

# Package ‘BioQC’

March 12, 2025

**Type** Package

**Title** Detect tissue heterogeneity in expression profiles with gene sets

**Version** 1.35.0

**Date** 2021-08-18

**Description** BioQC performs quality control of high-throughput expression data based on tissue gene signatures. It can detect tissue heterogeneity in gene expression data. The core algorithm is a Wilcoxon-Mann-Whitney test that is optimised for high performance.

**biocViews** GeneExpression,QualityControl,StatisticalMethod, GeneSetEnrichment

**Depends** R (>= 3.5.0), Biobase

**Imports** edgeR, Rcpp, methods, stats, utils

**Collate** AllClasses.R AllMethods.R as.GmtList.R GmtList-funcs.R readSignedGmt.R uniqGenesetsByNamespace.R appendGmtList.R utils.R entropy.R gini.R readGmt.R matchGenes.R wmwTest.R readCurrentSignatures.R prettySigNames.R leadingEdge.R

**Suggests** testthat, knitr, rmarkdown, lattice, latticeExtra, rbenchmark, gplots, gridExtra, org.Hs.eg.db, hgu133plus2.db, ggplot2, reshape2, plyr, ineq, covr, limma, RColorBrewer

**LinkingTo** Rcpp

**VignetteBuilder** knitr

**License** GPL (>=3) + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.1.1

**URL** <https://accio.github.io/BioQC>

**BugReports** <https://accio.github.io/BioQC/issues>

**git\_url** <https://git.bioconductor.org/packages/BioQC>

**git\_branch** devel

**git\_last\_commit** 33cb26a

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2025-03-12

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---

absLog10p	<i>Absolute base-10 logarithm of p-values</i>
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---

## Description

Absolute base-10 logarithm of p-values

## Usage

```
absLog10p(x)
```

## Arguments

x	Numeric vector or matrix
---	--------------------------

The function returns the absolute values of base-10 logarithm of p-values.

## Details

The logarithm transformation of p-values is commonly used to visualize results from statistical tests. Although it may cause misunderstanding and therefore its use is disapproved by some experts, it helps to visualize and interpret results of statistical tests intuitively.

The function transforms p-values with base-10 logarithm, and returns its absolute value. The choice of base 10 is driven by the simplicity of interpreting the results.

**Value**

Numeric vector or matrix.

**Author(s)**

Jitao David Zhang <jitao\_david.zhang@roche.com>

**Examples**

```
testp <- runif(1000, 0, 1)
testp.al <- absLog10p(testp)

print(head(testp))
print(head(testp.al))
```

---

appendGmtList	<i>Append a GmtList object to another one</i>
---------------	-----------------------------------------------

---

**Description**

Append a GmtList object to another one

**Usage**

```
appendGmtList(gmtList, newGmtList, ...)
```

**Arguments**

gmtList	A GmtList object
newGmtList	Another GmtList object to be appended
...	Further GmtList object to be appended

**Value**

A new GmtList list, with all elements in the input appended in the given order

**Examples**

```
test_gmt_file<- system.file("extdata/test.gmt", package="BioQC")
testGmtList1 <- readGmt(test_gmt_file, namespace="test1")
testGmtList2 <- readGmt(test_gmt_file, namespace="test2")
testGmtList3 <- readGmt(test_gmt_file, namespace="test3")
testGmtAppended <- appendGmtList(testGmtList1, testGmtList2, testGmtList3)
```

---

as.GmtList	<i>Convert a list of gene symbols into a gmtlist</i>
------------	------------------------------------------------------

---

**Description**

Convert a list of gene symbols into a gmtlist

**Usage**

```
as.GmtList(list, description = NULL, uniqGenes = TRUE, namespace = NULL)
```

**Arguments**

list	A named list with character vectors of genes. Names will become names of gene sets; character vectors will become genes
description	Character, description of gene-sets. The value will be expanded to the same length of the list.
uniqGenes	Logical, whether redundant genes should be made unique?
namespace	Character or NULL, namespace of the gene-set

**Examples**

```
testVec <- list(GeneSet1=c("AKT1", "AKT2"),
               GeneSet2=c("MAPK1", "MAPK3"),
               GeneSet3=NULL)
testVecGmtlist <- as.GmtList(testVec)
```

---

BaseIndexList-class	<i>An S4 class to hold a list of indices, with the possibility to specify the offset of the indices. IndexList and SignedIndexList extend this class</i>
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---

**Description**

An S4 class to hold a list of indices, with the possibility to specify the offset of the indices. IndexList and SignedIndexList extend this class

**Slots**

offset	An integer specifying the value of first element. Default 1
keepNA	Logical, whether NA is kept during construction
keepDup	Logical, whether duplicated values are kept during construction

---

entropy

*Shannon entropy*

---

### Description

Shannon entropy

### Usage

```
entropy(vector)
```

### Arguments

vector            A vector of numbers, or characters. Discrete probability of each item is calculated and the Shannon entropy is returned.

### Value

Shannon entropy

Shannon entropy can be used as measures of gene expression specificity, as well as measures of tissue diversity and specialization. See references below.

We use 2 as base for the entropy calculation, because in this base the unit of entropy is *bit*.

### Author(s)

Jitao David Zhang <jitao\_david.zhang@roche.com>

### References

Martinez and Reyes-Valdes (2008) Defining diversity, specialization, and gene specificity in transcriptomes through information theory. PNAS 105(28):9709–9714

### Examples

```
myVec0 <- 1:9
entropy(myVec0) ## log2(9)
myVec1 <- rep(1, 9)
entropy(myVec1)

entropy(LETTERS)
entropy(rep(LETTERS, 5))
```

---

entropyDiversity      *Entropy-based sample diversity*

---

## Description

Entropy-based sample diversity

## Usage

```
entropyDiversity(mat, norm = FALSE)
```

## Arguments

mat	A matrix (usually an expression matrix), with genes (features) in rows and samples in columns.
norm	Logical, whether the diversity should be normalized by $\log_2(\text{nrow}(\text{mat}))$ .

## Value

A vector as long as the column number of the input matrix

## References

Martinez and Reyes-Valdes (2008) Defining diversity, specialization, and gene specificity in transcriptomes through information theory. PNAS 105(28):9709–9714

## See Also

[entropy](#) and [sampleSpecialization](#)

## Examples

```
myMat <- rbind(c(3,4,5),c(6,6,6), c(0,2,4))
entropyDiversity(myMat)
entropyDiversity(myMat, norm=TRUE)

myRandomMat <- matrix(runif(1000), ncol=20)
entropyDiversity(myRandomMat)
entropyDiversity(myRandomMat, norm=TRUE)
```

---

entropySpecificity      *Entropy-based gene-expression specificity*

---

## Description

Entropy-based gene-expression specificity

## Usage

```
entropySpecificity(mat, norm = FALSE)
```

## Arguments

mat	A matrix (usually an expression matrix), with genes (features) in rows and samples in columns.
norm	Logical, whether the specificity should be normalized by $\log_2(\text{ncol}(\text{mat}))$ .

