

# Package ‘SOMNiBUS’

March 4, 2025

**Title** Smooth modeling of bisulfite sequencing

**Version** 1.14.2

**Description** This package aims to analyse count-based methylation data on predefined genomic regions, such as those obtained by targeted sequencing, and thus to identify differentially methylated regions (DMRs) that are associated with phenotypes or traits. The method is built a rich flexible model that allows for the effects, on the methylation levels, of multiple covariates to vary smoothly along genomic regions. At the same time, this method also allows for sequencing errors and can adjust for variability in cell type mixture.

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**URL** <https://github.com/kaiqiong/SOMNiBUS>

**BugReports** <https://github.com/kaiqiong/SOMNiBUS/issues>

**Depends** R (>= 4.1.0)

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**Suggests** BiocStyle, covr, devtools, dplyr, knitr, magick, rmarkdown, testthat, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Hsapiens.UCSC.hg19.knownGene, org.Hs.eg.db,

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binomRegMethModel	<i>A smoothed-EM algorithm to estimate covariate effects and test regional association in Bisulfite Sequencing-derived methylation data</i>
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## Description

This function fits a (dispersion-adjusted) binomial regression model to regional methylation data, and reports the estimated smooth covariate effects and regional p-values for the test of DMRs (differentially methylation regions). Over or under dispersion across loci is accounted for in the model by the combination of a multiplicative dispersion parameter (or scale parameter) and a sample-specific random effect.

This method can deal with outcomes, i.e. the number of methylated reads in a region, that are contaminated by known false methylation calling rate ( $p_0$ ) and false non-methylation calling rate ( $1-p_1$ ).

The covariate effects are assumed to smoothly vary across genomic regions. In order to estimate them, the algorithm first represents the functional parameters by a linear combination of a set of restricted cubic splines (with dimension  $n.k$ ), and a smoothness penalization term which depends on the smoothing parameters  $\lambda$  is also added to control smoothness. The estimation is performed by an iterated EM algorithm. Each M step constitutes an outer Newton's iteration to estimate smoothing parameters  $\lambda$  and an inner P-IRLS iteration to estimate spline coefficients  $\alpha$  for the covariate effects. Currently, the computation in the M step depends the implementation of `gam()` in package `mgcv`.

**Usage**

```

binomRegMethModel(
  data,
  n.k,
  p0 = 0.003,
  p1 = 0.9,
  Quasi = TRUE,
  epsilon = 10^(-6),
  epsilon.lambda = 10^(-3),
  maxStep = 200,
  binom.link = "logit",
  method = "REML",
  covs = NULL,
  RanEff = TRUE,
  reml.scale = FALSE,
  scale = -2,
  verbose = TRUE
)

```

**Arguments**

data	a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth_Counts (methylated counts), Total_Counts (read depths), Position (Genomic position for the CpG site) and ID (sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.
n.k	a vector of basis dimensions for the intercept and individual covariates. n.k specifies an upper limit of the degrees of each functional parameters. The length of n.k should equal to the number of covariates plus 1 (for the intercept). We recommend basis dimensions n.k, approximately equal to the number of unique CpGs in the region divided by 20. This parameter will be computed automatically, when several regions are generated by the partitioning function.
p0	the probability of observing a methylated read when the underlying true status is unmethylated. p0 is the rate of false methylation calls, i.e. false positive rate.
p1	the probability of observing a methylated read when the underlying true status is methylated. 1-p1 is the rate of false non-methylation calls, i.e. false negative rate.
Quasi	whether a Quasi-likelihood estimation approach will be used; in other words, whether a multiplicative dispersion is added in the model or not.
epsilon	numeric; stopping criterion for the closeness of estimates of spline coefficients from two consecutive iterations.
epsilon.lambda	numeric; stopping criterion for the closeness of estimates of smoothing parameter lambda from two consecutive iterations.
maxStep	the algorithm will step if the iteration steps exceed maxStep.
binom.link	the link function used in the binomial regression model; the default is the logit link.
method	the method used to estimate the smoothing parameters. The default is the 'REML' method which is generally better than prediction based criterion GCV. cp.

covs	a vector of covariate names. The covariates with names in covs will be included in the model and their covariate effects will be estimated. The default is to fit all covariates in dat
RanEff	whether sample-level random effects are added or not
reml.scale	whether a REML-based scale (dispersion) estimator is used. The default is Fletcher-based estimator.
scale	negative values mean scale parameter should be estimated; if a positive value is provided, a fixed scale will be used.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

### Value

This function return a list including objects:

