Package ‘SeqGSEA’

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Type Package

Title Gene Set Enrichment Analysis (GSEA) of RNA-Seq Data: integrating differential expression and splicing

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Description The package generally provides methods for gene set enrichment analysis of high-throughput RNA-Seq data by integrating differential expression and splicing. It uses negative binomial distribution to model read count data, which accounts for sequencing biases and biological variation. Based on permutation tests, statistical significance can also be achieved regarding each gene's differential expression and splicing, respectively.

License GPL (>= 3)

Depends Biobase, doParallel, DESeq

Imports methods, biomaRt

Suggests easyRNASeq, GenomicRanges

biocViews Sequencing, RNASEq, GeneSetEnrichment, GeneExpression, DifferentialExpression

NeedsCompilation no

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SeqGSEA-package

SeqGSEA: a Bioconductor package for gene set enrichment analysis of RNA-Seq data

Description

SeqGSEA is an R package for gene set enrichment analysis of RNA-Seq data with the ability to integrate differential expression and differential splice in functional analysis.

Details

Package: SeqGSEA
Type: Package
License: GPL (>= 3)

A User’s Guide is available as well as the usual help page documentation for each of the individual functions.

The most useful functions are listed below:

* ReadCountSet class
  * ReadCountSet-class
  * ReadCountSet
  * exonID
  * geneID
  * counts-methods
  * label
  * subsetByGenes

* SeqGeneSet class
  * SeqGeneSet-class
  * geneSetDescs
  * geneSetNames
  * geneSetSize
  * size

* Load data
  * newReadCountSet
  * loadExonCountData
  * newGeneSets
  * loadGenesets

* DE analysis
  * getGeneCount
SeqGSEA-package

- runDESeq
- DENBStat4GSEA
- DENBStatPermut4GSEA
- DENBTest
- DEpermutePval

* DS analysis
  - DSpermute4GSEA
  - DSpermutePval
  - exonTestability
  - geneTestability
  - estiExonNBstat
  - estiGeneNBstat

* GSEA main
  - GSEnrichAnalyze
  - calES
  - calES_perm
  - genePermuteScore
  - geneScore
  - rankCombine
  - normES
  - normFactor
  - scoreNormalization
  - signifES

* Result tables
  - GSEAresultTable
  - DSresultExonTable
  - DSresultGeneTable
  - topDEGenes
  - topDSExons
  - topDSGenes
  - topGeneSets

* Result displays
  - plotES
  - plotGeneScore
  - plotSig
  - plotSigGeneSet
  - writeSigGeneSet

* Miscellaneous
  - genpermuteMat
  - convertEnsembl2Symbol
  - convertSymbol2Ensembl
Author(s)

Xi Wang and Murray J. Cairns

Maintainer: Xi Wang <xi.wang@newcastle.edu.au>

References


calES

Calculate running enrichment scores of gene sets

Description

This is an internal function to calculate running enrichment scores of each gene set in the SeqGeneSet object specified.

Usage

```r
calES(gene.set, gene.score, weighted.type = 1)
```

Arguments

- `weighted.type`: gene score weight type.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

`GSEnrichAnalyze`, `calES.perm`

Examples

```r
data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
data(GS_example, package="SeqGSEA")
rES <- calES(GS_example, gene.score)
rES[1,]
```
**calES.perm**  
*Calculate enrichment scores for gene sets in the permutation data sets*

**Description**  
This is an internal function to calculate enrichment scores for gene sets in the permutation data sets.

**Usage**  
```r  
calES.perm(gene.set, gene.score.perm, weighted.type = 1)  
```

**Arguments**
- `gene.score.perm`: a matrix of gene scores on the permutation data sets.
- `weighted.type`: gene score weight type.

**Author(s)**
Xi Wang, xi.wang@newcastle.edu.au

**See Also**
`GSEnrichAnalyze`, `calES`,

**Examples**
```r  
data(DEscore.perm, package="SeqGSEA")  
data(DSscore.perm, package="SeqGSEA")  
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)  
data(GS_example, package="SeqGSEA")  
ES.perm <- calES.perm(GS_example, gene.score.perm)  
ES.perm[1:5,1:5]  
```

---

**convertEnsembl2Symbol**  
*Convert ensembl gene IDs to gene symbols*

**Description**  
Convert ensembl gene IDs to gene symbols

**Usage**  
```r  
convertEnsembl2Symbol(ensembl.genes)  
```

**Arguments**
- `ensembl.genes`: ensembl gene ID(s).
Value
A 2-column matrix showing the correspondence of ensembl gene IDs and gene symbols.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
convertSymbol2Ensembl

Examples
convertEnsembl2Symbol("ENSG00000162946") #DISC1

convertSymbol2Ensembl  Convert gene symbols to ensembl gene IDs

Description
Convert gene symbols to ensembl gene IDs

Usage
convertSymbol2Ensembl(symbols)

Arguments
symbols     gene symbol(s).

Value
A 2-column matrix showing the correspondence of gene symbols and ensembl gene IDs.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
convertEnsembl2Symbol

Examples
convertSymbol2Ensembl("DISC1") #ENSG00000162946
counts-methods  

Accessors for the 'counts' slot of a ReadCountSet object.

Description

Accessors for the 'counts' slot of a ReadCountSet object.

Usage

```r
## S4 method for signature 'ReadCountSet'
counts(object)
## S4 replacement method for signature 'ReadCountSet,matrix'
counts(object) <- value
```

Arguments

- **object**: a ReadCountSet object
- **value**: a matrix of read counts

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

Examples

```r
data(RCS_example, package="SeqGSEA")
readCounts <- counts(RCS_example)
head(readCounts)
```

DENBStat4GSEA  

Calculate NB-statistics quantifying differential expression for each gene

Description

Calculate NB-statistics quantifying differential expression between two groups of samples compared. The results will be used for GSEA run. Comparing with **DENBTest**, this function will not calculate NB test p-values.

This function only works with two-group comparison.

Usage

```r
DENBStat4GSEA(cds)
```

Arguments

- **cds**: A CountDataSet object with size factors and dispersion parameters estimated. Recommended to take the output of **runDESeq**.
A data frame containing each gene’s expression means and variances in each group, and each gene’s DE NB-statistics.

The results with the output of `DENBStatPermut4GSEA` can also be used to run `DEpermutePval`.

