

Package: wig (via r-universe)

September 3, 2024

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 7.2.1

Imports dplyr, magrittr, stringr, tibble

Suggests spelling

Language en-US

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

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

RemoteRef HEAD

RemoteSha 47d611b8f1d7e44af6bcf128e620667173715202

Contents

| | |
|------------------|----------|
| import_wig | 2 |
| Index | 3 |

| | |
|------------|---------------------------|
| import_wig | <i>Imports a WIG file</i> |
|------------|---------------------------|

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)
```

Index

`import_wig`, 2