

# Package ‘BioQC’

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**Type** Package

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

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**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.

**Depends** 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

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---

**absLog10p***Absolute base-10 logarithm of p-values*

---

**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                    *Append a GmtList object to another one*

---

### 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                    *Convert a list of gene symbols into a gmtlist*

---

### 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    *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*

---

**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 | <i>Entropy-based sample diversity</i> |
|------------------|---------------------------------------|

---

**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 | <i>Entropy-based gene-expression specificity</i> |
|--------------------|--|

---

**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))
```



---

|      |   |
|------|---|
| gini | <i>Calculate Gini Index of a numeric vector</i> |
|------|---|

---

**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 | <i>Convert a list to a GmtList object</i> |
|---------|---|

---

**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)
```

---

|                            |   |
|----------------------------|---|
| <code>GmtList-class</code> | <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.

---

|                                     |   |
|-------------------------------------|---|
| <code>gmtlist2signedGenesets</code> | <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 | <i>Gene-set names</i> |
|--------|-----------------------|

---

**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 | <i>Gene-set namespaces</i> |
|-------------|----------------------------|

---

**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 <code>function(x) x\$desc</code> 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 | <i>Convert a list to an IndexList object</i> |
|-----------|--|

---

**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 setValidity("BaseIndexList", "isValidBaseIndexList") 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 setValidity("GmtList", "isValidGmtList") to check integrity of GmtList objects. It can be very slow, therefore the feature is not turned on by default |
|--------|---|



---

isValidIndexList      *Function to validate an IndexList object*

---

**Description**

Function to validate an IndexList object

**Usage**

isValidIndexList(object)

**Arguments**

|        |  |
|--------|--|
| object | an IndexList object Use setValidity("BaseIndexList", "isValidBaseIndexList") 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**

|        |   |
|--------|---|
| object | A SignedGenesets object Use setValidity("SignedGenesets", "isValidSignedGenesets") 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**

|        |   |
|--------|---|
| object | a SignedIndexList object Use setValidity("SignedIndexList", "isValidSignedIndexList") 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=rownames(mat), row.names=rownames(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 | <i>Get offset from an IndexList object</i> |
|--------|--|

---

### 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<- | <i>Set the offset of an IndexList or a SignedIndexList object</i> |
|----------|---|

---

### 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)
```

---

|         |  |
|---------|--|
| 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 | <i>Set the namespace field in each gene-set within a GmtList</i> |
|--------------|--|

---

**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()
```

---

|         |  |
|---------|--|
| wmwTest | <i>Wilcoxon-Mann-Whitney rank sum test for high-throughput expression profiling data</i> |
|---------|--|

---

**Description**

We have implemented a highly efficient Wilcoxon-Mann-Whitney rank sum test for high-throughput expression profiling data. 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"),
  simplify = TRUE
)

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

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

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

## S4 method for signature 'eSet,GmtList'
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"),
```

```
    simplify = TRUE
  )

## S4 method for signature 'eSet,numeric'
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"),
  simplify = TRUE
)

## S4 method for signature 'eSet,logical'
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"),
  simplify = TRUE
)

## S4 method for signature 'eSet,list'
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"),
  simplify = TRUE
)

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

## S4 method for signature 'ANY,logical'
wmwTest(x, indexList, valType, simplify = TRUE)

## S4 method for signature 'ANY,list'
wmwTest(x, indexList, valType, simplify = TRUE)

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

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

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

## S4 method for signature 'eSet,SignedIndexList'
```

```

wmwTest(x, indexList, valType, simplify = TRUE)

## S4 method for signature 'eSet,SignedGenesets'
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"),
  simplify = TRUE
)

```

### Arguments

|                        |  |
|------------------------|--|
| <code>x</code>         | A numeric matrix. All other data types (e.g. numeric vectors or ExpressionSet objects) are coerced into matrix.  |
| <code>indexList</code> | 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.  |
| <code>col</code>       | a string sometimes used with a eSet  |
| <code>valType</code>   | The value type to be returned, allowed values include <code>p.greater</code> , <code>p.less</code> , <code>abs.log10p.greater</code> and <code>abs.log10p.less</code> (one-sided tests), <code>p.two.sided</code> , and <code>U</code> statistic, and their <code>log10</code> transformation variants. See details below. |
| <code>simplify</code>  | Logical. If not, the returning value is in matrix format; if set to <code>TRUE</code> , 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 `log10` 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 `log10`-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).

### 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.

### Author(s)

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### References

- Barry, W.T., Nobel, A.B., and Wright, F.A. (2008). A statistical framework for testing functional namespaces in microarray data. *\_Annals of Applied Statistics\_* 2, 286-315.
- Wu, D, and Smyth, GK (2012). Camera: a competitive gene set test accounting for inter-gene correlation. *\_Nucleic Acids Research\_* 40(17):e133
- Zar, JH (1999). *\_Biostatistical Analysis 4th Edition\_*. Prentice-Hall International, Upper Saddle River, New Jersey.

### 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")

## 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")

## 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 | <i>Wilcoxon-Mann-Whitney test in R</i> |
|------------|--|

---

**Description**

Wilcoxon-Mann-Whitney test in R

**Usage**

```
wmmTestInR(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))
wmmTestInR(testNums, testSub)
wmmTestInR(testNums, testSub, valType="p.two.sided")
wmmTestInR(testNums, testSub, valType="p.less")
wmmTestInR(testNums, testSub, valType="W")
```

---

|           |  |
|-----------|--|
| [.GmtList | <i>Subsetting GmtList object into another GmtList object</i> |
|-----------|--|

---

**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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