

Package ‘feather’

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Title R Bindings to the Feather 'API'

Version 0.4.0

Description Read and write feather files, a lightweight binary columnar data store designed for maximum speed.

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URL <https://github.com/wesm/feather>

BugReports <https://github.com/wesm/feather/issues>

Imports arrow ($\geq 0.17.0$)

Suggests hms, testthat ($\geq 3.0.0$), tibble

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.3

NeedsCompilation yes

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Repository CRAN

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|---------|---|
| feather | <i>Access a feather store like a data frame</i> |
|---------|---|

Description

These functions permit using a feather dataset much like a regular (read-only) data frame without reading everything into R.

Usage

```
feather(path)

feather_metadata(path)
```

Arguments

| | |
|------|----------------------|
| path | Path to feather file |
|------|----------------------|

Details

They work by using `arrow::read_feather()` to read the data in as an Arrow Table, an efficient data structure that supports many data-frame methods. See the [Arrow package documentation](#) for more information.

Value

An `arrow::Table`

| | |
|--------------|--------------------------------------|
| read_feather | <i>Read and write feather files.</i> |
|--------------|--------------------------------------|

Description

Read and write feather files.

Usage

```
read_feather(path, columns = NULL, ...)

write_feather(x, path, version = 1, ...)
```

Arguments

| | |
|---------|--|
| path | Path to feather file |
| columns | Columns to read (names or indexes), or a tidy selection specification of columns, as used in <code>dplyr::select()</code> . Default: Read all columns. |
| ... | Additional arguments passed to the <code>arrow::</code> functions |
| x | A data frame to write to disk |
| version | integer in <code>c(1, 2)</code> indicating the Feather format version to write. For compatibility, the default for <code>feather::write_feather()</code> is 1. |

Value

Both functions return a tibble/data frame. `write_feather` invisibly returns `x` (so you can use this function in a pipeline).

Examples

```
mtcars2 <- read_feather(feather_example("mtcars.feather"))
mtcars2
```

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