

# Package ‘multiWGCNA’

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## Contents

multiWGCNA-package . . . . .	2
bidirectionalBestMatches . . . . .	3
cleanDatExpr . . . . .	3
coexpressionLineGraph . . . . .	4
computeOverlapsFromWGCNA . . . . .	5
constructNetworks . . . . .	6
diffCoexpression . . . . .	7
diffModuleExpression . . . . .	8
drawMultiWGCNAnetwork . . . . .	9
GetDatExpr . . . . .	11
getPreservation . . . . .	11
iterate . . . . .	12
makeTraitTable . . . . .	13
moduleComparisonPlot . . . . .	13
moduleExpressionPlot . . . . .	14
moduleToModuleHeatmap . . . . .	15
name . . . . .	16
overlapComparisons . . . . .	16
performANOVA . . . . .	17
permutationTestResults . . . . .	18
preservationComparisonPlot . . . . .	18
preservationComparisons . . . . .	19
PreservationPermutationTest . . . . .	20
PreservationScoreDistribution . . . . .	22
runDME . . . . .	23
summarizeResults . . . . .	24
TOMFlowPlot . . . . .	25
topNGenes . . . . .	25
WGCNA-class . . . . .	26
<b>Index</b>	<b>27</b>

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multiWGCNA-package      *multiWGCNA: multiWGCNA*

---

## Description

An R package for deeping mining gene co-expression networks in multi-trait expression data. Provides functions for analyzing, comparing, and visualizing WGCNA networks across conditions. multiWGCNA was designed to handle the common case where there are multiple biologically meaningful sample traits, such as disease vs wildtype across development or anatomical region.

## Author(s)

**Maintainer:** Dario Tommasini <dtommasini@gmail.com> ([ORCID](#))

Authors:

- Brent Fogel [contributor]

---

 bidirectionalBestMatches

*Best matching modules*


---

### Description

Find all the modules from dataset1 that have a best match to a module in dataset2 if that module in dataset2 is also a best match to the module in dataset1

### Usage

```
bidirectionalBestMatches(comparisonList, plot = TRUE)
```

### Arguments

`comparisonList` a list with an element "overlap", which is a data.frame resulting from a call to `computeOverlapsFromWGCNA`

`plot` whether to generate a heatmap; default is TRUE

### Value

A ggplot object

### Author(s)

Dario Tommasini

### Examples

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
comparisonList = list()
comparisonList$overlaps = computeOverlapsFromWGCNA(astrocyte_networks$EAE, astrocyte_networks$WT)
bidirectionalBestMatches(comparisonList)
```

---

 cleanDatExpr

*cleanDatExpr*


---

### Description

A function that converts a data.frame where row 1 is gene symbols to a numeric matrix where columns are genes and rows are samples for compatibility with most WGCNA functions.

### Usage

```
cleanDatExpr(datExpr, checkGenesSamples = FALSE)
```

**Arguments**

`datExpr` a data.frame where columns are samples and rows are samples and the gene symbols are in the first row

`checkGenesSamples` call the WGCNA function `checkGenesSamples?`

**Value**

Returns a `datExpr` with rows as samples and columns as genes

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_se = eh_query[["EH8223"]]
datExpr = data.frame(X = rownames(assays(astrocyte_se)[[1]]), assays(astrocyte_se)[[1]])
cleanDatExpr(datExpr)
```

---

`coexpressionLineGraph` *Coexpression Line Graph*

---

**Description**

Plots a line graph showing the co-expression of selected genes across samples

**Usage**

```
coexpressionLineGraph(datExpr, splitBy = 1, fontSize = 2.15, colors = NULL)
```

**Arguments**

`datExpr` a data.frame with genes as rows and samples as columns

`splitBy` how much to split genes by on line graph

`fontSize` the font size of the gene labels

`colors` a vector of colors; default is random colors generated by `colors` function

**Value**

a ggplot object

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
datExpr = GetDatExpr(astrocyte_networks[[1]],
  genes = topNGenes(astrocyte_networks$EAE, "EAE_015", 20))
coexpressionLineGraph(datExpr) +
  geom_vline(xintercept = 20.5, linetype='dashed')
```

---

`computeOverlapsFromWGCNA`*computeOverlapsFromWGCNA*

---

**Description**

Computes overlap between the modules of two objects of class `WGCNA`

**Usage**

