresult objects, and it can take an arbitrary number of the later, making comparison between various results easier.

Note: One needs to type the complete attribute names (the exact name) of this function, like: topNodes = 5, rankOf = "resultFis", etc. This being the price paid for flexibility of specifying different number of topGOdata objects.

The showGroupDensity function analyse the distribution of the gene-wise scores for a specified GO term. The function will show the distribution of the genes in a GO term compared with the complementary set, using a lattice plot.

printGenes The function will generate a table with all the probes annotated to the specified GO term. Various type of identifiers, the gene name and the gene-wise statistics are provided in the table.

One or more GO identifiers can be given to the function using the whichTerms argument. When more than one GO is specified, the function returns a list of data.frames, otherwise only one data.frame is returned.

The function has a argument file which, when specified, will save the results into a file using the CSV format.

For the moment the function will work only when the chip used has an annotation package available in Bioconductor. It will not work with other type of custom annotations.

Value

A data.frame or a list of data.frames.

Author(s)

Adrian Alexa

See Also

groupStats-class, getSigGroups-methods

Examples

```
data(GOdata)


#######################################
## GenTable
#######################################

## load two topGOresult sample objects: resultFisher and resultKS
data(results.tGO)

## generate the result of Fisher's exact test
sig.tab <- GenTable(GOdata, Fis = resultFisher, topNodes = 20)
```

```
## results of both test
sig.tab <- GenTable(GOdata, resultFisher, resultKS, topNodes = 20)

## results of both test with specified names
sig.tab <- GenTable(GOdata, Fis = resultFisher, KS = resultKS, topNodes = 20)

## results of both test with specified names and specified ordering
sig.tab <- GenTable(GOdata, Fis = resultFisher,
                    KS = resultKS, orderBy = "KS",
                    ranksOf = "Fis", topNodes = 20)


#######################################
## showGroupDensity
#######################################

goID <- "GO:0006091"
print(showGroupDensity(GOdata, goID, ranks = TRUE))
print(showGroupDensity(GOdata, goID, ranks = FALSE, rm.one = FALSE))



#######################################
## printGenes
#######################################

## Not run:
library(hgu95av2.db)
goID <- "GO:0006629"

gt <- printGenes(GOdata, whichTerms = goID, chip = "hgu95av2.db", numChar = 40)

goIDs <- c("GO:0006629", "GO:0007076")
gt <- printGenes(GOdata, whichTerms = goIDs, chip = "hgu95av2.db", pvalCutOff = 0.01)

gt[goIDs[1]]

## End(Not run)
```

`elimCount-class` *Classes "elimCount" and "weight01Count"*

Description

Classes that extend the "classicCount" class by adding a slot representing the members that need to be removed.

Objects from the Class

Objects can be created by calls of the form `new("elimCount", testStatistic, name, allMembers, groupMembers, sigMembers, elim, cutOff, ...)`.

Slots

`elim`: Object of class `"integer"` ~~

`cutOff`: Object of class `"numeric"` ~~

`significant`: Object of class `"integer"` ~~

`name`: Object of class `"character"` ~~

`allMembers`: Object of class `"character"` ~~

`members`: Object of class `"character"` ~~

`testStatistic`: Object of class `"function"` ~~

`testStatPar`: Object of class `"list"` ~~

Extends

Class `"classicCount"`, directly. Class `"groupStats"`, by class "classicCount", distance 2.

Methods

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

Author(s)

Adrian Alexa

See Also

`classicScore-class`, `groupStats-class`, `getSigGroups-methods`

`elimExpr-class` *Class "elimExpr"*

Description

Classes that extend the "classicExpr" class by adding a slot representing the members that need to be removed.

Details

TODO: Some details here.....

Objects from the Class

Objects can be created by calls of the form `new("elimExpr", testStatistic, name, groupMembers, exprDat, pType, elim, cutOff, ...)`. ~~ describe objects here ~~

Slots

`cutOff`: Object of class "numeric" ~~

`elim`: Object of class "integer" ~~

`eData`: Object of class "environment" ~~

`pType`: Object of class "factor" ~~

`name`: Object of class "character" ~~

`allMembers`: Object of class "character" ~~

`members`: Object of class "character" ~~

`testStatistic`: Object of class "function" ~~

`testStatPar`: Object of class "list" ~~

Extends

Class "weight01Expr", directly. Class "classicExpr", by class "weight01Expr", distance 2. Class "groupStats", by class "weight01Expr", distance 3.

Methods

cutOff<- `signature(object = "elimExpr")`: ...

cutOff `signature(object = "elimExpr")`: ...

getSigGroups `signature(object = "topGOdata", test.stat = "elimExpr")`: ...

initialize `signature(.Object = "elimExpr")`: ...

Author(s)

Adrian Alexa

See Also

classicScore-class, groupStats-class, getSigGroups-methods

Examples

```
showClass("elimExpr")
```

elimScore-class *Classes "elimScore" and "weight01Score"*

Description

Classes that extend the "classicScore" class by adding a slot representing the members that need to be removed.

Details

TODO:

Objects from the Class

Objects can be created by calls of the form `new("elimScore", testStatistic, name, allMembers, groupMembers, score, alternative, elim, cutOff, ...)`. ~~ describe objects here ~~

Slots

`elim`: Object of class `"integer"` ~~

`cutOff`: Object of class `"numeric"` ~~

`score`: Object of class `"numeric"` ~~

`.alternative`: Object of class `"logical"` ~~

`name`: Object of class `"character"` ~~

`allMembers`: Object of class `"character"` ~~

`members`: Object of class `"character"` ~~

`testStatistic`: Object of class `"function"` ~~

`testStatPar`: Object of class `"list"` ~~

Extends

Class "classicScore", directly. Class "groupStats", by class "classicScore", distance 2.

