# Package 'cpp11bigwig'

January 7, 2025

Type Package **Title** Read bigWig and bigBed Files Version 0.1.0 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. License MIT + file LICENSE 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 Author Jay Hesselberth [aut, cre], RNA Bioscience Initiative [fnd, cph], Devon Ryan [cph] Maintainer Jay Hesselberth < jay.hesselberth@gmail.com> **Repository** CRAN

Date/Publication 2025-01-07 14:50:02 UTC

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read\_bigbed Read data from bigBed files.

#### Description

Read data from bigBed files.

## Usage

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

# Arguments

bbfile	filename for bigBed file
chrom	read data for specific chromosome
start	start position for data
end	end position for data
convert	convert bigBed values to individual columns

# 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")</pre>
```

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read\_bigwig

## 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")</pre>
```

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