Package ‘DMCHMM’

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Type Package
Title Differentially Methylated CpG using Hidden Markov Model
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Author Farhad Shokoohi
Maintainer Farhad Shokoohi <shokoohi@icloud.com>

Description A pipeline for identifying differentially methylated CpG sites using Hidden Markov Model in bisulfite sequencing data. DNA methylation studies have enabled researchers to understand methylation patterns and their regulatory roles in biological processes and disease. However, only a limited number of statistical approaches have been developed to provide formal quantitative analysis. Specifically, a few available methods do identify differentially methylated CpG (DMC) sites or regions (DMR), but they suffer from limitations that arise mostly due to challenges inherent in bisulfite sequencing data. These challenges include: (1) that read-depths vary considerably among genomic positions and are often low; (2) both methylation and autocorrelation patterns change as regions change; and (3) CpG sites are distributed unevenly. Furthermore, there are several methodological limitations: almost none of these tools is capable of comparing multiple groups and/or working with missing values, and only a few allow continuous or multiple covariates. The last of these is of great interest among researchers, as the goal is often to find which regions of the genome are associated with several exposures and traits. To tackle these issues, we have developed an efficient DMC identification method based on Hidden Markov Models (HMMs) called “DMCHMM” which is a three-step approach (model selection, prediction, testing) aiming to address the aforementioned drawbacks.

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DMCHMM-package

Differentially Methylated CpG using Hidden Markov Model

Description

DMCHMM is a novel profiling tool for identifying differentially methylated CpG sites using Hidden Markov Model in bisulfite sequencing data.

DMCHMM methods

cBSData, cBSDMCs, methHMEM, methHMMCMC, findDMCs, qqDMCs, manhattanDMCs, readBismark, writeBED.

DMCHMM objects

BSData-class, BSDMCs-class

BSData-class

Description

The BSData object is an S4 class that represents BS-Seq Data.

Arguments

methReads The matrix methReads contains the number of methylated reads spanning a CpG-site. The rows represent the CpG sites in rowRanges and the columns represent the samples in colData.

totalReads The matrix totalReads contains the number of reads spanning a CpG-site. The rows represent the CpG sites in rowRanges and the columns represent the samples in colData.

Value

A BSData-class object

Slots

methReads An integer matrix
totalReads An integer matrix

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>
See Also

SummarizedExperiment objects.

Examples

nr <- 500; nc <- 16
methc<-matrix(as.integer(runif(nr * nc, 0, nr)), nr)
methc<-matrix(rbinom(n=nr*nc,c(methc),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep("chr1", nr), IRanges(1:nr, width=1), strand="*")
names(r1) <- 1:nr
cd1<DataFrame(Group=rep(c("G1","G2"),each=nc/2),row.names=LETTERS[1:nc])
OBJ1<-cBSData(rowRanges=r1,methReads=methc,totalReads=metht,colData=cd1)
OBJ1

BSDMCs-class

BSDMCs object

Description

The BSDMCs object is an S4 class that represents differentially methylated CpG sites (DMCs) in BS-Seq Data.

Arguments

- **methReads**: The matrix `methReads` contains the number of methylated reads spanning a CpG-site. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`.
- **totalReads**: The matrix `totalReads` contains the number of reads spanning a CpG-site. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`.
- **methLevels**: The matrix `methLevels` contains the predicted methylation level obtained from Hidden Markov model. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`.
- **methStates**: The matrix `methStates` contains the state of methylation obtained from Hidden Markov model spanning a CpG-site. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`. The value of state is stored in metadata, named Beta.
- **methVars**: The matrix `methVars` contains the variances of the corresponding `methLevels` obtained from MCMC.