Methods

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

Author(s)

Adrian Alexa

See Also

classicScore-class, groupStats-class, getSigGroups-methods

Examples

```
##---- Should be DIRECTLY executable !! ----
```

`Gene set tests statistics` *Gene set tests statistics*

Description

Methods which implement and run a group test statistic for a class inheriting from `groupStats` class. See Details section for a description of each method.

Usage

```
GOFisherTest(object)
GOKSTest(object)
GOtTest(object)
GOglobalTest(object)
GOSumTest(object)
GOKSTiesTest(object)
```

Arguments

`object`	An object of class `groupStats` or decedent class.

Details

GOFisherTest: implements Fischer's exact test (based on contingency table) for `groupStats` objects dealing with "counts".

GOKSTest: implements the Kolmogorov-Smirnov test for `groupStats` objects dealing with gene "scores". This test uses the `ks.test` function and does not implement the running-sum-statistic test based on permutations.

GOtTest: implements the t-test for `groupStats` objects dealing with gene "scores". It should be used when the gene scores are t-statistics or any other score following a normal distribution.

GOglobalTest: implement Goeman's globaltest.

Value

All these methods return the p-value computed by the respective test statistic.

Author(s)

Adrian Alexa

See Also

`groupStats-class`, `getSigGroups-methods`

geneList *A toy example of a list of gene identifiers and the respective p-values*

Description

The geneList data is compiled from a differential expression analysis of the ALL dataset. It contains just a small number of genes with the corespondent p-values. The information on where to find the GO annotations is stored in the ALL object.

The topDiffGenes function included in this dataset will select the differentially expressed genes, at 0.01 significance level, from geneList.

Usage

```
data(geneList)
```

Source

Generated using the ALL gene expression data. See the "scripts" directory.

Examples

```
data(geneList)

## print the object
head(geneList)
length(geneList)

## the number of genes with a p-value less than 0.01
sum(topDiffGenes(geneList))
```

getPvalues *Convenient function to compute p-values from a gene expression matrix.*

Description

Warping function of "mt.teststat", for computing p-values of a gene expression matrix.

Usage

```
getPvalues(edata, classlabel, test = "t",
          alternative = c("greater", "two.sided", "less")[1], genesID = NULL,
           correction = c("none", "Bonferroni", "Holm", "Hochberg",
                          "SidakSS", "SidakSD", "BH", "BY")[8])
```

Arguments

edata	Gene expression matrix.
classlabel	The phenotype of the data
test	Which test statistic to use
alternative	The alternative of the test statistic
genesID	if a subset of genes is provided
correction	Multiple testing correction procedure

Value

An named numeric vector of p-values.

Author(s)

Adrian Alexa

See Also

GOKSTest, groupStats-class, getSigGroups-methods

Examples

```
library(ALL)
data(ALL)

## discriminate B-cell from T-cell
classLabel <- as.integer(sapply(ALL$BT, function(x) return(substr(x, 1, 1) == 'T')))

## Differentially expressed genes
geneList <- getPvalues(exprs(ALL), classlabel = classLabel,
                       alternative = "greater", correction = "BY")

hist(geneList, 50)
```

---

getSigGroups *Interfaces for running the enrichment tests*

Description

These function are used for dispatching the specific algorithm for a given topGOdata object and a test statistic.

Usage

```
getSigGroups(object, test.stat, ...)
runTest(object, algorithm, statistic, ...)
whichAlgorithms()
whichTests()
```

Arguments

object	An object of class topGOdata This object contains all data necessary for running the test.
test.stat	An object of class groupStats. This object defines the test statistic.
algorithm	Character string specifying which algorithm to use.
statistic	Character string specifying which test to use.
...	Other parameters. In the case of runTest they are used for defining the test statistic

Details

The runTest function can be used only with a predefined set of test statistics and algorithms. The algorithms and the statistical tests which are accessible via the runTest function are shown by the whichAlgorithms() and whichTests() functions.

The runTest function is a warping of the getSigGroups and the initialisation of a groupStats object functions.

...

Value

An object of class topGOresult.

Author(s)

Adrian Alexa

See Also

topGOdata-class, groupStats-class, topGOresult-class

Examples

```
## load a sample topGOdata object
data(GOdata)
GOdata

##############################
## getSigGroups interface
##############################

## define a test statistic
test.stat <- new("classicCount", testStatistic = GOFisherTest, name = "Fisher test")
## perform the test
resultFis <- getSigGroups(GOdata, test.stat)
resultFis



##############################
```

```
## runTest interface
##############################

## Enrichment analysis by using the "classic" method and Fisher's exact test
resultFis <- runTest(GOdata, algorithm = "classic", statistic = "fisher")
resultFis

## weight01 is the default algorithm
weight01.fisher <- runTest(GOdata, statistic = "fisher")
weight01.fisher


## not all combinations are possible!
# weight.ks <- runTest(GOdata, algorithm = "weight", statistic = "t")
```

GOdata *Sample topGOdata and topGOresult objects*

Description

The GOdata contains an instance of a topGOdata object. It can be used to run an enrichment analysis directly.

The resultFisher contains the results of an enrichment analysis.

Usage

```
data(GOdata)
```

Source

Generated using the ALL gene expression data. See topGOdata-class for code examples on how-to generate such an object.

Examples

```
data(GOdata)

## print the object
GOdata

data(results.tGO)

## print the object
resultFisher
```

groupGOTerms *Grouping of GO terms into the three ontologies*

Description

This function split the GOTERM environment into three different ontologies. The newly created environments contain each only the terms from one of the following ontologies 'BP', 'CC', 'MF'

Usage

```
groupGOTerms(where)
```

Arguments

where	The the environment where you want to bind the results.

Value

The function returns NULL.