Xi Wang, xi.wang@newcastle.edu.au


Examples

```r
data(RCS_example, package="SeqGSEA")
geneCounts <- getGeneCount(RCS_example)
label <- label(RCS_example)
DEG <- runDESeq(geneCounts, label)
DEGres <- DENBStat4GSEA(DEG)
head(DEGres)
```

**DENBStatPermut4GSEA**  
*Calculate NB-statistics quantifying DE for each gene in the permutation data sets*

Calculate NB-statistics quantifying differential expression for each gene in the permutation data sets. The results will be used for GSEA run.

**Usage**

`DENBStatPermut4GSEA(DEG, permuteMat)`

**Arguments**

- `DEG`: a CountDataSet object, can be the output of `runDESeq`.
- `permuteMat`: a permutation matrix generated by `genpermuteMat`.

**Value**

A matrix of NB-statistics. Each row corresponds to each gene, and each column to each permutation.
Note
The results with the output of `DENBStat4GSEA` can also be used to run `DEpermutePval`.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

References

See Also
`DENBStat4GSEA`, `runDESeq`, `DEpermutePval`, `genpermuteMat`

Examples
```r
data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
geneCounts <- getGeneCount(RCS_example)
label <- label(RCS_example)
DEG <- runDESeq(geneCounts, label)
DEpermNBstat <- DENBStatPermut4GSEA(DEG, permuteMat)
DEpermNBstat[1:10,1:10]
```

---

**DENBTest**

*Perform negative binomial exact test for differential expression*

**Description**
Perform negative binomial exact test for differential expression - a modified version of nbinomTest in DESeq package.

**Usage**
```
DENBTest(cds)
```

**Arguments**
- **cds**
  
  A CountDataSet object with size factors and dispersion parameters estimated. Recommended to take the output of `runDESeq`.

**Value**
A data frame of the test results. Information contains mean expression values, NB-statistics, (log) fold-changes, p-values, and adjusted p-values.

**Author(s)**
Xi Wang, xi.wang@newcastle.edu.au
DEpermutePval

References

See Also
runDESeq, DENBStat4GSEA

Examples
```
data(RCS_example, package="SeqGSEA")
geneCounts <- getGeneCount(RCS_example)
label <- label(RCS_example)
DEG <- runDESeq(geneCounts, label)
DEGres <- DENBTest(DEG)
head(DEGres)
```

DEpermutePval

Permutation for p-values in differential expression analysis

Description
Calculate permutation p-values in differential expression analysis for each genes.

Usage
```
DEpermutePval(DEGres, permuteNBstat)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEGres</td>
<td>the output of DENBStat4GSEA.</td>
</tr>
<tr>
<td>permuteNBstat</td>
<td>the output of DENBStatPermut4GSEA.</td>
</tr>
</tbody>
</table>

Value
A data frame containing the expression means and variances for each gene in each group compared, and NB-stats, permutation p-values and adjusted p-values for each gene.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
runDESeq, DENBStat4GSEA, DENBStatPermut4GSEA, DENBTest
Examples

```r
data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
geneCounts <- getGeneCount(RCS_example)
label <- label(RCS_example)
DEG <- runDESeq(geneCounts, label)
DEGres <- DENBStat4GSEA(DEG)
DEpermNBstat <- DENBStatPermut4GSEA(DEG, permuteMat)
DEGres <- DEpermutePval(DEGres, DEpermNBstat)
head(DEGres)
```

**DEscore**  
*Pre-calculated DE/DS scores*

**Description**

DEscore and DSscore are pre-calculated DE and DS scores, respectively; DEscore_perm and DSscore_perm are pre-calculated DE and DS scores on the permutation data sets, respectively; They are used in examples of the SeqGSEA package. Note that these scores are of no meaning but to demonstrate the usage of functions.

**Usage**

```r
data("DEscore") data("DEscore_perm")
data("DSscore") data("DSscore_perm")
```

**References**


**DSpermute4GSEA**  
*Compute NB-statistics quantifying differential splicing on the permutation data set.*

**Description**

This function is to calculate NB-statistics quantifying differential splicing for each gene on each permutation data set. The results will be used for GSEA run as DS background.

**Usage**

```r
DSpermute4GSEA(RCS, permuteMat)
```

**Arguments**

- **RCS**  
a ReadCountSet object after running `exonTestability`.
- **permuteMat**  
a permutation matrix generated by `genpermuteMat`.
DSpermutePval

Details
Parallel running configuration: TODO

Value
A ReadCountSet object with slot permute_NBstat_gene updated.

Note
Please run exonTestability before run this function.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

References

See Also
exonTestability, genpermuteMat, DENBStatPermut4GSEA, DSpermutePval

Examples

data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
RCS_example <- exonTestability(RCS_example)
RCS_example <- DSpermute4GSEA(RCS_example, permuteMat)
head(RCS_example@permute_NBstat_gene)

---

DSpermutePval

Permutation for p-values in differential splicing analysis

Description
Calculate permutation p-values in differential splicing analysis.

Usage
DSpermutePval(RCS, permuteMat)

Arguments

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<th>Argument</th>
<th>Description</th>
</tr>
</thead>
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<td>RCS</td>
<td>a ReadCountSet object after running estiExonNBstat and estiGeneNBstat.</td>
</tr>
<tr>
<td>permuteMat</td>
<td>a permutation matrix generated by genpermuteMat.</td>
</tr>
</tbody>
</table>

Details
Permutation p-values are computed based on NB-statistics for comparison of the studied groups and NB-statistics from the permutation data sets.
DSresultExonTable

Value

A ReadCountSet object with slots `permute_NBstat_exon`, `permute_NBstat_gene`, `featureData`, and `featureData_gene` updated.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

References


See Also

estiExonNBstat, estiGeneNBstat, genpermuteMat, DSpermute4GSEA

Examples

data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
RCS_example <- exonTestability(RCS_example)
RCS_example <- estiExonNBstat(RCS_example)
RCS_example <- estiGeneNBstat(RCS_example)
RCS_example <- DSpermutePval(RCS_example, permuteMat)
head(DSresultExonTable(RCS_example))
head(DSresultGeneTable(RCS_example))

---

DSresultExonTable  Form a table for DS analysis results at the Exon level

Description

Form a table for differential splicing analysis results at the Exon level.

Usage

DSresultExonTable(RCS)

Arguments

RCS  A ReadCountSet object with `DSpermutePval` done.

Details

A data frame containing each exon’s NB-statistics, p-values and adjusted p-values for differential splicing analysis.

Value

A matrix containing exon DS analysis results, including testability, NBstats, p-values and adjusted p-values.
Form a table for DS analysis results at the gene level

**Description**

Form a table for differential splicing analysis results at the gene level.

**Usage**

