

Package ‘cpp11bigwig’

May 8, 2026

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

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Contents

read_bigbed	2
read_bigwig	3

read_bigbed	<i>Read data from bigBed files.</i>
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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	<i>Read data from bigWig files.</i>
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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")
```

Index

`read_bigbed`, [2](#)
`read_bigwig`, [3](#)