Value

A BSDMCs-class object
cBSData-method

Slots

methReads  An integer matrix
totalReads  An integer matrix
methLevels  A numeric matrix
methStates  An integer matrix
methVars  A double matrix

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

nr <- 500; nc <- 16
metht <- matrix(as.integer(runif(nr * nc, 0, nr)), nr)
methc <- matrix(rbinom(n=nr*nc,c(metht),prob = runif(nr*nc)),nr,nc)
meths <- matrix(as.integer(runif(nr * nc, 0, 10)), nr)
methl <- methc/metht
methv <- matrix((runif(nr * nc, 0.1, 0.5)), nr)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ2 <- cBSDMCs(rowRanges=r1,methReads=methc,totalReads=metht,
methLevels=methl,methStates=meths,methVars=methv,colData=cd1)
OBJ2

Description

Creates a BSData-class object

Usage

cBSDData(
    methReads,
    totalReads,
    rowRanges,
    colData = DataFrame(row.names = colnames(methReads)),
    metadata = list(),
    ...
)

## S4 method for signature 'matrix,matrix,GRanges'
cBSDData(
    methReads,
    totalReads,
    rowRanges,
    colData = DataFrame(row.names = colnames(methReads)),
    metadata = list(),
    ...
```r
totalReads,
rowRanges,
colData = DataFrame(row.names = colnames(methReads)),
metadata = list(),
...
)
```

### Arguments

- **methReads**
The matrix `methReads` contains the number of methylated reads spanning a CpG-site. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`.

- **totalReads**
The matrix `totalReads` contains the number of reads spanning a CpG-site. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`.

- **rowRanges**
A GRanges or GRangesList object describing the ranges of interest. Names, if present, become the row names of the SummarizedExperiment object. The length of the GRanges or GRangesList must equal the number of rows of the matrices in assays. If `rowRanges` is missing, a SummarizedExperiment instance is returned.

- **colData**
Object of class "DataFrame" containing information on variable values of the samples

- **metadata**
An optional list of arbitrary content describing the overall experiment

- **other possible parameters**

### Details

The rows of a BSData object represent ranges (in genomic coordinates) of interest. The ranges of interest are described by a GRanges or a GRangesList object, accessible using the `rowRanges` function. The GRanges and GRangesList classes contain sequence (e.g., chromosome) name, genomic coordinates, and strand information. Each range can be annotated with additional data; this data might be used to describe the range or to summarize results (e.g., statistics of differential abundance) relevant to the range. Rows may or may not have row names; they often will not.

### Value

A BSData-class object

### Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

### Examples

```r
nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
```
**cBSDMCs-method**

```r
cBSDMCs <- 1:nc

cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSDData(rowRanges=r1,methReads=methc,totalReads=meth,t,colData=cd1)
OBJ1
```

---

### Description

Creates a BSDMCs-class object.

### Usage

```r
cBSDMCs(  
  methReads,  
  totalReads,  
  methLevels,  
  methStates,  
  methVars,  
  rowRanges,  
  colData = DataFrame(row.names = colnames(methReads)),  
  metadata = list(),  
  ...
)
```

```r
## S4 method for signature 'matrix,matrix,matrix,matrix,matrix,GRanges'
cBSDMCs(  
  methReads,  
  totalReads,  
  methLevels,  
  methStates,  
  methVars,  
  rowRanges,  
  colData = DataFrame(row.names = colnames(methReads)),  
  metadata = list(),  
  ...
)
```

### Arguments

- **methReads**: The matrix `methReads` contains the number of methylated reads spanning a CpG-site. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`.

- **totalReads**: The matrix `totalReads` contains the number of reads spanning a CpG-site. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`. 
methLevels The matrix methLevels contains the predicted methylation level spanning a CpG-site using Hidden Markov model. The rows represent the CpG sites in rowRanges and the columns represent the samples in colData.

methStates The matrix methStates contains the state of methylation obtained from Hidden Markov model spanning a CpG-site. The rows represent the CpG sites in rowRanges and the columns represent the samples in colData. The value of state is stored in metadata, named Beta.

methVars The matrix methVars contains the variances of the corresponding methLevels obtained from MCMC.

rowRanges A GRanges or GRangesList object describing the ranges of interest. Names, if present, become the row names of the SummarizedExperiment object. The length of the GRanges or GRangesList must equal the number of rows of the matrices in assays. If rowRanges is missing, a SummarizedExperiment instance is returned.

colData Object of class "DataFrame" containing information on variable values of the samples

metadata An optional list of arbitrary content describing the overall experiment

Details

The rows of a BSDMCs object represent ranges (in genomic coordinates) of interest. The ranges of interest are described by a GRanges or a GRangesList object, accessible using the rowRanges function. The GRanges and GRangesList classes contains sequence (e.g., chromosome) name, genomic coordinates, and strand information. Each range can be annotated with additional data; this data might be used to describe the range or to summarize results (e.g., statistics of differential abundance) relevant to the range. Rows may or may not have row names; they often will not.