- `est`: estimates of the spline basis coefficients alpha
- `lambda`: estimates of the smoothing parameters for each functional parameters
- `est.pi`: predicted methylation levels for each row in the input data
- `ite.points`: estimates of `est`, `lambda` at each EM iteration
- `cov1`: estimated variance-covariance matrix of the basis coefficients alphas
- `reg.out`: regional testing output obtained using Fletcher-based dispersion estimate; an additional 'ID' row would appear if `RanEff` is TRUE
- `reg.out.reml.scale`: regional testing output obtained using REML-based dispersion estimate;
- `reg.out.gam`: regional testing output obtained using (Fletcher-based) dispersion estimate from `mgcv` package;
- `phi_fletcher`: Fletcher-based estimate of the (multiplicative) dispersion parameter;
- `phi_reml`: REML-based estimate of the (multiplicative) dispersion parameter;
- `phi_gam`: Estimated dispersion parameter reported by `mgcv`;
- `SE.out`: a matrix of the estimated pointwise Standard Errors (SE); number of rows are the number of unique CpG sites in the input data and the number of columns equal to the total number of covariates fitted in the model (the first one is the intercept);
- `SE.out.REML.scale`: a matrix of the estimated pointwise Standard Errors (SE); the SE calculated from the REML-based dispersion estimates
- `uni.pos`: the genomic positions for each row of CpG sites in the matrix `SE.out`;
- `Beta.out`: a matrix of the estimated covariate effects  $\beta(t)$ , where  $t$  denotes the genomic positions;
- `ncovs`: number of functional paramters in the model (including the intercept);
- `sigma00`: estimated variance for the random effect if `RanEff` is TRUE; NA if `RanEff` is FALSE.

### Author(s)

Kaiqiong Zhao

### See Also

[gam](#)

**Examples**

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
out <- binomRegMethModel(
  data=RAdat.f, n.k=rep(5,3), p0=0.003307034, p1=0.9,
  epsilon=10^(-6), epsilon.lambda=10^(-3), maxStep=200
)
```

---

binomRegMethModelPlot *Plot the smooth covariate effect*

---

**Description**

This function accepts an output object from function `binomRegMethModel` and print out a plot of the estimated effect across the region for each test covariate.

**Usage**

```
binomRegMethModelPlot(
  BEM.obj,
  mfrow = NULL,
  same.range = FALSE,
  title = "Smooth covariate effects",
  covs = NULL,
  save = NULL,
  verbose = TRUE
)
```

**Arguments**

<code>BEM.obj</code>	an output object from function <code>binomRegMethModel</code>
<code>mfrow</code>	A vector of the form <code>c(nr, nc)</code> . Subsequent figures will be drawn in an <code>nr</code> -by- <code>nc</code> array on the device.
<code>same.range</code>	specify whether the plots should be in the same vertical scale
<code>title</code>	the text for the title
<code>covs</code>	a vector of covariate names. The covariates with names in <code>covs</code> will be included in the plot. When the value is set to <code>NULL</code> all the covariates and the Intercept will be represented. The default value is <code>NULL</code> .
<code>save</code>	file name to create on disk. When the value is set to <code>NULL</code> , the plot is not saved. The default value is <code>NULL</code> .
<code>verbose</code>	logical indicates if the algorithm should provide progress report information. The default value is <code>TRUE</code> .

**Value**

This function prints out a plot of smooth covariate effects and its pointwise confidence intervals

**Author(s)**

Kaiqiong Zhao, Audrey Lemaçon

**Examples**

```
#-----#
data(RAdat)
head(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
out <- binomRegMethModel(
  data=RAdat.f, n.k=rep(5, 3), p0=0.003307034, p1=0.9,
  epsilon=10^(-6), epsilon.lambda=10^(-3), maxStep=200,
  Quasi = FALSE, RanEff = FALSE
)
binomRegMethModelPlot(out, same.range=FALSE)
```

---

binomRegMethModelPred *A smoothed-EM algorithm to estimate covariate effects and test regional association in Bisulfite Sequencing-derived methylation data*

---

**Description**

This function returns the predicted methylation levels

**Usage**

```
binomRegMethModelPred(
  BEM.obj,
  newdata = NULL,
  type = "proportion",
  verbose = TRUE
)
```

**Arguments**

BEM.obj	an output from the function binomRegMethModel
newdata	the data set whose predictions are calculated; with columns 'Position', covariate names matching the BEM.obj
type	return the predicted methylation proportion or the predicted response (in logit or other binom.link scale)
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

**Value**

This function returns the predicted methylation levels

**Author(s)**

Kaiqiong Zhao

**Examples**

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
out <- binomRegMethModel(
  data=RAdat.f, n.k=rep(5, 3), p0=0.003307034, p1=0.9,
  epsilon=10^(-6), epsilon.lambda=10^(-3), maxStep=200,
  Quasi = FALSE, RanEff = FALSE
)
binomRegMethModelPred(out)
```

---

binomRegMethModelSim *Simulate Bisulfite sequencing data from specified smooth covariate effects*

---

**Description**

Simulate Bisulfite sequencing data from a Generalized Additive Model with functional parameters varying with the genomic position. Both the true methylated counts and observed methylated counts are generated, given the error/conversion rate parameters  $p_0$  and  $p_1$ . In addition, the true methylated counts can be simulated from a binomial or a dispersed binomial distribution (Beta-binomial distribution).

