Package: cpp11bigwig (via r-universe)

June 18, 2026

Type Package

Title Read bigWig and bigBed Files

Version 0.2.0

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.

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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, S4Vectors, tibble

Suggests testthat (>= 3.0.0)

LinkingTo cpp11

SystemRequirements libcurl (optional, for remote file access): libcurl-devel (rpm) or libcurl4-openssl-dev (deb)

Config/Needs/website rnabioco/rbitemplate

Config/testthat/edition 3

Encoding UTF-8

Config/roxygen2/version 8.0.0

NeedsCompilation yes

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Config/pak/sysreqs libssl-dev

Repository https://cran.r-universe.dev

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RemoteUrl https://github.com/cran/cpp11bigwig

RemoteRef HEAD

RemoteSha a1ef8b6f042885178facabfe0fe947f97156932e

Contents

`read_bigbed` *Read data from bigBed files.*

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`	path or URL for a bigBed file. Remote files (`http://`, `https://`, `ftp://`) are supported when the package was installed with libcurl available.
`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,
  fill = 0
)
```

Arguments

`bwfile`	path or URL for a bigWig file. Remote files (`http://`, `https://`, `ftp://`) are supported when the package was installed with libcurl available.
`chrom`	read data for specific chromosome
`start`	start position for data
`end`	end position for data
`as`	return data as a specific type. One of `"tbl"` (the default tibble), `"GRanges"`, or `"Rle"`. `"Rle"` returns a per-base run-length-encoded vector spanning the requested range (see Details).
`fill`	value used for bases with no data when `as = "Rle"`. Defaults to `0` (the convention for coverage); use `NA` to mark uncovered bases as missing. Ignored for other `as` values.

Details

When `as = "Rle"`, the result is an S4Vectors::Rle whose expanded length equals the queried range, i.e. `end - start` when both are supplied, otherwise the extent of the returned data for each chromosome. Bases with no data in the file are set to `fill`. bigWig coordinates are 0-based and half-open, so element `i` corresponds to genomic position `start + i - 1`. A single-chromosome query returns a bare `Rle`; a multi-chromosome query returns a named IRanges::RleList.

Value

A `tibble`, `GRanges`, or `Rle`/`RleList` depending on `as`.

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")

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

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