## Value

A vector of the length of the row number of the input matrix, namely the specificity score of genes.

## References

Martinez and Reyes-Valdes (2008) Defining diversity, specialization, and gene specificity in transcriptomes through information theory. PNAS 105(28):9709–9714

## See Also

[entropy](#)

## Examples

```
myMat <- rbind(c(3,4,5),c(6,6,6), c(0,2,4))
entropySpecificity(myMat)
entropySpecificity(myMat, norm=TRUE)

myRandomMat <- matrix(runif(1000), ncol=20)
entropySpecificity(myRandomMat)
entropySpecificity(myRandomMat, norm=TRUE)
```



---

filterBySize	<i>Filter a GmtList by size</i>
--------------	---------------------------------

---

**Description**

Filter a GmtList by size

**Usage**

```
filterBySize(x, min, max)
```

**Arguments**

x	A GmtList object
min	Numeric, gene-sets with fewer genes than min will be removed
max	Numeric, gene-sets with more genes than max will be removed

**Value**

A GmtList object with sizes (count of genes) between min and max (inclusive).

---

filterPmat	<i>Filter rows of p-value matrix under the significance threshold</i>
------------	-----------------------------------------------------------------------

---

**Description**

Filter rows of p-value matrix under the significance threshold

**Usage**

```
filterPmat(x, threshold)
```

**Arguments**

x	A matrix of p-values. It must be raw p-values and should not be transformed (e.g. logarithmic).
threshold	A numeric value, the minimal p-value used to filter rows. If missing, given the values of NA, NULL or number 0, no filtering will be done and the input matrix will be returned.

**Value**

Matrix of p-values. If no line is left, a empty matrix of the same dimension as input will be returned.

**Author(s)**

Jitao David Zhang <jitao\_david.zhang@roche.com>

**Examples**

```
set.seed(1235)
testMatrix <- matrix(runif(100,0,1), nrow=10)

## filtering
(testMatrix.filter <- filterPmat(testMatrix, threshold=0.05))
## more strict filtering
(testMatrix.strictfilter <- filterPmat(testMatrix, threshold=0.01))
## no filtering
(testMatrix.nofilter <- filterPmat(testMatrix))
```

---

getLeadingEdgeIndexFromVector

*Getting leading-edge indices from a vector*

---

**Description**

Getting leading-edge indices from a vector

**Usage**

```
getLeadingEdgeIndexFromVector(
  x,
  index,
  comparison = c("greater", "less"),
  reference = c("background", "geneset")
)

getLeadingEdgeIndexFromMatrix(
  x,
  index,
  comparison = c("greater", "less"),
  reference = c("background", "geneset")
)
```

**Arguments**

x	A numeric vector (getLeadingEdgeIndexFromVector) or a numeric matrix (getLeadingEdgeIndexFromMatrix).
index	An integer vector, indicating the indices of genes in a gene-set.
comparison	Character string, are values greater than or less than the reference value considered as leading-edge? This depends on the type of value requested by the user in <code>wmwTest</code> .

reference      Character string, which reference is used? If background, genes with expression higher than the median of the background are reported. Otherwise in the case of geneset, genes with expression higher than the median of the gene-set is reported. Default is background, which is consistent with the results of the Wilcoxon-Mann-Whitney tests.

### Value

An integer vector, indicating the indices of leading-edge genes.

### Functions

- `getLeadingEdgeIndexFromMatrix`: x is a matrix.

### See Also

[wmwTest](#)

### Examples

```
myProfile <- c(rnorm(5, 3), rnorm(15, -3), rnorm(100, 0))
getLeadingEdgeIndexFromVector(myProfile, 1:20)
getLeadingEdgeIndexFromVector(myProfile, 1:20, comparison="less")
getLeadingEdgeIndexFromVector(myProfile, 1:20, comparison="less", reference="geneset")
myProfile2 <- c(rnorm(15, 3), rnorm(5, -3), rnorm(100, 0))
myProfileMat <- cbind(myProfile, myProfile2)
getLeadingEdgeIndexFromMatrix(myProfileMat, 1:20)
getLeadingEdgeIndexFromMatrix(myProfileMat, 1:20, comparison="less")
getLeadingEdgeIndexFromMatrix(myProfileMat, 1:20, comparison="less", reference="geneset")
```

---

gini

*Calculate Gini Index of a numeric vector*

---

### Description

Calculate the Gini index of a numeric vector.

### Usage

```
gini(x)
```

### Arguments

x                      A numeric vector.

### Details

The Gini index (Gini coefficient) is a measure of statistical dispersion. A Gini coefficient of zero expresses perfect equality where all values are the same. A Gini coefficient of one expresses maximal inequality among values.

**Value**

A numeric value between 0 and 1.

**Author(s)**

Jitao David Zhang <jitao\_david.zhang@roche.com>

**References**

Gini. C. (1912) *Variability and Mutability*, C. Cuppini, Bologna 156 pages.

**Examples**

```
testValues <- runif(100)
gini(testValues)
```

---

GmtList

*Convert a list to a GmtList object*

---

**Description**

Convert a list to a GmtList object

**Usage**

```
GmtList(list)
```

**Arguments**

`list` A list of genesets; each geneset is a list of at least three fields: 'name', 'desc', and 'genes'. 'name' and 'desc' contains one character string ('desc' can be NULL while 'name' cannot), and 'genes' can be either NULL or a character vector. In addition, 'namespace' is accepted to represent the namespace.

For convenience, the function also accepts a list of character vectors, each containing a geneset. In this case, the function works as a wrapper of `as.GmtList`

**See Also**

If a list of gene symbols need to be converted into a GmtList, use `'as.GmtList'` instead

**Examples**

```
testList <- list(list(name="GS_A", desc=NULL, genes=LETTERS[1:3]),
                list(name="GS_B", desc="gene set B", genes=LETTERS[1:5]),
                list(name="GS_C", desc="gene set C", genes=NULL))
testGmt <- GmtList(testList)

# as wrapper of as.GmtList
testGeneList <- list(GS_A=LETTERS[1:3], GS_B=LETTERS[1:5], GS_C=NULL)
testGeneGmt <- GmtList(testGeneList)
```

---

GmtList-class	<i>An S4 class to hold geneset in the GMT file in a list, each item in the list is in in turn a list containing following items: name, desc, and genes.</i>
---------------	-------------------------------------------------------------------------------------------------------------------------------------------------------------

---

**Description**

An S4 class to hold geneset in the GMT file in a list, each item in the list is in in turn a list containing following items: name, desc, and genes.

---

gmtlist2signedGenesets	<i>Convert gmtlist into a list of signed genesets</i>
------------------------	-------------------------------------------------------

---

**Description**

Convert gmtlist into a list of signed genesets

**Usage**

```
gmtlist2signedGenesets(
  gmtlist,
  posPattern = "_UP$",
  negPattern = "_DN$",
  nomatch = c("ignore", "pos", "neg")
)
```

**Arguments**

gmtlist	A gmtlist object, probably read-in by readGmt
posPattern	Regular expression pattern of positive gene sets. It is trimmed from the original name to get the stem name of the gene set. See examples below.
negPattern	Regular expression pattern of negative gene sets. It is trimmed from the original name to get the stem name of the gene set. See examples below.
nomatch	Options to deal with gene sets that match neither positive nor negative patterns. ignore: they will be ignored (but not discarded, see details below); pos: they will be counted as positive signs; neg: they will be counted as negative signs

**Value**

An S4-object of SignedGenesets, which is a list of signed\_geneset, each being a two-item list; the first item is 'pos', containing a character vector of positive genes; and the second item is 'neg', containing a character vector of negative genes.

