

# Package ‘scmeth’

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**Type** Package

**Title** Functions to conduct quality control analysis in methylation data

**Version** 1.16.0

**Author** Divy Kangeyan <divyswar01@g.harvard.edu>

**Maintainer** Divy Kangeyan <divyswar01@g.harvard.edu>

**Depends** R (>= 3.5.0)

**Imports** knitr, rmarkdown, bsseq, AnnotationHub, GenomicRanges, reshape2, stats, utils, BSgenome, DelayedArray (>= 0.5.15), annotatr, SummarizedExperiment (>= 1.5.6), GenomeInfoDb, Biostrings, DT, HDF5Array (>= 1.7.5)

**Suggests** BSgenome.Mmusculus.UCSC.mm10, BSgenome.Hsapiens.NCBI.GRCh38, TxDb.Hsapiens.UCSC.hg38.knownGene, org.Hs.eg.db, Biobase, BiocGenerics, ggplot2, ggthemes

**Description** Functions to analyze methylation data can be found here.  
Some functions are relevant for single cell methylation data but most other functions can be used for any methylation data.  
Highlight of this workflow is the comprehensive quality control report.

**biocViews** DNAMethylation, QualityControl, Preprocessing, SingleCell, ImmunoOncology

**BugReports** <https://github.com/aryeelab/scmeth/issues>

**License** GPL-2

**LazyData** TRUE

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

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bsConversionPlot	<i>Bisulfite conversion rate visualization</i>
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### Description

Plot the bisulfite conversion rate for each sample based on the pheno data in the bs object

### Usage

```
bsConversionPlot(bs)
```

### Arguments

bs                    bsseq object

### Value

Plot showing bisulfite conversion rate for each sample

### Examples

```
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
bsConversionPlot(bs)
```

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chromosomeCoverage	<i>CpG coverage in each chromosome</i>
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**Description**

Provides Coverage metrics for each sample by the chromosome

**Usage**

```
chromosomeCoverage(bs)
```

**Arguments**

bs	bsseq object
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**Value**

matrix of chromosome coverage with column and rows indicating the samples and the chromosome respectively

**Examples**

```
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
chromosomeCoverage(bs)
```

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coverage	<i>Coverage for single cells</i>
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**Description**

Provides Coverage for each cell in a library pool

**Usage**

```
coverage(bs, subSample = 1e+06, offset = 50000)
```

**Arguments**

bs	bsseq object
subSample	number of CpGs to subsample. Default value is 1000000.
offset	how many CpGs to offset when subsampling Default value is set to be 50000, i.e. first 50000 CpGs will be ignored in subsampling.

**Value**

vector of coverage for the cells in bs object

**Examples**

```
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
coverage(bs)
```

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cpgDensity	<i>Provides Coverage by the CpG density. CpG Density is defined as the number of CpGs observed in certain base pair long region.</i>
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**Description**

Provides Coverage by the CpG density. CpG Density is defined as the number of CpGs observed in certain base pair long region.

**Usage**

```
cpgDensity(bs, organism, windowLength = 1000, small = FALSE)
```

**Arguments**

bs	bsseq object
organism	scientific name of the organism of interest, e.g. Mmusculus or Hsapiens
windowLength	Length of the window to calculate the density
small	Indicator for a small dataset, cpg density is calculated more memory efficiently for large dataset but for small dataset a different quicker method is used Default value for window length is 1000 basepairs.

**Value**

Data frame with sample name and coverage in repeat masker regions

**Examples**

```
library(BSgenome.Hsapiens.NCBI.GRCh38)
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
cpgDensity(bs, Hsapiens, 1000, small=TRUE)
```

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cpgDiscretization	<i>Discretize the CpG methylation values to align with single cell analysis</i>
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## Description

In single cell analysis overwhelmingly large number of CpGs have binary methylation. Due to errors in sequencing and amplification many CpGs tend to have non-binary methylation. Hence this function categorizes the non-binary CpGs as methylated if the methylation is above 0.8 and unmethylated if the methylation is below 0.2

## Usage

```
cpgDiscretization(bs, subSample = 1e+06, offset = 50000,  
  coverageVec = NULL)
```

## Arguments

bs	bsseq object
subSample	number of CpGs to subsample. Default value is 1000000.
offset	how many CpGs to offset when subsampling. Default value is set to be 50000, i.e. first 50000 CpGs will be ignored in subsampling.
coverageVec	If coverage vector is already calculated provide it to speed up the process

## Value

meth discretized methylation matrix  
discard total number of removed CpGs from each sample  
Percentage of CpGs discarded compared to the total number of CpGs

## Examples

```
directory <- system.file("extdata/bismark_data", package='scmeth')  
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)  
cpgDiscretization(bs)
```

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downsample                      *Downsample analysis*

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### Description

Downsample the CpG coverage matrix for saturation analysis

### Usage

```
downsample(bs, dsRates = c(0.01, 0.02, 0.05, seq(0.1, 0.9, 0.1)),
  subSample = 1e+06, offset = 50000)
```

### Arguments

bs	bsseq object
dsRates	downsampling rate. i.e. the probability of sampling a single CpG default is list of probabilities ranging from 0.01 to 1 0.01 0.02 0.05 0.10 0.20 0.30 0.40 0.50 0.60 0.70 0.80 0.90 For more continuous saturation curve dsRates can be changed to add more sampling rates
subSample	number of CpGs to subsample Default value is 1000000.
offset	how many CpGs to offset when subsampling Default value is set to be 50000, i.e. first 50000 CpGs will be ignored in subsampling.

