Biseq: A package for analyzing targeted bisulfite sequencing data

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Contents

1 Introduction 3

2 Data import and classes 4
  2.1 Sample data .............................................. 4
  2.2 Import of Bismark’s methylation output files .......... 4
  2.3 The BSraw and BSrel classes ......................... 4
    2.3.1 The BSraw class ... .............................. 4
    2.3.2 The BSrel class .................................. 7
  2.4 Data handling .......................................... 9

3 Quality control 11

4 Detection of DMRs within groups of samples 13
  4.1 Definition of CpG clusters .............................. 13
  4.2 Smooth methylation data ............................... 15
  4.3 Model and test group effect ........................... 17
  4.4 Test CpG clusters for differential methylation ...... 20
  4.5 Trim significant CpG clusters ........................ 24
  4.6 Definition of DMR boundaries .......................... 25

5 Detection of DMRs between two samples 27
6 Testing of predefined genomic regions 28
   6.1 Testing predefined genomic regions using the BiSeq method . . 28
   6.2 Testing predefined genomic regions using the Global Test . . . 29

7 Further data processing 30
1 Introduction

The BiSeq package provides useful classes and functions to handle and analyze targeted bisulfite sequencing (BS) data such as reduced representation bisulfite sequencing (RRBS) data. In particular, it implements an algorithm to detect differentially methylated regions (DMRs), as described in detail in [1]. The package takes already aligned BS data from one or multiple samples. Until now, it was used for the analysis of CpG methylation of human and mouse samples only.
2 Data import and classes

2.1 Sample data

As sample data we use a small part of a recently published data set, see [2]. It comprises RRBS data from 10 samples of CpG sites from genomic regions on p arms of chromosome 1 and 2 covered in at least one sample. Data was obtained from 5 bone marrow probes of patients with acute promyelocytic leukemia (APL) and 5 control samples (APL in remission). RRBS data was preprocessed with the Bismark software version 0.5 [3].

2.2 Import of Bismark’s methylation output files


> library(BiSeq)

readBismark imports the CpG context output files created by the methylation extractor of Bismark:

> readBismark(files, colData)

The argument files point to files created by Bismark’s `methylation_extractor` and `bismark2bedGraph` (see the man page of `readBismark` for details on how to retrieve the right input files). colData specifies the sample names and additional phenotype information. This method returns a BSraw object.

2.3 The BSraw and BSrel classes

The BiSeq package contains the classes BSraw and BSrel, both derived from RangedSummarizedExperiment.

2.3.1 The BSraw class

The BSraw class is a container for ’raw’ RRBS data. It comprises sample information together with CpG positions and numbers of reads spanning the CpG positions as well as the number of methylated reads.

A BSraw object consists of four slots:
1. A list of arbitrary content describing the overall experiment, accessible with `metadata`.

2. A `GRanges` of the positions of CpG-sites covered by BS in at least one sample, accessible with `rowRanges`.

3. A `DataFrame` of samples and the values of variables measured on those samples, accessible with `colData`.

4. An assays slot containing a `SimpleList` of two matrices, one containing the numbers of reads (accessible with `totalReads`) and the other the numbers of methylated reads (accessible with `methReads`).

A new `BSraw` object can also be created by hand:

```r
metadata <- list(Sequencer = "Instrument", Year = "2013")
rowRanges <- GRanges(seqnames = "chr1",
                     ranges = IRanges(start = c(1,2,3), end = c(1,2,3)))
colData <- DataFrame(group = c("cancer", "control"),
                     row.names = c("sample_1", "sample_2"))
totalReads <- matrix(c(rep(10L, 3), rep(5L, 3)), ncol = 2)
methReads <- matrix(c(rep(5L, 3), rep(5L, 3)), ncol = 2)
BSraw(metadata = metadata,
       rowRanges = rowRanges,
       colData = colData,
       totalReads = totalReads,
       methReads = methReads)
```

Nevertheless, users will most likely create `BSraw` objects when use `readBismark` to load data.

We load and show the APL data:

```r
> data(rrbs)
> rrbs
```

class: BSraw
dim: 10502 10
metadata(0):
assays(2): totalReads methReads
rownames(10502): 1456 1457 ... 4970981 4970982
rowData names(0):
colnames(10): APL1 APL2 ... APL11624 APL5894
colData names(1): group

We show the sample characteristics slot:

> colData(rrbs)

DataFrame with 10 rows and 1 column
  group  
  <factor>
  APL1     APL
  APL2     APL
  APL3     APL
  APL7     APL
  APL8     APL
  APL10961 control
  APL11436 control
  APL11523 control
  APL11624 control
  APL5894  control

The first CpG sites on chromosome 1 which were covered:

> head(rowRanges(rrbs))

GRanges object with 6 ranges and 0 metadata columns:
  seqnames ranges strand
  <Rle> <IRanges> <Rle>
  1456  chr1 [870425, 870425]  
  1457  chr1 [870443, 870443]  
  1458  chr1 [870459, 870459]  
  1459  chr1 [870573, 870573]  
  1460  chr1 [870584, 870584]  
  1461  chr1 [870599, 870599]  

seqinfo: 25 sequences from an unspecified genome; no seqlengths

The coverage of the first CpG sites per sample:
> head(totalReads(rrbs))