```
computeOverlapsFromWGCNA(dataset1, dataset2)
```

**Arguments**

<code>dataset1</code>	an object of class <code>WGCNA</code> to compare with <code>dataset2</code>
<code>dataset2</code>	an object of class <code>WGCNA</code> to compare with <code>dataset1</code>

**Value**

Returns a `data.frame` showing the overlap results for modules from `dataset1` with `dataset2`

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
computeOverlapsFromWGCNA(astrocyte_networks$EAE, astrocyte_networks$WT)
```

---

constructNetworks	<i>constructNetworks: Construct all the weighted gene correlation networks</i>
-------------------	--

---

### Description

A high level function that returns all networks possible for a given experimental design

### Usage

```
constructNetworks(
  datExpr,
  sampleTable,
  conditions1,
  conditions2,
  write = FALSE,
  alphaLevel = 0.05,
  plot = FALSE,
  ...
)
```

### Arguments

datExpr	either a SummarizedExperiment object or data.frame with genes are rows and samples as columns
sampleTable	data.frame with sample names in first column and sample traits in the second and third column. First column should be called "Sample"
conditions1	first design conditions, ie healthy/disease
conditions2	second design conditions, ie frontal lobe/temporal lobe
write	write results out to files?
alphaLevel	significance value passed to findBestTrait function, default is 0.05
plot	plot modules? Default is false
...	Arguments to pass to blockwiseModules function

### Value

A list of WGCNA objects, ie level one, two, and three networks.

### Author(s)

Dario Tommasini

### Examples

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
autism_se = eh_query[["EH8219"]]
set.seed(1)
autism_se = autism_se[sample(rownames(autism_se), 500),]
```

```

sampleTable = colData(autism_se)
conditions1 = unique(sampleTable[,2])
conditions2 = unique(sampleTable[,3])
autism_networks = constructNetworks(autism_se, sampleTable, conditions1[[1]], conditions2[[1]],
  networkType = "signed", TOMType = "unsigned",
  power = 10, minModuleSize = 100, maxBlockSize = 25000,
  reassignThreshold = 0, minKMEtoStay = 0, mergeCutHeight = 0,
  numericLabels = TRUE, pamRespectsDendro = FALSE,
  deepSplit = 4, verbose = 3)
autism_networks[["combined"]]

```

---

diffCoexpression      *Differential co-expression analysis*

---

## Description

Performs a differential co-expression analysis given an expression data.frame and a conditions vector

## Usage

```

diffCoexpression(
  datExpr,
  conditions,
  geneList = NULL,
  plot = FALSE,
  method = c("pearson", "spearman"),
  removeFreeNodes = TRUE,
  labelSize = 0.5,
  labelDist = 0,
  shape = "circle",
  degreeForSize = FALSE,
  label = FALSE,
  onlyPositive = FALSE,
  z.threshold = NULL,
  FDR.threshold = 0.05,
  nodeSize = 3
)

```

## Arguments

datExpr	a data.frame containing expression values
conditions	a vector containing conditions for the samples
geneList	vector of genes, will use all genes if NULL (default)
plot	plot a network?
method	either "pearson" or "spearman"
removeFreeNodes	remove free nodes from network?
labelSize	label size

labelDist	distance from labels to nodes
shape	shape of nodes
degreeForSize	should node size correspond to degree?
label	label nodes?
onlyPositive	only draw positive correlations?
z.threshold	z-score threshold
FDR.threshold	FDR threshold
nodeSize	size of node

**Value**

A list including a matrix of z-scores, a matrix of raw p-values, a matrix of adjusted p-values, and a summary data.frame

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_se = eh_query[["EH8223"]]
datExpr = assays(astrocyte_se)[[1]]
diffCoexpression(datExpr, c(rep(1,20), rep(2,16)),
  geneList = c("Gfap", "Vim", "Aspg", "Serpina3n", "Cp", "Osmr", "Cd44",
    "Cxcl10", "Hspb1", "Timp1", "S1pr3", "Steap4", "Lcn2"))
```

---

diffModuleExpression *Differential module expression*

---

**Description**

Runs (and plots) the differential module expression analysis

**Usage**

```
diffModuleExpression(
  WGCNAobject,
  geneList,
  design,
  plotTitle = NULL,
  mode = c("PC1", "Zscore"),
  testColumn = 2,
  refColumn = 3,
  test = c("ANOVA", "PERMANOVA"),
  plot = TRUE
)
```

**Arguments**

WGCNAobject	WGCNA object
geneList	vector of genes in WGCNAobject
design	the sampleTable
plotTitle	title for the plot
mode	either PC1 or Zscore, default is PC1
testColumn	the column of the sampleTable to be resolved
refColumn	the column of the sampleTable to be used as biological variation
test	statistical test to perform, either "ANOVA" or "PERMANOVA"
plot	generate a plot?