**Usage**

```
binomRegMethModelSim(
  n,
  posit,
  theta.0,
  beta,
  phi,
  random.eff = FALSE,
  mu.e = 0,
  sigma.ee = 1,
  p0 = 0.003,
  p1 = 0.9,
  X,
  Z,
  binom.link = "logit",
  verbose = TRUE
)
```

**Arguments**

n	sample size
posit	a numeric vector of size p (the number of CpG sites in the considered region) containing the genomic positions;
theta.0	numeric vector of size p which is a functional parameter for the intercept of the GAMM model.
beta	numeric vector of size p which is a functional parameter for the slope of cell type composition.

phi	a vector of length p determining the multiplicative dispersion parameter for each loci in a region. The dispersed-Binomial counts are simulated from beta-binomial distribution, so each element of phi has to be greater than 1.
random.eff	indicates whether adding the subject-specific random effect term e.
mu.e	number, the mean of the random effect.
sigma.ee	positive number, variance of the random effect
p0	the probability of observing a methylated read when the underlying true status is unmethylated. p0 is the rate of false methylation calls, i.e. false positive rate.
p1	the probability of observing a methylated read when the underlying true status is methylated. 1-p1 is the rate of false non-methylation calls, i.e. false negative rate.
X	the matrix of the read coverage for each CpG in each sample; a matrix of n rows and p columns.
Z	numeric matrix with p columns and n rows storing the covariate information.
binom.link	the link function used for simulation
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

### Value

The function returns a list of following objects

- S a numeric matrix of n rows and p columns containing the true methylation counts;
- Y a numeric matrix of n rows and p columns containing the observed methylation counts;
- theta a numeric matrix of n rows and p columns containing the methylation parameter (after the logit transformation);
- pi a numeric matrix of n rows and p columns containing the true methylation proportions used to simulate the data.

### Author(s)

Kaiqiong Zhao

### Examples

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
out <- binomRegMethModel(
  data=RAdat.f, n.k=rep(5, 3), p0=0, p1=1,
  epsilon=10^(-6), epsilon.lambda=10^(-3), maxStep=200, RanEff = FALSE
)
Z = as.matrix(RAdat.f[match(unique(RAdat.f$ID), RAdat.f$ID),
c('T_cell', 'RA')])
set.seed(123)
X = matrix(sample(80, nrow(Z)*length(out$uni.pos), replace = TRUE),
nrow = nrow(Z), ncol = length(out$uni.pos))+10
simdat = binomRegMethModelSim(n=nrow(Z), posit= out$uni.pos,
theta.0=out$Beta.out[,1], beta= out$Beta.out[,-1], random.eff=FALSE,
mu.e=0,sigma.ee=1, p0=0.003, p1=0.9,X=X , Z=Z, binom.link='logit',
phi = rep(1, length(out$uni.pos)))
```



---

 binomRegMethPredPlot *Plot the predicted methylation levels*


---

### Description

This function accepts the `data.frame` used as an input for the function `binomRegMethModelPred` with additional columns containing the predictions generated by the function `binomRegMethModelPred` and columns containing the name of each experimental group and returns a plot representing the predicted methylation levels according to each experimental group.

### Usage

```
binomRegMethPredPlot(
  pred,
  pred.type = "proportion",
  pred.col = "pred",
  group.col = NULL,
  title = "Predicted methylation levels",
  style = NULL,
  save = NULL,
  verbose = TRUE
)
```

### Arguments

<code>pred</code>	<code>data.frame</code> used as an input for the function <code>binomRegMethModelPred</code> (with columns 'Position', covariate names matching the original output from the function <code>binomRegMethModel</code> ) with additional columns containing the predictions generated by the function <code>binomRegMethModelPred</code> and columns containing the name of each experimental group. Rows without a valid group name (empty character "" or NA) are ignored
<code>pred.type</code>	type of prediction returned by the function <code>binomRegMethModelPred</code> : <code>proportion</code> or <code>link.scale</code> . The default value is "proportion".
<code>pred.col</code>	character defines the name of the column containing the prediction values. The default value is "pred".
<code>group.col</code>	character defines the name of the column containing the experimental groups. If the <code>group.col</code> is set to <code>NULL</code> , the resulting plot will be a simple scatter plot representing all predicted values disregarding any experimental design. The default value is <code>NULL</code> .
<code>title</code>	the text for the title
<code>style</code>	named list containing the wanted style (color and line type) for each experimental groups. The first level list is named according each experimental group and for each experimental group there is a list containing the color and the type of the line. The line types should be among the following types: <ul style="list-style-type: none"> <li>• <code>twodash</code>,</li> <li>• <code>solid</code>,</li> <li>• <code>longdash</code>,</li> <li>• <code>dotted</code>,</li> <li>• <code>dotdash</code>,</li> </ul>

- dashed,
- blank.

The function accepts color name and its hexadecimal code. The default value is NULL meaning that the colors will be chosen randomly and the line style will be set to solid.

save	file name to create on disk. When the value is set to NULL, the plot is not saved. The default value is NULL.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

### Value

This function prints out a plot of the predicted methylation levels according to preset experimental groups.

### Author(s)

Audrey Lemaçon

### Examples

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
BEM.obj <- binomRegMethModel(
  data=RAdat.f, n.k=rep(5, 3), p0=0.003307034, p1=0.9,
  epsilon=10^(-6), epsilon.lambda=10^(-3), maxStep=200,
  Quasi = FALSE, RanEff = FALSE, verbose = FALSE
)
pos <- BEM.obj$uni.pos
newdata <- expand.grid(pos, c(0, 1), c(0, 1))
colnames(newdata) <- c("Position", "T_cell", "RA")
my.pred <- binomRegMethModelPred(BEM.obj, newdata, type = "link.scale",
  verbose = FALSE)
newdata$group <- ""
newdata[(newdata$RA == 0 & newdata$T_cell == 0),]$group <- "CTRL MONO"
newdata[(newdata$RA == 0 & newdata$T_cell == 1),]$group <- "CTRL TCELL"
newdata[(newdata$RA == 1 & newdata$T_cell == 0),]$group <- "RA MONO"
newdata[(newdata$RA == 1 & newdata$T_cell == 1),]$group <- "RA TCELL"
pred <- cbind(newdata, Pred = my.pred)
style <- list("CTRL MONO" = list(color = "blue", type = "dashed"),
  "CTRL TCELL" = list(color = "green", type = "dashed"),
  "RA MONO" = list(color = "blue", type = "solid"),
  "RA TCELL" = list(color = "green", type = "solid"))
g <- binomRegMethPredPlot(pred, pred.col = "Pred", group.col = "group",
  style = style, save = NULL, verbose = FALSE)
```