<table>
<thead>
<tr>
<th></th>
<th>APL1</th>
<th>APL2</th>
<th>APL3</th>
<th>APL7</th>
<th>APL8</th>
<th>APL10961</th>
<th>APL11436</th>
<th>APL11523</th>
</tr>
</thead>
<tbody>
<tr>
<td>1456</td>
<td>39</td>
<td>6</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>48</td>
<td>31</td>
<td>65</td>
</tr>
<tr>
<td>1457</td>
<td>39</td>
<td>6</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>48</td>
<td>31</td>
<td>65</td>
</tr>
<tr>
<td>1458</td>
<td>39</td>
<td>6</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>48</td>
<td>27</td>
<td>65</td>
</tr>
<tr>
<td>1459</td>
<td>20</td>
<td>26</td>
<td>49</td>
<td>48</td>
<td>39</td>
<td>27</td>
<td>23</td>
<td>34</td>
</tr>
<tr>
<td>1460</td>
<td>20</td>
<td>26</td>
<td>49</td>
<td>48</td>
<td>39</td>
<td>27</td>
<td>23</td>
<td>34</td>
</tr>
<tr>
<td>1461</td>
<td>20</td>
<td>26</td>
<td>49</td>
<td>48</td>
<td>39</td>
<td>27</td>
<td>22</td>
<td>34</td>
</tr>
</tbody>
</table>

The number of methylated reads of the first CpG sites per sample:

> head(methReads(rrbs))

<table>
<thead>
<tr>
<th></th>
<th>APL1</th>
<th>APL2</th>
<th>APL3</th>
<th>APL7</th>
<th>APL8</th>
<th>APL10961</th>
<th>APL11436</th>
<th>APL11523</th>
</tr>
</thead>
<tbody>
<tr>
<td>1456</td>
<td>32</td>
<td>6</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>15</td>
<td>23</td>
<td>16</td>
</tr>
<tr>
<td>1457</td>
<td>33</td>
<td>6</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>18</td>
<td>10</td>
<td>19</td>
</tr>
<tr>
<td>1458</td>
<td>33</td>
<td>6</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>20</td>
<td>10</td>
<td>19</td>
</tr>
<tr>
<td>1459</td>
<td>13</td>
<td>20</td>
<td>34</td>
<td>41</td>
<td>32</td>
<td>3</td>
<td>8</td>
<td>8</td>
</tr>
<tr>
<td>1460</td>
<td>14</td>
<td>18</td>
<td>35</td>
<td>37</td>
<td>33</td>
<td>2</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>1461</td>
<td>14</td>
<td>16</td>
<td>35</td>
<td>40</td>
<td>31</td>
<td>5</td>
<td>5</td>
<td>5</td>
</tr>
</tbody>
</table>

2.3.2 The BSrel class

The BSrel is a container for ‘relative’ methylation levels of BS data. It comprises sample information together with CpG positions and the relative methylation values (between 0 and 1).
A \textit{BSrel} object consists of four slots:

1. A list of arbitrary content describing the overall experiment, accessible with \texttt{metadata}.

2. A \textit{GRanges} of the positions of CpG-sites covered by BS in at least one sample, accessible with \texttt{rowRanges}.

3. A \textit{DataFrame} of samples and the values of variables measured on those samples, accessible with \texttt{colData}.

4. An \texttt{assays} slot containing a \textit{SimpleList} of a matrix with the relative methylation levels (between 0 and 1), accessible with \texttt{methLevel}.

A new \textit{BSraw} object can be created by:

\begin{verbatim}
> methLevel <- matrix(c(rep(0.5, 3), rep(1, 3)), ncol = 2)
> BSrel(metadata = metadata,
       rowRanges = rowRanges,
       colData = colData,
       methLevel = methLevel)
\end{verbatim}

We can convert a \textit{BSraw} object to a \textit{BSrel} object easily:

\begin{verbatim}
> rrbs.rel <- rawToRel(rrbs)
> rrbs.rel
\end{verbatim}

\begin{verbatim}
class: BSrel
dim: 10502 10
metadata(0):
assays(1): methLevel
rownames(10502): 1456 1457 ... 4970981 4970982
rowData names(0):
colnames(10): APL1 APL2 ... APL11624 APL5894
colData names(1): group
\end{verbatim}

The relative methylation values of the first CpG sites:

\begin{verbatim}
> head(methLevel(rrbs.rel))
\end{verbatim}
2.4 Data handling

All methods for `RangedSummarizedExperiment` objects are applicable for `BSraw` and `BSrel` objects:

```r
> dim(rrbs)
[1] 10502 10

> colnames(rrbs)
[1] "APL1"  "APL2"  "APL3"  "APL7"  "APL8"
[6] "APL10961" "APL11436" "APL11523" "APL11624" "APL5894"
```

We can return subsets of samples or CpG sites:

```r
> rrbs[,"APL2"]
> ind.chr1 <- which(seqnames(rrbs) == "chr1")
> rrbs[ind.chr1,]
```