Value

A BSDMCs-class

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```r
set.seed(1980)
nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth),prob = runif(nr*nc)),nr,nc)
meths <- matrix(as.integer(runif(nr * nc, 0, 10)), nr)
methl <- meth/methc
methv <- matrix(runif(nr * nc, 0.1, 0.5)), nr)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*'
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
```
**Description**

combine two `BSData-class` or two `BSDMCs-class`

**Usage**

```r
combine(obj1, obj2)
```

## S4 method for signature 'BSData,BSData'

```r
combine(obj1, obj2)
```

## S4 method for signature 'BSDMCs,BSDMCs'

```r
combine(obj1, obj2)
```

**Arguments**

- `obj1`: A `BSData-class` or `BSDMCs-class`
- `obj2`: A `BSData-class` or `BSDMCs-class`

**Value**

A `BSData-class` or `BSDMCs-class`

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>

**Examples**

```r
set.seed(1980)

nr <- 150; nc <- 8
metht <- matrix(as.integer(runif(nr * nc*2, 0, nr)), nr)
methc <- matrix(rbinom(n=nr*nc,c(metht),prob = runif(nr*nc*2)),nr,nc*2)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep('G1',each=nc),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=r1,methReads=methc[,1:nc],totalReads=metht[,1:nc],colData=cd1)
cd2 <- DataFrame(Group=rep('G2',each=nc),row.names=LETTERS[nc+1:nc])
OBJ2 <- cBSData(rowRanges=r1,methReads=methc[,nc+1:nc],totalReads=metht[,nc+1:nc],colData=cd2)
OBJ3 <- combine(OBJ1, OBJ2)
OBJ3
```
Description

A part of BS-Seq data for three cell type: WGBS data were derived from whole blood collected on a cohort of healthy individuals from Sweden. Cell lines were separated into T-cells (19 samples), monocytes (13 samples) and B-cells (8 samples). Sequencing was performed on the Illumina HiSeq2000/2500 system for each of the 40 samples, separately. For illustration only 3 samples each containing 30,440 CpG sites around BLK gene are provided here. The whole data are analyzed in the cited paper.

Format

BED files

Details

The data is part of whole blood from Sweden.

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Source

Genomic Quebec

findDMCs-method

Description

finds the DMCs after smoothing using HMM

Usage

findDMCs(
  object,
  formula,
  FDRthreshold,
  Methylthreshold,
  mc.cores,
  windowsize,
  weightfunction
)
findDMCs-method

## S4 method for signature 'BSDMCs'
findDMCs(
  object,
  formula,
  FDRthreshold,
  Methylthreshold,
  mc.cores,
  windowsize,
  weightfunction
)

Arguments

object  A BSDData-class or BSDMCs-class object
formula  A formula
FDRthreshold  A numeric value
Methylthreshold  A positive numeric value; the default is 0.001
mc.cores  An integer greater than 0
windowsize  An integer value for partitioning data into windows of size windowsize.
weightfunction  A function to create weights using variance obtained form the MCMC algorithm

Value

BSDMCs-class object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

set.seed(1980)
nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth),prob = runif(nr+nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2), row.names=LETTERS[1:nc])
OBJ1 <- cBSDData(rowRanges=r1,methReads=methc,totalReads=meth, colData=cd1)
OBJ2 <- methHMEM(OBJ1, MaxK=2, mc.cores=2)
OBJ3 <- methHMMCMC(OBJ2, mc.cores=2)
OBJ4 <- findDMCs(OBJ3, mc.cores=2)
head(metadata(OBJ4)$DMCHMM)
Description

Creates a Manhattan plot based on the p-values obtained from `findDMCs` method

Usage

```r
manhattanDMCs(object, col, chrlabs, suggestiveline, genomewideline, highlight, logp, annotatePval, annotateTop, ...)
```

## S4 method for signature 'BSDMCs'