---

formatFromBismark	<i>Parsing output from the Bismark alignment suite</i>
-------------------	--

---

## Description

This function reads and converts Bismark's '[genome wide cytosine report](#)' and '[coverage](#)' into a list of `data.frames` (one per chromosome) to a format compatible with SOMNiBUS' main functions `runSOMNiBUS` and `binomRegMethModel`.

## Usage

```
formatFromBismark(..., verbose = TRUE)
```

## Arguments

...	parameters from <code>bsseq::read.bismark()</code> function
verbose	logical indicates the level of information provided by the algorithm during the process. The default value is TRUE.

## Value

This function returns a list of `data.frames` (one per chromosome). Each `data.frame` contains rows as individual CpGs appearing in all the samples. The first 4 columns contain the information of `Meth_Counts` (methylated counts), `Total_Counts` (read depths), `Position` (Genomic position for the CpG site) and `ID` (sample ID). The additional information (such as disease status, sex, age) extracted from the BSseq object are listed in column 5 and onwards and will be considered as covariate information by SOMNiBUS algorithms.

## Author(s)

Audrey Lemaçon

## See Also

[read.bismark](#) for parsing output from the Bismark alignment suite.

Other Parsing functions: [formatFromBSseq\(\)](#)

## Examples

```
infile <- system.file("extdata/test_data.fastq_bismark.bismark.cov.gz",  
package = "bsseq")  
dat <- formatFromBismark(infile, verbose = FALSE)
```

---

formatFromBSseq	<i>Parsing output from the BSseq package</i>
-----------------	--

---

## Description

This function reads and converts a BSseq object into a list of data.frames (one per chromosome) to a format compatible with SOMNiBUS' main functions runSOMNiBUS and binomRegMethModel.

## Usage

```
formatFromBSseq(bsseq_dat, verbose = TRUE)
```

## Arguments

bsseq_dat	an object of class BSseq.
verbose	logical indicates the level of information provided by the algorithm during the process. The default value is TRUE.

## Value

This function returns a list of data.frames (one per chromosome). Each data.frame contains rows as individual CpGs appearing in all the samples. The first 4 columns contain the information of Meth\_Counts (methylated counts), Total\_Counts (read depths), Position (Genomic position for the CpG site) and ID (sample ID). The additional information (such as disease status, sex, age) extracted from the BSseq object are listed in column 5 and onwards and will be considered as covariate information by SOMNiBUS algorithms.

## Author(s)

Audrey Lemaçon

## See Also

[BSseq](#) for the BSseq class.

Other Parsing functions: [formatFromBismark\(\)](#)

## Examples

```
M <- matrix(1:9, 3,3)
colnames(M) <- c("A1", "A2", "A3")
BStest <- bsseq::BSseq(pos = 1:3, chr = c("chr1", "chr2", "chr1"),
M = M, Cov = M + 2)
dat <- formatFromBSseq(BStest, verbose = FALSE)
```

---

RAdat

*A simulated methylation dataset based on a real data.*

---

### Description

A dataset containing methylation levels on one targeted region on chromosome 4 near gene BANK1 from cases with rheumatoid arthritis (RA) and controls.

### Usage

RAdat

### Format

A data frame of 5289 rows and 6 columns. Each row represents a CpG site for a sample. Columns include in order:

**Meth\_Counts** Number of methylated reads

**Total\_Counts** Total number of reads; read-depth

**Position** Genomic position (in bp) for the CpG site

**ID** indicates which sample the CpG site belongs to

**T\_cell** whether a sample is from T cell or monocyte

**RA** whether a sample is an RA patient or control

### Details

This example data include methylation levels of cell type separated blood samples of 22 rheumatoid arthritis (RA) patients and 21 healthy individuals. In the data set, 123 CpG sites are measured and there are 25 samples from circulating T cells and 18 samples from monocytes.

It should be noted that this data example is only for illustration purposes. The forward and reverse reads were not merged in this dataset. Try not to overinterpret the results of this simple example.

### Source

simulation is based a real data set provided by Dr. Marie Hudson (McGill University).

---

RAdat2

*A simulated methylation dataset based on a real data.*

---

### Description

This example data include methylation levels on a region with 208 CpGs for 116 blood samples.