We can also subset by overlaps with a `GRanges` object:

```r
> region <- GRanges(seqnames="chr1",
  ranges=IRanges(start = 875200, end = 875500))
```
> findOverlaps(rrbs, region)
> subsetByOverlaps(rrbs, region)

We can sort \textit{BSraw} and \textit{BSrel} objects into ascending order of CpG sites positions on chromosomes:

> sort(rrbs)

\textit{BSraw} and \textit{BSrel} objects can be combined and splitted:

> combine(rrbs[1:10,1:2], rrbs[1:1000, 3:10])
> split(rowRanges(rrbs),
>       f = as.factor(as.character(seqnames(rrbs)))))
3 Quality control

Via two very simple methods it is possible to compare the sample’s coverages. `covStatistics` lists the number of CpG sites that were covered per sample together with the median of the coverage of these CpG sites. `covBoxplots` represent the coverage distributions per sample.

```r
> covStatistics(rrbs)

$Covered_CpG_sites

<table>
<thead>
<tr>
<th></th>
<th>APL1</th>
<th>APL2</th>
<th>APL3</th>
<th>APL7</th>
<th>APL8</th>
<th>APL10961</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>5217</td>
<td>4240</td>
<td>4276</td>
<td>3972</td>
<td>3821</td>
<td>5089</td>
</tr>
<tr>
<td>APL11436</td>
<td>APL11523</td>
<td>APL11624</td>
<td>APL5894</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>5169</td>
<td>6922</td>
<td>6483</td>
<td>7199</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

$Median_coverage

<table>
<thead>
<tr>
<th></th>
<th>APL1</th>
<th>APL2</th>
<th>APL3</th>
<th>APL7</th>
<th>APL8</th>
<th>APL10961</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>12</td>
<td>5</td>
<td>12</td>
<td>15</td>
<td>11</td>
<td>10</td>
</tr>
<tr>
<td>APL11436</td>
<td>APL11523</td>
<td>APL11624</td>
<td>APL5894</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>8</td>
<td>4</td>
<td>5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
```
> covBoxplots(rrbs, col = "cornflowerblue", las = 2)

Figure 1: Sample wise coverage distributions
4 Detection of DMRs within groups of samples

The algorithm to detect differentially methylated regions (DMRs) within two groups of samples (e.g. cancer and control) is described in detail in [1]. To better understand this User’s guide it is helpful to know the rough procedure. The DMR detection is a five-steps approach:

1. Definition of CpG clusters
2. Smooth methylation data within CpG clusters
3. Model and test group effect for each CpG site within CpG clusters
4. Apply hierarchical testing procedure:
   (a) Test CpG clusters for differential methylation and control weighted FDR on cluster
   (b) Trim rejected CpG clusters and control FDR on single CpGs
5. Define DMR boundaries

Please see [1] for more details.

4.1 Definition of CpG clusters

In order to smooth the methylation data we first have to detect CpG clusters (regions with a high spatial density of covered CpG sites). Within a BSraw object clusterSites searches for agglomerations of CpG sites across all samples. In a first step the data is reduced to CpG sites covered in round(perc.samples*ncol(object)) samples (here: 4 samples), these are called ‘frequently covered CpG sites’. In a second step regions are detected where not less than min.sites frequently covered CpG sites are sufficiently close to each other (max.dist. Note, that the frequently covered CpG sites are considered to define the boundaries of the CpG clusters only. For the subsequent analysis the methylation data of all CpG sites within these clusters are used.

We perform the analysis on a subset of our data to save time:
> rrbs.small <- rrbs[1:1000,]
> rrbs.clust.unlim <- clusterSites(object = rrbs.small,
    groups = colData(rrbs)$group,
    perc.samples = 4/5,
    min.sites = 20,
    max.dist = 100)

rrbs.clust.unlim is a again BSraw object but restricted to CpG sites within CpG clusters. Each CpG site is assigned to a cluster:

> head(rowRanges(rrbs.clust.unlim))

GRanges object with 6 ranges and 1 metadata column:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>cluster.id</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1</td>
<td>[872335, 872335]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
<tr>
<td>chr1</td>
<td>[872369, 872369]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
<tr>
<td>chr1</td>
<td>[872370, 872370]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
<tr>
<td>chr1</td>
<td>[872385, 872385]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
<tr>
<td>chr1</td>
<td>[872386, 872386]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
<tr>
<td>chr1</td>
<td>[872412, 872412]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
</tbody>
</table>

The underlying CpG clusters can also be converted to a GRanges object with the start and end positions:

> clusterSitesToGR(rrbs.clust.unlim)

GRanges object with 6 ranges and 1 metadata column:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>cluster.id</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1</td>
<td>[872335, 872616]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
<tr>
<td>chr1</td>
<td>[875227, 875470]</td>
<td>*</td>
<td>chr1_2</td>
</tr>
<tr>
<td>chr1</td>
<td>[875650, 876028]</td>
<td>*</td>
<td>chr1_3</td>
</tr>
<tr>
<td>chr1</td>
<td>[876807, 877458]</td>
<td>*</td>
<td>chr1_4</td>
</tr>
<tr>
<td>chr1</td>
<td>[877684, 877932]</td>
<td>*</td>
<td>chr1_5</td>
</tr>
<tr>
<td>chr2</td>
<td>[ 45843, 46937]</td>
<td>*</td>
<td>chr2_1</td>
</tr>
</tbody>
</table>

seqinfo: 25 sequences from an unspecified genome; no seqlengths
4.2 Smooth methylation data