Gene set names are detected whether they are positive or negative. If neither positive nor negative, nomatch will determine how will they be interpreted. In case of pos (or neg), such genesets will be treated as positive (or negative) gene sets. In case nomatch is set to ignore, the gene set will appear in the returned values with both positive and negative sets set to NULL.

**Examples**

```
testInputList <- list(list(name="GeneSetA_UP", genes=LETTERS[1:3]),
                     list(name="GeneSetA_DN", genes=LETTERS[4:6]),
                     list(name="GeneSetB", genes=LETTERS[2:4]),
                     list(name="GeneSetC_DN", genes=LETTERS[1:3]),
                     list(name="GeneSetD_UP", genes=LETTERS[1:3]))
testOutputList.ignore <- gmtlist2signedGenesets(testInputList, nomatch="ignore")
testOutputList.pos <- gmtlist2signedGenesets(testInputList, nomatch="pos")
testOutputList.neg <- gmtlist2signedGenesets(testInputList, nomatch="neg")
```

---

 gsDesc

*Gene-set descriptions*


---

**Description**

Gene-set descriptions

**Usage**

```
gsDesc(x)
```

**Arguments**

x                    A GmtList object

**Value**

Descriptions as a vector of character strings of the same length as x

---

gsGeneCount	<i>Gene-set gene counts</i>
-------------	-----------------------------

---

**Description**

Gene-set gene counts

gsSize is the synonym of gsGeneCount

**Usage**

```
gsGeneCount(x, uniqGenes = TRUE)
```

```
gsSize(x, uniqGenes = TRUE)
```

**Arguments**

x                    A GmtList or similar object

uniqGenes           Logical, whether only unique genes are counted

**Value**

Gene counts (aka gene-set sizes) as a vector of integer of the same length as x

---

gsGenes	<i>Gene-set member genes</i>
---------	------------------------------

---

**Description**

Gene-set member genes

**Usage**

```
gsGenes(x)
```

**Arguments**

x                    A GmtList object

**Value**

A list of genes as character strings of the same length as x

gsName *Gene-set names*

---

**Description**

Gene-set names

**Usage**

gsName(x)

**Arguments**

x                    A GmtList object

**Value**

Names as a vector of character strings of the same length as x

---

gsNamespace *Gene-set namespaces*

---

**Description**

Gene-set namespaces

**Usage**

gsNamespace(x)

**Arguments**

x                    A GmtList object

**Value**

Namespaces as a vector of character strings of the same length as x



---

gsNamespace<-                    *gsNamespace<- is the synonym of setGsNamespace*

---

**Description**

gsNamespace<- is the synonym of setGsNamespace

**Usage**

```
gsNamespace(x) <- value
```

**Arguments**

x	A GmtList object
value	namespace in setGsNamespace. It can be either a function that applies to a gene-set list element of the object (for instance function(x) x\$desc to extract description), or a vector of the same length of x, or in the special case NULL, which will erase the field namespace.

---

hasNamespace                    *Whether namespace is set*

---

**Description**

Whether namespace is set

**Usage**

```
hasNamespace(x)
```

**Arguments**

x	A GmtList object
---	------------------

**Value**

Logical, whether all gene-sets have the field namespace set

---

IndexList

---

*Convert a list to an IndexList object*


---

**Description**

Convert a list to an IndexList object

**Usage**

```
IndexList(object, ..., keepNA = FALSE, keepDup = FALSE, offset = 1L)
```

```
## S4 method for signature 'numeric'
```

```
IndexList(object, ..., keepNA = FALSE, keepDup = FALSE, offset = 1L)
```

```
## S4 method for signature 'logical'
```

```
IndexList(object, ..., keepNA = FALSE, keepDup = FALSE, offset = 1L)
```

```
## S4 method for signature 'list'
```

```
IndexList(object, keepNA = FALSE, keepDup = FALSE, offset = 1L)
```

**Arguments**

object	Either a list of unique integer indices, NULL and logical vectors (of same lengths), or a numerical vector or a logical vector. NA is discarded.
...	If object isn't a list, additional vectors can go here.
keepNA	Logical, whether NA indices should be kept or not. Default: FALSE (removed)
keepDup	Logical, whether duplicated indices should be kept or not. Default: FALSE (removed)
offset	Integer, the starting index. Default: 1 (as in the convention of R)

**Value**

The function returns a list of vectors

**Examples**

```
testList <- list(GS_A=c(1,2,3,4,3),
                GS_B=c(2,3,4,5),
                GS_C=NULL,
                GS_D=c(1,3,5,NA),
                GS_E=c(2,4))
testIndexList <- IndexList(testList)
IndexList(c(FALSE, TRUE, TRUE), c(FALSE, FALSE, TRUE), c(TRUE, FALSE, FALSE), offset=0)
IndexList(list(A=1:3, B=4:5, C=7:9))
IndexList(list(A=1:3, B=4:5, C=7:9), offset=0)
```

---

IndexList-class	<i>An S4 class to hold a list of integers as indices, with the possibility to specify the offset of the indices</i>
-----------------	---------------------------------------------------------------------------------------------------------------------

---

**Description**

An S4 class to hold a list of integers as indices, with the possibility to specify the offset of the indices

**Slots**

offset An integer specifying the value of first element. Default 1

keepNA Logical, whether NA is kept during construction

keepDup Logical, whether duplicated values are kept during construction

---

isValidBaseIndexList	<i>Function to validate a BaseIndexList object</i>
----------------------	----------------------------------------------------

---

**Description**

Function to validate a BaseIndexList object

**Usage**

```
isValidBaseIndexList(object)
```

**Arguments**

object	A BaseIndexList object Use <code>setValidity("BaseIndexList", "isValidBaseIndexList")</code> to check integrity of BaseIndexList objects. It can be very slow, therefore the feature is not turned on by default
--------	------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

---

isValidGmtList	<i>Function to validate a GmtList object</i>
----------------	----------------------------------------------

---

**Description**

Function to validate a GmtList object

**Usage**

```
isValidGmtList(object)
```

**Arguments**

object	A GmtList object Use <code>setValidity("GmtList", "isValidGmtList")</code> to check integrity of GmtList objects. It can be very slow, therefore the feature is not turned on by default
--------	------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

---

isValidIndexList	<i>Function to validate an IndexList object</i>
------------------	-------------------------------------------------

---

**Description**

Function to validate an IndexList object

**Usage**

```
isValidIndexList(object)
```

**Arguments**

object	an IndexList object Use <code>setValidity("BaseIndexList", "isValidBaseIndexList")</code> to check integrity of IndexList objects. It can be very slow, therefore the feature is not turned on by default
--------	-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