```r
DSresultGeneTable(RCS)
```

**Arguments**

- **RCS**  
  A ReadCountSet object with `DSpermutePval` done.

**Value**

A data frame containing each gene’s NB-statistics, p-values and adjusted p-values for differential splicing analysis.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**See Also**

`DSresultExonTable`, `DSpermutePval`

**Examples**

```r
data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
RCS_example <- exonTestability(RCS_example)
RCS_example <- estiExonNBstat(RCS_example)
RCS_example <- estiGeneNBstat(RCS_example)
RCS_example <- DSpermutePval(RCS_example, permuteMat)
head(DSresultExonTable(RCS_example))
```
Description
Calculate NB-statistics quantifying differential splicing for individual exons between two groups of samples compared.

Usage
estiExonNBstat(RCS)

Arguments
RCS a ReadCountSet object after running exonTestability.

Value
A ReadCountSet object with the slot featureData updated.

Note
Please run exonTestability before you run this function.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

References

See Also
exonTestability, estiGeneNBstat

Examples
```r
data(RCS_example, package="SeqGSEA")
RCS_example <- exonTestability(RCS_example, cutoff=5)
RCS_example <- estiExonNBstat(RCS_example)
head(fData(RCS_example))
```
estiGeneNBstat  

**Description**

Calculate NB-statistics quantifying differential splicing for each gene between two groups of samples compared. The results will be used for GSEA run (as DS-scores).

**Usage**

estiGeneNBstat(RCS)

**Arguments**

- **RCS**
  
a ReadCountSet object after running estiExonNBstat.

**Value**

A ReadCountSet object with slot `featureData_gene` updated.

**Note**

Please run estiExonNBstat before run this function.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**References**


**See Also**

estiExonNBstat

**Examples**

data(RCS_example, package="SeqGSEA")
RCS_example <- exonTestability(RCS_example, cutoff=5)
RCS_example <- estiExonNBstat(RCS_example)
RCS_example <- estiGeneNBstat(RCS_example)
head(RCS_example@featureData_gene)
**exonID**

*Accessor to the exonID slot of ReadCountSet objects*

**Description**
Accessor to the exonID slot of ReadCountSet objects

**Usage**

```r
exonID(RCS)
exonID(RCS) <- value
```

**Arguments**

- `RCS`: a ReadCountSet object
- `value`: a vector of exon IDs

**Value**
A character vector of exon IDs; or a ReadCountSet object.

**Author(s)**
Xi Wang, xi.wang@newcastle.edu.au

**See Also**

`newReadCountSet`, `geneID`

**Examples**

```r
data(RCS_example, package="SeqGSEA")
exonID(RCS_example)
```

---

**exonTestability**

*Check exon testability*

**Description**
Check exon testability, filtering out exons with very few (default: 5) read counts

**Usage**

```r
exonTestability(RCS, cutoff = 5)
```

**Arguments**

- `RCS`: a ReadCountSet object.
- `cutoff`: exons with read counts less than this cutoff are to be marked as untestable.
**geneID**

Value

a ReadCountSet object with slot `fData` updated.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

geneTestability

Examples

data(RCS_example, package="SeqGSEA")
RCS_example <- exonTestability(RCS_example, cutoff=5)
head(fData(RCS_example))

geneID  

Accessor to the geneID slot of ReadCountSet objects

Description

Accessor to the geneID slot of ReadCountSet objects

Usage

geneID(RCS)
geneID(RCS) <- value

Arguments

- **RCS**  
a ReadCountSet object
- **value**  
a vector of gene IDs

Value

A character vector of gene IDs, which can be duplicated; or a ReadCountSet object.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

newReadCountSet, exonID

Examples

data(RCS_example, package="SeqGSEA")
geneID(RCS_example)
geneList

Get the gene list in a SeqGeneSet object

Description

Get the gene list in a SeqGeneSet object

Usage

geneList(GS)

Arguments

GS
A SeqGeneSet object.

Details

TBA

Value

A vector of gene IDs.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

loadGenesets, SeqGeneSet-class

Examples

##
gs <- newGeneSets(GS=list(1:10, 6:15, 11:20),
geneList=paste("Gene", 1:22, sep=""),
GSNames=c("gs1","gs2","gs3"),
GSDescs=c("test1","test2","test3"),
nname="gs examples")
genelist(gs)
## End
**genePermuteScore**

*Calculate gene scores on permutation data sets*

**Description**

Calculate gene scores on permutation data sets

**Usage**

```r
genePermuteScore(DEscoreMat, DSscoreMat = NULL, method = c("linear", "quadratic", "rank"), DEweight = 0.5)
```

**Arguments**

- **DEscoreMat**: normalized DE scores on permutation data sets.
- **DSscoreMat**: normalized DS scores on permutation data sets.
- **method**: one of the integration methods: linear, quadratic, or rank; default: linear.
- **DEweight**: any number between 0 and 1 (included), the weight of differential expression scores (the weight for differential splice is (1-DEweight)).

**Details**

The integration methods including "linear", "quadratic", and "rank" are detailed in Wang and Cairns (2013). Here the rank method refers only to the method using data-set-specific ranks.

For DE-only analysis, just specify DEweight to be 1, and the DSscoreMat value can be NULL.

**Value**

A gene score matrix.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**References**


**See Also**

geneScore

**Examples**

```r
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
# linear combination with weight for DE 0.3
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
# DE only analysis
gene.score.perm <- genePermuteScore(DEscore.perm, DEweight=1)
```
geneScore

*Calculate gene scores by integrating DE and DS scores*

**Description**

Calculate gene scores by integrating DE and DS scores

**Usage**

```r
geneScore(DEscore, DSscore = NULL, method = c("linear", "quadratic", "rank"), DEweight = 0.5)
```

**Arguments**

- `DEscore`: normalized DE scores.
- `DSscore`: normalized DS scores.
- `method`: one of the integration methods: linear, quadratic, or rank; default: linear.
- `DEweight`: any number between 0 and 1 (included), the weight of differential expression scores (the weight for differential splice is (1-DEweight)).

**Details**

The integration methods including "linear", "quadratic", and "rank" are detailed in Wang and Cairns (2013). Here the rank method refers only to the method using data-set-specific ranks.

For DE-only analysis, just specify DEweight to be 1, and the DSscore value can be NULL.

**Value**

A vector of gene scores.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**References**


**See Also**

genePermuteScore

**Examples**