In the smoothing step CpG sites with high coverages get high weights. To reduce bias due to unusually high coverages we limit the coverage, e.g. to the 90% quantile:

```r
> ind.cov <- totalReads(rrbs.clust.unlim) > 0
> quant <- quantile(totalReads(rrbs.clust.unlim)[ind.cov], 0.9)
> quant

90%
32

> rrbs.clust.lim <- limitCov(rrbs.clust.unlim, maxCov = quant)
```

We then smooth the methylation values of CpG sites within the clusters with the default bandwidth \( h = 80 \) base pairs. It is possible - and recommended - to parallelize this step by setting `mc.cores`, to 6 cores for instance, if there are 6 available.

```r
> predictedMeth <- predictMeth(object = rrbs.clust.lim)
```

`predictedMeth` is a `BSrel` object with smoothed relative methylation levels for each CpG site within CpG clusters:

```r
> predictedMeth

class: BSrel
dim: 344 10
metadata(0):
assays(1): methLevel
rownames(344): 1 2 ... 343 344
rowData names(1): cluster.id
colnames(10): APL1 APL2 ... APL11624 APL5894
colData names(1): group
```

The effect of the smoothing step can be shown with the `plotMeth` function:
> covBoxplots(rrbs.clust.lim, col = "cornflowerblue", las = 2)

Figure 2: Sample wise coverage distributions after coverage limitation
> plotMeth(object.raw = rrbs[,6],
object.rel = predictedMeth[,6],
region = region,
lwd.lines = 2,
col.points = "blue",
cex = 1.5)

Figure 3: Raw data together with smoothed methylation levels

4.3 Model and test group effect

We observe a differential methylation between cancer and control for some CpG sites:
To detect the CpG sites where the DNA methylation differs between APL and control samples we model the methylation within a beta regression with the group as explanatory variable and use the Wald test to test if there is a
group effect:

> ## To shorten the run time set mc.cores, if possible!
> betaResults <- betaRegression(formula = ~group,
>     link = "probit",
>     object = predictedMeth,
>     type = "BR")

> ## OR:
> data(betaResults)

betaResults is a data.frame containing model and test information for each
CpG site:

> head(betaResults)

<table>
<thead>
<tr>
<th>chr</th>
<th>pos</th>
<th>p.val</th>
<th>meth.group1</th>
<th>meth.group2</th>
<th>meth.diff</th>
<th>estimate</th>
<th>std.error</th>
<th>pseudo.R.sqrt</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1</td>
<td>872335</td>
<td>0.0011317652</td>
<td>0.9525098</td>
<td>0.8635983</td>
<td>-0.08891149</td>
<td>-0.5730618</td>
<td>0.1760266</td>
<td>0.6304051</td>
</tr>
<tr>
<td>chr1</td>
<td>872369</td>
<td>0.0007678027</td>
<td>0.9414368</td>
<td>0.8444060</td>
<td>-0.09703074</td>
<td>-0.5542171</td>
<td>0.1647422</td>
<td>0.6291904</td>
</tr>
<tr>
<td>chr1</td>
<td>872370</td>
<td>0.0008347451</td>
<td>0.9414314</td>
<td>0.8448725</td>
<td>-0.09655890</td>
<td>-0.5522164</td>
<td>0.1652843</td>
<td>0.6246474</td>
</tr>
<tr>
<td>chr1</td>
<td>872385</td>
<td>0.0010337477</td>
<td>0.9412217</td>
<td>0.8521862</td>
<td>-0.08903549</td>
<td>-0.5192564</td>
<td>0.1582531</td>
<td>0.6108452</td>
</tr>
<tr>
<td>chr1</td>
<td>872386</td>
<td>0.0010975571</td>
<td>0.9410544</td>
<td>0.8526863</td>
<td>-0.08836810</td>
<td>-0.5156622</td>
<td>0.1579728</td>
<td>0.6090794</td>
</tr>
<tr>
<td>chr1</td>
<td>872412</td>
<td>0.0035114839</td>
<td>0.9378250</td>
<td>0.8718024</td>
<td>-0.06602261</td>
<td>-0.4018161</td>
<td>0.1376551</td>
<td>0.5851744</td>
</tr>
</tbody>
</table>

cluster.id

| chr 1.1 | chr1_1 |
| chr 1.2 | chr1_1 |
| chr 1.3 | chr1_1 |
| chr 1.4 | chr1_1 |
| chr 1.5 | chr1_1 |
| chr 1.6 | chr1_1 |

By setting type = "BR" the maximum likelihood with bias reduction is
called. This is especially useful, when the sample size is small, see [4]. The
mean of the response (methylation) is linked to a linear predictor described by 
~ \( x_1 + x_2 \) using a link function while the precision parameter is assumed to
be constant. Sometimes the variance of DNA methylation is dependent on the
group factor, e.g. the methylation variance in cancer samples is often higher
than in normal samples. These additional regressors can be linked to the
precision parameter within the formula of type 
~ \( x_1 + x_2 \mid y_1 + y_2 \) where
the regressors in the two parts can be overlapping, see the documentation in
the \textit{betareg} package.

