

# Package: cpp11bigwig (via r-universe)

January 8, 2025

**Type** Package

**Title** Read bigWig and bigBed Files

**Version** 0.1.0.9000

**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

**LazyData** TRUE

**RoxygenNote** 7.3.2

**Roxygen** list(markdown = TRUE)

**Config/pak/sysreqs** libssl-dev

**Repository** <https://rnabioco.r-universe.dev>

**RemoteUrl** <https://github.com/rnabioco/cpp11bigwig>

**RemoteRef** HEAD

**RemoteSha** 5a52aebef0f3f50798c9e862271f17a16ccd8932

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

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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")
```

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