**Value**

a data.frame with the resulting p-values

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_se = eh_query[["EH8223"]]
sampleTable = colData(astrocyte_se)
astrocyte_networks = eh_query[["EH8222"]]
diffModuleExpression(astrocyte_networks[["combined"]],
  topNGenes(astrocyte_networks$combined, "combined_013"),
  sampleTable,
  test = "ANOVA",
  plotTitle = "combined_013",
  plot = TRUE)
```

---

drawMultiWGCNAnetwork *Draw multiWGCNA network*

---

**Description**

Draw a network where nodes are modules and edges represent significant gene overlap. Modules are sorted by levels 1, 2, and 3.

**Usage**

```
drawMultiWGCNAnetwork(
  WGCNAlist,
  comparisonList,
  moduleOfInterest,
  design,
  overlapCutoff = 0,
  padjCutoff = 1,
  removeOutliers = TRUE,
  alpha = 1e-50,
```

```

    layout = NULL,
    hjust = 0.4,
    vjust = 0.3,
    width = 0.5,
    colors = NULL
  )

```

### Arguments

WGCNAlist	list of WGCNA objects
comparisonList	the list of overlap comparisons ie from iterate(myNetworks, overlapComparisons, ...)
moduleOfInterest	module of interest, ie "combined_001"
design	the sampleTable design matrix
overlapCutoff	cutoff to remove module correspondences with less than this number of genes
padjCutoff	cutoff to remove module correspondences above this significance value
removeOutliers	remove outlier modules?
alpha	alpha level of significance
layout	layout of network to be passed to plot function of igraph object, defaults to multiWGCNA custom layout
hjust	horizontal justification of labels
vjust	vertical justification of labels
width	width of labels
colors	colors to use for modules, should be the same length as the number of WGCNA objects in the WGCNAlist. Defaults to random colors for each condition.

### Value

an igraph plot

### Author(s)

Dario Tommasini

### Examples

```

library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_se = eh_query[["EH8223"]]
sampleTable = colData(astrocyte_se)
astrocyte_networks = eh_query[["EH8222"]]
results = list()
results$overlaps = iterate(astrocyte_networks, overlapComparisons, plot=FALSE)
drawMultiWGCNAnetwork(astrocyte_networks,
  results$overlaps,
  "combined_013",
  sampleTable)

```

---

GetDatExpr	<i>Get expression data</i>
------------	----------------------------

---

**Description**

Returns the expression data frame a WGCNA object as a data.frame

**Usage**

```
GetDatExpr(object, genes = NULL)
```

**Arguments**

object	An object of class WGCNA
genes	a list of genes to subset to; default is NULL

**Value**

a data.frame

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
datExpr = GetDatExpr(astrocyte_networks[[1]],
  genes = topNGenes(astrocyte_networks$EAE, "EAE_015", 20))
coexpressionLineGraph(datExpr) +
  geom_vline(xintercept = 20.5, linetype='dashed')
```

---

getPreservation	<i>getPreservation</i>
-----------------	------------------------

---

**Description**

Performs a network preservation analysis

**Usage**

```
getPreservation(reference, test, nPermutations = 100, write = FALSE)
```

**Arguments**

reference	reference network of class WGCNA
test	test network of class WGCNA
nPermutations	number of permutations to perform; at least 50 permutations
write	write to file?