\section*{4.4 Test CpG clusters for differential methylation}

The aim is to detect CpG clusters containing at least one differentially methy-
lated location. To do so the P values \( p \) from the Wald tests are transformed
to Z scores: 
\[ z = \Phi^{-1}(1 - p), \]
which are normally distributed under Null hypothesis (no group effect). As cluster test statistic a standardized Z score
average is used. To estimate the standard deviation of the Z scores we have
to estimate the correlation and hence the variogram of methylation between
two CpG sites within a cluster. The estimation of the standard deviation
requires that the distribution of the Z scores follows a standard normal dis-
tribution. However, if methylation in both groups differs for many CpG sites
the density distribution of P values shows a peak near 0. To ensure that the
P values are roughly uniformly distributed to get a variance of the Z scores
that is Gaussian with variance 1 we recommend to estimate the variogram
(and hence the correlation of Z scores) under the null hypothesis. To do so
we model the beta regression again for resampled data:

\begin{verbatim}
> ## Both resampled groups should have the same number of
cancer and control samples:
predictedMethNull <- predictedMeth[,c(1:4, 6:9)]
colData(predictedMethNull)$group.null <- rep(c(1,2), 4)
> ## To shorten the run time, please set \texttt{mc.cores}, if possible!
> betaResultsNull <- betaRegression(formula = ~group.null,
link = "probit",
object = predictedMethNull,
type="BR")

> ## OR:
data(betaResultsNull)
\end{verbatim}
We estimate the variogram for the Z scores obtained for the resampled data:

```r
> vario <- makeVariogram(betaResultsNull)
> ## OR:
> data(vario)
```

Based on the variogram plot we evaluate the sill (usually near 1) of the variogram and smooth the curve:

```r
> plot(vario$variogram$v)
> vario.sm <- smoothVariogram(vario, sill = 0.9)
> lines(vario.sm$variogram[,c("h", "v.sm")],
       col = "red", lwd = 1.5)
> grid()
```

![Figure 5: Estimated variogram together with the smoothed curve](image-url)
The `vario.sm` object is a list of two:

```r
> names(vario.sm)
[1] "variogram" "pValsList"
```

```r
> head(vario.sm$variogram)
     h   v.sm
1 1 0.0000000000
2 2 0.0000000000
3 3 0.0000000000
4 4 0.0004532616
5 5 0.0019789519
6 6 0.0038612942
```

```r
> head(vario.sm$pValsList[[1]])
         chr pos  p.val meth.group1 meth.group2
chr1.1   chr1 872335 0.8567258  0.9191601
chr1.2   chr1 872369 0.7910594 0.9056264
chr1.3   chr1 872370 0.7855283 0.9060236
chr1.4   chr1 872386 0.7462536 0.9080750
chr1.5   chr1 872387 0.7462667 0.9081423
chr1.6   chr1 872412 0.8575813 0.9093737
     meth.diff estimate    std.error pseudo.R.sqrt
chr1.1   0.007573505 -0.05244358  0.2904759  0.006696118
chr1.2   0.012429670 -0.07781982  0.2937315  0.013223677
chr1.3   0.012708263 -0.07993265  0.2937384  0.013863179
chr1.4   0.014497213 -0.09359431  0.2892434  0.020416968
chr1.5   0.014453228 -0.09334700  0.2884945  0.020484807
chr1.6   0.007222875 -0.04562887  0.2542651  0.006457349
          cluster.id       z.score pos.new
chr1.1   chr1_1     -1.0657239    1
chr1.2   chr1_1     -0.8101026   35
chr1.3   chr1_1     -0.7910010   36
chr1.4   chr1_1     -0.6627467   51
chr1.5   chr1_1     -0.6627876   52
chr1.6   chr1_1     -1.0695155   78
```
We replace the `pValsList` object (which consists of the test results of the resampled data) by the test results of interest (for group effect):

```r
> ## auxiliary object to get the pValsList for the test
> ## results of interest:
> vario.aux <- makeVariogram(betaResults, make.variogram=FALSE)
> vario.sm$pValsList <- vario.aux$pValsList
> head(vario.sm$pValsList[[1]])
```