### Usage

RAdat2

**Format**

A data frame of 6064 rows and 13 columns. Each row represents a CpG site for a sample. Columns include in order:

- Meth\_Counts** Number of methylated reads
- Total\_Counts** Total number of reads; read-depth
- Position** Genomic position (in bp) for the CpG site
- ID** indicates which sample the CpG site belongs to
- ACPA4** binary indicator for a biomarker anti-citrullinated protein antibody
- Age** Age
- Sex** 2-female; 1-male
- Smoking** 1-current or ex-smoker; 0-non-smoker
- Smoking\_NA** 1-Smoking info is NA; 0-Smoking info is available
- PC1** PC1 for the cell type proportions
- PC2** PC2 for the cell type proportions
- PC3** PC3 for the cell type proportions
- PC4** PC4 for the cell type proportions

**Source**

simulation is based a real data set provided by PI Dr. Sasha Bernatsky (McGill University)

---

runSOMNiBUS

*Wrapper function running the smoothed-EM algorithm to estimate covariate effects and test regional association in Bisulfite Sequencing-derived methylation data*

---

**Description**

This function splits the methylation data into regions (according to different approaches) and, for each region, fits a (dispersion-adjusted) binomial regression model to regional methylation data, and reports the estimated smooth covariate effects and regional p-values for the test of DMRs (differentially methylation regions). Over or under dispersion across loci is accounted for in the model by the combination of a multiplicative dispersion parameter (or scale parameter) and a sample-specific random effect.

This method can deal with outcomes, i.e. the number of methylated reads in a region, that are contaminated by known false methylation calling rate ( $p_0$ ) and false non-methylation calling rate ( $1-p_1$ ).

The covariate effects are assumed to smoothly vary across genomic regions. In order to estimate them, the algorithm first represents the functional parameters by a linear combination of a set of restricted cubic splines (with dimension  $n.k$ ), and a smoothness penalization term which depends on the smoothing parameters  $\lambda$  is also added to control smoothness. The estimation is performed by an iterated EM algorithm. Each M step constitutes an outer Newton's iteration to estimate smoothing parameters  $\lambda$  and an inner P-IRLS iteration to estimate spline coefficients  $\alpha$  for the covariate effects. Currently, the computation in the M step depends the implementation of `gam()` in package `mgcv`.

**Usage**

```
runSOMNiBUS(
  dat,
  split = list(approach = "region"),
  min.cpgs = 50,
  max.cpgs = 2000,
  n.k,
  p0 = 0.003,
  p1 = 0.9,
  Quasi = TRUE,
  epsilon = 10(-6),
  epsilon.lambda = 10(-3),
  maxStep = 200,
  binom.link = "logit",
  method = "REML",
  covs = NULL,
  RanEff = TRUE,
  reml.scale = FALSE,
  scale = -2,
  verbose = TRUE
)
```

**Arguments**

dat	a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth_Counts (methylated counts), Total_Counts (read depths), Position (Genomic position for the CpG site) and ID (sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.
split	<p>this list must contain at least the element approach which corresponds to the partitioning approach used to split the data into independent regions. The partitioning methods available are:</p> <ul style="list-style-type: none"> <li>• "region" (partitioning based on the spacing of CpGs),</li> <li>• "density" (partitioning based on CpG density),</li> <li>• "chromatin" (partitioning based on chromatin states),</li> <li>• "gene" (partitioning based on gene regions),</li> <li>• "granges" (partitioning based on user-specific annotations provided as a GenomicRanges object),</li> <li>• "bed" (partitioning based on user-specific annotations provided in a BED file).</li> </ul> <p>This list should also contain additional parameters specific to each partitioning approach (see the documentation of each approach for details).</p>
min.cpgs	positive integer defining the minimum number of CpGs within a region for the algorithm to perform optimally. The default value is 50.
max.cpgs	positive integer defining the maximum number of CpGs within a region for the algorithm to perform optimally. The default value is 2000.
n.k	a vector of basis dimensions for the intercept and individual covariates. n.k specifies an upper limit of the degrees of each functional parameters. The length of n.k should equal to the number of covariates plus 1 (for the intercept). We recommend basis dimensions n.k, approximately equal to the number of unique

	CpGs in the region divided by 20. This parameter will be computed automatically, when several regions are generated by the partitioning function.
<code>p0</code>	the probability of observing a methylated read when the underlying true status is unmethylated. <code>p0</code> is the rate of false methylation calls, i.e. false positive rate.
<code>p1</code>	the probability of observing a methylated read when the underlying true status is methylated. $1-p1$ is the rate of false non-methylation calls, i.e. false negative rate.
<code>Quasi</code>	whether a Quasi-likelihood estimation approach will be used; in other words, whether a multiplicative dispersion is added in the model or not.
<code>epsilon</code>	numeric; stopping criterion for the closeness of estimates of spline coefficients from two consecutive iterations.
<code>epsilon.lambda</code>	numeric; stopping criterion for the closeness of estimates of smoothing parameter <code>lambda</code> from two consecutive iterations.
<code>maxStep</code>	the algorithm will step if the iteration steps exceed <code>maxStep</code> .
<code>binom.link</code>	the link function used in the binomial regression model; the default is the logit link.
<code>method</code>	the method used to estimate the smoothing parameters. The default is the 'REML' method which is generally better than prediction based criterion <code>GCV.cp</code> .
<code>covs</code>	a vector of covariate names. The covariates with names in <code>covs</code> will be included in the model and their covariate effects will be estimated. The default is to fit all covariates in <code>dat</code>
<code>RanEff</code>	whether sample-level random effects are added or not
<code>reml.scale</code>	whether a REML-based scale (dispersion) estimator is used. The default is Fletcher-based estimator.
<code>scale</code>	negative values mean scale parameter should be estimated; if a positive value is provided, a fixed scale will be used.
<code>verbose</code>	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