**Value**

a data.frame summarizing results of preservation analysis

**Author(s)**

Dario Tommasini

---

iterate	<i>iterate: Iterate function across networks</i>
---------	--

---

**Description**

A high level function that iterates functions across a list of WGCNA objects

**Usage**

```
iterate(WGCNAlist, FUN, ...)
```

**Arguments**

WGCNAlist	a vector of objects of type WGCNAobject
FUN	function to iterate, either overlapComparisons or preservationComparisons
...	arguments to be passed on to overlapComparisons or preservationComparisons

**Value**

a comparison list from overlapComparisons or preservationComparisons

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
results = list()
iterate(astrocyte_networks, overlapComparisons, plot=FALSE)
```

---

makeTraitTable	<i>Generate a trait table from a sample table</i>
----------------	---

---

**Description**

Generates a WGCNA-compatible trait table from a sampleTable dataframe

**Usage**

```
makeTraitTable(inputTable, column, detectNumbers = FALSE)
```

**Arguments**

inputTable	the sampleTable data.frame
column	the column from the sampleTable to use as traits
detectNumbers	whether to consider traits with numbers as numerical rather than categorical variables

**Value**

a data.frame with integer values denoting the categorical sample traits

**Examples**

```
sampleTable = data.frame(Sample = c(paste0("EAE", 1:10), paste0("WT", 1:10)),
                        Disease = c(rep("EAE", 10), rep("WT", 10)),
                        Region = c(rep(c("Cb1", "Sc"), 5)))
makeTraitTable(sampleTable, 2)
```

---

moduleComparisonPlot	<i>Module comparison plot</i>
----------------------	-------------------------------

---

**Description**

A plotting function that returns a heatmap and barplot for a module

**Usage**

```
moduleComparisonPlot(overlapDf, dataset1, dataset2)
```

**Arguments**

overlapDf	a data.frame resulting from a call to computeOverlapsFromWGCNA
dataset1	an object of class WGCNA to compare with dataset2
dataset2	an object of class WGCNA to compare with dataset1

**Value**

Returns a ggplot object (flowplot and heatmap) showing the module correspondence between two objects of class WGCNA

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
overlapDf = computeOverlapsFromWGCNA(astrocyte_networks$EAE, astrocyte_networks$WT)
moduleComparisonPlot(overlapDf, astrocyte_networks$EAE, astrocyte_networks$WT)
```

---

moduleExpressionPlot *Plots an expression profile for a module*

---

**Description**

A plotting function that returns a heatmap and barplot for a module

**Usage**

```
moduleExpressionPlot(
  WGCNAobject,
  geneList,
  mode = c("PC1", "averageZscore"),
  legend = FALSE,
  title = NULL,
  clusterGenes = FALSE
)
```

**Arguments**

WGCNAobject	an object of class WGCNAobject
geneList	a vector of gene names to be extracted from WGCNAobject
mode	use first principal component or averageZscore?
legend	plot legend?
title	title of the plot
clusterGenes	cluster heatmap genes by hierarchical clustering?

**Value**

a patchworked ggplot object

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
moduleExpressionPlot(astrocyte_networks[["combined"]],
  geneList = topNGenes(astrocyte_networks$combined, "combined_013"))
```

---

moduleToModuleHeatmap *Module to module heatmap*

---

**Description**

Returns a heatmap where color corresponds to FDR-adjusted overlap (hypergeometric test) and the label corresponds to the number of overlapping genes

**Usage**

```
moduleToModuleHeatmap(
  comparisonDf,
  dataset1 = NULL,
  dataset2 = NULL,
  trait1 = NULL,
  trait2 = NULL,
  list1 = NULL,
  list2 = NULL,
  filterByTrait = FALSE,
  alphaLevel = 0.05
)
```

**Arguments**

comparisonDf	the data.frame output of computeOverlapFromWGCNA
dataset1	optional; WGCNA object for dataset 1
dataset2	optional; WGCNA object for dataset 2
trait1	optional; subset to modules correlated to this trait for dataset 1
trait2	optional; subset to modules correlated to this trait for dataset 2
list1	subset to this list of modules for dataset 1
list2	subset to this list of modules for dataset 2
filterByTrait	only plot for modules that correlate with some trait?
alphaLevel	the alpha level of significance for module-trait correlation, defaults to 0.05

**Value**

A ggplot object

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
overlapDf = computeOverlapsFromWGCNA(astrocyte_networks$EAE, astrocyte_networks$WT)
moduleToModuleHeatmap(overlapDf)
```

---

name	<i>name: Name of WGCNAobject</i>
------	----------------------------------

---

**Description**

Returns the name of a WGCNAobject.

**Usage**

```
name(WGCNAobject)
```

**Arguments**

WGCNAobject    an object of class WGCNA

**Value**

Returns the name of the WGCNA object, ie "EAE" for astrocyte\_networks\$EAE.