<table>
<thead>
<tr>
<th>chr</th>
<th>pos</th>
<th>p.val</th>
<th>meth.group1</th>
<th>meth.group2</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1.1</td>
<td>chr1</td>
<td>872335</td>
<td>0.0011317652</td>
<td>0.9525098</td>
</tr>
<tr>
<td>chr1.2</td>
<td>chr1</td>
<td>872369</td>
<td>0.0007678027</td>
<td>0.9414368</td>
</tr>
<tr>
<td>chr1.3</td>
<td>chr1</td>
<td>872370</td>
<td>0.0008347451</td>
<td>0.9414314</td>
</tr>
<tr>
<td>chr1.4</td>
<td>chr1</td>
<td>872385</td>
<td>0.0010337477</td>
<td>0.9412217</td>
</tr>
<tr>
<td>chr1.5</td>
<td>chr1</td>
<td>872386</td>
<td>0.0010975571</td>
<td>0.9410544</td>
</tr>
<tr>
<td>chr1.6</td>
<td>chr1</td>
<td>872412</td>
<td>0.0035114839</td>
<td>0.9378250</td>
</tr>
</tbody>
</table>

```r
meth.diff estimate std.error pseudo.R.sqrt
chr1.1 0.08891149 -0.5730618 0.1760266 0.6304051
chr1.2 0.09703074 -0.5542171 0.1647422 0.6291904
chr1.3 0.09655890 -0.5522164 0.1652843 0.6246474
chr1.4 0.08903549 -0.5192564 0.1582531 0.6108452
chr1.5 0.0836810 -0.5156622 0.1579728 0.6090794
chr1.6 0.06602261 -0.4018161 0.1376551 0.5851744
```

`vario.sm` now contains the smoothed variogram under the Null hypothesis together with the P values (and Z scores) from the Wald test, that the group has no effect on methylation. The correlation of the Z scores between two locations in a cluster can now be estimated:

```r
> locCor <- estLocCor(vario.sm)
```

We test each CpG cluster for the presence of at least one differentially methylated location at $q$ what can be interpreted as the size-weighted FDR on clusters:
> clusters.rej <- testClusters(locCor,
   FDR.cluster = 0.1)

3 CpG clusters rejected.

> clusters.rej$clusters.reject

GRanges object with 3 ranges and 2 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>X</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Rle</td>
<td>Rle</td>
<td>character</td>
</tr>
<tr>
<td>[1]</td>
<td>chr1 [872335, 872616]</td>
<td>*</td>
<td>chr1_1</td>
</tr>
<tr>
<td>[2]</td>
<td>chr1 [875227, 875470]</td>
<td>*</td>
<td>chr1_2</td>
</tr>
<tr>
<td>[3]</td>
<td>chr2 [ 45843, 46937]</td>
<td>*</td>
<td>chr2_1</td>
</tr>
</tbody>
</table>

p.value

<numeric>

[1] 6.867163e-03
[3] 1.881082e-09

-------

seqinfo: 2 sequences from an unspecified genome; no seqlengths

4.5 Trim significant CpG clusters

We then trim the rejected CpG clusters that is to remove the not differentially methylated CpG sites at $q_1$ what can be interpreted as the location-wise FDR:

> clusters.trimmed <- trimClusters(clusters.rej,
   FDR.loc = 0.05)

> head(clusters.trimmed)

<table>
<thead>
<tr>
<th>chr</th>
<th>pos</th>
<th>p.val</th>
<th>meth.group1</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1_1.chr1.1</td>
<td>chr1 872335   0.0011317652  0.9525098</td>
<td></td>
<td></td>
</tr>
<tr>
<td>chr1_1.chr1.2</td>
<td>chr1 872369   0.0007678027  0.9414368</td>
<td></td>
<td></td>
</tr>
<tr>
<td>chr1_1.chr1.3</td>
<td>chr1 872370   0.0008347451  0.9414314</td>
<td></td>
<td></td>
</tr>
<tr>
<td>chr1_1.chr1.4</td>
<td>chr1 872385   0.0009755571  0.9410544</td>
<td></td>
<td></td>
</tr>
<tr>
<td>chr1_1.chr1.5</td>
<td>chr1 872386   0.0009755571  0.9410544</td>
<td></td>
<td></td>
</tr>
<tr>
<td>chr1_1.chr1.6</td>
<td>chr1 872387   0.0009755571  0.9410544</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>meth.group2 meth.diff estimate std.error</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1_1.chr1.1</td>
</tr>
</tbody>
</table>
clusters.trimmed is a data.frame object containing all differentially methylated CpG sites. The p.li column contains the P values estimated in the cluster trimming step, see [1].

4.6 Definition of DMR boundaries

We can now define the boundaries of DMRs as rejected CpG sites within which rejected CpG sites solely are located. Within the DMRs the distance between neighbored rejected CpG sites should not exceed max.dist base pairs (usually the same as for max.dist in clusterSites), otherwise, the DMR is splitted. DMRs are also splitted if the methylation difference switches from positive to negative, or vice versa, if diff.dir = TRUE. That way we ensure that within a DMR all CpG sites are hypermethylated, and hypomethylated respectively.

```r
> DMRs <- findDMRs(clusters.trimmed,
                    max.dist = 100,
                    diff.dir = TRUE)
> DMRs
```

25
GRanges object with 4 ranges and 4 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1</td>
<td>[872335, 872386]</td>
<td>*</td>
</tr>
<tr>
<td>chr1</td>
<td>[875227, 875470]</td>
<td>*</td>
</tr>
<tr>
<td>chr2</td>
<td>[46126, 46718]</td>
<td>*</td>
</tr>
<tr>
<td>chr2</td>
<td>[46915, 46937]</td>
<td>*</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>median.p</th>
<th>median.meth.group1</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0010337476937105</td>
<td>0.94143135870377</td>
</tr>
<tr>
<td>6.67719258580069e-06</td>
<td>0.502443544206678</td>
</tr>
<tr>
<td>3.9604046820675e-05</td>
<td>0.438629367812053</td>
</tr>
<tr>
<td>0.0148459621327497</td>
<td>0.13636374336524</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>median.meth.group2</th>
<th>median.meth.diff</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.852186207117906</td>
<td>0.089035493038882</td>
</tr>
<tr>
<td>0.182082007625853</td>
<td>0.319474180010203</td>
</tr>
<tr>
<td>0.0776818250851119</td>
<td>0.355363178661131</td>
</tr>
<tr>
<td>0.0369197526986237</td>
<td>0.099443990666616</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome; no seqlengths
5 Detection of DMRs between two samples