```r
data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
# linear combination with weight for DE 0.3
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
# DE only analysis
gene.score <- geneScore(DEscore, DEweight = 1)
```
**geneSetDescs**

*Get the descriptions of gene sets in a SeqGeneSet object*

**Description**
Get the descriptions of gene sets in a SeqGeneSet object

**Usage**
geneSetDescs(GS)

**Arguments**
- **GS**
  - a SeqGeneSet object.

**Details**
Gene sets with size less than `GSSizeMin` or more than `GSSizeMax` are not included.

**Value**
A vector of descriptions of each gene set in the SeqGeneSet object.

**Author(s)**
Xi Wang, xi.wang@newcastle.edu.au

**See Also**
geneSetNames, geneSetSize, SeqGeneSet-class, loadGenesets

**Examples**
data(GS_example, package="SeqGSEA")
geneSetDescs(GS_example)

**geneSetNames**

*Get the names of gene set in a SeqGeneSet object*

**Description**
Get the names of gene set in a SeqGeneSet object

**Usage**
geneSetNames(GS)

**Arguments**
- **GS**
  - a SeqGeneSet object.
Details

Gene sets with size less than GSSizeMin or more than GSSizeMax are not included.

Value

A vector of gene set names in this SeqGeneSet object.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

geneSetDescs, geneSetSize, SeqGeneSet-class, loadGenesets

Examples

data(GS_example, package="SeqGSEA")
geneSetNames(GS_example)

geneSetSize

Get the numbers of genes in each gene set in a SeqGeneSet object

Description

Get the numbers of genes in each gene set in a SeqGeneSet object

Usage

geneSetSize(GS)

Arguments

GS a SeqGeneSet object.

Details

Gene sets with size less than GSSizeMin or more than GSSizeMax are not included.

Value

A vector of integers indicating the number of genes in each gene set in this SeqGeneSet object.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

geneSetNames, geneSetDescs, SeqGeneSet-class, loadGenesets
geneTestability

Examples

data(GS_example, package="SeqGSEA")
geneSetSize(GS_example)

geneTestability Check gene testability

Description
This function is to determine each gene’s testability. A gene is testable if at least one of its exons are testable.

Usage
geneTestability(RCS)

Arguments
RCS a ReadCountSet object after exon testability checked, usually the output of exonTestability.

Details
This result can be applied to filter out genes not expressed.

Value
A logical vector indicating which genes are testable, i.e., having at least one exon testable.

Note
Please run exonTestability before run this function.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
exonTestability, subsetByGenes

Examples

data(RCS_example, package="SeqGSEA")
RCS_example <- exonTestability(RCS_example, cutoff=5)
geneTestable <- geneTestability(RCS_example)
head(geneTestable)
genpermuteMat Generate permutation matrix

Description
Generate permutation matrix from ReadCountSet objects or from label vectors.

Usage
genpermuteMat(obj, times = 1000, seed = NULL)

Arguments
- obj: a ReadCountSet object or a label vector. This function needs the original sample label information to generate permutation matrix.
- times: an integer indication the times of permutation.
- seed: an integer or NULL, to produce the random seed (an integer vector) for generating random permutation matrix: the same seed generates the same permutation matrix, which is introduced for reproducibility.

Value
A sample label shuffled matrix, rows corresponding to samples and columns for each permutation.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
DSpermute4GSEA, DENBStatPermut4GSEA

Examples
data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10, seed=0)
RCS_example <- exonTestability(RCS_example)
RCS_example <- DSpermute4GSEA(RCS_example, permuteMat)

getGeneCount Calculate read counts of genes from a ReadCountSet object

Description
Calculate read counts of genes from a ReadCountSet object

Usage
getGeneCount(RCS)
**GSEAresultTable**

**Arguments**
- RCS: a ReadCountSet object

**Details**
This function can be used to get gene read counts from exon read counts.

**Value**
a matrix of gene read counts for each gene (row) and each sample (col).

**Author(s)**
Xi Wang, xi.wang@newcastle.edu.au

**See Also**
- loadExonCountData, runDESeq

**Examples**
```r
data(RCS_example, package="SeqGSEA")
geneCounts <- getGeneCount(RCS_example)
```

---

**GSEAresultTable**

*Form a table for GSEA results*

**Description**
Form a table for GSEA results.

**Usage**
```r
GSEAresultTable(gene.set, GSDesc = FALSE)
```

**Arguments**
- gene.set: a SeqGeneSet object after running GSEnrichAnalyze.
- GSDesc: logical indicating whether to output gene set descriptions. default: FALSE

**Value**
A data frame containing columns of GSName, GSSize, ES, ES.pos, pval, FDR, and FWER.

**Author(s)**
Xi Wang, xi.wang@newcastle.edu.au

**See Also**
- GSEnrichAnalyze, topGeneSets
GSEnrichAnalyze

Main function of gene set enrichment analysis

Description

The main function of gene set enrichment analysis

Usage

GSEnrichAnalyze(gene.set, gene.score, gene.score.perm, weighted.type = 1)

Arguments

gene.set       a SeqGeneSet object.
gene.score     a vector of integrated gene scores in the same order as genes listed in the geneList
               slot of gene.set.
gene.score.perm a matrix of integrated gene scores on permutation data sets; row: genes; col: permutation.
weighted.type  weight type for gene scores; default: 1.

Value

A SeqGeneSet object with many slots updated, such as GSEA.ES and GSEA.pval.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

References


See Also

normES, signifES
Examples

data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
data(GS_example, package="SeqGSEA")
GS_example <- GSEnrichAnalyze(GS_example, gene.score, gene.score.perm)
topGeneSets(GS_example, 5)

---

GS_example

**SeqGeneSet object example**

Description

An exemplified SeqGeneSet object to demonstrate functions in the SeqGSEA package. This object was generated with collection #6 (C6) gene sets of the Molecular Signatures Database (MSigDB) v3.1.

Usage

data("GS_example")

References


---

label

**Get the labels of samples in a ReadCountSet object**

Description

Get the labels of samples in a ReadCountSet object

Usage

label(RCS)

Arguments

RCS a ReadCountSet object

Author(s)

Xi Wang, xi.wang@newcastle.edu.au
loadExonCountData

See Also

newReadCountSet

Examples

data(RCS_example, package="SeqGSEA")
label(RCS_example)

loadExonCountData (Load Exon Count Data)

Description

This function is used to load (sub-)exon count data. Exon count data can be got by the Python script count_in_exons.py.

Usage

loadExonCountData(case.files, control.files)

Arguments

case.files a character vector containing the exon count file names for case samples
control.files a character vector containing the exon count file names for control samples

Details

You may need the Python script count_in_exons.py (released with this package) to generate your exon count files from read mapping results (say BAM files). The detailed usage can be obtained by simply typing python \path\to\count_in_exons.py. Users can also use other scripts or software for exon read counting.

The format of the exon count file is:

GeneName1:001[tab]Count11
GeneName1:002[tab]Count12
...
GeneName1:00N[tab]Count1N
GeneName2:001[tab]Count21
...

Value

This function returns a ReadCountSet object.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

newReadCountSet, ReadCountSet-class
loadGenesets

Examples

library(SeqGSEA)
dat.dir = system.file("extdata", package="SeqGSEA", mustWork=TRUE)
case.pattern <- "^SC"
ctrl.pattern <- "^SN"
case.files <- dir(dat.dir, pattern=case.pattern, full.names = TRUE)
control.files <- dir(dat.dir, pattern=ctrl.pattern, full.names = TRUE)

## Not run:
RCS <- loadExonCountData(case.files, control.files)
RCS

## End (Not run)

loadGenesets

Load gene sets from files

Description

This function is to load annotation of gene sets from files. The files are in the format of Molecular
Signatures Database (MSigDB), and those files can be downloaded at http://www.broadinstitute.
org/gsea/msigdb/index.jsp.

Usage

loadGenesets(geneset.file, geneIDs, geneID.type = c("gene.symbol", "ensembl"),
genesetsize.min = 5, genesetsize.max = 1000)

Arguments

geneset.file the file containing the gene set annotation.
geneIDs gene IDs that have expression values in the studied data set.
geneID.type indicating the type of gene IDs, gene symbol or emsembl gene IDs.
genesetsize.min the minimum number of genes in a gene set that will be treated in the analysis.
genesetsize.max the maximum number of genes in a gene set that will be treated in the analysis.

Details

TBA

Value

A SeqGeneSet object.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au
newGeneSets

Initialize a new SeqGeneSet object

Description

This is an internal function to generate a new SeqGeneSet object.

Usage

newGeneSets(GS, GSNames, GSDescs, geneList, name = NA_character_,
sourceFile = NA_character_, GSSizeMin = 5, GSSizeMax = 1000)

Arguments

- **GS**: a list, each element is an integer vector, indicating the indexes of genes in each gene set. See Details below.
- **GSNames**: a character string vector, each is the name of each gene set.
- **GSDescs**: a character string vector, each is the description of each gene set.
- **geneList**: a character string vector of gene IDs. See Details below.
- **name**: the name of this category of gene sets.
- **sourceFile**: the source file name of this category of gene sets.
- **GSSizeMin**: the minimum number of genes in a gene set to be analyzed. Default: 5
- **GSSizeMax**: the maximum number of genes in a gene set to be analyzed. Default: 1000

Details

TBA

Value

A SeqGeneSet object.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au
newReadCountSet

**Description**

This is a internal function to generate a new ReadCountSet object.

**Usage**

