

Package ‘DMCHMM’

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Type Package

Title Differentially Methylated CpG using Hidden Markov Model

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Description A pipeline for identifying differentially methylated CpG sites using Hidden Markov Model in bisulfite sequencing data.

Depends R (>= 3.5.0), SummarizedExperiment, methods, S4Vectors, BiocParallel, GenomicRanges, IRanges, fdrtool

Imports utils, stats, grDevices, rtracklayer, multcomp, calibrate, graphics

Suggests testthat, knitr

VignetteBuilder knitr

biocViews DifferentialMethylation, Sequencing, HiddenMarkovModel, Coverage

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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

[cBSDData](#), [cBSDMCs](#), [methHMEM](#), [methHMMCMC](#), [findDMCs](#), [qqDMCs](#), [manhattanDMCs](#), [readBismark](#), [writeBED](#).

DMCHMM objects

[BSDData-class](#), [BSDMCs-class](#)

| | |
|--------------|----------------------|
| BSData-class | <i>BSData object</i> |
|--------------|----------------------|

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
metht<-matrix(as.integer(runif(nr * nc, 0, nr)), 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)
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 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. |

Value

A `BSDMCs-class` object

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

```

cBSData-method

*cBSData method***Description**

Creates a [BSData-class](#) object

Usage

```

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

```

```

## S4 method for signature 'matrix,matrix,GRanges'
cBSData(methReads, 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 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 `BSDData-class` object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```
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 <- cBSDData(rowRanges=r1,methReads=methc,totalReads=metht,colData=cd1)
OBJ1
```

cBSDMCs-method

cBSDMCs method

Description

Creates a `BSDMCs-class` object

Usage

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

```
## 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

| | |
|-------------------------|--|
| <code>methReads</code> | 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> . |
| <code>totalReads</code> | 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> . |
| <code>methLevels</code> | 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> . |
| <code>methStates</code> | 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 <code>Beta</code> . |

| | |
|-----------|--|
| 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 |
| ... | other possible parameters |

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

```
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='*')
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
```

combine-method

combine method

Description

combine two [BSDData-class](#) or two [BSDMCs-class](#)

Usage

```
combine(obj1, obj2)

## S4 method for signature 'BSDData,BSDData'
combine(obj1, obj2)

## S4 method for signature 'BSDMCs,BSDMCs'
combine(obj1, obj2)
```

Arguments

```
obj1          A BSDData-class or BSDMCs-class
obj2          A BSDData-class or BSDMCs-class
```

Value

A [BSDData-class](#) or [BSDMCs-class](#)

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```
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 <- cBSDData(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 <- cBSDData(rowRanges=r1,methReads=methc[,nc+1:nc],totalReads=
metht[,nc+1:nc],colData=cd2)
OBJ3 <- combine(OBJ1, OBJ2)
OBJ3
```

data

data

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

findDMCs method

Description

finds the DMCs after smoothing using HMM

Usage

```
findDMCs(object, formula, FDRthreshold, Methylthreshold, mc.cores,  
weightfunction)
```

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

Arguments

| | |
|-----------------|--|
| object | A BSDData-class or BSDMCs-class object |
| formula | A formula |
| FDRthreshold | A numeric value |
| Methylthreshold | A numeric value |
| mc.cores | An integer greater than 0 |
| weightfunction | A function to create weights using variance obtained from the MCMC algorithm |

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 <- cBSDData(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)
head(metadata(OBJ4)$DMCHMM)

```

manhattanDMCs-method *manhattanDMCs method*

Description

Creates a Manhattan plot based on the p-values obtained from [findDMCs](#) method

Usage

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

```
## S4 method for signature 'BSDMCs'
manhattanDMCs(object, col, chrlabs, suggestiveline,
  genomewideline, highlight, logp, annotatePval, annotateTop, ...)
```

Arguments

| | |
|----------------|---|
| object | A BSDData-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 -log ₁₀ (1e-5). Set to FALSE to disable. |
| genomewideline | Where to draw a "genome-wide significant" line. Default -log ₁₀ (5e-8). Set to FALSE to disable. |
| highlight | A character vector of SNPs in your dataset to highlight. These SNPs should all be in your dataset. |
| logp | If TRUE, the -log ₁₀ 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
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 <- cBSDData(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)
manhattanDMCs(OBJ4)
```

methHMEM-method

methHMEM method

Description

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

Usage

```
methHMEM(object, MaxK, MaxEmitter, epsEM, useweight, mc.cores)
```

```
## S4 method for signature 'BSDData'
methHMEM(object, MaxK, MaxEmitter, epsEM, useweight,
  mc.cores)
```

Arguments

| | |
|------------|--|
| object | A BSDData-class or BSDMCs-class object |
| MaxK | An integer value |
| MaxEmitter | 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 <- cBSDData(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)
```

