Package ‘DMCFB’

April 3, 2024

Type     Package
Title    Differentially Methylated Cytosines via a Bayesian Functional Approach
Version  1.16.1

Description  DMCFB is a pipeline for identifying differentially methylated cytosines using a Bayesian functional regression model in bisulfite sequencing data. By using a functional regression data model, it tries to capture position-specific, group-specific and other covariates-specific methylation patterns as well as spatial correlation patterns and unknown underlying models of methylation data. It is robust and flexible with respect to the true underlying models and inclusion of any covariates, and the missing values are imputed using spatial correlation between positions and samples. A Bayesian approach is adopted for estimation and inference in the proposed method.

Depends  R (>= 4.3.0), SummarizedExperiment, methods, S4Vectors, BiocParallel, GenomicRanges, IRanges
Imports  utils, stats, speedglm, MASS, data.table, splines, arm, rtracklayer, benchmarkme, tibble, matrixStats, fastDummies, graphics
Suggests testthat, knitr, rmarkdown, BiocStyle
VignetteBuilder knitr
biocViews DifferentialMethylation, Sequencing, Coverage, Bayesian, Regression
License  GPL-3
Encoding UTF-8
LazyData true

BugReports https://github.com/shokoohi/DMCFB/issues
RoxygenNote 7.3.1
git_url https://git.bioconductor.org/packages/DMCFB
git_branch RELEASE_3_18
git_last_commit d224bf2
DMCFB-package

Description

DMCFB is a profiling tool for identifying differentially methylated cytosines using Functional Bayesian Model in bisulfite sequencing data.

DMCFB methods

findDMCFB, plotDMCFB, cBSDMC, readBismark.

BSDMC objects

BSDMC-class
**BSDMC-class**

**BSDMC object**

**Description**

The BSDMC 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 Bayesian functional regression models. The rows represent the CpG sites in `rowRanges` and the columns represent the samples in `colData`.

**Value**

A BSDMC-class object

**Slots**

- `methReads`: An integer matrix
- `totalReads`: An integer matrix
- `methLevels`: A numeric matrix

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>

**See Also**

RangedSummarizedExperiment-class GRanges-class

**Examples**

```r
nr <- 500
cc <- 16
meth <- matrix(as.integer(runif(nr * cc, 0, nr)), nr)
methc <- matrix(rbinom(n = nr * cc, c(meth), prob = runif(nr * cc)), nr, cc)
meths <- matrix(as.integer(runif(nr * cc, 0, 10)), nr)
methl <- methc / meth
methv <- matrix((runif(nr * cc, 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 <- cBSDMC(
    rowRanges = r1, methReads = methc, totalReads = metht,
    methLevels = methl, methStates = meths, methVars = methv, colData = cd1
)
OBJ2

---

cBSDMC-method

cBSDMC method

Description

Creates a BSDMC-class object

Usage

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

## S4 method for signature 'matrix,matrix,matrix,GRanges'
cBSDMC(
    methReads,
    totalReads,
    methLevels,
    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 Bayesian functional regression models. 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  A list of storing MCMC samples or DMCs

Details

The rows of a BSDMC 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 BSDMC-class

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:nc
cdl <- DataFrame(
    Group = rep(c("G1", "G2"), each = nc / 2),
    row.names = LETTERS[1:nc]
)
OBJ2 <- cBSDMC(
    rowRanges = r1, methReads = methc, totalReads = meth,
    methLevels = methl, methStates = meths, methVars = methv, colData = cdl
)
combine-method

combine two BSDMC-class or two BSDMC-class

Usage

combine(obj1, obj2)

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

Arguments

obj1 A BSDMC-class
obj2 A BSDMC-class

Value

A BSDMC-class or BSDMC-class

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

set.seed(1980)
nr <- 150
nc <- 8
meth <- matrix(as.integer(runif(nr * nc * 2, 0, nr)), nr)
methc <- matrix(
  rbinom(n = nr * nc, c(meth), prob = runif(nr * nc * 2)),
  nr, nc * 2
)
methl <- methc / meth
r1 <- GRanges(rep("chr1", nr), IRanges(1:nr, width = 1), strand = "x")
names(r1) <- 1:nr
cd1 <- DataFrame(Group = rep("G1", each = nc), row.names = LETTERS[1:nc])
OBJ1 <- cBSDMC(
  rowRanges = r1, methReads = methc[, 1:nc], totalReads = methl[, 1:nc],
  methLevels = methl[, 1:nc], colData = cd1
)
cd2 <- DataFrame(
  Group = rep("G2", each = nc),
findDMCFB-method