```
newReadCountSet(readCounts, exonIDs, geneIDs)
```

**Arguments**

- `readCounts`: a data frame, read counts for each exon of each samples. Must have colnames, which indicate the label of samples.
- `exonIDs`: a character vector indicating exon IDs.
- `geneIDs`: a character vector indicating gene IDs.

**Value**

A object of the ReadCountSet class.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**See Also**

`loadExonCountData`, `ReadCountSet-class`
Examples

```r
counts <- cbind(t(sapply(1:10, function(x) {rnbinom(5, size=10, prob=runif(1))} ) ,
                t(sapply(1:10, function(x) {rnbinom(5, size=10, prob=runif(1))} ))
colnames(counts) <- c(paste("S", 1:5, sep=""), paste("C", 1:5, sep=""))
geneIDs <- c(rep("G1", 4), rep("G2", 6))
exonIDs <- c(paste("E", 1:4, sep=""), paste("E", 1:6, sep=""))
##
RCS <- newReadCountSet(counts, exonIDs, geneIDs)
RCS
## End
```

### normES

#### Normalize enrichment scores

This is an internal function to normalize enrichment scores. For advanced users only.

**Usage**

```r
normES(gene.set)
```

**Arguments**

- `gene.set` a SeqGeneSet object after running `calES` and `calES.perm`.

**Value**

A SeqGeneSet object with ES scores normalized.

**Author(s)**

Xi Wang. xi.wang@newcastle.edu.au

**See Also**

`GSEnrichAnalyze, signifES`

### normFactor

#### Get normalization factors for normalization DE or DS scores

Get normalization factors from permutation scores for normalization DE or DS scores

**Usage**

```r
normFactor(permStat)
```
plotES

Plot the distribution of enrichment scores

Description

This function is to plot the distribution of enrichment scores, with comparison with permutation enrichment scores.

Usage

plotES(gene.set, pdf = NULL)

Arguments

gene.set a SeqGeneSet object after running GSEnrichAnalyze.

pdf whether to save the plot to PDF file; if yes, provide the name of the PDF file.
plotGeneScore

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

GSEnrichAnalyze, plotSigGeneSet

Examples

data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
data(GS_example, package="SeqGSEA")
GS_example <- GSEnrichAnalyze(GS_example, gene.score, gene.score.perm)
plotES(GS_example)

plotGeneScore

Plot gene (DE/DS) scores

Description

This function is to plot gene scores, as well as DE scores and DS scores

Usage

plotGeneScore(score, perm.score = NULL, pdf = NULL,
main = c("Overall", "Expression", "Splicing"))

Arguments

score the gene/DE/DS score vector.
perm.score a matrix of the corresponding gene/DE/DS scores on the permutation data sets.
pdf if a PDF file name provided, plot will be save to that file.
main the key words representing the type of scores that will be shown in the plot main title.

Details

The plot shows the ranked scores from the largest to the smallest. Lines also show the maximum and average scores, values shown on the top left.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au
plotSig

Examples

data(DEscore, package="SeqGSEA")
plotGeneScore(DEscore, main="Expression")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
plotGeneScore(gene.score)

data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
data(GS_example, package="SeqGSEA")

plotSig(GS_example)

plotSig

Plot showing SeqGeneSet’s p-values/FDRs vs. NESs

Description

The function is to generate a plot of p-values (FDRs) versus normalized enrichment scores (NES). It also shows the distribution of p-values (FDRs) in this gene set category.

Usage

plotSig(gene.set, pdf = NULL)

Arguments

gene.set a SeqGeneSet object after running GSEnrichAnalyze.

pdf whether to save the plot to PDF file; if yes, provide the name of the PDF file.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

GSEnrichAnalyze, plotSigGeneSet

Examples

data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
data(GS_example, package="SeqGSEA")
GS_example <- GSEnrichAnalyze(GS_example, gene.score, gene.score.perm)
plotSig(GS_example)
plotSigGeneSet

Plot gene set details

Description
This function is to generate a two-panel plot showing detailed information of the gene set specified. One panel is showing the running enrichment scores and the position where the ES appear. The other panel shows the significance level of the ES, comparing with permutation ESs.

Usage
plotSigGeneSet(gene.set, i, gene.score, pdf = NULL)

Arguments
gene.set a SeqGeneSet object after running GSEnrichAnalyze.
i the i-th gene set in the SeqGeneSet object. topGeneSets is useful to find the most significantly overrepresented gene set.
gene.score the gene score vector containing gene scores for each gene.
pdf whether to save the plot to PDF file; if yes, provide the name of the PDF file.

Details
See writeSigGeneSet, which writes the detailed gene set information to a file or to the screen.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
GSEnrichAnalyze, topGeneSets, plotSig, plotES, writeSigGeneSet

Examples
data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
data(GS_example, package="SeqGSEA")
GS_example <- GSEnrichAnalyze(GS_example, gene.score, gene.score.perm)
topGeneSets(GS_example, n=5)
plotSigGeneSet(GS_example, 9, gene.score) # 9th gene set is the most significant one.
Integration of differential expression and differential splice scores with a rank-based strategy

**Description**

Integration of differential expression and differential splice scores with a rank-based strategy, which simultaneously integrates observed scores and permutation scores using the same ranks.

**Usage**