### Value

Data frame with the CpG coverage for each sample at each sampling rate

### Examples

```
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
scmeth::downsample(bs)
```

---

featureCoverage                      *Coverage based on the genomic feature*

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### Description

Provides Coverage metrics for the sample by each genomic features provided by the user

### Usage

```
featureCoverage(bs, features, genomebuild)
```

**Arguments**

bs	bsseq object
features	list of genomic features, e.g. genes_exons, genes_introns, cpg_islands, cpg_shelves Names are based on the annotatr packages, so all the features provided by the annotatr package will be supported in this function
genomebuild	reference alignment, i.e. mm10 or hg38

**Value**

a data frame with genomic feature names and the number of CpG covered in each feature

**Examples**

```
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
featureCoverage(bs, c('cpg_islands', 'cpg_shores'), 'hg38')
```

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mbiasplot	<i>Methylation bias plot</i>
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**Description**

Plot the methylation at each position of the read to observe any biases in the methylation based on the read position

**Usage**

```
mbiasplot(dir = NULL, mbiasFiles = NULL)
```

**Arguments**

dir	directory name with mbias files
mbiasFiles	list of mbias files

**Value**

Returns a list containing the methylation across the read position in original top and original bottom strand both in forward and reverse reads for multiple samples

**Examples**

```
mbiasFile <- '2017-04-21_HG23KBCXY_2_AGGCAGAA_TATCTC_pe.M-bias.txt'
mbiasplot(mbiasFiles=system.file("extdata", mbiasFile, package='scmeth'))
```

methylationDist      *Provide graphics for methylation distribution*

---

**Description**

Plot the methylation distribution for the cells in bsseq object

**Usage**

```
methylationDist(bs)
```

**Arguments**

bs                    bsseq object

**Value**

mean methylation for each sample

**Examples**

```
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
methylationDist(bs)
```

---

readmetrics            *Provide graphics for read information*

---

**Description**

Plot the mapped and unmapped reads

**Usage**

```
readmetrics(bs)
```

**Arguments**

bs                    bsseq object

**Value**

Plot showing the mapped and unmapped read information for each cell

**Examples**

```
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
readmetrics(bs)
```



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repMask	<i>Provides Coverage metrics in the repeat masker region</i>
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**Description**

Provides Coverage metrics in the repeat masker region

**Usage**

```
repMask(bs, organism, genome)
```

**Arguments**

bs	bsseq object
organism	scientific name of the organism of interest, e.g. Mmusculus or Hsapiens
genome	reference alignment, i.e. mm10 or hg38

**Value**

Data frame with sample name and coverage in repeat masker regions

**Examples**

```
library(BSgenome.Mmusculus.UCSC.mm10)
library(AnnotationHub)
load(system.file("extdata", 'bsObject.rda', package='scmeth'))
repMask(bs, Mmusculus, 'mm10')
```

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report	<i>Generates an inclusive report on methylation analysis</i>
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**Description**

This function uses most of the functions in this package to generate a report for the user

**Usage**

```
report(bsObj, outdirectory, organism, genome, mbiasDir = NULL,
       subSample = 1e+06, offset = 50000, small = FALSE)
```

**Arguments**

bsObj	bsseq object
outdir	name of the output directory where the report will be saved
organism	scientific name of the organism of interest, e.g. Mmusculus or Hsapiens
genome	reference alignment, e.g. mm10 or hg38 the report will have graphics on read information
mbiasDir	Optional argument to provide directory name that has the mbias files or the list of mbias files
subSample	number of CpGs to subsample Default value is 1000000.
offset	how many CpGs to offset when subsampling Default value is set to be 50000, i.e. first 50000 CpGs will be ignored in subsampling.
small	Indicator for a small dataset, cpg density is calculated more

**Value**

Report will be an html file

**Examples**

```
library(BSgenome.Hsapiens.NCBI.GRCh38)
directory <- system.file("extdata/bismark_data", package='scmeth')
bs <- HDF5Array::loadHDF5SummarizedExperiment(directory)
mbiasDirectory=system.file("extdata", package='scmeth')
outdir <- system.file(package='scmeth')
report(bs, outDir, Hsapiens, 'hg38', mbiasDir=mbiasDirectory, small=TRUE)
```

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scmeth	<i>scmeth: a package to conduct quality control analysis for methylation data. Most functions can be applied to both bulk and single-cell methylation while other functions are specific to single-cell methylation data. scmeth is especially customized to use the output from the FireCloud implementation of methylation pipeline to produce comprehensive quality control report</i>
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**Description**

scmeth: a package to conduct quality control analysis for methylation data. Most functions can be applied to both bulk and single-cell methylation while other functions are specific to single-cell methylation data. scmeth is especially customized to use the output from the FireCloud implementation of methylation pipeline to produce comprehensive quality control report

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