---

`isValidSignedGenesets` *Function to validate a SignedGenesets object*

---

**Description**

Function to validate a SignedGenesets object

**Usage**

`isValidSignedGenesets(object)`

**Arguments**

<code>object</code>	A SignedGenesets object Use <code>setValidity("SignedGenesets", "isValidSignedGenesets")</code> to check integrity of SignedGenesets objects. It can be very slow, therefore the feature is not turned on by default
---------------------	----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

---

`isValidSignedIndexList`  
*Function to validate a SignedIndexList object*

---

**Description**

Function to validate a SignedIndexList object

**Usage**

`isValidSignedIndexList(object)`

**Arguments**

<code>object</code>	a SignedIndexList object Use <code>setValidity("SignedIndexList", "isValidSignedIndexList")</code> to check integrity of SignedIndexList objects. It can be very slow, therefore the feature is not turned on by default
---------------------	--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

---

`matchGenes`*Match genes in a list-like object to a vector of genesymbols*

---

**Description**

Match genes in a list-like object to a vector of genesymbols

**Usage**

```
matchGenes(list, object, ...)  
  
## S4 method for signature 'GmtList,character'  
matchGenes(list, object)  
  
## S4 method for signature 'GmtList,matrix'  
matchGenes(list, object)  
  
## S4 method for signature 'GmtList,eSet'  
matchGenes(list, object, col = "GeneSymbol")  
  
## S4 method for signature 'character,character'  
matchGenes(list, object)  
  
## S4 method for signature 'character,matrix'  
matchGenes(list, object)  
  
## S4 method for signature 'character,eSet'  
matchGenes(list, object)  
  
## S4 method for signature 'character,DGEList'  
matchGenes(list, object, col = "GeneSymbol")  
  
## S4 method for signature 'GmtList,DGEList'  
matchGenes(list, object, col = "GeneSymbol")  
  
## S4 method for signature 'SignedGenesets,character'  
matchGenes(list, object)  
  
## S4 method for signature 'SignedGenesets,matrix'  
matchGenes(list, object)  
  
## S4 method for signature 'SignedGenesets,eSet'  
matchGenes(list, object, col = "GeneSymbol")  
  
## S4 method for signature 'SignedGenesets,DGEList'  
matchGenes(list, object, col = "GeneSymbol")
```

**Arguments**

list	A GmtList, list, character or SignedGenesets object
object	Gene symbols to be matched; they can come from a vector of character strings, or a column in the fData of an eSet object.
...	additional arguments like col
col	Column name of fData in an eSet object, or genes in an DGEList object, to specify where gene symbols are stored. The default value is set to "GeneSymbol"

**Value**

An IndexList object, which is essentially a list of the same length as input (length of 1 in case characters are used as input), with matching indices.

**Examples**

```
## test GmtList, character
testGenes <- sprintf("gene%d", 1:10)
testGeneSets <- GmtList(list(gs1=c("gene1", "gene2"), gs2=c("gene9", "gene10"), gs3=c("gene100")))
matchGenes(testGeneSets, testGenes)

## test GmtList, matrix
testGenes <- sprintf("gene%d", 1:10)
testGeneSets <- GmtList(list(gs1=c("gene1", "gene2"), gs2=c("gene9", "gene10"), gs3=c("gene100")))
testGeneExprs <- matrix(rnorm(100), nrow=10, dimnames=list(testGenes, sprintf("sample%d", 1:10)))
matchGenes(testGeneSets, testGeneExprs)

## test GmtList, eSet
testGenes <- sprintf("gene%d", 1:10)
testGeneSets <- GmtList(list(gs1=c("gene1", "gene2"), gs2=c("gene9", "gene10"), gs3=c("gene100")))
testGeneExprs <- matrix(rnorm(100), nrow=10, dimnames=list(testGenes, sprintf("sample%d", 1:10)))
testFeat <- data.frame(GeneSymbol=rownames(testGeneExprs), row.names=testGenes)
testPheno <- data.frame(SampleId=colnames(testGeneExprs), row.names=colnames(testGeneExprs))
testEset <- ExpressionSet(assayData=testGeneExprs,
  featureData=AnnotatedDataFrame(testFeat),
  phenoData=AnnotatedDataFrame(testPheno))
matchGenes(testGeneSets, testGeneExprs)
## force using row names
matchGenes(testGeneSets, testEset, col=NULL)

## test GmtList, DGEList
if(requireNamespace("edgeR")) {
  mat <- matrix(rnbinom(100, mu=5, size=2), ncol=10)
  rownames(mat) <- sprintf("gene%d", 1:nrow(mat))
  y <- edgeR::DGEList(counts=mat, group=rep(1:2, each=5))

  ## if genes are not set, row names of the count matrix will be used for lookup
  myGeneSet <- GmtList(list(gs1=rownames(mat)[1:2], gs2=rownames(mat)[9:10], gs3="gene100"))
  matchGenes(myGeneSet, y)
}
```

```
matchGenes(c("gene1", "gene2"), y)
## alternatively, use 'col' parameter to specify the column in 'genes'
y2 <- edgeR::DGEList(counts=mat,
  group=rep(1:2, each=5),
  genes=data.frame(GeneIdentifier=row.names(mat), row.names=row.names(mat)))
matchGenes(myGeneSet, y2, col="GeneIdentifier")
}

## test character, character
matchGenes(c("gene1", "gene2"), testGenes)

## test character, matrix
matchGenes(c("gene1", "gene2"), testGeneExprs)

## test character, eset
matchGenes(c("gene1", "gene2"), testEset)
```

---

offset

*Get offset from an IndexList object*

---

## Description

Get offset from an IndexList object

## Usage

```
offset(object)
```

```
## S4 method for signature 'BaseIndexList'
offset(object)
```

## Arguments

object            An IndexList object

## Examples

```
myIndexList <- IndexList(list(1:5, 2:7, 3:8), offset=1L)
offset(myIndexList)
```



---

```
offset<-
```

*Set the offset of an IndexList or a SignedIndexList object*

---

**Description**

Set the offset of an IndexList or a SignedIndexList object

**Usage**

```
`offset<-`(object, value)

## S4 replacement method for signature 'IndexList,numeric'
offset(object) <- value

## S4 replacement method for signature 'SignedIndexList,numeric'
offset(object) <- value
```

**Arguments**

object	An IndexList or a SignedIndexList object
value	The value, that the offset of object is set too. If it isn't an integer, it's coerced into an integer.