```r
rankCombine(DEscore, DSscore, DEscoreMat, DSscoreMat, DEweight = 0.5)
```

**Arguments**

- `DEscore`: differential expression scores, normalized.
- `DSscore`: differential splice scores, normalized.
- `DEscoreMat`: differential expression scores in permuted data sets, normalized.
- `DSscoreMat`: differential splice scores in permuted data sets, normalized.
- `DEweight`: any number between 0 and 1 (included), the weight of differential expression scores (so the weight for differential splice is (1-DEweight)).

**Details**

This integration method is also known as integration with global ranks. See Wang and Cairns (2013) for details.

**Value**

A list with two elements `geneScore` and `genePermuteScore`.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**References**


**See Also**

- `geneScore`
- `genePermuteScore`

**Examples**

```r
data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
combine <- rankCombine(DEscore, DSscore, DEscore.perm, DSscore.perm, DEweight=0.3)
gene.score <- combine$geneScore
gene.score.perm <- combine$genePermuteScore
```
An exemplified ReadCountSet object to demonstrate functions in the SeqGSEA package. This object is comprised of 20 samples across 5,000 exons, a part of the prostate cancer RNA-Seq data set from Kannan et al (2011). Please note that the count data in this example object is incomplete.

Usage

```r
data("RCS_example")
```

References


Objects from the Class

Objects can be created by calls of the form `newReadCountSet`.

Slots

- `featureData_gene`: Object of class "data.frame". Data for each genes.
- `permute_NBstat_exon`: Object of class "matrix". NB statistics of exons on the permutation data sets.
- `permute_NBstat_gene`: Object of class "matrix". NB statistics of genes on the permutation data sets.
- `assayData`: Object of class "AssayData". The read count data.
- `phenoData`: Object of class "AnnotatedDataFrame". Data for each samples.
- `featureData`: Object of class "AnnotatedDataFrame". Data for each exons.
- `experimentData`: Object of class "MIAxE". Experiment data.
- `annotation`: Object of class "character". Not used.
- `__classVersion__`: Object of class "Versions". Version information.
**Methods**

- **counts**  Get counts from a ReadCountSet object. See `counts`.
- **counts<-** Set counts to a ReadCountSet object. See `counts`.

**Extends**

Class "eSet", directly.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**References**


**See Also**

`newReadCountSet`, `loadExonCountData`, `exonID`, `geneID`, `counts-methods`, `label`, `subsetByGenes`

**Examples**

```r
showClass("ReadCountSet")
```

---

**runDESeq**

*Run DESeq for differential expression analysis*

**Description**

This function provides a wrapper to run DESeq for differential expression analysis. It includes two steps, `DESeq::estimateSizeFactors` and `DESeq::estimateDispersions`.

**Usage**