```r
row.names = LETTERS[nc + 1:nc]
)
OBJ2 <- cBSDMC(
  rowRanges = r1, methReads = methc[, nc + 1:nc], totalReads =
  metht[, nc + 1:nc], methLevels = methl[, nc + 1:nc], colData = cd2
)
OBJ3 <- combine(OBJ1, OBJ2)
OBJ3
```

findDMCFB-method  findDMCFB method

---

**Description**

DMC identification via Bayesian functional regression models

**Usage**

```r
findDMCFB(
  object,
  bwa,
  bwb,
  nBurn,
  nMC,
  nThin,
  alpha,
  sdv,
  nCores,
  pSize,
  sfiles
)
```

```r
## S4 method for signature 'BSDMC'
findDMCFB(
  object,
  bwa,
  bwb,
  nBurn,
  nMC,
  nThin,
  alpha,
  sdv,
  nCores,
  pSize,
  sfiles
)
```
findDMCFB-method

Arguments

object  
A BSDMC-class object

bwa  
An integer value specifying the band-width size of B-spline basis matrix for a natural cubic spline for the group-specific effects of the Bayesian functional regression model

bwb  
An integer value specifying the band-width size of B-spline basis matrix for a natural cubic spline for the individual-specific effects of the Bayesian functional regression model

nBurn  
An integer value specifying the number of burn-in samples

nMC  
An integer value specifying the number of MCMC samples after burn-in

nThin  
An integer value specifying the thinning number in MCMC

alpha  
A numeric value specifying the level of \( \alpha \) in credible interval \((1 - \alpha)\%

sdv  
An double value specifying the standard deviation of priors

nCores  
An integer value specifying the number of machine cores for parallel computing

pSize  
An integer value specifying the number of cytosines in a regrion to be used in a Bayesian functiona regression model for DMC detection

sfiles  
A logical value indicating whether files to be saved or not.

Value

BSDMC-class object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

```r
set.seed(1980)
nr <- 1000
nc <- 4
metht <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n = nr * nc, c(metht), prob = runif(nr * nc)), nr, nc)
methl <- methc / metht
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 <- cBSDMC(
  rowRanges = r1, methReads = methc, totalReads = metht,
  methLevels = methl, colData = cd1
)
OBJ2 <- findDMCFB(OBJ1,
  bwa = 10, bwb = 10, nBurn = 50, nMC = 50, nThin = 1,
  alpha = 0.05, nCores = 2, pSize = 500, sfiles = FALSE
)```
methLevels-method

Description

Returns methLevels stored in BSDMC-class
Assigns methLevels to BSDMC-class

Usage

methLevels(object)
methLevels(object) <- value

## S4 method for signature 'BSDMC'
methLevels(object)

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

Arguments

object A BSDMC-class object
value An integer matrix

Value

A matrix
A BSDMC-class object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>

Examples

nr <- 150
cc <- 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)
methl <- methc / meth
r1 <- GRanges(rep("chr1", nr), IRanges(1:nr, width = 1), strand = "*")
names(r1) <- 1:nr
c1 <- DataFrame(
  Group = rep(c("G1", "G2"), each = nc / 2),
)
methReads-method

Description

Returns methReads stored in BSDMC-class

Assigns methReads to BSDMC-class

Usage

methReads(object)

methReads(object) <- value

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

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

Arguments

object     A BSDMC-class object
value      An integer matrix

Value

A matrix

A BSDMC-class object

Author(s)

Farhad Shokoohi <shokoohi@icloud.com>
Examples

```r
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)
methl <- methc / metht
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 <- cBSDMC(
  rowRanges = r1, methReads = methc, totalReads = metht,
  methLevels = methl, colData = cd1
)
methReads(OBJ1)
methReads(OBJ1) <- methc
```

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`.

- **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 Bayesian functional regression models. 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**: A list of storing MCMC samples or DMCs.

