

# Package ‘multiWGCNA’

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|                    |                               |
|--------------------|-------------------------------|
| multiWGCNA-package | <i>multiWGCNA: multiWGCNA</i> |
|--------------------|-------------------------------|

---

## 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 | <i>cleanDatExpr</i> |
|--------------|---------------------|

---

**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 | <i>Coexpression Line Graph</i> |
|-----------------------|--------------------------------|

---

**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**

|          |   |
|----------|---|
| dataset1 | an object of class WGCNA to compare with dataset2 |
| dataset2 | an object of class WGCNA to compare with dataset1 |

**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

|                              |   |
|------------------------------|---|
| <code>datExpr</code>         | a data.frame containing expression values             |
| <code>conditions</code>      | a vector containing conditions for the samples        |
| <code>geneList</code>        | vector of genes, will use all genes if NULL (default) |
| <code>plot</code>            | plot a network?                                       |
| <code>method</code>          | either "pearson" or "spearman"                        |
| <code>removeFreeNodes</code> | remove free nodes from network?                       |
| <code>labelSize</code>       | label size  |
| <code>labelDist</code>       | distance from labels to nodes                         |
| <code>shape</code>           | shape of nodes  |
| <code>degreeForSize</code>   | should node size correspond to degree?                |
| <code>label</code>           | label nodes?  |
| <code>onlyPositive</code>    | only draw positive correlations?                      |
| <code>z.threshold</code>     | z-score threshold                                     |
| <code>FDR.threshold</code>   | FDR threshold   |
| <code>nodeSize</code>        | 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("multiWGCAdata"))
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

*Get expression data*

---

**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`

*getPreservation*

---

**Description**

Performs a network preservation analysis

**Usage**

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

**Arguments**

|                            |   |
|----------------------------|---|
| <code>reference</code>     | reference network of class WGCNA                            |
| <code>test</code>          | test network of class WGCNA                                 |
| <code>nPermutations</code> | number of permutations to perform; at least 50 permutations |
| <code>write</code>         | 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 *Module comparison plot*

---

**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 | <i>Perform ANOVA</i> |
|--------------|----------------------|

---

**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 | <i>Permutation test results</i> |
|------------------------|---------------------------------|

---

**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("multiWGCNAdat"))
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("multiWGCNAdat"))
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(17000,3000),],
    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

*Run differential module expression*

---

**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**

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

**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

*TOMFlowPlot*

---

**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

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