

# Package: feather (via r-universe)

September 29, 2024

**Title** R Bindings to the Feather 'API'

**Version** 0.3.5.9000

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

**Encoding** UTF-8

**License** Apache License 2.0

**LazyData** true

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

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

**Imports** arrow (>= 0.17.0)

**Suggests** hms, testthat, tibble

**RoxygenNote** 7.1.0.9000

**Roxygen** list(markdown = TRUE)

**Repository** <https://wesm.r-universe.dev>

**RemoteUrl** <https://github.com/wesm/feather>

**RemoteRef** HEAD

**RemoteSha** 3635466429b5ef7910da606267d0a339cf1c9821

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feather	<i>Access a feather store like a data frame</i>
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### 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
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### 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`

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read_feather	<i>Read and write feather files.</i>
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### Description

Read and write feather files.

### Usage

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

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

**Arguments**

<code>path</code>	Path to feather file
<code>columns</code>	Columns to read (names or indexes), or a <a href="#">tidy selection specification</a> of columns, as used in <code>dplyr::select()</code> . Default: Read all columns.
<code>...</code>	Additional arguments passed to the <code>arrow::</code> functions
<code>x</code>	A data frame to write to disk
<code>version</code>	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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