Author(s)

Adrian Alexa

See Also

topGOdata-class, GOTERM

Examples

```
groupGOTerms()
```

groupStats-class *Class "groupStats"*

Description

A virtual class containing basic gene set information: the gene universe, the member of the current group, the test statistic defined for this group, etc.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

`name`: Object of class `"character"` ~~

`allMembers`: Object of class `"character"` ~~

`members`: Object of class `"character"` ~~

`testStatistic`: Object of class `"function"` ~~

`testStatPar`: Object of class `"ANY"` ~~

Methods

allMembers<- `signature(object = "groupStats")`: ...

allMembers `signature(object = "groupStats")`: ...

initialize `signature(.Object = "groupStats")`: ...

members<- `signature(object = "groupStats")`: ...

members `signature(object = "groupStats")`: ...

Name<- `signature(object = "groupStats")`: ...

Name `signature(object = "groupStats")`: ...

numAllMembers `signature(object = "groupStats")`: ...

numMembers `signature(object = "groupStats")`: ...

runTest `signature(object = "groupStats")`: ...

testStatistic `signature(object = "groupStats")`: ...

Author(s)

Adrian Alexa

See Also

`classicCount-class`, `getSigGroups-methods`

---

inducedGraph *The subgraph induced by a set of nodes.*

Description

Given a set of nodes (GO terms) this function is returning the subgraph containing these nodes and their ancestors.

Usage

```
inducedGraph(dag, startNodes)
nodesInInducedGraph(dag, startNodes)
```

Arguments

dag	An object of class graphNEL containing a directed graph.
startNodes	A character vector giving the starting nodes.

Value

An object of class graphNEL-class is returned.

Author(s)

Adrian Alexa

See Also

topGOdata-class, reverseArch,

Examples

```
data(GOdata)

## the GO graph
g <- graph(GOdata)
g

## select 10 random nodes
sn <- sample(nodes(g), 10)


## the subgraph induced by these nodes
sg <- inducedGraph(g, sn)
sg
```

---

parentChild-class *Classes "parentChild" and "pC"*

Description

Classes that extend the "classicCount" class by adding support for the parent-child test.

Objects from the Class

Objects can be created by calls of the form new("parentChild", testStatistic, name, groupMembers, parents, sigMembers, joinFun, ...).

Slots

`splitIndex`: Object of class "integer" ~~

`joinFun`: Object of class "character" ~~

`significant`: Object of class "integer" ~~

`name`: Object of class "character" ~~

`allMembers`: Object of class "character" ~~

`members`: Object of class "character" ~~

`testStatistic`: Object of class "function" ~~

`testStatPar`: Object of class "list" ~~

Extends

Class "classicCount", directly. Class "groupStats", by class "classicCount", distance 2.

Methods

allMembers<- `signature(object = "parentChild")`: ...

allMembers `signature(object = "parentChild")`: ...

allParents `signature(object = "parentChild")`: ...

getSigGroups `signature(object = "topGOdata", test.stat = "parentChild")`: ...

initialize `signature(.Object = "parentChild")`: ...

joinFun `signature(object = "parentChild")`: ...

numAllMembers `signature(object = "parentChild")`: ...

numSigAll `signature(object = "parentChild")`: ...

sigAllMembers `signature(object = "parentChild")`: ...

sigMembers<- `signature(object = "parentChild")`: ...

updateGroup `signature(object = "parentChild", name = "missing", members = "character")`: ...

Author(s)

Adrian Alexa

See Also

classicCount-class, groupStats-class, getSigGroups-methods

Examples

```
showClass("parentChild")
showClass("pC")
```

printGraph-methods *Visualisation functions*

Description

Functions to plot the subgraphs induced by the most significant GO terms

Usage

```
showSigOfNodes(GOdata, termsP.value, firstSigNodes = 10, reverse = TRUE,
               sigForAll = TRUE, wantedNodes = NULL, putWN = TRUE,
               putCL = 0, type = NULL, showEdges = TRUE,  swPlot = TRUE,
               useFullNames = TRUE, oldSigNodes = NULL,
               useInfo = c("none", "pval", "counts", "def", "np", "all")[1],
               plotFunction = GOplot, .NO.CHAR = 20)

printGraph(object, result, firstSigNodes, refResult, ...)
```

Arguments

object	an object of class topGOdata.
GOdata	an object of class topGOdata.
result	an object of class topGOresult.
firstSigNodes	the number of top scoring GO terms which ....
refResult	an object of class topGOresult.
termsP.value	named vector of p-values.
reverse	the direction of the edges.
sigForAll	if TRUE the score/p-value of all nodes in the DAG is shown, otherwise only the score for the sigNodes
wantedNodes	the nodes that we want to find, we will plot this nodes with a different color. The vector contains the names of the nodes
putWN	the graph is generated with using the firstSigNodes and the wantedNodes.
putCL	we generate the graph from the nodes given by all previous parameters, plus their children. if putCL = 1 than only the children are added, if putCL = n we get the nodes form the next n levels.
type	used for plotting pie charts
showEdges	if TRUE the edge are shown
swPlot	if true the graph is ploted, if not no plotting is done.
useInfo	additional info to be ploted to each node.
oldSigNodes	used to plot the (new) sigNodes in the same color range as the old ones
useFullNames	argument for internal use ..
plotFunction	argument for internal use ..

.NO.CHAR	argument for internal use ..
...	Extra arguments for printGraph can be:
	fn.prefix character string giving the file name prefix.
	useInfo as in showSigOfNodes function.
	pdfSW logical attribute switch between PDF or PS formats.

Details

There are two functions available. The showSigOfNodes will plot the induced subgraph to the current graphic device. The printGraph is a warping function for showSigOfNodes and will save the resulting graph into a PDF or PS file.

In the plots, the significant nodes are represented as rectangles. The plotted graph is the upper induced graph generated by these significant nodes.

