Package ‘cpp11bigwig’

December 11, 2025

Type Package

Title Read bigWig and bigBed Files

Version 0.1.3

Description Read bigWig and bigBed files using ``libBigWig'' <https://github.com/dpryan79/libBigWig>. Provides lightweight access to the binary bigWig and bigBed formats developed by the UCSC Genome Browser group.

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URL https://rnabioco.github.io/cpp11bigwig/, https://github.com/rnabioco/cpp11bigwig

BugReports https://github.com/rnabioco/cpp11bigwig/issues

Imports GenomicRanges, IRanges, tibble

Suggests testthat (>= 3.0.0)

LinkingTo cpp11

Config/Needs/website rnabioco/rbitemplate

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation yes

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Repository CRAN

Date/Publication 2025-12-11 06:10:39 UTC

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Description

Columns are automatically typed based on the autoSql schema embedded in the bigBed file. Integer types (`uint`, `int`) become R integers, floating point types (`float`, `double`) become R doubles, and all other types (including array types like `int[blockCount]`) remain as character strings.

Usage

```
read_bigbed(bbfile, chrom = NULL, start = NULL, end = NULL)
```

Arguments

`bbfile`	filename for bigBed file
`chrom`	read data for specific chromosome
`start`	start position for data
`end`	end position for data

Value

`tibble`

See Also

https://github.com/dpryan79/libBigWig

https://github.com/brentp/bw-python

Examples

```
bb <- system.file("extdata", "test.bb", package = "cpp11bigwig")

read_bigbed(bb)

read_bigbed(bb, chrom = "chr10")
```

`read_bigwig` *Read data from bigWig files.*

Description

Read data from bigWig files.

Usage

```
read_bigwig(bwfile, chrom = NULL, start = NULL, end = NULL, as = NULL)
```

Arguments

`bwfile`	filename for bigWig file
`chrom`	read data for specific chromosome
`start`	start position for data
`end`	end position for data
`as`	return data as a specific type. The default is a tibble (`tbl`) or GRanges (`gr`)

Value

`tibble`

See Also

https://github.com/dpryan79/libBigWig

https://github.com/brentp/bw-python

Examples

```
bw <- system.file("extdata", "test.bw", package = "cpp11bigwig")

read_bigwig(bw)

read_bigwig(bw, chrom = "10")

read_bigwig(bw, chrom = "1", start = 100, end = 130)

read_bigwig(bw, as = "GRanges")
```

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