```r
manhattanDMCs(object, col, chrlabs, suggestiveline, genomewideline, highlight, logp, annotatePval, annotateTop, ...)
```

Arguments

- `object` A `BSData-class` or `BSDMCs-class` object
- `col` A character vector indicating which colors to alternate.
- `chrlabs` A character vector equal to the number of chromosomes specifying the chromosome labels (e.g., `c(1:22, "X", "Y", "MT")`).
- `suggestiveline` Where to draw a "suggestive" line. Default `-log10(1e-5)`. Set to `FALSE` to disable.
- `genomewideline` Where to draw a "genome-wide significant" line. Default `-log10(5e-8)`. Set to `FALSE` to disable.
methHMEM-method

highlight      A character vector of SNPs in your dataset to highlight. These SNPs should all be in your dataset.

logp          If TRUE, the -log10 of the p-value is plotted. It isn’t very useful to plot raw p-values, but plotting the raw value could be useful for other genome-wide plots, for example, peak heights, bayes factors, test statistics, other “scores,” etc.

annotatePval  If set, SNPs below this p-value will be annotated on the plot.

annotateTop   If TRUE, only annotates the top hit on each chromosome that is below the annotatePval threshold.

...           other possible parameters

Value

A Manhattan plot

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

set.seed(1980)
nr <- 150; nc <- 8
methh <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(methh),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=r1,methReads=methc,totalReads=methh,colData=cd1)
OBJ2 <- methHMEM(OBJ1, MaxK=2, mc.cores=2)
OBJ3 <- methHMEMC(OBJ2, mc.cores=2)
OBJ4 <- findDMCs(OBJ3, mc.cores=2)
manhattanDMCs(OBJ4)

Description

Estimates the HMM methylation paths and the HMM order for each sample using the EM algorithm

Usage

methHMEM(object, MaxK, MaxEmiter, epsEM, useweight, mc.cores)

## S4 method for signature 'BSData'
methHMEM(object, MaxK, MaxEmiter, epsEM, useweight, mc.cores)
methHMMCMC-method

Arguments

object A BSData-class or BSDMCs-class object
MaxK An integer value
MaxEmiter An integer value
epsEM A positive numeric value
useweight A logical value
mc.cores An integer greater than 0

Value

BSDMCs-class object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

set.seed(1980)
nr <- 150; nc <- 8
metht <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(metht),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=r1,methReads=methc,totalReads=metht,colData=cd1)
OBJ2 <- methHMEM(OBJ1, MaxK=2, mc.cores=2)
OBJ2

methHMMCMC-method methHMMCMC method

Description

Estimates the HMM methylation paths and the HMM order for each sample using the MCMC algorithm

Usage

methHMMCMC(object, useweight, nburn, nthin, nsamp, mc.cores)

## S4 method for signature 'BSDMCs'
methHMMCMC(object, useweight, nburn, nthin, nsamp, mc.cores)
**methLevels-method**

**Arguments**

- **object**: A BSDData-class or BSDMCs-class object
- **useweight**: A logical value
- **nburn**: An integer value
- **nthin**: An integer value
- **nsamp**: An integer value
- **mc.cores**: An integer greater than 0

**Value**

BSDMCs-class object

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>

**Examples**

```r
set.seed(1980)
nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=r1,methReads=methc,totalReads=meth, colData=cd1)
OBJ2 <- methHMEM(OBJ1, MaxK=2, mc.cores=2)
OBJ3 <- methHMMCMC(OBJ2, mc.cores=2)
OBJ3
```

**Description**

Returns methLevels stored in BSDMCs-class

Assigns methLevels to BSDMCs-class

**Usage**

```r
methLevels(object)

methLevels(object) <- value
```

## S4 method for signature 'BSDMCs'
methLevels(object)
## S4 replacement method for signature 'BSDMCs,matrix'
methLevels(object) <- value

**Arguments**

- `object`: A BSDData-class or BSDMCs-class object
- `value`: An integer matrix

**Value**

A matrix

A BSDMCs-class object

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>

**Examples**