Author(s)

Adrian Alexa

See Also

groupStats-class, getSigGroups-methods

Examples

```
## Not run:
data(GOdata)
data(results.tGO)

showSigOfNodes(GOdata, score(resultFisher), firstSigNodes = 5, useInfo = 'all')
printGraph(GOdata, resultFisher, firstSigNodes = 5,
           fn.prefix = "sampleFile", useInfo = "all", pdfSW = TRUE)

## End(Not run)
```

---

topGOdata-class *Class "topGOdata"*

Description

TODO: The node attributes are environments containing the genes/probes annotated to the respective node

If genes is a numeric vector than this should represent the gene's score. If it is factor it should discriminate the genes in interesting genes and the rest

TODO: it will be a good idea to replace the allGenes and allScore with an ExpressionSet class. In this way we can use tests like global test, globalAncova.... – ALL variables starting with . are just for internal class usage (private)

Objects from the Class

Objects can be created by calls of the form `new("topGOdata", ontology, allGenes, geneSelectionFun, description, annotationFun, ...)`. ~~ describe objects here ~~

Slots

`description`: Object of class `"character"` ~~

`ontology`: Object of class `"character"` ~~

`allGenes`: Object of class `"character"` ~~

`allScores`: Object of class `"ANY"` ~~

`geneSelectionFun`: Object of class `"function"` ~~

`feasible`: Object of class `"logical"` ~~

`nodeSize`: Object of class `"integer"` ~~

`graph`: Object of class `"graphNEL"` ~~

`expressionMatrix`: Object of class `"matrix"` ~~

`phenotype`: Object of class `"factor"` ~~

Methods

allGenes `signature(object = "topGOdata")`: ...

attrInTerm `signature(object = "topGOdata", attr = "character", whichGO = "character")`: ...

attrInTerm `signature(object = "topGOdata", attr = "character", whichGO = "missing")`: ...

countGenesInTerm `signature(object = "topGOdata", whichGO = "character")`: ...

countGenesInTerm `signature(object = "topGOdata", whichGO = "missing")`: ...

description<- `signature(object = "topGOdata")`: ...

description `signature(object = "topGOdata")`: ...

feasible<- `signature(object = "topGOdata")`: ...

feasible `signature(object = "topGOdata")`: ...

geneScore `signature(object = "topGOdata")`: ...

geneSelectionFun<- `signature(object = "topGOdata")`: ...

geneSelectionFun `signature(object = "topGOdata")`: ...

genes `signature(object = "topGOdata")`: A method for obtaining the list of genes, as a character vector, which will be used in the further analysis.

numGenes `signature(object = "topGOdata")`: A method for obtaining the number of genes, which will be used in the further analysis. It has the same effect as: `lenght(genes(object))`.

sigGenes `signature(object = "topGOdata")`: A method for obtaining the list of significant genes, as a character vector.

genesInTerm `signature(object = "topGOdata", whichGO = "character")`: ...

genesInTerm `signature(object = "topGOdata", whichGO = "missing")`: ...

getSigGroups signature(object = "topGOdata", test.stat = "classicCount"): ...

getSigGroups signature(object = "topGOdata", test.stat = "classicScore"): ...

graph<- signature(object = "topGOdata"): ...

graph signature(object = "topGOdata"): ...

initialize signature(.Object = "topGOdata"): ...

ontology<- signature(object = "topGOdata"): ...

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

termStat signature(object = "topGOdata", whichGO = "character"): ...

termStat signature(object = "topGOdata", whichGO = "missing"): ...

updateGenes signature(object = "topGOdata", geneList = "numeric", geneSelFun = "function"): ...

updateGenes signature(object = "topGOdata", geneList = "factor", geneSelFun = "missing"): ...

updateTerm<- signature(object = "topGOdata", attr = "character"): ...

usedGO signature(object = "topGOdata"): ...

Author(s)

Adrian Alexa

See Also

buildLevels, annFUN

Examples

```
## load the dataset
data(geneList)
library(package = affyLib, character.only = TRUE)

## the distribution of the adjusted p-values
hist(geneList, 100)

## how many differentially expressed genes are:
sum(topDiffGenes(geneList))

## build the topGOdata class
GOdata <- new("topGOdata",
              ontology = "BP",
              allGenes = geneList,
              geneSel = topDiffGenes,
              description = "GO analysis of ALL data: DE B-cell vs T-cell",
              annot = annFUN.db,
              affyLib = affyLib)

## display the GOdata object
GOdata
```

```
############################################################
## Examples on how to use the methods
############################################################

## description of the experiment
description(GOdata)

## obtain the genes that will be used in the analysis
a <- genes(GOdata)
str(a)
numGenes(GOdata)

## obtain the score (p-value) of the genes
selGenes <- names(geneList)[sample(1:length(geneList), 10)]
gs <- geneScore(GOdata, whichGenes = selGenes)
print(gs)

## if we want an unnamed vector containing all the feasible genes
gs <- geneScore(GOdata, use.names = FALSE)
str(gs)

## the list of significant genes
sg <- sigGenes(GOdata)
str(sg)
numSigGenes(GOdata)

## to update the gene list
.geneList <- geneScore(GOdata, use.names = TRUE)
GOdata ## more available genes
GOdata <- updateGenes(GOdata, .geneList, topDiffGenes)
GOdata ## the available genes are now the feasible genes

## the available GO terms (all the nodes in the graph)
go <- usedGO(GOdata)
length(go)

## to list the genes annotated to a set of specified GO terms
sel.terms <- sample(go, 10)
ann.genes <- genesInTerm(GOdata, sel.terms)
str(ann.genes)

## the score for these genes
ann.score <- scoresInTerm(GOdata, sel.terms)
str(ann.score)

## to see the number of annotated genes
num.ann.genes <- countGenesInTerm(GOdata)
str(num.ann.genes)

## to summarise the statistics
termStat(GOdata, sel.terms)
```

topGOresult-class *Class "topGOresult"*

Description

Class instance created by getSigGroups-methods or by runTest

Objects from the Class

Objects can be created by calls of the form new("topGOresult", description, score, testName, algorithm, geneData).

