

Package: RBedMethyl (via r-universe)

October 11, 2026

Type Package

Title Disk-backed Representation of ONT bedMethyl Files

Version 1.1.2

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)

RxygenNote 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

Config/pak/sysreqs make libbz2-dev liblzma-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

Date/Publication 2026-10-01 12:11:33 UTC

RemoteUrl <https://github.com/bioc/RBedMethyl>

RemoteRef HEAD

RemoteSha 493883f6cf20b9520bbe00842b5e5628e9aaa71d

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[,RBedMethyl,missing,missing,missing-method
<i>Subset rows</i>

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.

bedMethylFields	<i>List retrievable bedMethyl fields</i>
-----------------	--

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
<i>Per-site methylation fraction</i>

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	<i>Filter by coverage</i>
------------------	---------------------------

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	<i>RBedMethyl class</i>
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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	<i>Read an ONT modkit bedMethyl file</i>
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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	<i>Subset by assay predicate</i>
----------	----------------------------------

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	<i>Subset by chromosomes</i>
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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	<i>Subset by region</i>
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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	<i>Summarize by regions</i>
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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)
```

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