**Examples**

```
myIndexList <- IndexList(list(1:5, 2:7, 3:8), offset=1L)
offset(myIndexList)
offset(myIndexList) <- 3
offset(myIndexList)
```

---

```
prettySigNames
```

*Prettify default signature names*

---

**Description**

Prettify default signature names

**Usage**

```
prettySigNames(names, includeNamespace = TRUE)
```

**Arguments**

names	Character strings, signature names
includeNamespace	Logical, whether the namespace of the signatures should be included

**Value**

Character strings, pretty signature names

**Examples**

```
sig <- readCurrentSignatures()
prettyNames <- prettySigNames(names(sig))
```

---

readCurrentSignatures *Load current BioQC signatures*

---

**Description**

Load current BioQC signatures

**Usage**

```
readCurrentSignatures(uniqGenes = TRUE, namespace = NULL)
```

**Arguments**

uniqGenes	Logical, whether duplicated genes should be removed, passed to <a href="#">readGmt</a> .
namespace	Character, namespace of the gene-set, or codeNULL, passed to <a href="#">readGmt</a>

**Value**

A GmtList

**See Also**

[readGmt](#)

**Examples**

```
readCurrentSignatures()
```

---

readGmt	<i>Read in gene-sets from a GMT file</i>
---------	------------------------------------------

---

## Description

Read in gene-sets from a GMT file

## Usage

```
readGmt(..., uniqGenes = TRUE, namespace = NULL)
```

## Arguments

...	Named or unnamed character string vector, giving file names of one or more GMT format files.
uniqGenes	Logical, whether duplicated genes should be removed
namespace	Character, namespace of the gene-set. It can be used to specify namespace or sources of the gene-sets. If NULL is given, so no namespace is used and all gene-sets are assumed to come from the same unspecified namespace. The option can be helpful when gene-sets from multiple namespaces are jointly used.

## Value

A GmtList object, which is a S4-class wrapper of a list. Each element in the object is a list of (at least) three items:

- gene-set name (field name), character string, accessible with `gsName`
- gene-set description (field desc), character string, accessible with `gsDesc`
- genes (field genes), a vector of character strings, accessible with `gsGenes`
- namespace (field namespace), accessible with `gsNamespace`

## Note

Currently, when namespace is set as NULL, no namespace is used. This may change in the future, since we may use file base name as the default namespace.

## Examples

```
gmt_file <- system.file("extdata/exp.tissuemark.affy.roche.symbols.gmt", package="BioQC")
gmt_list <- readGmt(gmt_file)
gmt_nonUniqGenes_list <- readGmt(gmt_file, uniqGenes=FALSE)
gmt_namespace_list <- readGmt(gmt_file, uniqGenes=FALSE, namespace="myNamespace")

## suppose we have two lists of gene-sets to read in
test_gmt_file <- system.file("extdata/test.gmt", package="BioQC")
gmt_twons_list <- readGmt(gmt_file, test_gmt_file, namespace=c("BioQC", "test"))
## alternatively
gmt_twons_list <- readGmt(BioQC=gmt_file, test=test_gmt_file)
```

---

readSignedGmt	<i>Read signed GMT files</i>
---------------	------------------------------

---

## Description

Read signed GMT files

## Usage

```
readSignedGmt(  
  filename,  
  posPattern = "_UP$",  
  negPattern = "_DN$",  
  nomatch = c("ignore", "pos", "neg"),  
  uniqGenes = TRUE,  
  namespace = NULL  
)
```

## Arguments

filename	A gmt file
posPattern	Pattern of positive gene sets
negPattern	Pattern of negative gene sets
nomatch	options to deal with gene sets that match to neither posPattern nor negPattern patterns
uniqGenes	Logical, whether genes should be made unique
namespace	Character string or NULL, namespace of gene-sets

## See Also

[gmtlist2signedGenesets](#) for parameters posPattern, negPattern, and nomatch

## Examples

```
testGmtFile <- system.file("extdata/test.gmt", package="BioQC")  
testSignedGenesets.ignore <- readSignedGmt(testGmtFile, nomatch="ignore")  
testSignedGenesets.pos <- readSignedGmt(testGmtFile, nomatch="pos")  
testSignedGenesets.neg <- readSignedGmt(testGmtFile, nomatch="neg")
```

---

sampleSpecialization *Entropy-based sample specialization*

---

**Description**

Entropy-based sample specialization

**Usage**

```
sampleSpecialization(mat, norm = TRUE)
```

**Arguments**

mat	A matrix (usually an expression matrix), with genes (features) in rows and samples in columns.
norm	Logical, whether the specialization should be normalized by $\log_2(\text{ncol}(\text{mat}))$ .

**Value**

A vector as long as the column number of the input matrix

**References**

Martinez and Reyes-Valdes (2008) Defining diversity, specialization, and gene specificity in transcriptomes through information theory. PNAS 105(28):9709–9714

**See Also**

[entropy](#) and [entropyDiversity](#)

**Examples**

```
myMat <- rbind(c(3,4,5),c(6,6,6), c(0,2,4))
sampleSpecialization(myMat)
sampleSpecialization(myMat, norm=TRUE)

myRandomMat <- matrix(runif(1000), ncol=20)
sampleSpecialization(myRandomMat)
sampleSpecialization(myRandomMat, norm=TRUE)
```

---

setDescAsNamespace      *Set gene-set description as namespace*

---

### Description

Set gene-set description as namespace

### Usage

```
setDescAsNamespace(x)
```

### Arguments

x                      A `GmtList` object  
 This function wraps `setNamespace` to set gene-set description as namespace

### See Also

[setNamespace](#)

---

setNamespace              *Set the namespace field in each gene-set within a GmtList*

---

### Description

Set the namespace field in each gene-set within a `GmtList`

### Usage

```
setNamespace(x, namespace)
```

### Arguments

x                      A `GmtList` object encoding a list of gene-sets

namespace            It can be either a function that applies to a gene-set list element of the object (for instance `function(x) x$desc` to extract description), or a vector of the same length of x, or in the special case `NULL`, which will erase the field namespace.

Note that using vectors as namespace leads to poor performance when the input object has many gene-sets.

**Examples**

```

myGmtList <- GmtList(list(list(name="GeneSet1", desc="Namespace1", genes=LETTERS[1:3]),
  list(name="GeneSet2", desc="Namespace1", genes=rep(LETTERS[4:6],2)),
  list(name="GeneSet1", desc="Namespace1", genes=LETTERS[4:6]),
  list(name="GeneSet3", desc="Namespace2", genes=LETTERS[1:5])))
hasNamespace(myGmtList)
myGmtList2 <- setNamespace(myGmtList, namespace=function(x) x$desc)
gsNamespace(myGmtList2)
## the function can provide flexible ways to encode the gene-set namespace
myGmtList3 <- setNamespace(myGmtList, namespace=function(x) gsub("Namespace", "C", x$desc))
gsNamespace(myGmtList3)
## using vectors
myGmtList4 <- setNamespace(myGmtList, namespace=c("C1", "C1", "C1", "C2"))
gsNamespace(myGmtList4)
myGmtList2null <- setNamespace(myGmtList2, namespace=NULL)
hasNamespace(myGmtList2null)

```

---

show,GmtList-method    *Show method for GmtList*

---

**Description**

Show method for GmtList

**Usage**

```

## S4 method for signature 'GmtList'
show(object)

```

**Arguments**

object                    An object of the class GmtList

---

show,IndexList-method    *Show method for IndexList*

---

**Description**

Show method for IndexList

**Usage**

```

## S4 method for signature 'IndexList'
show(object)

```

**Arguments**

object                    An object of the class IndexList

---

show, SignedGenesets-method  
*Show method for SignedGenesets*

---

**Description**

Show method for SignedGenesets

**Usage**

```
## S4 method for signature 'SignedGenesets'  
show(object)
```

**Arguments**

object            An object of the class SignedGenesets

---

show, SignedIndexList-method  
*Show method for SignedIndexList*

---

**Description**

Show method for SignedIndexList

**Usage**

```
## S4 method for signature 'SignedIndexList'  
show(object)
```

**Arguments**

object            An object of the class SignedIndexList



---

SignedGenesets      *Convert a list to a SignedGenesets object*

---

### Description

Convert a list to a SignedGenesets object

### Usage

```
SignedGenesets(list)
```

### Arguments

**list**      A list of genesets; each geneset is a list of at least three fields: 'name', 'pos', and 'neg'. 'name' contains one non-null character string, and both 'pos' and 'neg' can be either NULL or a character vector.

