Package 'RBedMethyl'

November 12, 2026

Type Package

Title Disk-backed Representation of ONT bedMethyl Files

Version 1.0.0

Description Bioconductor-native infrastructure for handling large nanoporetech modkit bedMethyl pileup files from ONT data using HDF5Array and DelayedArray.

URL https://github.com/CMG-UA/RBedMethyl

BugReports https://github.com/CMG-UA/RBedMethyl/issues

License GPL (>= 2)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

VignetteBuilder knitr

biocViews DNAMethylation, DifferentialMethylation, Epigenetics, Infrastructure, DataImport, Software

LazyData false

Imports methods, HDF5Array, rhdf5, DelayedArray, DelayedMatrixStats, SummarizedExperiment, bsseq, GenomicRanges, S4Vectors, IRanges, data.table

Suggests BiocStyle, knitr, rmarkdown, testthat

git_url https://git.bioconductor.org/packages/RBedMethyl

git_branch RELEASE_3_23

git_last_commit 08623bb

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

Author Vasileios Lemonidis [aut, cre, cph] (ORCID: <https://orcid.org/0000-0002-6446-3536>), Center for Oncological Research, University of Antwerp [cph, fnd], Stichting Tegen Kanker [fnd]

Maintainer Vasileios Lemonidis <vasileios.lemonidis@uantwerpen.be>

Contents

bedMethylFields . . . 2
beta,RBedMethyl,missing-method . . . 2
filterByCoverage . . . 3
RBedMethyl-class . . . 4
readBedMethyl . . . 4
subsetBy . . . 5
subsetByChromosomes . . . 6
subsetByRegion . . . 6
subsetByRegion,RBedMethyl,GRanges,missing,missing-method . . . 7
summarizeByRegion . . . 8
[,RBedMethyl,missing,missing,missing-method . . . 8

Index **10**

`bedMethylFields` *List retrievable bedMethyl fields*

Description

Returns a data.frame describing retrievable bedMethyl fields and their types.

Usage

```
bedMethylFields()
```

Value

A `data.frame` with columns `field`, `type`, and `description`.

Examples

```
bedMethylFields()
```

`beta,RBedMethyl,missing-method`
Per-site methylation fraction

Description

Compute per-site methylation fraction for an `RBedMethyl` object. Requires the `mod_reads` assay to be loaded.

Usage

```
## S4 method for signature 'RBedMethyl,missing'
beta(a, b)
```

Arguments

a	An RBedMethyl object.
b	Unused, kept for base::beta compatibility.

Value

Numeric vector of per-site methylation fractions.

---

filterByCoverage *Filter by coverage*

Description

Filter an RBedMethyl object by minimum coverage.

Usage

```
filterByCoverage(x, min_cov)
```

Arguments

x	An RBedMethyl object.
min_cov	Minimum coverage threshold.

Value

A filtered RBedMethyl object.

Examples

```
lines <- c(
  paste("chr1", 0, 1, "m", 0, "+", 0, 1, 0, 10, 0.5, 5, 5, 0, 0, 0, 0, 0, sep = "\t"),
  paste("chr1", 10, 11, "m", 0, "+", 10, 11, 0, 20, 0.25, 5, 15, 0, 0, 0, 0, 0, sep = "\t")
)
tmp <- tempfile(fileext = ".bed")
writeLines(lines, tmp)
bm <- readBedMethyl(tmp, mod = "m", fields = c("coverage", "pct", "mod_reads"))
bm2 <- filterByCoverage(bm, min_cov = 15)
length(RBedMethyl::beta(bm2))
```

RBedMethyl-class *RBedMethyl class*

Description

Disk-backed representation of nanoporetech modkit bedMethyl data from ONT sequencing.

Slots

`assays` A `SimpleList` of assay arrays.

`chrom_levels` Character vector of chromosome names.

`strand_levels` Character vector of strand levels.

`chr_index` Matrix of chromosome row ranges (start/end).

`index` Integer vector of active row indices.