## Value

This function returns a list of models (one by independent region) including objects:

- `est`: estimates of the spline basis coefficients `alpha`
- `lambda`: estimates of the smoothing parameters for each functional parameters
- `est.pi`: predicted methylation levels for each row in the input data
- `ite.points`: estimates of `est`, `lambda` at each EM iteration
- `cov1`: estimated variance-covariance matrix of the basis coefficients `alphas`
- `reg.out`: regional testing output obtained using Fletcher-based dispersion estimate; an additional 'ID' row would appear if `RanEff` is TRUE
- `reg.out.reml.scale`: regional testing output obtained using REML-based dispersion estimate;
- `reg.out.gam`: regional testing output obtained using (Fletcher-based) dispersion estimate from `mgcv` package;
- `phi_fletcher`: Fletcher-based estimate of the (multiplicative) dispersion parameter;
- `phi_reml`: REML-based estimate of the (multiplicative) dispersion parameter;



- `phi_gam`: Estimated dispersion parameter reported by `mgcv`;
- `SE.out`: a matrix of the estimated pointwise Standard Errors (SE); number of rows are the number of unique CpG sites in the input data and the number of columns equal to the total number of covariates fitted in the model (the first one is the intercept);
- `SE.out.REML.scale`: a matrix of the estimated pointwise Standard Errors (SE); the SE calculated from the REML-based dispersion estimates
- `uni.pos`: the genomic positions for each row of CpG sites in the matrix `SE.out`;
- `Beta.out`: a matrix of the estimated covariate effects  $\beta(t)$ , where  $t$  denotes the genomic positions;
- `ncovs`: number of functional parameters in the model (including the intercept);
- `sigma00`: estimated variance for the random effect if `RanEff` is TRUE; NA if `RanEff` is FALSE.

### Author(s)

Audrey Lemaçon

### Examples

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
outs <- runSOMNiBUS(
  dat=RAdat.f, split = list(approach = "region", gap = 1e6), min.cpgs = 5,
  n.k = rep(5,3), p0 = 0.003, p1 = 0.9
)
```

---

splitDataByBed

*Split methylation data into regions based on the genomic annotations*

---

### Description

This function splits the methylation data into regions based on the genomic annotation provided under the form of a 1-based BED file

### Usage

```
splitDataByBed(
  dat,
  chr,
  bed,
  gap = -1,
  min.cpgs = 50,
  max.cpgs = 2000,
  verbose = TRUE
)
```

**Arguments**

dat	a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth_Counts (methylated counts), Total_Counts (read depths), Position (Genomic position for the CpG site) and ID (sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.
chr	character vector containing the chromosome information. Its length should be equal to the number of rows in dat.
bed	character, path to the 1-based BED file containing the annotations
gap	integer defining the maximum gap that is allowed between two regions to be considered as overlapping. According to the GenomicRanges::findOverlaps function, the gap between 2 ranges is the number of positions that separate them. The gap between 2 adjacent ranges is 0. By convention when one range has its start or end strictly inside the other (i.e. non-disjoint ranges), the gap is considered to be -1. Decimal values will be rounded to the nearest integer. The default value is -1 (meaning strict overlapping).
min.cpgs	positive integer defining the minimum number of CpGs within a region for the algorithm to perform optimally. The default value is 50.
max.cpgs	positive integer defining the maximum number of CpGs within a region for the algorithm to perform optimally. The default value is 2000.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

**Value**

A named list of data.frame containing the data of each independent region.

**Author(s)**

Audrey Lemaçon

---

splitDataByChromatin *Split methylation data into regions based on the chromatin states*

---

**Description**

This function splits the methylation data into regions based on the chromatin states predicted by ChromHMM software (Ernst and Kellis (2012)). The annotations come from the Bioconductor package annotatr. Chromatin states determined by chromHMM are available in hg19 for nine cell lines (Gm12878, H1hesc, Hepg2, Hmec, Hsmm, Huvec, K562, Nhek, and Nhlf).

**Usage**