- **object**: A `BSDMC-class` object.
<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>value</td>
<td>An integer matrix</td>
</tr>
<tr>
<td>name</td>
<td>A character list</td>
</tr>
<tr>
<td>obj1</td>
<td>A BSDMC-class</td>
</tr>
<tr>
<td>obj2</td>
<td>A BSDMC-class</td>
</tr>
<tr>
<td>files</td>
<td>A character list</td>
</tr>
<tr>
<td>file</td>
<td>A character</td>
</tr>
<tr>
<td>nCores</td>
<td>An integer value specifying the number of machine cores for parallel computing</td>
</tr>
<tr>
<td>mc.cores</td>
<td>An integer greater than 0</td>
</tr>
<tr>
<td>pSize</td>
<td>An integer value specifying the number of cytosines in a region to be used in a Bayesian functiona regression model for DMC detection</td>
</tr>
<tr>
<td>bwa</td>
<td>An integer value specifying the band-width size of B-spline basis matrix for a natural cubic spline for the group-specific effects of the Bayesian functional regression model</td>
</tr>
<tr>
<td>bwb</td>
<td>An integer value specifying the band-width size of B-spline basis matrix for a natural cubic spline for the individual-specific effects of the Bayesian functional regression model</td>
</tr>
<tr>
<td>nBurn</td>
<td>An integer value specifying the number of burn-in samples</td>
</tr>
<tr>
<td>nThin</td>
<td>An integer value specifying the thinning number in MCMC</td>
</tr>
<tr>
<td>nMC</td>
<td>An integer value specifying the number of MCMC samples after burn-in</td>
</tr>
<tr>
<td>sdv</td>
<td>An double value specifying the standard deviation of priors</td>
</tr>
<tr>
<td>alpha</td>
<td>A numeric value specifying the level of $\alpha$ in credible interval $(1 - \alpha)%$</td>
</tr>
<tr>
<td>col</td>
<td>A character vector indicating which colors to alternate.</td>
</tr>
<tr>
<td>sfiles</td>
<td>A logical value indicating whether files to be saved or not.</td>
</tr>
<tr>
<td>region</td>
<td>An integer vector of length two specifying which subset of the object to be plotted</td>
</tr>
<tr>
<td>nSplit</td>
<td>A integer value specifying the number of subsets must be done for plotting the results of DMC identification</td>
</tr>
<tr>
<td>parList</td>
<td>A list specifying plots parameters, see par</td>
</tr>
<tr>
<td>...</td>
<td>other possible parameters</td>
</tr>
</tbody>
</table>

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>
plotDMCFB-method

Description
Plotting the results of DMC identification stored in a BSDMC-class object.

Usage
plotDMCFB(object, region, nSplit, parList)

## S4 method for signature 'BSDMC'
plotDMCFB(object, region, nSplit, parList)

Arguments
- object: A BSDMC-class object
- region: An integer vector of length two specifying which subset of the object to be plotted.
- nSplit: A integer value specifying the number of subsets must be done for plotting the results of DMC identification.
- parList: A list specifying plots parameters, see par.

Value
Plot

Author(s)
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Examples
```r
set.seed(1980)
nr <- 1000
nc <- 4
metht <- matrix(as.integer(runif(nr * nc, 0, 100)), nr)
methc <- matrix(rbinom(n = nr * nc, c(metht), prob = runif(nr * nc)), nr, nc)
methl <- methc / metht
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]
)
OBJ1 <- cBSDMC(
  rowRanges = r1, methReads = methc, totalReads = metht,
  methLevels = methl, colData = cd1
)
OBJ2 <- findDMCFB(OBJ1, bwa = 10, bwb = 10, nBurn = 50, nMC = 50, nThin = 1, alpha = 0.05, nCores = 2, pSize = 500, sfiles = FALSE)
plotDMCFB(OBJ2)

### 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 BSDMC-class object

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

```r
fn <- list.files(system.file("extdata", package = "DMCFB"))
fn.f <- list.files(system.file("extdata", package = "DMCFB"),
  full.names = TRUE)
OBJ <- readBismark(fn.f, fn, mc.cores=1)
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**

**totalReads method**

---

**Description**

Returns `totalReads` stored in `BSDMC-class`

Assigns `totalReads` to `BSDMC-class`

**Usage**

```r
totalReads(object)
```

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

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

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

**Arguments**

- `object`  
  A `BSDMC-class` object

- `value`  
  An integer matrix

**Value**

A matrix

A `BSDMC-class` object

**Author(s)**

Farhad Shokoohi <shokoohi@icloud.com>
Examples

```r	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)
methl <- methc / metht
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 <- cBSDMC(
  rowRanges = r1, methReads = methc, totalReads = metht,
  methLevels = methl, colData = cd1
)
totalReads(OBJ1)
totalReads(OBJ1) <- metht
```
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