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

```

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 <- cBSDData(rowRanges=r1,methReads=methc,totalReads=metht,colData=cd1)
OBJ2 <- methHMEM(OBJ1, MaxK=2, mc.cores=2)
OBJ3 <- methHMMCMC(OBJ2, mc.cores=2)
OBJ3

```

methLevels-method *methLevels method*

Description

Returns methLevels stored in [BSDMCs-class](#)

Assigns methLevels to [BSDMCs-class](#)

Usage

```

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

```

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='*')
names(r1) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1', 'G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ2 <- cBDMCs(rowRanges=r1,methReads=methc,totalReads=metht,
methLevels=methl,methStates=meths,methVars=methv,colData=cd1)
methLevels(OBJ2)
methLevels(OBJ2) <- methl

```

methReads-method

*methReads method***Description**

Returns methReads stored in [BSDData-class](#)

Assigns methReads to [BSDData-class](#)

Returns methReads stored in [BDMCs-class](#)

Assigns methReads to [BDMCs-class](#)

Usage

```
methReads(object)
```

```
methReads(object) <- value
```

```
methReads(object)
```

```
methReads(object) <- value
```

```
## S4 method for signature 'BSDData'
```

```
methReads(object)
```

```
## S4 replacement method for signature 'BSDData,matrix'
```

```
methReads(object) <- value
```

```
## S4 method for signature 'BDMCs'
```

```
methReads(object)
```

```
## S4 replacement method for signature 'BDMCs,matrix'
```

```
methReads(object) <- value
```

Arguments

object A [BSDData-class](#) or [BDMCs-class](#) object

value An integer matrix

Value

A matrix
 A [BSDData-class](#) object
 A matrix
 A [BSDMCs-class](#) object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```
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 <- cBSDData(rowRanges=r1,methReads=methc,totalReads=metht,colData=cd1)
methReads(OBJ1)
methReads(OBJ1) <- methc
```

methStates-method

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, 100)), 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)
methStates(OBJ2)
methStates(OBJ2)<- meths
```

params

params

Description

parameters name and their descriptions

Arguments

| | |
|------------|---|
| methReads | 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> . |
| totalReads | 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> . |
| methLevels | 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> . |
| methVars | The matrix <code>methVars</code> contains the variances of the corresponding <code>methLevels</code> obtained from MCMC. |
| methStates | 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 metadata, named <code>Beta</code> . |
| 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 <code>rowRanges</code> 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 |
| object | A BSData-class or BSDMCs-class object |
| value | An integer matrix |
| obj1 | A BSData-class or BSDMCs-class |
| obj2 | A BSData-class or BSDMCs-class |
| files | A character list |
| file | A character |
| name | A character list |
| MaxK | An integer value |
| MaxEmitter | An integer value |
| epsEM | A positive numeric value |
| useweight | A logical value |
| mc.cores | An integer greater than 0 |
| nburn | An integer value |
| nthin | An integer value |
| nsamp | An integer value |
| formula | A formula |
| FDRthreshold | A numeric value |
| Methylthreshold | A numeric value |
| weightfunction | A function to create weights using variance obtained from the MCMC algorithm |
| ... | other possible parameters |
| 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 $-\log_{10}(1e-5)$. Set to FALSE to disable. |
| genomewideline | Where to draw a "genome-wide significant" line. Default $-\log_{10}(5e-8)$. Set to FALSE to disable. |
| highlight | A character vector of SNPs in your dataset to highlight. These SNPs should all be in your dataset. |
| logp | If TRUE, the $-\log_{10}$ 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. |

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

`qqDMCs-method`*qqDMCs method*

Description

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

Usage

```
qqDMCs(object, ...)
```

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

Arguments

| | |
|---------------------|--|
| <code>object</code> | A <code>BSDData-class</code> or <code>BSDMCs-class</code> object |
| <code>...</code> | other possible parameters |

Value

A QQ plot

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 <- cBSDData(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)
```

| | |
|--------------------|---------------------------|
| readBismark-method | <i>readBismark method</i> |
|--------------------|---------------------------|

Description

reads BS-Seq data

Usage

```
readBismark(files, colData)

## S4 method for signature 'character,DataFrame'
readBismark(files, colData)

## S4 method for signature 'character,data.frame'
readBismark(files, colData)

## S4 method for signature 'character,character'
readBismark(files, colData)
```

Arguments

| | |
|---------|--|
| files | A character list |
| colData | Object of class "DataFrame" containing information on variable values of the samples |

Value

A [BSData-class](#) object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```
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)
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 | <i>totalReads method</i> |
|-------------------|--------------------------|

Description

Returns totalReads stored in [BSData-class](#)

Assigns totalReads to [BSData-class](#)

Returns totalReads stored in [BSDMCs-class](#)

Assigns totalReads to [BSDMCs-class](#)

Usage

```
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

```
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)
totalReads(OBJ1)
totalReads(OBJ1) <- metht
```

writeBED-method

writeBED method

Description

write BS-Seq data to BED files

Usage

```
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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