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
name(astrocyte_networks$EAE)
```

---

overlapComparisons	<i>Overlap comparisons</i>
--------------------	----------------------------

---

**Description**

Compares modules between two objects of type WGCNAobjects within a WGCNAobject list given the indices. Recommended to be used in conjunction with the iterate function.

**Usage**

```

overlapComparisons(
  comparisonList,
  WGCNAlist,
  first,
  second,
  element,
  plot = TRUE,
  write = FALSE
)

```

**Arguments**

comparisonList	a list passed by the iterate function
WGCNAlist	list of objects of class WGCNA
first	index of first WGCNA object
second	index of second WGCNA object
element	element position in the comparison list (passed by iterate function)
plot	generate plots?
write	write results to file?

**Value**

A list, in which the first element is a data.frame showing the overlap results and the second element is a data.frame showing the best matching modules between the two WGCNA objects.

**Author(s)**

Dario Tommasini

**Examples**

```

library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
results = list()
results$overlaps = iterate(astrocyte_networks, overlapComparisons, plot=FALSE)

```

---

performANOVA

*Perform ANOVA*

---

**Description**

Test association between module expression to traits using ANOVA

**Usage**

```
performANOVA(datExpr, design, testCondition, refCondition, alphaLevel = 0.05)
```

**Arguments**

datExpr	expression data.frame
design	the sampleTable
testCondition	test column in sampleTable
refCondition	reference column in sampleTable
alphaLevel	the significance level

**Value**

a data.frame with p-values for each association

---

permutationTestResults  
*Permutation test results*

---

**Description**

The results of running the PreservationPermutationTest in the astrocyte vignette. This is provided since this function is quite slow. Please see the astrocyte vignette for more details.

**Usage**

```
data(permutationTestResults)
```

**Format**

A list of data.frames containing preservation results for each permutation

---

preservationComparisonPlot  
*Preservation Comparison Scatterplot*

---

**Description**

A plotting function that draws a scatterplot of preservation scores between two WGCNA objects

**Usage**

```
preservationComparisonPlot(
  preservationList,
  dataset1,
  dataset2,
  alphaLevel = 0.05,
  outliers = FALSE
)
```

**Arguments**

preservationList	a list resulting from a call to preservationComparisons
dataset1	an object of class WGCNAobject to compare with dataset2
dataset2	an object of class WGCNAobject to compare with dataset1
alphaLevel	alpha level of significance, default is 0.05
outliers	leave outlier modules? By default these are removed

**Value**

a ggplot object

**Author(s)**

Dario Tommasini

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
results = list()
results$preservation=iterate(astrocyte_networks[c("EAE", "WT")],
  preservationComparisons,
  write=FALSE,
  plot=FALSE,
  nPermutations=2)
preservationComparisonPlot(results$preservation$EAE_vs_WT,
  astrocyte_networks$EAE,
  astrocyte_networks$WT)
```

---

preservationComparisons

*Preservation comparisons*

---

**Description**

A high level function that performs a perservation comparison between two WGCNAobjects in a WGCNAlist, usually supplied by iterate function

**Usage**

```
preservationComparisons(
  comparisonList,
  WGCNAlist,
  first,
  second,
  element,
  plot = FALSE,
```

```
write = FALSE,  
alphaLevel = 0.05,  
nPermutations = 100  
)
```

### Arguments

`comparisonList` a list passed by the iterate function  
`WGCNAlist` list of objects of type `WGCNAobject`  
`first` index of first `WGCNAobject`  
`second` index of second `WGCNAobject`  
`element` element position in the comparison list (passed by iterate function)  
`plot` generate plots?  
`write` write results to file?  
`alphaLevel` alpha level of significance for module-trait correlation  
`nPermutations` number of permutations, defaults to 100

### Value

a list of preservation comparisons results across levels 1, 2, 3

### Author(s)

Dario Tommasini

### Examples

```
library(ExperimentHub)  
eh = ExperimentHub()  
eh_query = query(eh, c("multiWGCNAdata"))  
astrocyte_networks = eh_query[["EH8222"]]  
results = list()  
iterate(astrocyte_networks[c("EAE", "WT")],  
preservationComparisons,  
write=FALSE,  
plot=FALSE,  
nPermutations=2)
```

---

PreservationPermutationTest

*PreservationPermutationTest*

---

### Description

Performs a permutation test to determine if a null distribution of expected preservation scores for modules in this dataset if the labels were randomly assigned. Please look at the astrocyte vignette for more info.