If there are two samples only to be compared we can use the `compareTwoSamples` function which determines the differences per CpG site and aggregates the sites surpassing the minimum difference `minDiff`:

```r
> DMRs.2 <- compareTwoSamples(object = predictedMeth,
    sample1 = "APL1",
    sample2 = "APL10961",
    minDiff = 0.3,
    max.dist = 100)
```

Some of the DMRs detected within these two samples overlap with the groupwise DMRs:

```r
> sum(overlapsAny(DMRs.2, DMRs))

[1] 1
```
6 Testing of predefined genomic regions

There are sometimes biological and/or technical reasons for testing predefined genomic regions for differential methylation. For example, one might want to test for methylation differences in known CpG islands or promoter regions. In this scenario it is not of interest which exact CpG sites are differentially methylated. The methods of choice for testing genomic regions are BiSeq and the global test (which we also implemented in this package) [5]. Here, we want to give a short guidance on how to use the BiSeq package in order to test predefined genomic regions using BiSeq and the global test.

6.1 Testing predefined genomic regions using the BiSeq method

Testing predefined genomic regions using the BiSeq method is mostly equivalent to the procedure shown above for DMR detection. Instead of the definition of CpG clusters (which we described in section 4.1) we will just add the region information to the CpG sites in the BSraw object. In this example, we assume that we want to test gene promoters for differential methylation.

We filter out all CpG sites of the BSraw object that do not fall into any promoter region. The remaining CpG sites get the promoter identifier in a column named cluster.id:

```r
> data(promoters)
> data(rrbs)
> rrbs.red <- subsetByOverlaps(rrbs, promoters)
> ov <- findOverlaps(rrbs.red, promoters)
> rowRanges(rrbs.red)$cluster.id[queryHits(ov)] <- promoters$acc_no[subjectHits(ov)]
> head(rowRanges(rrbs.red))
```

GRanges object with 6 ranges and 1 metadata column:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>cluster.id</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;character&gt;</td>
</tr>
<tr>
<td>chr2</td>
<td>[46089, 46089]</td>
<td>+</td>
<td>NM_001077710</td>
</tr>
<tr>
<td>chr2</td>
<td>[46095, 46095]</td>
<td>+</td>
<td>NM_001077710</td>
</tr>
<tr>
<td>chr2</td>
<td>[46104, 46104]</td>
<td>+</td>
<td>NM_001077710</td>
</tr>
<tr>
<td>chr2</td>
<td>[46111, 46111]</td>
<td>+</td>
<td>NM_001077710</td>
</tr>
<tr>
<td>chr2</td>
<td>[46113, 46113]</td>
<td>+</td>
<td>NM_001077710</td>
</tr>
</tbody>
</table>

28
From here on we can use the same pipeline as usual: Smoothing and modeling (sections 4.2 and 4.3) of the DNA methylation data and subsequent testing of the regions (section 4.4).

### 6.2 Testing predefined genomic regions using the Global Test

Goeman et al. [6] proposed a score test for testing high dimensional alternatives. The approach is implemented in the R/Bioconductor package `globaltest`. The BiSeq package offers a wrapper function to apply Goeman’s Global Test directly to RRBS data given as a `BSrel` object:

```r
> data(promoters)
> data(rrbs)
> rrbs <- rawToRel(rrbs)
> promoters <- promoters[overlapsAny(promoters, rrbs)]
> gt <- globalTest(group~1,
                    rrbs,
                    subsets = promoters)
> head(gt)

          p-value Statistic Expected Std.dev #Cov
1 0.00975 2.50e+01 11.1 4.89 206
2 0.05381 2.05e+01 11.1 5.61  67
3 0.05381 2.05e+01 11.1 5.61  67
4 1.00000 1.85e-31 11.1 14.81   8
5 1.00000 1.85e-31 11.1 14.81   8
6 0.06744 1.84e+01 11.1 4.88 149
```

If the parameter `subsets` is not given, the null hypothesis is that no CpG site (rather than region) is associated with the given response variable.
7 Further data processing

The plotMethMap function is helpful to evaluate DMRs graphically. Via \texttt{zlim = c(0,1)} that is passed to the heatmap function we ensure that green stands for a relative methylation of 0 and red stands for a relative methylation of 1:

```r
> rowCols <- c("magenta", "blue")[as.numeric(colData(predictedMeth)$group)]
> plotMethMap(predictedMeth,
  region = DMRs[3],
  groups = colData(predictedMeth)$group,
  intervals = FALSE,
  zlim = c(0,1),
  RowSideColors = rowCols,
  labCol = "", margins = c(0, 6))
```