```r
set.seed(1980)
nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth),prob = runif(nr*nc)),nr,nc)
meths <- matrix(as.integer(runif(nr * nc, 0, 10)), nr)
methl <- methc/meth
methv <- matrix((runif(nr * nc, 0.1, 0.5)), nr)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ2 <- cBSDMCs(rowRanges=r1,methReads=methc,totalReads=metht,
methLevels=methl,methStates=meths,methVars=methv,colData=cd1)
methLevels(OBJ2)
methLevels(OBJ2) <- methl
```

---

**Description**

Returns methReads stored in BSDData-class

Assigns methReads to BSDData-class

Returns methReads stored in BSDMCs-class

Assigns methReads to BSDMCs-class
methReads-method

Usage

methReads(object)

methReads(object) <- value

methReads(object)

methReads(object) <- value

## S4 method for signature 'BSData'
methReads(object)

## S4 replacement method for signature 'BSData,matrix'
methReads(object) <- value

## S4 method for signature 'BSDMCs'
methReads(object)

## S4 replacement method for signature 'BSDMCs,matrix'
methReads(object) <- value

Arguments

object       A BSData-class or BSDMCs-class object
value        An integer matrix

Value

A matrix
A BSData-class object
A matrix
A BSDMCs-class object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=r1,methReads=methc,totalReads=methc,colData=cd1)
methReads(OBJ1)
methReads(OBJ1) <- methc
methStates-method

Description

Returns methStates stored in BSDMCs-class

Assigns methStates to BSDMCs-class

Usage

methStates(object)

methStates(object) <- value

## S4 method for signature 'BSDMCs'
methStates(object)

## S4 replacement method for signature 'BSDMCs,matrix'
methStates(object) <- value

Arguments

object A BSDData-class or BSDMCs-class object

value An integer matrix

Value

A matrix

A BSDMCs-class object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

set.seed(1980)
nr <- 150; nc <- 8
metht <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(metht),prob = runif(nr*nc)),nr,nc)
meths <- matrix(as.integer(runif(nr * nc, 0, 10)), nr)
methl <- methc/metht
methv <- matrix((runif(nr * nc, 0.1, 0.5)), nr)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='x')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ2 <- cBSDMCs(rowRanges=r1,methReads=methc,totalReads=methht,
methLevels=methl,methStates=meths,methVars=methv,colData=cd1)
methVars-method

methStates(OBJ2)
methStates(OBJ2) <- meths

Description

Returns `methVars` stored in `BSDMCs-class`
Assigns `methVars` to `BSDMCs-class`

Usage

methVars(object)
methVars(object) <- value

## S4 method for signature 'BSDMCs'
methVars(object)

## S4 replacement method for signature 'BSDMCs,matrix'
methVars(object) <- value

Arguments

object A `BSData-class` or `BSDMCs-class` object
value An integer matrix

Value

A matrix
A `BSDMCs-class` object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```r
set.seed(1980)
nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n = nr * nc, c(meth), prob = runif(nr * nc)), nr, nc)
meths <- matrix(as.integer(runif(nr * nc, 0, 10)), nr)
methl <- methc/meth
methv <- matrix((runif(nr * nc, 0.1, 0.5)), nr)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
```
```r
params

Description

parameters name and their descriptions

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>methReads</td>
<td>The matrix <code>methReads</code> contains the number of methylated reads spanning a CpG-site. The rows represent the CpG sites in <code>rowRanges</code> and the columns represent the samples in <code>colData</code>.</td>
</tr>
<tr>
<td>totalReads</td>
<td>The matrix <code>totalReads</code> contains the number of reads spanning a CpG-site. The rows represent the CpG sites in <code>rowRanges</code> and the columns represent the samples in <code>colData</code>.</td>
</tr>
<tr>
<td>methLevels</td>
<td>The matrix <code>methLevels</code> contains the predicted methylation level spanning a CpG-site using Hidden Markov model. The rows represent the CpG sites in <code>rowRanges</code> and the columns represent the samples in <code>colData</code>.</td>
</tr>
<tr>
<td>methVars</td>
<td>The matrix <code>methVars</code> contains the variances of the corresponding <code>methLevels</code> obtained from MCMC.</td>
</tr>
<tr>
<td>methStates</td>
<td>The matrix <code>methStates</code> contains the state of methylation obtained from Hidden Markov model spanning a CpG-site. The rows represent the CpG sites in <code>rowRanges</code> and the columns represent the samples in <code>colData</code>. The value of state is stored in <code>metadata</code>, named Beta.</td>
</tr>
<tr>
<td>rowRanges</td>
<td>A <code>GRanges</code> or <code>GRangesList</code> object describing the ranges of interest. Names, if present, become the row names of the <code>SummarizedExperiment</code> object. The length of the <code>GRanges</code> or <code>GRangesList</code> must equal the number of rows of the matrices in assays. If <code>rowRanges</code> is missing, a <code>SummarizedExperiment</code> instance is returned.</td>
</tr>
<tr>
<td>colData</td>
<td>Object of class &quot;DataFrame&quot; containing information on variable values of the samples</td>
</tr>
<tr>
<td>metadata</td>
<td>An optional list of arbitrary content describing the overall experiment</td>
</tr>
<tr>
<td>obj1</td>
<td>A <code>BSData-class</code> or <code>BSDMCs-class</code> object</td>
</tr>
<tr>
<td>obj2</td>
<td>A <code>BSData-class</code> or <code>BSDMCs-class</code> object</td>
</tr>
<tr>
<td>files</td>
<td>A character list</td>
</tr>
</tbody>
</table>
```
params