Slots

description: character string containing a short description on how the object was build.

score: named numerical vector containing the p-values or the scores of the tested GO terms.

testName: character string containing the name of the test statistic used.

algorithm: character string containing the name of the algorithm used.

geneData: list containing summary statistics on the genes/gene universe/annotations.

Methods

score: method to access the score slot.

testName: method to access the testName slot.

algorithm: method to access the algorithm slot.

geneData: method to access the geneData slot.

show: method to print the object.

combineResults: method to aggregate two or more topGOresult objects. method = c("gmean", "mean", "median", "min", "max") provides the way the object scores (which most of the time are p-values) are combined..

Author(s)

Adrian Alexa

See Also

groupStats-class, getSigGroups-methods

Examples

```
data(results.tGO)

s <- score(resultFisher)

go <- sort(names(s))
go.sub<- sample(go, 100)
go.mixed <- c(sample(go, 50), sample(ls(GOCCTerm), 20))
go.others <- sample(ls(GOCCTerm), 100)


str(go)
str(go.sub)
str(go.mixed)
str(go.others)

str(score(resultFisher, whichGO = go))
str(score(resultFisher, whichGO = go.sub))
str(score(resultFisher, whichGO = go.mixed))
str(score(resultFisher, whichGO = go.others))

avgResult <- combineResults(resultFisher, resultKS)
avgResult
combineResults(resultFisher, resultKS, method = "min")
```

---

weightCount-class *Class "weightCount"*

Description

~~ A concise (1-5 lines) description of what the class is. ~~

Details

TODO: Some details here.....

Objects from the Class

Objects can be created by calls of the form `new("weightCount", testStatistic, name, allMembers, groupMembers, sigMembers, weights, sigRatio, penalise, ...)`.

Slots

`weights`: Object of class `"numeric"` ~~

`sigRatio`: Object of class `"function"` ~~

`penalise`: Object of class `"function"` ~~

`roundFun`: Object of class `"function"` ~~

`significant`: Object of class `"integer"` ~~

`name`: Object of class `"character"` ~~

`allMembers`: Object of class `"character"` ~~

`members`: Object of class `"character"` ~~

`testStatistic`: Object of class `"function"` ~~

`testStatPar`: Object of class `"list"` ~~

Extends

Class `"classicCount"`, directly. Class `"groupStats"`, by class "classicCount", distance 2.

Methods

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

Author(s)

Adrian Alexa

See Also

`groupStats-class`, `getSigGroups-methods`

Index

∗ **classes**
  classicCount-class, 6
  classicExpr-class, 7
  classicScore-class, 8
  elimCount-class, 13
  elimExpr-class, 14
  elimScore-class, 16
  groupStats-class, 22
  parentChild-class, 24
  topGOdata-class, 27
  topGOresult-class, 31
  weightCount-class, 32
∗ **datasets**
  geneList, 18
  GOdata, 21
∗ **graphs**
  Determines the levels of a Directed Acyclic Graph (DAG), 9
  getPvalues, 18
  inducedGraph, 23
  topGOdata-class, 27
∗ **methods**
  dignostic-methods, 11
  getSigGroups, 19
  printGraph-methods, 26
∗ **misc**
  annFUN, 3
  Gene set tests statistics, 17
  groupGOTerms, 22
∗ **package**
  topGO-package, 2

affyLib *(geneList)*, 18
algorithm *(topGOresult-class)*, 31
algorithm,topGOresult-method *(topGOresult-class)*, 31
algorithm<- *(topGOresult-class)*, 31
algorithm<-,topGOresult-method *(topGOresult-class)*, 31
allGenes *(topGOdata-class)*, 27
allGenes,topGOdata-method *(topGOdata-class)*, 27
allMembers *(groupStats-class)*, 22
allMembers,elimScore-method *(elimScore-class)*, 16
allMembers,groupStats-method *(groupStats-class)*, 22
allMembers,parentChild-method *(parentChild-class)*, 24
allMembers,weight01Expr-method *(elimExpr-class)*, 14
allMembers,weight01Score-method *(elimScore-class)*, 16
allMembers,weightCount-method *(weightCount-class)*, 32
allMembers<- *(groupStats-class)*, 22
allMembers<-,classicExpr-method *(classicExpr-class)*, 7
allMembers<-,groupStats-method *(groupStats-class)*, 22
allMembers<-,parentChild-method *(parentChild-class)*, 24
allMembers<-,pC-method *(parentChild-class)*, 24
allParents *(parentChild-class)*, 24
allParents,parentChild-method *(parentChild-class)*, 24
allScore *(classicScore-class)*, 8
allScore,classicScore,logical-method *(classicScore-class)*, 8
allScore,classicScore,missing-method *(classicScore-class)*, 8
allScore,elimScore,logical-method *(elimScore-class)*, 16
allScore,elimScore,missing-method *(elimScore-class)*, 16
allScore,weight01Score,logical-method *(elimScore-class)*, 16
allScore,weight01Score,missing-method