**Usage**

```

PreservationPermutationTest(
  referenceDatExpr,
  design,
  constructNetworksIn,
  testPreservationIn,
  nPermutations = 100,
  nPresPermutations = 100,
  ...
)

```

**Arguments**

```

referenceDatExpr      the combined datExpr
design                 the sampleTable
constructNetworksIn  the condition to use for network construction, e.g. for the astrocyte data, this is
                     "EAE"
testPreservationIn   the condition to use for testing preservation, e.g. for the astrocyte data, this was
                     "WT"
nPermutations         the number of permutations to perform for permutation test
nPresPermutations    the number of permutations to perform in modulePreservation function
...                  arguments to pass to blockwiseModules function for network construction (should
                     be the same as used for constructing the original network)

```

**Value**

A list of data.frames with preservation results for each permutation

**Author(s)**

Dario Tommasini

**Examples**

```

## Not run:
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
astrocyte_se = eh_query[["EH8223"]]
sampleTable = colData(astrocyte_se)
results = list()
results$permutation.test = PreservationPermutationTest(astrocyte_networks$combined@datExpr[sample(17000, 300,
                                                    sampleTable,
                                                    constructNetworksIn = "EAE", # Construct networks using EAE samples
                                                    testPreservationIn = "WT", # Test preservation of disease samples in WT samples
                                                    nPermutations = 10, # Number of permutations for permutation test
                                                    nPresPermutations = 10, # Number of permutations for modulePreservation function
                                                    networkType = "signed", TOMType = "unsigned"),

```

```

power = 12, minModuleSize = 100, maxBlockSize = 25000,
reassignThreshold = 0, minKMEtoStay = 0, mergeCutHeight = 0,
  numericLabels = TRUE, pamRespectsDendro = FALSE,
    deepSplit = 4, verbose = 3
  )

## End(Not run)

```

---

PreservationScoreDistribution

*PreservationScoreDistribution*

---

### Description

Extracts the preservation score distribution from the results of `PreservationPermutationTest`.

### Usage

```
PreservationScoreDistribution(preservationData, moduleOfInterestSize)
```

### Arguments

```

preservationData
    the results from PreservationPermutationTest
moduleOfInterestSize
    the number of genes in your module of interest

```

### Value

A data.frame with Z-summary preservation scores of the module from each permutation and the corresponding module size

### Author(s)

Dario Tommasini

### Examples

```

# Remove outlier modules
permutationTestResultsFiltered = lapply(permutationTestResults, function(x) x[!x$is.outlier.module,])

# Find preservation score distribution for a given module size
scores.summary = PreservationScoreDistribution(permutationTestResultsFiltered,
  moduleOfInterestSize = 303)

```

---

runDME	<i>Run differential module expression</i>
--------	---

---

**Description**

A wrapper to run `diffModuleExpression` on all the modules in a network

**Usage**

```
runDME(  
  WGCNAobject,  
  design,  
  alphaLevel = 0.05,  
  testCondition = NULL,  
  refCondition = NULL,  
  p.adjust = "fdr",  
  plot = FALSE,  
  test = c("ANOVA", "PERMANOVA"),  
  write = FALSE,  
  out = NULL  
)
```

**Arguments**

<code>WGCNAobject</code>	object of class <code>WGCNA</code> with the modules to run DME on
<code>design</code>	the <code>sampleTable</code>
<code>alphaLevel</code>	level of significance
<code>testCondition</code>	the column of the <code>sampleTable</code> to be resolved
<code>refCondition</code>	the column of the <code>sampleTable</code> to be used as biological variation
<code>p.adjust</code>	adjust for multiple comparisons, argument to pass to <code>p.adjust</code> function
<code>plot</code>	generate a plot?
<code>test</code>	statistical test to perform, either "ANOVA" or "PERMANOVA"
<code>write</code>	write results to a file?
<code>out</code>	file name for DME plots, only used if <code>write</code> is <code>TRUE</code>