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>file</td>
<td>A character</td>
</tr>
<tr>
<td>name</td>
<td>A character list</td>
</tr>
<tr>
<td>MaxK</td>
<td>An integer value</td>
</tr>
<tr>
<td>MaxEmiter</td>
<td>An integer value</td>
</tr>
<tr>
<td>epsEM</td>
<td>A positive numeric value</td>
</tr>
<tr>
<td>useweight</td>
<td>A logical value</td>
</tr>
<tr>
<td>mc.cores</td>
<td>An integer greater than 0</td>
</tr>
<tr>
<td>nburn</td>
<td>An integer value</td>
</tr>
<tr>
<td>nthin</td>
<td>An integer value</td>
</tr>
<tr>
<td>nsamp</td>
<td>An integer value</td>
</tr>
<tr>
<td>formula</td>
<td>A formula</td>
</tr>
<tr>
<td>FDRthreshold</td>
<td>A numeric value</td>
</tr>
<tr>
<td>Methylthreshold</td>
<td>A positive numeric value; the default is 0.001</td>
</tr>
<tr>
<td>weightfunction</td>
<td>A function to create weights using variance obtained form the MCMC algorithm</td>
</tr>
<tr>
<td>...</td>
<td>other possible parameters</td>
</tr>
<tr>
<td>col</td>
<td>A character vector indicating which colors to alternate.</td>
</tr>
<tr>
<td>chrlabs</td>
<td>A character vector equal to the number of chromosomes specifying the chromo-</td>
</tr>
<tr>
<td></td>
<td>some labels (e.g., c(1:22, &quot;X&quot;, &quot;Y&quot;, &quot;MT&quot;)).</td>
</tr>
<tr>
<td>suggestiveline</td>
<td>Where to draw a &quot;suggestive&quot; line. Default -log10(1e-5). Set to FALSE to</td>
</tr>
<tr>
<td></td>
<td>disable.</td>
</tr>
<tr>
<td>genomewideline</td>
<td>Where to draw a &quot;genome-wide significant&quot; line. Default -log10(5e-8). Set</td>
</tr>
<tr>
<td></td>
<td>to FALSE to disable.</td>
</tr>
<tr>
<td>highlight</td>
<td>A character vector of SNPs in your dataset to highlight. These SNPs should</td>
</tr>
<tr>
<td></td>
<td>all be in your dataset.</td>
</tr>
<tr>
<td>logp</td>
<td>If TRUE, the -log10 of the p-value is plotted. It isn’t very useful to plot</td>
</tr>
<tr>
<td></td>
<td>raw p-values, but plotting the raw value could be useful for other genome-</td>
</tr>
<tr>
<td></td>
<td>wide plots, for example, peak heights, bayes factors, test statistics, other</td>
</tr>
<tr>
<td></td>
<td>&quot;scores,&quot; etc.</td>
</tr>
<tr>
<td>annotatePval</td>
<td>If set, SNPs below this p-value will be annotated on the plot.</td>
</tr>
<tr>
<td>annotateTop</td>
<td>If TRUE, only annotates the top hit on each chromosome that is below the</td>
</tr>
<tr>
<td></td>
<td>annotatePval threshold.</td>
</tr>
<tr>
<td>windowsize</td>
<td>An integer value for partitioning data into windows of size windowsize.</td>
</tr>
</tbody>
</table>