### See Also

GmtList

### Examples

```
testList <- list(list(name="GS_A", pos=NULL, neg=LETTERS[1:3]),
                 list(name="GS_B", pos=LETTERS[1:5], neg=LETTERS[7:9]),
                 list(name="GS_C", pos=LETTERS[1:5], neg=NULL),
                 list(name="GS_D", pos=NULL, neg=NULL))
testSigndGS <- SignedGenesets(testList)
```

---

SignedGenesets-class      *An S4 class to hold signed genesets, each item in the list is in in turn a list containing following items: name, pos, and neg.*

---

### Description

An S4 class to hold signed genesets, each item in the list is in in turn a list containing following items: name, pos, and neg.

---

SignedIndexList      *Convert a list into a SignedIndexList*

---

### Description

Convert a list into a SignedIndexList

### Usage

```
SignedIndexList(object, ...)
```

```
## S4 method for signature 'list'
```

```
SignedIndexList(object, keepNA = FALSE, keepDup = FALSE, offset = 1L)
```

### Arguments

object	A list of lists, each with two elements named 'pos' or 'neg', can be logical vectors or integer indices
...	additional arguments, currently ignored
keepNA	Logical, whether NA indices should be kept or not. Default: FALSE (removed)
keepDup	Logical, whether duplicated indices should be kept or not. Default: FALSE (removed)
offset	offset; 1 if missing

### Value

A SignedIndexList, a list of lists, containing two vectors named 'positive' and 'negative', which contain the indices of genes that are either positively or negatively associated with a certain phenotype

### Examples

```
myList <- list(a = list(pos = list(1, 2, 2, 4), neg = c(TRUE, FALSE, TRUE)),
              b = list(NA), c = list(pos = c(c(2, 3), c(1, 3))))
SignedIndexList(myList)
```

```
## a special case of input is a single list with two elements, \code{pos} and \code{neg}
SignedIndexList(myList[[1]])
```

---

`SignedIndexList-class` *An S4 class to hold a list of signed integers as indices, with the possibility to specify the offset of the indices*

---

### Description

An S4 class to hold a list of signed integers as indices, with the possibility to specify the offset of the indices

### Slots

`offset` An integer specifying the value of first element. Default 1  
`keepNA` Logical, whether NA is kept during construction  
`keepDup` Logical, whether duplicated values are kept during construction

---

`simplifyMatrix` *Simplify matrix in case of single row/columns*

---

### Description

Simplify matrix in case of single row/columns

### Usage

```
simplifyMatrix(matrix)
```

### Arguments

`matrix` A matrix of any dimension  
 If only one row/column is present, the dimension is dropped and a vector will be returned

### Examples

```
testMatrix <- matrix(round(rnorm(9),2), nrow=3)
simplifyMatrix(testMatrix)
simplifyMatrix(testMatrix[1L,,drop=FALSE])
simplifyMatrix(testMatrix[,1L,drop=FALSE])
```

---

uniqGenesetsByNamespace

*Make names of gene-sets unique by namespace, and member genes of gene-sets unique*

---

## Description

Make names of gene-sets unique by namespace, and member genes of gene-sets unique

## Usage

```
uniqGenesetsByNamespace(gmtList)
```

## Arguments

`gmtList` A `GmtList` object, probably from `readGmt`. The object must have namespaces defined by `setNamespace`.

The function make sure that

- names of gene-sets within each namespace are unique, by merging gene-sets with duplicated names
- genes within each gene-set are unique, by removing duplicated genes

Gene-sets with duplicated names and different desc are merged, desc are made unique, and in case of multiple values, concatenated (with | as the collapse character).

## Value

A `GmtList` object, with unique gene-sets and unique gene lists. If not already present, a new item namespace is appended to each list element in the `GmtList` object, recording the namespace used to make gene-sets unique. The order of the returned `GmtList` object is given by the unique gene-set name of the input object.

## Examples

```
myGmtList <- GmtList(list(list(name="GeneSet1", desc="Namespace1", genes=LETTERS[1:3]),
  list(name="GeneSet2", desc="Namespace1", genes=rep(LETTERS[4:6],2)),
  list(name="GeneSet1", desc="Namespace1", genes=LETTERS[4:6]),
  list(name="GeneSet3", desc="Namespace2", genes=LETTERS[1:5])))

print(myGmtList)
myGmtList <- setNamespace(myGmtList, namespace=function(x) x$desc)
myUniqGmtList <- uniqGenesetsByNamespace(myGmtList)
print(myUniqGmtList)
```

---

valTypes	<i>prints the options of valTypes of wmwTest</i>
----------	--------------------------------------------------

---

**Description**

prints the options of valTypes of wmwTest

**Usage**

```
valTypes()
```

---

wmwLeadingEdge	<i>Identify BioQC leading-edge genes of one gene-set</i>
----------------	----------------------------------------------------------

---

**Description**

Identify BioQC leading-edge genes of one gene-set

**Usage**

```
wmwLeadingEdge(
  matrix,
  indexVector,
  valType = c("p.greater", "p.less", "p.two.sided", "U", "abs.log10p.greater",
    "log10p.less", "abs.log10p.two.sided", "Q", "r", "f", "U1", "U2"),
  thr = 0.05,
  reference = c("background", "geneset")
)
```

**Arguments**

matrix	A numeric matrix
indexVector	An integer vector, giving indices of a gene-set of interest
valType	Value type, consistent with the types in wmwTest
thr	Threshold of the value, greater or less than which the gene-set is considered significantly enriched in one sample
reference	Character string, which reference is used? If background, genes with expression higher than the median of the background are reported. Otherwise in the case of geneset, genes with expression higher than the median of the gene-set is reported. Default is background, which is consistent with the results of the Wilcoxon-Mann-Whitney tests.

**Value**

A list of integer vectors.