**Value**

a `data.frame` summarizing the results of the analysis

**Author(s)**

Dario Tommasini

## Examples

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNadata"))
astrocyte_se = eh_query[["EH8223"]]
sampleTable = colData(astrocyte_se)
astrocyte_networks = eh_query[["EH8222"]]
runDME(astrocyte_networks[["combined"]],
  design = sampleTable,
  p.adjust = "fdr",
  refCondition = "Region",
  testCondition = "Disease")
```

---

summarizeResults

*summarizeResults: Summarize results from a results list object*

---

## Description

Prints (or writes) a summary of the results from a results list object

## Usage

```
summarizeResults(
  myNetworks,
  results,
  alphaLevel = 0.05,
  write = FALSE,
  outputFile = "results.txt"
)
```

## Arguments

myNetworks	a list of WGCNAobjects
results	results list
alphaLevel	alpha level of significance
write	write to file?
outputFile	name of output file, defaults to results.txt

## Value

prints a summary of results from the multiWGCNA analysis

---

TOMFlowPlot	<i>TOMFlowPlot</i>
-------------	--------------------

---

**Description**

Plots a sankey flow diagram showing the movement of genes from one WGCNA to another WGCNA. Uses the ggalluvial framework.

**Usage**

```
TOMFlowPlot(
  WGCNAlist,
  networks,
  toms,
  genes_to_label,
  alpha = 0.1,
  color = "black",
  width = 0.05
)
```

**Arguments**

WGCNAlist	list of WGCNA objects
networks	list of network names of length 2
toms	a list of TOM distance objects of length 2
genes_to_label	genes to label across two networks
alpha	alpha of flows
color	color of flows
width	width of the strata

**Value**

a ggplot object

**Author(s)**

Dario Tommasini

---

topNGenes	<i>topNGenes: Top N genes of a module</i>
-----------	---

---

**Description**

Returns the top N number of genes of a module. All genes returned if no number is specified. Genes are in order of intramodular connectivity.

**Usage**

```
topNGenes(WGCNAobject, module, nGenes = NULL)
```

**Arguments**

WGCNAobject     an object of class WGCNA  
 module            the name of the module in WGCNAobject  
 nGenes            an integer from 1 to module size; returns all genes if left NULL

**Value**

a character vector of the genes/probes in the module

**Examples**

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_networks = eh_query[["EH8222"]]
topNGenes(astrocyte_networks$EAE, "EAE_015", nGenes = 10)
```

---

WGCNA-class

*The WGCNA Class*


---

**Description**

The WGCNA class is the main class used in multiWGCNA to store results from a weighted gene co-expression network analysis. These include the original unaltered expression data used as input, connectivity metrics, module assignment, input sample conditions, trait

**Value**

NA

**Slots**

datExpr    The expression data, connectivity data, and module assignment  
 conditions    A data.frame with integer conditions for WGCNA  
 trait        A data.frame showing pearson correlation values to traits  
 moduleEigengenes    A data.frame of module eigengenes for each module across samples  
 outlierModules    A vector of modules classified by our algorithm as being driven by sample outliers

# Index

- \* **datasets**
  - permutationTestResults, [18](#)
- \* **internal**
  - multiWGCNA-package, [2](#)
- bidirectionalBestMatches, [3](#)
- cleanDatExpr, [3](#)
- coexpressionLineGraph, [4](#)
- computeOverlapsFromWGCNA, [5](#)
- constructNetworks, [6](#)
- diffCoexpression, [7](#)
- diffModuleExpression, [8](#)
- drawMultiWGCNAnetwork, [9](#)
- GetDatExpr, [11](#)
- getPreservation, [11](#)
- iterate, [12](#)
- makeTraitTable, [13](#)
- moduleComparisonPlot, [13](#)
- moduleExpressionPlot, [14](#)
- moduleToModuleHeatmap, [15](#)
- multiWGCNA (multiWGCNA-package), [2](#)
- multiWGCNA-package, [2](#)
- name, [16](#)
- overlapComparisons, [16](#)
- performANOVA, [17](#)
- permutationTestResults, [18](#)
- preservationComparisonPlot, [18](#)
- preservationComparisons, [19](#)
- PreservationPermutationTest, [20](#)
- PreservationScoreDistribution, [22](#)
- runDME, [23](#)
- summarizeResults, [24](#)
- TOMFlowPlot, [25](#)
- topNGenes, [25](#)
- WGCNA-class, [26](#)