(elimScore-class), 16
alternative,elimScore-method
(elimScore-class), 16
annFUN, 3, *29*
attrInTerm (topGOdata-class), 27
attrInTerm,topGOdata,character,character-method
(topGOdata-class), 27
attrInTerm,topGOdata,character,missing-method
(topGOdata-class), 27

buildLevels, *29*
buildLevels (Determines the levels of
a Directed Acyclic Graph
(DAG)), 9

classicCount, *14*, *25*, *33*
classicCount-class, 6
classicExpr, *15*
classicExpr-class, 7
classicScore, *16*
classicScore-class, 8
combineResults (topGOresult-class), 31
contTable (classicCount-class), 6
contTable,classicCount-method
(classicCount-class), 6
contTable,elimCount-method
(elimCount-class), 13
countGenesInTerm (topGOdata-class), 27
countGenesInTerm,topGOdata,character-method
(topGOdata-class), 27
countGenesInTerm,topGOdata,missing-method
(topGOdata-class), 27
cutOff (elimCount-class), 13
cutOff,elimCount-method
(elimCount-class), 13
cutOff,elimExpr-method
(elimExpr-class), 14
cutOff,elimScore-method
(elimScore-class), 16
cutOff<- (elimCount-class), 13
cutOff<-,elimCount-method
(elimCount-class), 13
cutOff<-,elimExpr-method
(elimExpr-class), 14
cutOff<-,elimScore-method
(elimScore-class), 16

depth (elimCount-class), 13
depth,leaCount-method
(elimCount-class), 13
depth,leaExpr-method (elimExpr-class),
14
depth,leaScore-method
(elimScore-class), 16
depth<- (elimCount-class), 13
depth<-,leaCount-method
(elimCount-class), 13
depth<-,leaExpr-method
(elimExpr-class), 14
depth<-,leaScore-method
(elimScore-class), 16
description (topGOdata-class), 27
description,topGOdata-method
(topGOdata-class), 27
description,topGOresult-method
(topGOresult-class), 31
description<- (topGOdata-class), 27
description<-,topGOdata,ANY-method
(topGOdata-class), 27
description<-,topGOresult,ANY-method
(topGOresult-class), 31
Determines the levels of a Directed
Acyclic Graph (DAG), 9
dignostic-methods, 11

elim (elimCount-class), 13
elim,elimCount-method
(elimCount-class), 13
elim,elimScore-method
(elimScore-class), 16
elim,weight01Count-method
(elimCount-class), 13
elim,weight01Expr-method
(elimExpr-class), 14
elim,weight01Score-method
(elimScore-class), 16
elim<- (elimCount-class), 13
elim<-,elimCount-method
(elimCount-class), 13
elim<-,elimScore-method
(elimScore-class), 16
elim<-,weight01Count-method
(elimCount-class), 13
elim<-,weight01Expr-method
(elimExpr-class), 14
elim<-,weight01Score-method
(elimScore-class), 16

elimCount-class, 13
elimExpr-class, 14
elimScore-class, 16
emptyExpr,classicExpr-method
(classicExpr-class), 7
expressionMatrix (topGOdata-class), 27
expressionMatrix,topGOdata-method
(topGOdata-class), 27

feasible (topGOdata-class), 27
feasible,topGOdata-method
(topGOdata-class), 27
feasible<- (topGOdata-class), 27
feasible<-,topGOdata-method
(topGOdata-class), 27

Gene set tests statistics, 17
geneData (topGOresult-class), 31
geneData,topGOresult-method
(topGOresult-class), 31
geneData<- (topGOresult-class), 31
geneData<-,topGOresult-method
(topGOresult-class), 31
geneList, 18
genes (topGOdata-class), 27
genes,topGOdata-method
(topGOdata-class), 27
geneScore (topGOdata-class), 27
geneScore,topGOdata,character-method
(topGOdata-class), 27
geneScore,topGOdata,missing-method
(topGOdata-class), 27
geneScore,topGOdata-method
(topGOdata-class), 27
geneSelectionFun (topGOdata-class), 27
geneSelectionFun,topGOdata-method
(topGOdata-class), 27
geneSelectionFun<- (topGOdata-class), 27
geneSelectionFun<-,topGOdata-method
(topGOdata-class), 27
genesInTerm (topGOdata-class), 27
genesInTerm,topGOdata,character-method
(topGOdata-class), 27
genesInTerm,topGOdata,missing-method
(topGOdata-class), 27
GenTable (dignostic-methods), 11
GenTable,topGOdata-method
(dignostic-methods), 11

getGraphRoot (Determines the levels of
a Directed Acyclic Graph
(DAG)), 9
getNoOfLevels (Determines the levels
of a Directed Acyclic Graph
(DAG)), 9
getPvalues, 18
getSigGroups, 19
getSigGroups,topGOdata,classicCount-method
(getSigGroups), 19
getSigGroups,topGOdata,classicExpr-method
(getSigGroups), 19
getSigGroups,topGOdata,classicScore-method
(getSigGroups), 19
getSigGroups,topGOdata,elimCount-method
(getSigGroups), 19
getSigGroups,topGOdata,elimExpr-method
(getSigGroups), 19
getSigGroups,topGOdata,elimScore-method
(getSigGroups), 19
getSigGroups,topGOdata,leaCount-method
(getSigGroups), 19
getSigGroups,topGOdata,leaExpr-method
(getSigGroups), 19
getSigGroups,topGOdata,leaScore-method
(getSigGroups), 19
getSigGroups,topGOdata,parentChild-method
(getSigGroups), 19
getSigGroups,topGOdata,pC-method
(getSigGroups), 19
getSigGroups,topGOdata,weight01Count-method
(getSigGroups), 19
getSigGroups,topGOdata,weight01Expr-method
(getSigGroups), 19
getSigGroups,topGOdata,weight01Score-method
(getSigGroups), 19
getSigGroups,topGOdata,weightCount-method
(getSigGroups), 19
getSigGroups-methods (getSigGroups), 19
getSigRatio (weightCount-class), 32
getSigRatio,weightCount-method
(weightCount-class), 32
GOBPTerm (groupGOTerms), 22
GOCCTerm (groupGOTerms), 22
GOdata, 21
GOFisherTest (Gene set tests
statistics), 17
GOFisherTest,classicCount-method