```
splitDataByChromatin(
  dat,
  chr,
  cell.line,
  states,
  gap = -1,
```

```

    min.cpgs = 50,
    max.cpgs = 2000,
    verbose = TRUE
)

```

### Arguments

dat	a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth_Counts (methylated counts), Total_Counts (read depths), Position (Genomic position for the CpG site) and ID(sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.
chr	character vector containing the chromosome information. Its length should be equal to the number of rows in dat.
cell.line	character defining the cell line of interest. Nine cell lines are available: <ul style="list-style-type: none"> <li>• "gm12878": Lymphoblastoid cells GM12878,</li> <li>• "h1hesc": Embryonic cells H1 hESC,</li> <li>• "hepg2": Liver carcinoma HepG2,</li> <li>• "hmec", Mammary epithelial cells HMEC,</li> <li>• "hsmm", Skeletal muscle myoblasts HSMM,</li> <li>• "huvec": Umbilical vein endothelial HUVEC,</li> <li>• "k562": Myelogenous leukemia K562,</li> <li>• "nhek": Keratinocytes NHEK,</li> <li>• "nh1f": Normal human lung fibroblasts NHLF.</li> </ul>
states	character vector defining the chromatin states of interest among the following available options: <ul style="list-style-type: none"> <li>• "ActivePromoter": Active Promoter</li> <li>• "WeakPromoter": Weak Promoter</li> <li>• "PoisedPromoter": Poised Promoter</li> <li>• "StrongEnhancer": Strong Enhancer</li> <li>• "WeakEnhancer": Weak/poised Enhancer</li> <li>• "Insulator": Insulator</li> <li>• "TxnTransition": Transcriptional Transition</li> <li>• "TxnElongation": Transcriptional Elongation</li> <li>• "WeakTxn": Weak Transcribed</li> <li>• "Repressed": Polycomb-Repressed</li> <li>• "Heterochrom": Heterochromatin; low signal</li> <li>• "RepetitiveCNV": Repetitive/Copy Number Variation Use state="all" to select all the states simultaneously.</li> </ul>
gap	this integer defines the maximum gap that is allowed between two regions to be considered as overlapping. According to the GenomicRanges::findOverlaps function, the gap between 2 ranges is the number of positions that separate them. The gap between 2 adjacent ranges is 0. By convention when one range has its start or end strictly inside the other (i.e. non-disjoint ranges), the gap is considered to be -1. Decimal values will be rounded to the nearest integer. The default value is -1.
min.cpgs	positive integer defining the minimum number of CpGs within a region for the algorithm to perform optimally. The default value is 50.

max.cpgs	positive integer defining the maximum number of CpGs within a region for the algorithm to perform optimally. The default value is 2000.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

**Value**

A list of data.frame containing the data of each independent region.

**Author(s)**

Audrey Lemaçon

**Examples**

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
results <- splitDataByChromatin(dat = RAdat.f,
cell.line = "huvec", chr = rep(x = "chr4", times = nrow(RAdat.f)),
states = "Insulator", verbose = FALSE)
```

---

splitDataByDensity      *Split methylation data into regions based on the density of CpGs*

---

**Description**

This function splits the methylation data into regions based on the density of CpGs.

**Usage**

```
splitDataByDensity(
  dat,
  window.size = 100,
  by = 1,
  min.density = 5,
  gap = 10,
  min.cpgs = 50,
  max.cpgs = 2000,
  verbose = TRUE
)
```

**Arguments**

dat                    a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth\_Counts (methylated counts), Total\_Counts (read depths), Position (Genomic position for the CpG site) and ID (sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.

window.size	this positive integer defines the size of the sliding window in bp. Decimal values will be rounded to the nearest integer. The value should be greater than 10. The default value is 100 (100 bp)
by	positive integer defines by how many base pairs the window moves at each increment. Decimal values will be rounded to the nearest integer. The default value is 1 (1 bp).
min.density	positive integer defines the minimum density threshold for each window. Decimal values will be rounded to the nearest integer. The default value is 5 (5 CpGs/window.size).
gap	positive integer defining the gap width beyond which we consider that two regions are independent. Decimal values will be rounded to the nearest integer. The default value is 10 (10bp).
min.cpgs	positive integer defining the minimum number of CpGs within a region for the algorithm to perform optimally. The default value is 50.
max.cpgs	positive integer defining the maximum number of CpGs within a region for the algorithm to perform optimally. The default value is 2000.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

**Value**

A named list of data.frame containing the data of each independent region.

**Author(s)**

Audrey Lemaçon

**Examples**

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
results <- splitDataByDensity(dat = RAdat.f, window.size = 100, by = 1,
min.density = 5, gap = 10, min.cpgs = 50, verbose = FALSE)
```

---

splitDataByGene

*Split methylation data into regions based on the genes annotations*


---

**Description**

This function splits the methylation data into regions based on the genes. The annotations are coming from the Bioconductor package annotatr.

**Usage**

