Package 'wig'

October 12, 2022

Type Package

Title Import WIG Data into R in Long Format

Version 0.1.0

Description Import WIG data into R in long format.

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URL <https://github.com/ramiromagno/wig>

BugReports <https://github.com/ramiromagno/wig/issues>

Encoding UTF-8

RoxygenNote 7.1.2

Imports dplyr, magrittr, stringr, tibble

Suggests spelling

Language en-US

NeedsCompilation no

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import_wig	*Imports a WIG file*

Description

import_wig reads a WIG (wiggle) file and expands the data into long format, i.e., the each observation in the returned tibble pertains the position of one single base.

Usage

```
import_wig(file_path, n = -1L)
```

Arguments

file_path	A path to a WIG file.
n	The (maximal) number of lines to read. Negative values indicate that one should read up to the end of input on the connection.

Value

A tibble of three variables: chr, chromosome; pos, genomic position; and val, value. Chromosome positions are 1-relative, i.e. the first base is 1, as specified in WIG files.

Examples

```
# Import a WIG file
wig_file <- system.file(
              "extdata",
              file = 'hg19-pik3ca.wig',
              package = "wig",
              mustWork = TRUE)

import_wig(wig_file)
```

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