(classicCount-class), 6
GOFisherTest,elimCount-method
(elimCount-class), 13
GOglobalTest (Gene set tests
statistics), 17
GOglobalTest,classicExpr-method
(classicExpr-class), 7
GOKSTest, *19*
GOKSTest (Gene set tests statistics), 17
GOKSTest,classicScore-method
(classicScore-class), 8
GOKSTiesTest (Gene set tests
statistics), 17
GOKSTiesTest,classicScore-method
(classicScore-class), 8
GOMFTerm (groupGOTerms), 22
GOplot (printGraph-methods), 26
GOSumTest (Gene set tests statistics),
17
GOSumTest,classicScore-method
(classicScore-class), 8
GOTERM, *22*
GOtTest (Gene set tests statistics), 17
GOtTest,classicScore-method
(classicScore-class), 8
graph (topGOdata-class), 27
graph,topGOdata-method
(topGOdata-class), 27
graph<- (topGOdata-class), 27
graph<-,topGOdata-method
(topGOdata-class), 27
groupGOTerms, 22
groupStats, *7*, *14–16*, *25*, *33*
groupStats-class, 22

inducedGraph, *10*, 23
initialize,classicCount-method
(classicCount-class), 6
initialize,classicExpr-method
(classicExpr-class), 7
initialize,classicScore-method
(classicScore-class), 8
initialize,elimCount-method
(elimCount-class), 13
initialize,elimExpr-method
(elimExpr-class), 14
initialize,elimScore-method
(elimScore-class), 16
initialize,groupStats-method
(groupStats-class), 22
initialize,leaCount-method
(elimCount-class), 13
initialize,leaExpr-method
(elimExpr-class), 14
initialize,leaScore-method
(elimScore-class), 16
initialize,parentChild-method
(parentChild-class), 24
initialize,pC-method
(parentChild-class), 24
initialize,topGOdata-method
(topGOdata-class), 27
initialize,topGOresult-method
(topGOresult-class), 31
initialize,weight01Count-method
(elimCount-class), 13
initialize,weight01Expr-method
(elimExpr-class), 14
initialize,weight01Score-method
(elimScore-class), 16
initialize,weightCount-method
(weightCount-class), 32
inverseList (annFUN), 3

joinFun (parentChild-class), 24
joinFun,parentChild-method
(parentChild-class), 24

leaCount-class (elimCount-class), 13
leaExpr-class (elimExpr-class), 14
leaScore-class (elimScore-class), 16

members (groupStats-class), 22
members,elimScore-method
(elimScore-class), 16
members,groupStats,missing-method
(groupStats-class), 22
members,weight01Expr,missing-method
(elimExpr-class), 14
members,weight01Score,missing-method
(elimScore-class), 16
members,weightCount-method
(weightCount-class), 32
members<- (groupStats-class), 22
members<-,groupStats-method
(groupStats-class), 22
membersExpr (classicExpr-class), 7

membersExpr,classicExpr-method
(classicExpr-class), 7
membersScore (classicScore-class), 8
membersScore,classicScore-method
(classicScore-class), 8
membersScore,elimScore-method
(elimScore-class), 16
membersScore,weight01Score-method
(elimScore-class), 16

Name (groupStats-class), 22
Name,groupStats-method
(groupStats-class), 22
Name,weightCount-method
(weightCount-class), 32
Name<- (groupStats-class), 22
Name<-,groupStats-method
(groupStats-class), 22
nodesInInducedGraph (inducedGraph), 23
numAllMembers (groupStats-class), 22
numAllMembers,elimCount-method
(elimCount-class), 13
numAllMembers,elimScore-method
(elimScore-class), 16
numAllMembers,groupStats-method
(groupStats-class), 22
numAllMembers,parentChild-method
(parentChild-class), 24
numAllMembers,weight01Count-method
(elimCount-class), 13
numAllMembers,weight01Expr-method
(elimExpr-class), 14
numAllMembers,weight01Score-method
(elimScore-class), 16
numAllMembers,weightCount-method
(weightCount-class), 32
numGenes (topGOdata-class), 27
numGenes,topGOdata-method
(topGOdata-class), 27
numMembers (groupStats-class), 22
numMembers,elimCount-method
(elimCount-class), 13
numMembers,elimScore-method
(elimScore-class), 16
numMembers,groupStats-method
(groupStats-class), 22
numMembers,weight01Count-method
(elimCount-class), 13
numMembers,weight01Expr-method
(elimExpr-class), 14
numMembers,weight01Score-method
(elimScore-class), 16
numMembers,weightCount-method
(weightCount-class), 32
numSigAll (classicCount-class), 6
numSigAll,classicCount-method
(classicCount-class), 6
numSigAll,elimCount-method
(elimCount-class), 13
numSigAll,parentChild-method
(parentChild-class), 24
numSigAll,weight01Count-method
(elimCount-class), 13
numSigAll,weightCount-method
(weightCount-class), 32
numSigGenes (topGOdata-class), 27
numSigGenes,topGOdata-method
(topGOdata-class), 27
numSigMembers (classicCount-class), 6
numSigMembers,classicCount-method
(classicCount-class), 6
numSigMembers,elimCount-method
(elimCount-class), 13
numSigMembers,weight01Count-method
(elimCount-class), 13
numSigMembers,weightCount-method
(weightCount-class), 32

ontology (topGOdata-class), 27
ontology,topGOdata-method
(topGOdata-class), 27
ontology<- (topGOdata-class), 27
ontology<-,topGOdata-method
(topGOdata-class), 27

parentChild-class, 24
pC-class (parentChild-class), 24
penalise (weightCount-class), 32
penalise,weightCount,numeric,numeric-method
(weightCount-class), 32
permSumStats (Gene set tests
statistics), 17
phenotype (topGOdata-class), 27
phenotype,topGOdata-method
(topGOdata-class), 27
print,topGOdata-method
(topGOdata-class), 27

