

Package ‘RBedMethyl’

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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

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Suggests BiocStyle, knitr, rmarkdown, testthat

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

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	<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)
```

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

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