`mod` Modification code.

readBedMethyl *Read an ONT modkit bedMethyl file*

Description

Create an `RBedMethyl` object backed by HDF5Array from a nanoporetech modkit bedMethyl file (headerless).

Usage

```
readBedMethyl(
  bedmethyl,
  mod = "m",
  chunk_size = 5e+06,
  h5file = NULL,
  check_sorted = TRUE,
  fields = c("coverage", "mod_reads")
)
```

Arguments

`bedmethyl`	Path to a nanoporetech modkit bedMethyl file (optionally gzipped).
`mod`	Modification code to retain (`"m"` or `"h"`).
`chunk_size`	Reserved for future use.
`h5file`	Path to the HDF5 file to create. Defaults to a deterministic path in `tempdir()` derived from the input `bedmethyl` filename, so subsequent calls reuse the same file.
`check_sorted`	Logical, check that records are sorted by chrom and chromStart.
`fields`	Character vector of numeric fields to load. Defaults to `c("coverage", "mod_reads")`.

Value

An RBedMethyl object.

Examples

```
lines <- c(
  paste("chr1", 0, 1, "m", 0, "+", 0, 1, 0, 10, 0.5, 5, 5, 0, 0, 0, 0, 0, sep = "\t"),
  paste("chr1", 10, 11, "m", 0, "+", 10, 11, 0, 20, 0.25, 5, 15, 0, 0, 0, 0, 0, sep = "\t")
)
tmp <- tempfile(fileext = ".bed")
writeLines(lines, tmp)
bm <- readBedMethyl(tmp, mod = "m", fields = c("coverage", "pct", "mod_reads"))
bm
```

---

subsetBy *Subset by assay predicate*

Description

Subset an RBedMethyl object using a predicate over an assay.

Usage

```
subsetBy(x, column, FUN)
```

Arguments

x	An RBedMethyl object.
column	Assay name to filter on (must be loaded).
FUN	Predicate function returning a logical vector.

Value

A filtered RBedMethyl object.

Examples

```
lines <- c(
  paste("chr1", 0, 1, "m", 0, "+", 0, 1, 0, 10, 0.5, 5, 5, 0, 0, 0, 0, 0, sep = "\t"),
  paste("chr1", 10, 11, "m", 0, "+", 10, 11, 0, 20, 0.25, 5, 15, 0, 0, 0, 0, 0, sep = "\t")
)
tmp <- tempfile(fileext = ".bed")
writeLines(lines, tmp)
bm <- readBedMethyl(tmp, mod = "m", fields = c("coverage", "pct", "mod_reads"))
bm2 <- subsetBy(bm, "coverage", function(v) v >= 15)
length(RBedMethyl::beta(bm2))
```

subsetByChromosomes *Subset by chromosomes*

Description

Subset an RBedMethyl object by one or more chromosomes.

Usage

```
subsetByChromosomes(x, chr)
```

Arguments

x	An RBedMethyl object.
chr	Character vector of chromosome names.

Value

A filtered RBedMethyl object.

Examples

```
lines <- c(
  paste("chr1", 0, 1, "m", 0, "+", 0, 1, 0, 10, 0.5, 5, 5, 0, 0, 0, 0, 0, sep = "\t"),
  paste("chr2", 10, 11, "m", 0, "+", 10, 11, 0, 20, 0.25, 5, 15, 0, 0, 0, 0, 0, sep = "\t")
)
tmp <- tempfile(fileext = ".bed")
writeLines(lines, tmp)
bm <- readBedMethyl(tmp, mod = "m", fields = c("coverage", "pct", "mod_reads"))
bm2 <- subsetByChromosomes(bm, c("chr1"))
length(RBedMethyl::beta(bm2))
```

subsetByRegion *Subset by region*

Description

Subset an RBedMethyl object by genomic interval.

Usage

```
subsetByRegion(x, chr, start, end)
```

Arguments

x	An RBedMethyl object.
chr	Chromosome name.
start	Region start (0-based, half-open).
end	Region end.

Value

A filtered RBedMethyl object.