print,topGOresult-method
(topGOresult-class), 31
printGenes (dignostic-methods), 11
printGenes,topGOdata,character,character-method
(dignostic-methods), 11
printGenes,topGOdata,character,missing-method
(dignostic-methods), 11
printGenes-methods (dignostic-methods),
11
printGraph (printGraph-methods), 26
printGraph,topGOdata,topGOresult,numeric,missing-method
(printGraph-methods), 26
printGraph,topGOdata,topGOresult,numeric,topGOresult-method
(printGraph-methods), 26
printGraph-methods, 26
pType (classicExpr-class), 7
pType,classicExpr-method
(classicExpr-class), 7
pType<- (classicExpr-class), 7
pType<-,classicExpr-method
(classicExpr-class), 7

rankMembers (classicScore-class), 8
rankMembers,classicScore-method
(classicScore-class), 8
rankMembers,elimScore-method
(elimScore-class), 16
rankMembers,weight01Score-method
(elimScore-class), 16
readMappings (annFUN), 3
resultFisher (GOdata), 21
resultKS (GOdata), 21
reverseArch, *24*
reverseArch (Determines the levels of
a Directed Acyclic Graph
(DAG)), 9
roundFun (weightCount-class), 32
roundFun,weightCount-method
(weightCount-class), 32
runTest (getSigGroups), 19
runTest,groupStats,missing,missing-method
(groupStats-class), 22
runTest,groupStats-method
(groupStats-class), 22
runTest,topGOdata,character,character-method
(getSigGroups), 19
runTest,topGOdata,missing,character-method
(getSigGroups), 19

score (topGOresult-class), 31
score,topGOresult-method
(topGOresult-class), 31
score<- (classicScore-class), 8
score<-,classicScore-method
(classicScore-class), 8
score<-,elimScore-method
(elimScore-class), 16
score<-,topGOresult-method
(topGOresult-class), 31
scoreOrder (classicScore-class), 8
scoreOrder,classicScore-method
(classicScore-class), 8
scoresInTerm (topGOdata-class), 27
scoresInTerm,topGOdata,character-method
(topGOdata-class), 27
scoresInTerm,topGOdata,missing-method
(topGOdata-class), 27
show,topGOdata-method
(topGOdata-class), 27
show,topGOresult-method
(topGOresult-class), 31
showGroupDensity (dignostic-methods), 11
showSigOfNodes (printGraph-methods), 26
sigAllMembers (classicCount-class), 6
sigAllMembers,classicCount-method
(classicCount-class), 6
sigAllMembers,elimCount-method
(elimCount-class), 13
sigAllMembers,parentChild-method
(parentChild-class), 24
sigAllMembers,weight01Count-method
(elimCount-class), 13
sigGenes (topGOdata-class), 27
sigGenes,topGOdata-method
(topGOdata-class), 27
sigMembers (classicCount-class), 6
sigMembers,classicCount-method
(classicCount-class), 6
sigMembers,elimCount-method
(elimCount-class), 13
sigMembers,weight01Count-method
(elimCount-class), 13
sigMembers<- (classicCount-class), 6
sigMembers<-,classicCount-method
(classicCount-class), 6
sigMembers<-,elimCount-method
(elimCount-class), 13

sigMembers<-,parentChild-method
(parentChild-class), 24
sigMembers<-,pC-method
(parentChild-class), 24
significant (weightCount-class), 32
significant,weightCount-method
(weightCount-class), 32
sigRatio (weightCount-class), 32
sigRatio,weightCount-method
(weightCount-class), 32
sigRatio<- (weightCount-class), 32
sigRatio<-,weightCount-method
(weightCount-class), 32

termStat (topGOdata-class), 27
termStat,topGOdata,character-method
(topGOdata-class), 27
termStat,topGOdata,missing-method
(topGOdata-class), 27
testName (topGOresult-class), 31
testName,topGOresult-method
(topGOresult-class), 31
testName<- (topGOresult-class), 31
testName<-,topGOresult-method
(topGOresult-class), 31
testStatistic (groupStats-class), 22
testStatistic,groupStats-method
(groupStats-class), 22
testStatistic,weightCount-method
(weightCount-class), 32
testStatPar (groupStats-class), 22
testStatPar,groupStats-method
(groupStats-class), 22
testStatPar,weightCount-method
(weightCount-class), 32
topDiffGenes (geneList), 18
topGO (topGO-package), 2
topGO-package, 2
topGOdata-class, 27
topGOresult-class, 31

updateGenes (topGOdata-class), 27
updateGenes,topGOdata,factor,missing-method
(topGOdata-class), 27
updateGenes,topGOdata,numeric,function-method
(topGOdata-class), 27
updateGroup (groupStats-class), 22
updateGroup,groupStats,character,character-method
(groupStats-class), 22
updateGroup,parentChild,missing,character-method
(parentChild-class), 24
updateGroup,pC,missing,character-method
(parentChild-class), 24
updateGroup,pC,missing,missing-method
(parentChild-class), 24
updateGroup,weightCount,character,character-method
(weightCount-class), 32
updateTerm<- (topGOdata-class), 27
updateTerm<-,topGOdata,character-method
(topGOdata-class), 27
usedGO (topGOdata-class), 27
usedGO,topGOdata-method
(topGOdata-class), 27

weight01Count-class (elimCount-class),
13
weight01Expr, *15*
weight01Expr-class (elimExpr-class), 14
weight01Score-class (elimScore-class),
16
weightCount-class, 32
Weights (weightCount-class), 32
Weights,weightCount,logical-method
(weightCount-class), 32
Weights,weightCount,missing-method
(weightCount-class), 32
Weights,weightCount-method
(weightCount-class), 32
Weights<- (weightCount-class), 32
Weights<-,weightCount-method
(weightCount-class), 32
whichAlgorithms (getSigGroups), 19
whichTests (getSigGroups), 19