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. 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.

Depends R (>= 4.1.0), SummarizedExperiment, methods, S4Vectors, BiocParallel, GenomicRanges, IRanges, fdrtool

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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)**

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**BSDMCs-class**

### 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

---

**Examples**

```r
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
```

---

**See Also**

SummarizedExperiment objects.
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

```r
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)
rl <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(rl) <- 1:nr
cdl <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ2 <- cBSDMCs(rowRanges=rl,methReads=methc,totalReads=metht,
methLevels=methl,methStates=meths,methVars=methv,colData=cdl)
OBJ2
```

Description

Creates a BSData-class object

Usage

```r
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 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

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=metht,colData=cd1)
OBJ1

---

cBSDMCs-method  cBSDMCs method

**Description**

Creates a BSDMCs-class object

**Usage**

```r
 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'

```r
 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.

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

set.seed(1980)
nr <- 150; nc <- 8
meth1 <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n=nr*nc,c(meth1),prob = runif(nr*nc)),nr,nc)
meths <- matrix(as.integer(runif(nr * nc, 0, 10)), nr)
methl <- methc/meth1
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])
combine-method

OBJ2 <- cBSDMCs(rowRanges=r1,methReads=methc,totalReads=metht, methLevels=methl,methStates=meths,methVars=methv,colData=cd1)
OBJ2

Description
combine two BSData-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
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)

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Source

Genomic Quebec

Description

finds the DMCs after smoothing using HMM

Usage

```r
findDMCs(
  object,  # object
  formula,  # formula
  FDRthreshold,  # FDR threshold
  Methylthreshold,  # Methyl threshold
  mc.cores,  # number of cores
  windowsize,  # window size
  weightfunction
)
```
### S4 method for signature 'BSDMCs'

```r
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

```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,coData=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.
**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**

```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)
rl <- GRanges(rep('chr1', nr), IRanges(1:nr, width=1), strand='*')
names(rl) <- 1:nr
cd1 <- DataFrame(Group=rep(c('G1','G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ1 <- cBSData(rowRanges=rl,methReads=methc,totalReads=metht,colData=cd1)
OBJ2 <- methHMEM(OBJ1, MaxK=2, mc.cores=2)
OBJ3 <- methHMMC(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**

```r
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 BSDData-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

```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)
OBJ2
```

Description

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

Usage

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

```r
## 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

```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)
OBJ3
```

Description

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

Usage

```r
methLevels(object)
methLevels(object) <- value
```

```r
## S4 method for signature 'BSDMCs'
methLevels(object)
```
## S4 replacement method for signature 'BSDMCs,matrix'
methLevels(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
cd1 <- DataFrame(Group=rep(c('G1', 'G2'),each=nc/2),row.names=LETTERS[1:nc])
OBJ2 <- cBSDMCs(rowRanges=r1,methReads=methc,totalReads=meth,methLevels=methl,methStates=meths,methVars=methv,colData=cd1)
methLevels(OBJ2)
methLevels(OBJ2) <- methl
```

### Description

Returns methReads stored in BSData-class
Assigns methReads to BSData-class
Returns methReads stored in BSDMCs-class
Assigns methReads to BSDMCs-class
Usage

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  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
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='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=meth, methLevels=methl,methStates=meths,methVars=methv,colData=cd1)
methStates(OBJ2)
methStates(OBJ2) <- meths

methVars-method

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 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
params

Description

parameters name and their descriptions

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

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

Arguments

- `object` A `BSData-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
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
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
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)
```

```r
totalReads(object) <- value
```

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

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

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

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

Arguments

<table>
<thead>
<tr>
<th>argument</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>A <strong>BSData-class</strong> or <strong>BSDMCs-class</strong> object</td>
</tr>
<tr>
<td>value</td>
<td>An integer matrix</td>
</tr>
</tbody>
</table>

Value

A matrix
A **BSData-class** object
A matrix
A **BSDMCs-class** object
writeBED-method

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=metht,colData=cd1)
totalReads(OBJ1)
totalReads(OBJ1) <- meth
totalReads(OBJ1)

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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