Figure 6: Methylation map of smoothed methylation data within a detected DMR together with hierarchical clustering of the samples

To represent the smoothed methylation curves we can use the plotSmooth-
Meth function:

```r
> plotSmoothMeth(object.rel = predictedMeth,
    region = DMRs[3],
    groups = colData(predictedMeth)$group,
    group.average = FALSE,
    col = c("magenta", "blue"),
    lwd = 1.5)
> legend("topright",
    legend=levels(colData(predictedMeth)$group),
    col=c("magenta", "blue"),
    lty=1, lwd = 1.5)
```

Figure 7: The smoothed methylation curves for all samples within a detected DMR
We can annotate the detected DMRs by means of a `GRanges` object, e.g. a list of promoter regions. In case of an overlapping of both `GRanges` objects the DMR is marked as `TRUE`, or with the respective identifier in the promoter list:

```r
> data(promoters)
> head(promoters)

GRanges object with 6 ranges and 1 metadata column:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>acc_no</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;character&gt;</td>
</tr>
<tr>
<td>[1]</td>
<td>chr1 [66998824, 67000324]</td>
<td>*</td>
<td>NM_032291</td>
</tr>
</tbody>
</table>

seqinfo: 24 sequences from an unspecified genome; no seqlengths

> DMRs.anno <- annotateGRanges(object = DMRs, regions = promoters, name = 'Promoter', regionInfo = 'acc_no')

> DMRs.anno

GRanges object with 4 ranges and 5 metadata columns:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>median.p</th>
<th>median.meth.group1</th>
<th>median.meth.group2</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt;</td>
<td>&lt;Rle&gt;</td>
<td>&lt;numeric&gt;</td>
<td>&lt;numeric&gt;</td>
<td>&lt;numeric&gt;</td>
</tr>
<tr>
<td>[1]</td>
<td>chr1 [872335, 872386]</td>
<td>*</td>
<td>1.033748e-03</td>
<td>0.9414314</td>
<td>0.85218621</td>
</tr>
<tr>
<td>[2]</td>
<td>chr1 [875227, 875470]</td>
<td>*</td>
<td>6.677193e-06</td>
<td>0.5024435</td>
<td>0.18208201</td>
</tr>
<tr>
<td>[3]</td>
<td>chr2 [46126, 46718]</td>
<td>*</td>
<td>3.960405e-05</td>
<td>0.4386294</td>
<td>0.07768183</td>
</tr>
<tr>
<td>[4]</td>
<td>chr2 [46915, 46937]</td>
<td>*</td>
<td>1.484596e-02</td>
<td>0.1363637</td>
<td>0.03691975</td>
</tr>
</tbody>
</table>
```

32
<table>
<thead>
<tr>
<th>median.meth.diff</th>
<th>Promoter</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;numeric&gt;</td>
<td>&lt;character&gt;</td>
</tr>
<tr>
<td>[1] 0.08903549</td>
<td>&lt;NA&gt;</td>
</tr>
<tr>
<td>[2] 0.31947418</td>
<td>&lt;NA&gt;</td>
</tr>
<tr>
<td>[3] 0.35536318</td>
<td>NM_001077710</td>
</tr>
<tr>
<td>[4] 0.09944399</td>
<td>NM_001077710</td>
</tr>
</tbody>
</table>

seqinfo: 2 sequences from an unspecified genome; no seqlengths

plotBindingSites plots the average methylation around given genomic regions, e.g. protein binding sites. Here, we compare the methylation in and around promoter regions between APL and controls:
> plotBindingSites(object = rrbs,
    regions = promoters,
    width = 4000,
    group = colData(rrbs)$group,
    col = c("magenta", "blue"),
    lwd = 1.5)
>
> legend("top",
    legend=levels(colData(rrbs)$group),
    col=c("magenta", "blue"),
    lty=1, lwd = 1.5)

Figure 8: Methylation around 1,000 promoters; Position 0 refers to the centers of the promoters

The raw and relative methylation data can also be viewed in the Integra-
tive Genomics Viewer (IGV; freely available for download from [www.broadinstitute.org/igv](http://www.broadinstitute.org/igv)) [7]. To do so we first write the methylation information of each sample within the $BS_{raw}$ or $BS_{rel}$ object to a bed file:

```r
> track.names <- paste(colData(rrbs)$group, 
"_",
gsub("APL", ",", colnames(rrbs)), 
sep="")
> writeBED(object = rrbs, 
name = track.names, 
file = paste(colnames(rrbs), ".bed", sep = ""))
> writeBED(object = predictedMeth, 
name = track.names, 
file = paste(colnames(predictedMeth), ".bed", sep = ""))
```

We can load the bed files of the raw data in the IGV. The integers beneath the CpG marks represent the numbers of sequencing reads covering the CpG sites:

![IGV snapshot of the raw data in and around a detected DMR](image)

**Figure 9:** IGV snapshot of the raw data in and around a detected DMR
We can also load the smoothed methylation levels:

![Figure 10: IGV snapshot of the smoothed data in and around a detected DMR](image)

Figure 10: IGV snapshot of the smoothed data in and around a detected DMR.
References