```
splitDataByGene(
  dat,
  chr,
  organism = "human",
  build = "hg38",
```

```

types = "promoter",
gap = -1,
min.cpgs = 50,
max.cpgs = 2000,
verbose = TRUE
)

```

### Arguments

dat	a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth_Counts (methylated counts), Total_Counts (read depths), Position (Genomic position for the CpG site) and ID(sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.
chr	character vector containing the chromosome information. Its length should be equal to the number of rows in dat.
organism	character defining the organism of interest Only Homo sapiens ("human") is available. Additional packages are required for Mus musculus ("mouse"), Rattus norvegicus ("rat") and Drosophila melanogaster ("fly"). The matching is case-insensitive. The default value is "human".
build	character defining the version of the genome build on which the methylation data have been mapped. By default, the build is set to "hg38", however the build "hg19" is also available for Homo sapiens: Once the additional packages are installed, the following organisms and builds are available: <ul style="list-style-type: none"> <li>• "mm9" and "mm10" for Mus musculus;</li> <li>• "rn4", "rn5" and "rn6" for Rattus norvegicus;</li> <li>• "dm3" and "dm6" for Drosophila melanogaster;</li> </ul>
types	character vector defining the type of genic annotations to use among the following options: <ul style="list-style-type: none"> <li>• "upstream" for the annotations included 1-5Kb upstream of the TSS;</li> <li>• "promoter" for the annotations included &lt; 1Kb upstream of the TSS;</li> <li>• "threeprime" for the annotations included in 3' UTR;</li> <li>• "fiveprime" for the annotations included in the 5' UTR;</li> <li>• "exon" for the annotations included in the exons;</li> <li>• "intron" for the annotations included in the introns;</li> <li>• "all" for all the annotations aforementioned. The default value is "promoter".</li> </ul>
gap	this integer defines the maximum gap allowed between two regions to be considered as overlapping. According to the GenomicRanges::findOverlaps function, the gap between 2 ranges is the number of positions that separate them. The gap between 2 adjacent ranges is 0. By convention when one range has its start or end strictly inside the other (i.e. non-disjoint ranges), the gap is considered to be -1. Decimal values will be rounded to the nearest integer. The default value is -1.
min.cpgs	positive integer defining the minimum number of CpGs within a region for the algorithm to perform optimally. The default value is 50.
max.cpgs	positive integer defining the maximum number of CpGs within a region for the algorithm to perform optimally. The default value is 2000.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

**Value**

A named list of data.frame containing the data of each independent region.

**Author(s)**

Audrey Lemaçon

**Examples**

```
#-----#
data(RAdat)
# Add a column containing the chromosome information
RAdat$Chr <- "chr4"
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
results <- splitDataByGene(dat = RAdat.f,
chr = rep(x = "chr1", times = nrow(RAdat.f)), verbose = FALSE)
```

---

splitDataByGRanges      *Split methylation data into regions based on the genomic annotations*

---

**Description**

This function splits the methylation data into regions based on the genomic annotations provided under the form of a GenomicRanges object.

**Usage**

```
splitDataByGRanges(
  dat,
  chr,
  annots,
  gap = -1,
  min.cpgs = 50,
  max.cpgs = 2000,
  verbose = TRUE
)
```

**Arguments**

dat	a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth_Counts (methylated counts), Total_Counts (read depths), Position (Genomic position for the CpG site) and ID (sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.
chr	character vector containing the chromosome information. Its length should be equal to the number of rows in dat.
annots	GenomicRanges object containing the annotations

gap	integer defining the maximum gap that is allowed between two regions to be considered as overlapping. According to the <code>GenomicRanges::findOverlaps</code> function, the gap between 2 ranges is the number of positions that separate them. The gap between 2 adjacent ranges is 0. By convention when one range has its start or end strictly inside the other (i.e. non-disjoint ranges), the gap is considered to be -1. Decimal values will be rounded to the nearest integer. The default value is -1 (meaning strict overlapping).
min.cpgs	positive integer defining the minimum number of CpGs within a region for the algorithm to perform optimally. The default value is 50.
max.cpgs	positive integer defining the maximum number of CpGs within a region for the algorithm to perform optimally. The default value is 2000.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

**Value**

A named list of `data.frame` containing the data of each independent region.

**Author(s)**

Audrey Lemaçon

**Examples**

```
#-----#
data(RAdat)
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])
annot <- GenomicRanges::GRanges(seqnames = "chr1", IRanges::IRanges(
  start = c(102711720,102711844,102712006,102712503,102712702),
  end = c(102711757,102711909,102712195,102712637,102712712)
))
results <- splitDataByGRanges(dat = RAdat.f,
  chr = rep(x = "chr1", times = nrow(RAdat.f)),
  annots = annot, gap = -1, min.cpgs = 5)
```

---

splitDataByRegion

*Split methylation data into regions based on the spacing of CpGs*

---

**Description**

This function splits the methylation data into regions based on the spacing of CpGs.

**Usage**

```
splitDataByRegion(
  dat,
  gap = 1e+06,
  min.cpgs = 50,
  max.cpgs = 2000,
  verbose = TRUE
)
```



**Arguments**

dat	a data frame with rows as individual CpGs appearing in all the samples. The first 4 columns should contain the information of Meth_Counts (methylated counts), Total_Counts (read depths), Position (Genomic position for the CpG site) and ID (sample ID). The covariate information, such as disease status or cell type composition, are listed in column 5 and onwards.
gap	positive integer defining the gap width beyond which we consider that two regions are independent. Odd and decimal values will be rounded to the next even numbers (e.g. 8.2 and 8.7 become gaps of 8 and 10 respectively). The default value is 1e+6 (1Mb).
min.cpgs	positive integer defining the minimum number of CpGs within a region for the algorithm to perform optimally. The default value is 50.
max.cpgs	positive integer defining the maximum number of CpGs within a region for the algorithm to perform optimally. The default value is 2000.
verbose	logical indicates if the algorithm should provide progress report information. The default value is TRUE.

**Value**

A named list of data.frame containing the data of each independent region.

**Author(s)**

Audrey Lemaçon

**Examples**

```
#-----#  
data(RAdat)  
RAdat.f <- na.omit(RAdat[RAdat$Total_Counts != 0, ])  
results <- splitDataByRegion( dat=RAdat.f, gap = 1e6, min.cpgs = 5,  
verbose = FALSE)
```

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