

# Package ‘DMCHMM’

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**Type** Package

**Title** Differentially Methylated CpG using Hidden Markov Model

**Version** 1.8.0

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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](#)

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

```

cBSDData-method

*cBSDData method***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(), ...)

```

**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 <a href="#">GRanges</a> or <a href="#">GRangesList</a> object describing the ranges of interest. Names, if present, become the row names of the <a href="#">SummarizedExperiment</a> object. The length of the <a href="#">GRanges</a> or <a href="#">GRangesList</a> must equal the number of rows of the matrices in assays. If rowRanges is missing, a <a href="#">SummarizedExperiment</a> 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 <a href="#">GRanges</a> or <a href="#">GRangesList</a> object describing the ranges of interest. Names, if present, become the row names of the <a href="#">SummarizedExperiment</a> object. The length of the <a href="#">GRanges</a> or <a href="#">GRangesList</a> must equal the number of rows of the matrices in assays. If rowRanges is missing, a <a href="#">SummarizedExperiment</a> 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 'BSData,BSData'
combine(obj1, obj2)

## S4 method for signature 'BSDMCs,BSDMCs'
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**

```
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
```

---

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	<i>findDMCs method</i>
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---

**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 <a href="#">BSDData-class</a> or <a href="#">BSDMCs-class</a> 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 <a href="#">BSDData-class</a> or <a href="#">BSDMCs-class</a> 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., <code>c(1:22, "X", "Y", "MT")</code> ).
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 <code>annotatePval</code> 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 <a href="#">BSDData-class</a> or <a href="#">BSDMCs-class</a> 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 <a href="#">BSDData-class</a> or <a href="#">BSDMCS-class</a> 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	<i>methLevels method</i>
-------------------	--------------------------

---

## 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 <a href="#">GRanges</a> or <a href="#">GRangesList</a> object describing the ranges of interest. Names, if present, become the row names of the <a href="#">SummarizedExperiment</a> object. The length of the <a href="#">GRanges</a> or <a href="#">GRangesList</a> must equal the number of rows of the matrices in assays. If <code>rowRanges</code> is missing, a <a href="#">SummarizedExperiment</a> 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 <a href="#">BSData-class</a> or <a href="#">BSDMCs-class</a> object
value	An integer matrix
obj1	A <a href="#">BSData-class</a> or <a href="#">BSDMCs-class</a>
obj2	A <a href="#">BSData-class</a> or <a href="#">BSDMCs-class</a>
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., <code>c(1:22, "X", "Y", "MT")</code> ).
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 <code>annotatePval</code> threshold.

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>

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qqDMCs-method	<i>qqDMCs method</i>
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## 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

object	A <a href="#">BSDData-class</a> or <a href="#">BSDMCs-class</a> object
...	other possible parameters

## Value

A QQ plot

## Author(s)

Farhad Shokoohi <[shokoohi@icloud.com](mailto: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)
```

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readBismark-method	<i>readBismark method</i>
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## 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>
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---

### 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 <- cBSDData(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 'BSDData,character,character'
writeBED(object, name, file)
```

```
## S4 method for signature 'BSDData,character,missing'
writeBED(object, name)
```

```
## S4 method for signature 'BSDData,missing,character'
writeBED(object, file)
```

```
## S4 method for signature 'BSDData,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 <a href="#">BSDData-class</a> or <a href="#">BSDMCs-class</a> object
name	A character list
file	A character

**Value**

BED files

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>

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