BioQC leading-edge genes are defined as those features whose expression is higher than the median expression of the background in a sample. The function identifies leading-edge genes of a given dataset (specified by the index vector) in a number of samples (specified by the matrix, with genes/features in rows and samples in columns) in three steps. The function calls `wmwTest` to run BioQC and identify samples in which the gene-set is significantly enriched. The enrichment criteria is specified by `valType` and `thr`. Then the function identifies genes in the gene-set that have greater or less expression than the median value of the reference in those samples showing significant enrichment. Finally, it reports either leading-edge genes in individual samples, or the intersection/union of leading-edge genes in multiple samples.

**See Also**

[wmwTest](#)

**Examples**

```
myProfile <- c(rnorm(5, 3), rnorm(15, -3), rnorm(100, 0))
myProfile2 <- c(rnorm(15, 3), rnorm(5, -3), rnorm(100, 0))
myProfile3 <- c(rnorm(10, 5), rnorm(10, 0), rnorm(100, 0))
myProfileMat <- cbind(myProfile, myProfile2, myProfile3)
wmwLeadingEdge(myProfileMat, 1:20, valType="p.greater")
wmwLeadingEdge(myProfileMat, 1:20, valType="log10p.less")
wmwLeadingEdge(myProfileMat, 1:20, valType="U", reference="geneset")
wmwLeadingEdge(myProfileMat, 1:20, valType="abs.log10p.greater")
```

---

wmwTest

*Wilcoxon-Mann-Whitney rank sum test for high-throughput expression profiling data*

---

**Description**

`wmwTest` is a highly efficient Wilcoxon-Mann-Whitney rank sum test for high-dimensional data, such as gene expression profiling. For datasets with more than 100 features (genes), the function can be more than 1,000 times faster than its R implementations (`wilcox.test` in `stats`, or `rankSumTestWithCorrelation` in `limma`).

**Usage**

```
wmwTest(
  x,
  indexList,
  col = "GeneSymbol",
  valType = c("p.greater", "p.less", "p.two.sided", "U", "abs.log10p.greater",
    "log10p.less", "abs.log10p.two.sided", "Q", "r", "f", "U1", "U2"),
  simplify = TRUE
```

```
)

## S4 method for signature 'matrix,IndexList'
wmwTest(x, indexList, valType = "p.greater", simplify = TRUE)

## S4 method for signature 'numeric,IndexList'
wmwTest(x, indexList, valType = "p.greater", simplify = TRUE)

## S4 method for signature 'matrix,GmtList'
wmwTest(x, indexList, valType = "p.greater", simplify = TRUE)

## S4 method for signature 'eSet,GmtList'
wmwTest(
  x,
  indexList,
  col = "GeneSymbol",
  valType = "p.greater",
  simplify = TRUE
)

## S4 method for signature 'eSet,numeric'
wmwTest(
  x,
  indexList,
  col = "GeneSymbol",
  valType = "p.greater",
  simplify = TRUE
)

## S4 method for signature 'eSet,logical'
wmwTest(
  x,
  indexList,
  col = "GeneSymbol",
  valType = "p.greater",
  simplify = TRUE
)

## S4 method for signature 'eSet,list'
wmwTest(
  x,
  indexList,
  col = "GeneSymbol",
  valType = "p.greater",
  simplify = TRUE
)

## S4 method for signature 'ANY,numeric'
```

```

wmmTest(x, indexList, valType = "p.greater", simplify = TRUE)

## S4 method for signature 'ANY,logical'
wmmTest(x, indexList, valType = "p.greater", simplify = TRUE)

## S4 method for signature 'ANY,list'
wmmTest(x, indexList, valType = "p.greater", simplify = TRUE)

## S4 method for signature 'matrix,SignedIndexList'
wmmTest(x, indexList, valType, simplify = TRUE)

## S4 method for signature 'matrix,SignedGenesets'
wmmTest(x, indexList, valType, simplify = TRUE)

## S4 method for signature 'numeric,SignedIndexList'
wmmTest(x, indexList, valType, simplify = TRUE)

## S4 method for signature 'eSet,SignedIndexList'
wmmTest(x, indexList, valType, simplify = TRUE)

## S4 method for signature 'eSet,SignedGenesets'
wmmTest(
  x,
  indexList,
  col = "GeneSymbol",
  valType = c("p.greater", "p.less", "p.two.sided", "U", "abs.log10p.greater",
    "log10p.less", "abs.log10p.two.sided", "Q", "r", "f", "U1", "U2"),
  simplify = TRUE
)

```

## Arguments

x	A numeric matrix. All other data types (e.g. numeric vectors or ExpressionSet objects) are coerced into matrix.
indexList	A list of integer indices (starting from 1) indicating signature genes. Can be of length zero. Other data types (e.g. a list of numeric or logical vectors, or a numeric or logical vector) are coerced into such a list. See details below for a special case using GMT files.
col	a string sometimes used with a eSet
valType	The value type to be returned, allowed values include p.greater, p.less, abs.log10p.greater and abs.log10p.less (one-sided tests), p.two.sided, and U statistic (or more specifically, either U1 or U2), and a few other variants. See details below.
simplify	Logical. If not, the returning value is in matrix format; if set to TRUE, the results are simplified into vectors when possible (default).



## Details

The basic application of the function is to test the enrichment of gene sets in expression profiling data or differentially expressed data (the matrix with feature/gene in rows and samples in columns).

A special case is when `x` is an `eSet` object (e.g. `ExpressionSet`), and `indexList` is a list returned from `readGmt` function. In this case, the only requirement is that one column named `GeneSymbol` in the `featureData` contain gene symbols used in the GMT file. The same applies to signed Gmt files. See the example below.

Besides the conventional value types such as `'p.greater'`, `'p.less'`, `'p.two.sided'`, and `'U'` (the U-statistic), `wmwTest` (from version 0.99-1) provides further value types: `abs.log10p.greater` and `log10p.less` perform  $\log_{10}$  transformation on respective  $p$ -values and give the transformed value a proper sign (positive for greater than, and negative for less than); `abs.log10p.two.sided` transforms two-sided  $p$ -values to non-negative values; and `Q` score reports absolute  $\log_{10}$ -transformation of  $p$ -value of the two-side variant, and gives a proper sign to it, depending on whether it is rather greater than (positive) or less than (negative).

From version 1.19.1, the rank-biserial correlation coefficient (`'r'`) and the common language effect size (`'f'`) are supported value types.

Before version 1.19.3, the `'U'` statistic returned is in fact `'U2'`. From version 1.19.3, `'U1'` is returned when `'U'` is used, and users can specify additional parameter values `'U1'` and `'U2'`. The sum of `'U1'` and `'U2'` is the product of the sizes of two vectors to be compared.

## Value

A numeric matrix or vector containing the statistic.

