

Package: cpp11bigwig (via r-universe)

October 15, 2026

Type Package

Title Read bigWig and bigBed Files

Version 0.3.1.9000

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.

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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

LazyData TRUE

Roxygen list(markdown = TRUE)

Config/roxygen2/version 8.0.0

Config/pak/sysreqs libssl-dev

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

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bigbed_info	<i>Report header metadata for a bigBed file.</i>
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Description

Reads the bigBed header without loading any intervals. This is useful for identifying the BED variant a file holds before reading it: a genuine BED12 has defined_field_count == 12, whereas a bed9+3 file (9 standard BED columns plus 3 custom fields) has defined_field_count == 9 and field_count == 12.

Usage

bigbed_info(bbfile)

Arguments

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

Value

A named list with elements version, n_chroms, field_count, defined_field_count, n_bases_covered, and autosql (the embedded autoSql schema string, or "" when the file has none).

See Also

[read_bigbed\(\)](#), [bigwig_info\(\)](#)

Examples

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

info <- bigbed_info(bb)
info$defined_field_count
```

bigwig_info*Report header metadata and summary statistics for a bigWig file.*

Description

Reads the bigWig header without loading any intervals. The summary statistics (min, max, mean, std) are the file-level values stored in the header and computed over all covered bases.

Usage

```
bigwig_info(bwfile)
```

Arguments

bwfile path or URL for a bigWig file. Remote files (<http://>, <https://>, <ftp://>) are supported when the package was installed with libcurl available.

Value

A named list with elements version, n_levels, n_chroms, n_bases_covered, min, max, mean, and std.

See Also

[read_bigwig\(\)](#), [bigbed_info\(\)](#)

Examples

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

bigwig_info(bw)
```

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	chromosome(s) to read. Either a character vector of chromosome names, or a GenomicRanges::GRanges of query regions (in which case start/end are ignored). As with read_bigwig() , GRanges 1-based coordinates are converted to bigBed's 0-based half-open coordinates.
start	start position(s) for data. May be a vector describing several ranges, recycled against chrom/end.
end	end position(s) for data. May be a vector describing several ranges, recycled against chrom/start.

Details

When a bigBed file has no embedded autoSql schema (for example one produced by bedToBigBed without `-as`), columns are still recovered using the standard BED field names (`name`, `score`, `strand`, `thickStart`, `thickEnd`, `itemRgb`, `blockCount`, `blockSizes`, `blockStarts`) derived from the file's field counts. Any additional (`bedN+`) fields beyond the standard BED columns are returned as generic `fieldN` character columns. Because those names are inferred rather than declared by the file, a `message()` is emitted in this case; silence it with [base::suppressMessages\(\)](#).

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")

# query several chromosomes in one call
read_bigbed(bb, chrom = c("chr1", "chr10"))

# restrict each query to a window
read_bigbed(bb, chrom = c("chr1", "chr10"), start = c(0, 0), end = c(5e6, 5e6))

# pass a GRanges of regions; 1-based coords are converted automatically
gr <- GenomicRanges::GRanges(
  c("chr1", "chr10"),
  IRanges::IRanges(start = 1, width = 1e7)
)
```

```
read_bigbed(bb, chrom = gr)
```

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,
  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	chromosome(s) to read. Either a character vector of chromosome names, or a GenomicRanges::GRanges of query regions (in which case start/end are ignored; see Details).
start	start position(s) for data. May be a vector, recycled against chrom/end to describe several ranges.
end	end position(s) for data. May be a vector, recycled against chrom/start to describe several ranges.
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

Multiple ranges can be queried in one call by passing equal-length (or length-1, recycled) chrom, start, and end vectors, where range *i* is (chrom[*i*], start[*i*], end[*i*]). Alternatively, pass a [GenomicRanges::GRanges](#) as chrom; its regions are used directly. Because GRanges is 1-based and inclusive while bigWig is 0-based and half-open, a region is converted as start(gr) - 1 to end(gr).

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-range query returns a bare `Rle`; a multi-range (or multi-chromosome) query returns a named `IRanges::RleList` with one element per range.

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")

# query several ranges in one call with equal-length vectors
read_bigwig(bw, chrom = c("1", "10"), start = c(0, 0), end = c(50, 50))

# multiple windows on the same chromosome (chrom recycles)
read_bigwig(bw, chrom = "1", start = c(0, 100), end = c(50, 130))

# a multi-range "Rle" query returns a named RleList, one element per range
read_bigwig(bw, chrom = "1", start = c(0, 100), end = c(50, 130), as = "Rle")

# pass a GRanges of regions; 1-based coords are converted automatically
gr <- GenomicRanges::GRanges(
  c("1", "10"),
  IRanges::IRanges(start = c(1, 1), end = c(50, 50))
)
read_bigwig(bw, chrom = gr)
```

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