```r
runDESeq(geneCounts, label)
```

**Arguments**

- **geneCounts**  a matrix containing read counts for each gene, can be the output of `getGeneCount`.
- **label**  the sample classification labels.

**Value**

A CountDataSet object with size factors and dispersion parameters been estimated.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au
runSeqGSEA

An all-in function that allows end users to apply SeqGSEA to their data with one step.

Description

This function provides typical SeqGSEA analysis pipelines for end users to apply the SeqGSEA method in the easiest fashion. It assumes the pipelines start with exon reads counts, even for the DE-only analysis. Users should specify their file locations and a few parameters before running this pipeline.

It allows DE-only analysis, which will skip the DS analysis portion, and it also allows users to try different weights in integrating DE and DS scores, which will save time in computing the DE and DS scores.

The function returns a list of SeqGSEA analysis results in the format of GSEAresultTable, and generates a few plots and writes a few files, whose name prefix can be specified. The output files will either be in PDF format or TXT format, and generated by plotGeneScore, writeScores, plotES, plotSig, plotSigGeneSet, and writeSigGeneSet.

Usage

runSeqGSEA(data.dir, case.pattern, ctrl.pattern, geneset.file, output.prefix, topGS=10, geneID.type=c("gene.symbol", "ensembl"), nCores=1, perm.times=1000, seed=NULL, minExonReadCount=5, integrationMethod=c("linear", "quadratic", "rank"), DEweight=c(0.5), DEonly=FALSE, minGSsize=5, maxGSsize=1000, GSEA.WeightedType=1)

Arguments

data.dir a character vector, the path to your count data directory.
case.pattern a character vector, the unique pattern in the file names of case samples. E.g. if file names starting with "SC", the pattern writes "^SC".
ctrl.pattern a character vector, the unique pattern in the file names of control samples.
output.prefix a character vector, the path with prefix for output files.
### runSeqGSEA

**topGS**  
an integer, this number of top ranked gene sets will be output with details; if geneset.file contains less than this number of gene sets, all gene sets’ result details will be output. Default: 10.

**geneID.type**  
the gene ID type in geneset.file. Currently only support "gene.symbol" and "ensembl". Default: gene.symbol.

**nCores**  
an integer. The number of cores for running SeqGSEA. Default: 1

**perm.times**  
an integer. The number of times for permutation, which will be used for normalizing DE and DS scores and for GSEA significance analysis. Recommended values are greater than 1000. Default: 1000.

**seed**  
an integer or NULL, used for setting the seeds to generate random numbers. The same seed will guarantee the same analysis results given by SeqGSEA. Default: NULL.

**minExonReadCount**  
an integer. An exon with total read count across all samples less than this number will be marked as untestable and be excluded in SeqGSEA analysis. Default: 5.

**integrationMethod**  
one of the three integration methods for DE and DS score integration: linear, quadratic, or rank. Default: linear.

**DEweight**  
a real number between 0 and 1 OR a vector of those. Each number is the DE weight in DE and DS integration. If using a vector of real numbers, SeqGSEA will run with each of them individually. Default: 0.5.

**DEonly**  
logical, whether to run SeqGSEA only considering DE. Default: FALSE

**minGSsize**  
an integer. The minimum gene set size: gene sets with genes less than this number will be skipped. Default: 5.

**maxGSsize**  
an integer. The maximum gene set size: gene sets with genes greater than this number will be skipped. Default: 1000.

**GSEA.WeightedType**  
the weight type of the main GSEA algorithm, can be 0 (unweighted = Kolmogorov-Smirnov), 1 (weighted), and 2 (over-weighted). Default: 1. It is recommended not to change it.

### Value

A list of SeqGSEA analysis results in the format of `GSEAresultTable`, which allows users for meta-analysis.

### Author(s)

Xi Wang, xi.wang@mdc-berlin.de

### References


### See Also

`GSEAresultTable`, `geneScore`, `GSEnrichAnalyze`
scoreNormalization

Description
Normalization of DE/DS scores or permutation DE/DS scores.

Usage
scoreNormalization(scores, norm.factor)

Arguments
scores a vector (a nX1 matrix) of a matrix of scores, rows corresponding to genes and columns corresponding to a study or permutation.
norm.factor normalization factor, output of the function normFactor.

Value
A normalized vector or matrix depending on the input: with the same dimensions as the input.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au
References


See Also

normFactor

Examples

data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
RCS_example <- exonTestability(RCS_example)
RCS_example <- estiExonNBstat(RCS_example)
RCS_example <- estiGeneNBstat(RCS_example)
RCS_example <- DSpermute4GSEA(RCS_example, permuteMat)
## (not run)
DSscore.normFac <- normFactor(RCS_example@permute_NBstat_gene)
DSscore <- scoreNormalization(RCS_example@featureData_gene$NBstat, DSScore.normFac)
DSscore.perm <- scoreNormalization(RCS_example@permute_NBstat_gene, DSScore.normFac)
## End (not run)

---

SeqGeneSet-class

Class "SeqGeneSet"

Description

SeqGeneSet class

Objects from the Class

Objects can be created by calls of the function newGeneSets.

Slots

name: Object of class "character" the name of this gene set category
sourceFile: Object of class "character" the source file of gene set category
geneList: Object of class "character" the gene ID list indicating genes involved in this GSEA
GS: Object of class "list" a list of gene indexes corresponding to geneList, each element in the list indicating which genes are in each gene set of this SeqGeneSet object
GSNames: Object of class "character". Gene set names.
GSDescs: Object of class "character". Gene set descriptions.
GSSize: Object of class "numeric". Gene set sizes.
GSSizeMin: Object of class "numeric". The minimum gene set size to be analyzed.
GSSizeMax: Object of class "numeric". The maximum gene set size to be analyzed.
GS.Excluded: Object of class "list". Gene sets excluded to be analyzed.
GSNames.Excluded: Object of class "character". Gene set names excluded to be analyzed.
GSDescs.Excluded: Object of class "character". Gene set descriptions excluded to be analyzed.
signifES

GSEA.ES: Object of class "numeric". Enrichment scores.
GSEA.ES.pos: Object of class "numeric". The positions where enrichment scores appear.
GSEA.ES.perm: Object of class "matrix". The enrichment scores of the permutation data sets.
GSEA.score.cumsum: Object of class "matrix". Running enrichment scores.
GSEA.normFlag: Object of class "logical". Logical indicating whether GSEA.ES has been normalized.
GSEA.pval: Object of class "numeric". P-values of each gene set.
GSEA.FWER: Object of class "numeric". Family-wise error rate of each gene set.
GSEA.FDR: Object of class "numeric". False discovery rate of each gene set.
version: Object of class "Versions". Version information.

Methods

- Get a sub-list of gene sets, and return a SeqGeneSet object.
- show Show basic information of the SeqGeneSet object.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

References


See Also

newGeneSets, size, geneSetNames, geneSetDescs, geneSetSize

Examples

showClass("SeqGeneSet")

---

signifES  

*Calculate significance of ESs*

Description

The is an internal function to calculate significance of ESs of each gene set. For advanced users only.

Usage

signifES(gene.set)

Arguments

gene.set a GeneSet object after running normES.
Value
A SeqGeneSet object with gene set enrichment significance metrics calculated.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
GSEnrichAnalyze, normES

Example
```r
data(GS_example, package="SeqGSEA")
size(GS_example)
```
subsetByGenes

Get a new ReadCountSet with specified gene IDs.

Description

Get a new ReadCountSet with specified gene IDs.

Usage

subsetByGenes(RCS, genes)

Arguments

RCS  a ReadCountSet object.

genes  a list of gene IDs.

Value

This function returns a new ReadCountSet object, with changes in slots assayData, featureData, featureData_gene, and permute_NBstat_exon and permute_NBstat_gene if they have been calculated.

Author(s)

Xi Wang, xi.wang@newcastle.edu.au

See Also

newReadCountSet, ReadCountSet

Examples

data(RCS_example, package="SeqGSEA")
RCS_example
genes <- c("ENSG00000000938", "ENSG00000000005")
RCS_sub <- subsetByGenes(RCS_example, genes)
RCS_sub

topDEGenes

Extract top differentially expressed genes.

Description

This function is to extract top n differentially expressed genes, ranked by either DESeq p-values, DESeq adjusted p-values, permutation p-values, permutation adjusted p-values, or NB-statistics.

Usage

topDEGenes(DEGres, n = 20,
            sortBy = c("padj", "pval", "perm.pval", "perm.padj", "NBstat", "foldChange"))
topDSExons

**Arguments**

- **DEGres**: DE analysis results.
- **n**: the number of top DE genes.
- **sortBy**: indicating which method to rank genes.

**Details**

If the `sortBy` method is not among the column names, the function will result in an error.

**Value**

A table for top n DE genes with significance metrics.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**See Also**

`topDSGenes`, `topDSExons`

**Examples**