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>
Description

Creates a Q-Q plot based on the p-values obtained from `findDMCs` method

Usage

```r
qqDMCs(object, ...)
```  
```
## S4 method for signature 'BSDMCs'
qqDMCs(object, ...)
```

Arguments

- `object` A `BSDData-class` or `BSDMCs-class` object
- `...` other possible parameters

Value

A QQ plot

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```r
set.seed(1980)
nr <- 150; nc <- 8
metht <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(metht),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=r1,methReads=methc,totalReads=metht,colData=cd1)
OBJ2 <- methHMEM(OBJ1, MaxK=2, mc.cores=2)
OBJ3 <- methHMMCMC(OBJ2, mc.cores=2)
OBJ4 <- findDMCs(OBJ3, mc.cores=2)
qqDMCs(OBJ4)
```
**Description**
reads BS-Seq data

**Usage**
```r
readBismark(files, colData, mc.cores)
## S4 method for signature 'character,DataFrame,numeric'
readBismark(files, colData, mc.cores)
## S4 method for signature 'character,data.frame,numeric'
readBismark(files, colData, mc.cores)
## S4 method for signature 'character,character,numeric'
readBismark(files, colData, mc.cores)
```

**Arguments**
- `files`: A character list
- `colData`: Object of class "DataFrame" containing information on variable values of the samples
- `mc.cores`: An integer greater than 0

**Value**
A `BSData-class` object

**Author(s)**
Farhad Shokoohi <shokoohi@icloud.com>

**Examples**
```r
fn <- list.files(system.file('extdata', package = 'DMCHMM'))
fn.f <- list.files(system.file('extdata', package = 'DMCHMM'), full.names = TRUE)
OBJ <- readBismark(fn.f, fn, mc.cores = 2)
cdOBJ <- DataFrame(Cell = factor(c('BC', 'TC', 'Mono'),
labels = c('BC', 'TC', 'Mono'), row.names = c('BCU1568', 'BCU173', 'BCU551'))
colData(OBJ) <- cdOBJ
OBJ
```
totalReads-method

Description

Returns totalReads stored in **BSData-class**
Assigns totalReads to **BSData-class**

Returns totalReads stored in **BSDMCs-class**
Assigns totalReads to **BSDMCs-class**

Usage

```r
totalReads(object)

totalReads(object) <- value

totalReads(object)

totalReads(object) <- value

## S4 method for signature 'BSData'
totalReads(object)

## S4 replacement method for signature 'BSData,matrix'
totalReads(object) <- value

## S4 method for signature 'BSDMCs'
totalReads(object)

## S4 replacement method for signature 'BSDMCs,matrix'
totalReads(object) <- value
```

Arguments

- **object**: A **BSData-class** or **BSDMCs-class** object
- **value**: An integer matrix

Value

A matrix
A **BSData-class** object
A matrix
A **BSDMCs-class** object
**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>

**Examples**

```r	nr <- 150; nc <- 8
meth <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth),prob = runif(nr*nc)),nr,nc)
r1 <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=r1,methReads=methc,totalReads=metht,colData=cd1)
totalReads(OBJ1)
totalReads(OBJ1) <- metht
```

**Description**

write BS-Seq data to BED files

**Usage**

```r
writeBED(object, name, file)
## S4 method for signature 'BSData,character,character'
writeBED(object, name, file)
## S4 method for signature 'BSData,character,missing'
writeBED(object, name)
## S4 method for signature 'BSData,missing,character'
writeBED(object, file)
## S4 method for signature 'BSData,missing,missing'
writeBED(object)
## S4 method for signature 'BSDMCs,character,character'
writeBED(object, name, file)
## S4 method for signature 'BSDMCs,character,missing'
writeBED(object, name)
## S4 method for signature 'BSDMCs,missing,character'
writeBED(object, file)
## S4 method for signature 'BSDMCs,missing,missing'
writeBED(object)
```

Arguments

object  A BSData-class or BSDMCs-class object
name    A character list
file    A character

Value

BED files

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>
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