Examples

```
lines <- c(
  paste("chr1", 0, 1, "m", 0, "+", 0, 1, 0, 10, 0.5, 5, 5, 0, 0, 0, 0, 0, sep = "\t"),
  paste("chr1", 10, 11, "m", 0, "+", 10, 11, 0, 20, 0.25, 5, 15, 0, 0, 0, 0, 0, sep = "\t")
)
tmp <- tempfile(fileext = ".bed")
writeLines(lines, tmp)
bm <- readBedMethyl(tmp, mod = "m", fields = c("coverage", "pct", "mod_reads"))
bm2 <- subsetByRegion(bm, "chr1", 0, 5)
length(RBedMethyl::beta(bm2))
```

---

subsetByRegion,RBedMethyl,GRanges,missing,missing-method

Subset by GRanges

Description

Subset an RBedMethyl object by overlaps with a GRanges.

Usage

```
## S4 method for signature 'RBedMethyl,GRanges,missing,missing'
subsetByRegion(x, chr, start, end)
```

Arguments

x	An RBedMethyl object.
chr	A GRanges object of regions.
start	Unused (for signature compatibility).
end	Unused (for signature compatibility).

Value

A filtered RBedMethyl object.

summarizeByRegion *Summarize by regions*

Description

Summarize methylation by a set of regions.

Usage

```
summarizeByRegion(x, regions)
```

Arguments

x	An RBedMethyl object.
regions	A GRanges of regions.

Value

A DataFrame with coverage, mod_reads, beta, and n_sites.

Examples

```
lines <- c(
  paste("chr1", 0, 1, "m", 0, "+", 0, 1, 0, 10, 0.5, 5, 5, 0, 0, 0, 0, 0, sep = "\t"),
  paste("chr1", 10, 11, "m", 0, "+", 10, 11, 0, 20, 0.25, 5, 15, 0, 0, 0, 0, 0, sep = "\t")
)
tmp <- tempfile(fileext = ".bed")
writeLines(lines, tmp)
bm <- readBedMethyl(tmp, mod = "m", fields = c("coverage", "pct", "mod_reads"))
regions <- GenomicRanges::GRanges(
  seqnames = "chr1",
  ranges = IRanges::IRanges(start = 1, end = 12)
)
summarizeByRegion(bm, regions)
```

[,RBedMethyl,missing,missing,missing-method *Subset rows*

Description

Subset an RBedMethyl object by integer, logical, or GRanges index.

Usage

```
## S4 method for signature 'RBedMethyl,missing,missing,missing'
x[i, j, ..., drop = TRUE]
```

Arguments

x	An RBedMethyl object.
i	Integer, logical, or GRanges index.
j	Unused.
...	Unused.
drop	Unused.

Value

A filtered RBedMethyl object.

Index

[,RBedMethyl,ANY,missing,missing-method
(,RBedMethyl,missing,missing,missing-method), 8
[,RBedMethyl,missing,missing,missing-method, 8
[,RBedMethyl-method
(,RBedMethyl,missing,missing,missing-method), 8

bedMethylFields, 2
beta,RBedMethyl,missing-method, 2
beta,RBedMethyl-method
(beta,RBedMethyl,missing-method), 2

filterByCoverage, 3
filterByCoverage,RBedMethyl-method
(filterByCoverage), 3

RBedMethyl-class, 4
readBedMethyl, 4

subsetBy, 5
subsetBy,RBedMethyl-method (subsetBy), 5
subsetByChromosomes, 6
subsetByChromosomes,RBedMethyl-method
(subsetByChromosomes), 6
subsetByRegion, 6
subsetByRegion,RBedMethyl,character,numeric,numeric-method
(subsetByRegion), 6
subsetByRegion,RBedMethyl,GRanges,missing,missing-method, 7
subsetByRegion,RBedMethyl,GRanges-method
(subsetByRegion,RBedMethyl,GRanges,missing,missing-method), 7
subsetByRegion,RBedMethyl-method
(subsetByRegion), 6
summarizeByRegion, 8
summarizeByRegion,RBedMethyl-method
(summarizeByRegion), 8