## Methods (by class)

- `x = matrix, indexList = IndexList`: `x` is a matrix and `indexList` is a `IndexList`
- `x = numeric, indexList = IndexList`: `x` is a numeric and `indexList` is a `IndexList`
- `x = matrix, indexList = GmtList`: `x` is a matrix and `indexList` is a `GmtList`
- `x = eSet, indexList = GmtList`: `x` is a `eSet` and `indexList` is a `GmtList`
- `x = eSet, indexList = numeric`: `x` is a `eSet` and `indexList` is a numeric
- `x = eSet, indexList = logical`: `x` is a `eSet` and `indexList` is a logical
- `x = eSet, indexList = list`: `x` is a `eSet` and `indexList` is a list
- `x = ANY, indexList = numeric`: `x` is ANY and `indexList` is a numeric
- `x = ANY, indexList = logical`: `x` is ANY and `indexList` is a logical
- `x = ANY, indexList = list`: `x` is ANY and `indexList` is a list
- `x = matrix, indexList = SignedIndexList`: `x` is a matrix and `indexList` is a `SignedIndexList`
- `x = matrix, indexList = SignedGenesets`: `x` is a `eSet` and `indexList` is a `SignedIndexList`
- `x = numeric, indexList = SignedIndexList`: `x` is a numeric and `indexList` is a `SignedIndexList`
- `x = eSet, indexList = SignedIndexList`: `x` is a `eSet` and `indexList` is a `SignedIndexList`
- `x = eSet, indexList = SignedGenesets`: `x` is a `eSet` and `indexList` is a `SignedIndexList`

**Note**

The function has been optimized for expression profiling data. It avoids repetitive ranking of data as done by native R implementations and uses efficient C code to increase the performance and control memory use. Simulation studies using expression profiles of 22000 genes in 2000 samples and 200 gene sets suggested that the C implementation can be >1000 times faster than the R implementation. And it is possible to further accelerate by parallel calling the function with `mclapply` in the multicore package.

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**References**

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**See Also**

`codewilcox.test` in the `stats` package, and `rankSumTestWithCorrelation` in the `limma` package.

**Examples**

```
## R-native data structures
set.seed(1887)
rd <- rnorm(1000)
r1 <- sample(c(TRUE, FALSE), 1000, replace=TRUE)
wmmTest(rd, r1, valType="p.two.sided")
wmmTest(rd, which(r1), valType="p.two.sided")
rd1 <- rd + ifelse(r1, 0.5, 0)
wmmTest(rd1, r1, valType="p.greater")
wmmTest(rd1, r1, valType="U")
rd2 <- rd - ifelse(r1, 0.2, 0)
wmmTest(rd2, r1, valType="p.greater")
wmmTest(rd2, r1, valType="p.two.sided")
wmmTest(rd2, r1, valType="p.less")
wmmTest(rd2, r1, valType="r")
wmmTest(rd2, r1, valType="f")

## matrix forms
rmat <- matrix(c(rd, rd1, rd2), ncol=3, byrow=FALSE)
wmmTest(rmat, r1, valType="p.two.sided")
wmmTest(rmat, r1, valType="p.greater")

wmmTest(rmat, which(r1), valType="p.two.sided")
```

```

wmmTest(rmat, which(r1), valType="p.greater")

## other valTypes
wmmTest(rmat, which(r1), valType="U")
wmmTest(rmat, which(r1), valType="abs.log10p.greater")
wmmTest(rmat, which(r1), valType="log10p.less")
wmmTest(rmat, which(r1), valType="abs.log10p.two.sided")
wmmTest(rmat, which(r1), valType="Q")
wmmTest(rmat, which(r1), valType="r")
wmmTest(rmat, which(r1), valType="f")

## using ExpressionSet
data(sample.ExpressionSet)
testSet <- sample.ExpressionSet
fData(testSet)$GeneSymbol <- paste("GENE_", 1:nrow(testSet), sep="")
mySig1 <- sample(c(TRUE, FALSE), nrow(testSet), prob=c(0.25, 0.75), replace=TRUE)
wmmTest(testSet, which(mySig1), valType="p.greater")

## using integer
exprs(testSet)[,1L] <- exprs(testSet)[,1L] + ifelse(mySig1, 50, 0)
wmmTest(testSet, which(mySig1), valType="p.greater")

## using lists
mySig2 <- sample(c(TRUE, FALSE), nrow(testSet), prob=c(0.6, 0.4), replace=TRUE)
wmmTest(testSet, list(first=mySig1, second=mySig2))
## using GMT file
gmt_file <- system.file("extdata/exp.tissuemark.affy.roche.symbols.gmt", package="BioQC")
gmt_list <- readGmt(gmt_file)

gss <- sample(unlist(sapply(gmt_list, function(x) x$genes)), 1000)
eset<-new("ExpressionSet",
          exprs=matrix(rnorm(10000), nrow=1000L),
          phenoData=new("AnnotatedDataFrame", data.frame(Sample=LETTERS[1:10])),
          featureData=new("AnnotatedDataFrame", data.frame(GeneSymbol=gss)))
esetWmmRes <- wmmTest(eset, gmt_list, valType="p.greater")
summary(esetWmmRes)

## using signed GMT file
signed_gmt_file <- system.file("extdata/test.gmt", package="BioQC")
signed_gmt <- readSignedGmt(signed_gmt_file)
esetSignedWmmRes <- wmmTest(eset, signed_gmt, valType="p.greater")

esetMat <- exprs(eset); rownames(esetMat) <- fData(eset)$GeneSymbol
esetSignedWmmRes2 <- wmmTest(esetMat, signed_gmt, valType="p.greater")

```

---

wmmTestInR

*Wilcoxon-Mann-Whitney test in R*


---

## Description

Wilcoxon-Mann-Whitney test in R

**Usage**

```
wmwTestInR(x, sub, valType = c("p.greater", "p.less", "p.two.sided", "W"))
```

**Arguments**

x	A numerical vector
sub	A logical vector or integer vector to subset x. Numbers in sub are compared with numbers out of sub
valType	Type of returned-value. Supported values: p.greater, p.less, p.two.sided, and W statistic (note it is different from the U statistic)

**Examples**

```
testNums <- 1:10
testSub <- rep_len(c(TRUE, FALSE), length.out=length(testNums))
wmwTestInR(testNums, testSub)
wmwTestInR(testNums, testSub, valType="p.two.sided")
wmwTestInR(testNums, testSub, valType="p.less")
wmwTestInR(testNums, testSub, valType="W")
```

---

[.GmtList

*Subsetting GmtList object into another GmtList object*


---

**Description**

Subsetting GmtList object into another GmtList object

**Usage**

```
## S3 method for class 'GmtList'
x[i, drop = FALSE]
```

**Arguments**

x	A GmtList object
i	Index to subset
drop	In case only one element remains, should a list representing the single geneset returned? Default: FALSE

**Examples**

```
myGmtList <- GmtList(list(gs1=letters[1:3], gs2=letters[3:4], gs3=letters[4:5]))
myGmtList[1:2]
myGmtList[1] ## default behaviour: not dropping
myGmtList[1,drop=TRUE] ## force dropping
```

---

`[[.GmtList`*Subsetting GmtList object to fetch one gene-set*

---

**Description**

Subsetting GmtList object to fetch one gene-set

**Usage**

```
## S3 method for class 'GmtList'  
x[[i]]
```

**Arguments**

x	A GmtList object
i	The index to subset

**Examples**

```
myGmtList <- GmtList(list(gs1=letters[1:3], gs2=letters[3:4], gs3=letters[4:5]))  
myGmtList[[1]]
```

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