```r
data(RCS_example, package="SeqGSEA")
geneCounts <- getGeneCount(RCS_example)
label <- label(RCS_example)
DEG <- runDESeq(geneCounts, label)
permuteMat <- genpermuteMat(RCS_example, times=10)
DEGres <- DENBTest(DEG)
DEpermNBstat <- DENBStatPermut4GSEA(DEG, permuteMat)
DEGres <- DEpermutePval(DEGres, DEpermNBstat)

# Extract top 10 DE genes

DEGres <- topDEGenes(DEGres, n = 10, sortBy = "NBstat")
```

`topDSExons`  
Extract top differentially spliced exons

**Description**

This function is to extract top n differentially spliced exons, ranked by p-values or NB-stats.

**Usage**

```r
topDSExons(RCS, n = 20, sortBy = c("pvalue", "NBstat"))
```

**Arguments**

- **RCS**: a `ReadCountSet` object after running `DSpermutePval`.
- **n**: the number of top genes.
- **sortBy**: indicating whether p-value or NBstat to be used for ranking genes.
Value
A table for top n exons. Columns include: geneID, exonID, testable, NBstat, pvalue, padjust, and meanCounts.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
topDSGenes, DSpermutePval

Examples
```r
data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
RCS_example <- exonTestability(RCS_example)
RCS_example <- estiExonNBstat(RCS_example)
RCS_example <- estiGeneNBstat(RCS_example)
RCS_example <- DSpermutePval(RCS_example, permuteMat)
topDSExons(RCS_example, 10, "NB")
```

---

topDSGenes

*Extract top differentially spliced genes*

Description
This function to extract top n differentially spliced genes, ranked by p-values or NBstats.

Usage
topDSGenes(RCS, n = 20, sortBy = c("pvalue", "NBstat"))

Arguments
- **RCS**: a ReadCountSet object after running DSpermutePval.
- **n**: the number of top genes.
- **sortBy**: indicating whether p-value or NBstat to be used for ranking genes.

Value
A table for top n genes. Columns include: geneID, NBstat, pvalue, and padjust.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
topDSExons, DSpermutePval
**topGeneSets**

**Examples**

```r
data(RCS_example, package="SeqGSEA")
permuteMat <- genpermuteMat(RCS_example, times=10)
RCS_example <- exonTestability(RCS_example)
RCS_example <- estiExonNBstat(RCS_example)
RCS_example <- estiGeneNBstat(RCS_example)
RCS_example <- DSpermutePval(RCS_example, permuteMat)
topDSGenes(RCS_example, 10, "NB")
```

**topGeneSets**

*Extract top significant gene sets*

**Description**

This function is to extract n top significant gene sets overrepresented in the samples studied, ranked by FDR, p-values, or FWER.

**Usage**

```r
topGeneSets(gene.set, n = 20, sortBy = c("FDR", "pvalue", "FWER"), GSDesc = FALSE)
```

**Arguments**

- `gene.set`: an object of class SeqGeneSet after GSEA runs.
- `n`: the number of top gene sets.
- `sortBy`: indicating which method to rank gene sets.
- `GSDesc`: logical indicating whether or not to output gene set descriptions.

**Value**

A data frame for top n gene sets detected with respect to the ranking method specified. Information includes: GSName, GSSize, ES, ES.pos, pval, FDR, and FWER.

**Author(s)**

Xi Wang. xi.wang@newcastle.edu.au

**See Also**

`GSEnrichAnalyze`, `GSEAResultTable`

**Examples**

```r
data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
data(GS_example, package="SeqGSEA")
GS_example <- GSEnrichAnalyze(GS_example, gene.score, gene.score.perm)
topGeneSets(GS_example, n=5)
```
writeScores     Write DE/DS scores and gene scores

Description
This function is to write DE and DS scores, and optionally gene scores.

Usage
writeScores(DEscore, DSscore, geneScore=NULL, geneScoreAttr=NULL, file="")

Arguments
- DEscore: normalized DE scores.
- DSscore: normalized DS scores.
- geneScore: gene scores integrated from DE and DS scores.
- geneScoreAttr: the parameters for integrating DE and DS scores.
- file: output file name, if not specified print to screen.

Author(s)
Xi Wang, xi.wang@newcastle.edu.au

See Also
DEscore, geneScore

Examples
data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
genе.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
writeScores(DEscore, DSscore)  # without gene scores
writeScores(DEscore, DSscore, geneScore = gene.score, geneScoreAttr = "linear,0.3")  # gene scores with attr.

writeSigGeneSet     Write gene set supporting information

Description
This function is to write the specified gene set (whose index is i) with significance information, including p-value and FDR, and gene scores for each gene in this set.

Usage
writeSigGeneSet(gene.set, i, gene.score, file = "")
writeSigGeneSet

**Arguments**

- `gene.set` an object of class SeqGeneSet with `GSEnrichAnalyze` done.
- `i` the i-th gene set in the SeqGeneSet object. `topGeneSets` is useful to find the most significantly overrepresented gene set.
- `gene.score` the vector of gene scores for running GSEA.
- `file` output file name, if not specified print to screen.

**Details**

See `plotSigGeneSet`, which shows graphic information of the gene set specified.

**Author(s)**

Xi Wang, xi.wang@newcastle.edu.au

**See Also**

`GSEnrichAnalyze`, `topGeneSets`, `plotSigGeneSet`

**Examples**

data(DEscore, package="SeqGSEA")
data(DSscore, package="SeqGSEA")
gene.score <- geneScore(DEscore, DSscore, method="linear", DEweight = 0.3)
data(DEscore.perm, package="SeqGSEA")
data(DSscore.perm, package="SeqGSEA")
gene.score.perm <- genePermuteScore(DEscore.perm, DSscore.perm, method="linear", DEweight=0.3)
data(GS_example, package="SeqGSEA")
GS_example <- GSEnrichAnalyze(GS_example, gene.score, gene.score.perm)
topGeneSets(GS_example, n=5)
writeSigGeneSet(GS_example, 9, gene.score) # 9th gene set is the most significant one.
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