

# Package ‘hdfqlr’

June 11, 2021

**Title** Interface to 'HDFq1' API

**Version** 0.6-2

**Description** Provides an interface to 'HDFq1' <<https://www.hdfq1.com/>> and helper functions for reading data from and writing data to 'HDF5' files. 'HDFq1' provides a high-level language for managing 'HDF5' data that is platform independent. For more information, see the reference manual <<https://www.hdfq1.com/resources/HDFq1ReferenceManual.pdf>>.

**Depends** R (>= 3.4)

**Imports** utils, methods

**Suggests** bit64 (>= 0.9), knitr (>= 1.22), ggplot2 (>= 3.2), microbenchmark (>= 1.4), testthat (>= 2.1.0), rmarkdown (>= 2.8)

**SystemRequirements** HDFq1 (>= 2.1.0)

**License** GPL (>= 3)

**Encoding** UTF-8

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-06-11 04:50:02 UTC

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hdfq1r	<i>hdfq1r: an HDF API based on HDFq1</i>
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### Description

This package provides an R interface to HDF files using the [HDFq1](#).

### Package options

hdfq1r uses the following [options\(\)](#) to configure behavior:

- `hdfq1r.dir`: The HDFq1 install directory.

Alternatively, the HDFq1 install directory can be saved to an environment variable `HDFQ1_DIR`.

### Author(s)

**Maintainer:** Michael Koohafkan <[michael.koohafkan@gmail.com](mailto:michael.koohafkan@gmail.com)>

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hql	<i>HDFq1 Wrapper Constants and Functions</i>
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### Description

Access the constants and functions provided by the HDFq1 wrapper. The wrapper contents are stored in an environment when the HDFq1 library is loaded and used internally by hdfq1r to perform operations.

### Usage

hql

### Format

An object of class environment of length 1.

### Details

This environment is exported so that users can directly use the HDFq1 wrapper functions. The intended method of use is to [attach\(\)](#) the environment to the search path. For more information on what is provided by the wrapper, consult the [HDFq1 reference manual](#).

**Examples**

```
## Not run:  
  attach(hql$wrapper)  
  
## End(Not run)
```

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hql_create	<i>Create HDF Files, Datasets or Attribute</i>
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**Description**

Create HDF files and groups.

**Usage**

```
hql_create_file(file, overwrite = FALSE, parallel = FALSE)  
  
hql_create_group(group, overwrite = FALSE)
```

**Arguments**

file	The HDF file to create.
overwrite	If TRUE, overwrite existing file, group, attribute, or dataset.
parallel	If TRUE, use parallel capabilities.
group	The group to create.

**Functions**

- hql\_create\_file: Create HDF file.
- hql\_create\_group: Create HDF group.

**Examples**

```
if(hql_is_loaded()) {  
  tf = tempfile(fileext = ".h5")  
  hql_create_file(tf)  
  
  hql_use_file(tf)  
  hql_create_group("group1")  
  
  hql_close_file(tf)  
}
```

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hql_drop	<i>Drop HDF groups, datasets, and attributes</i>
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**Description**

Drop a dataset, attribute, or group from an HDF file.

**Examples**

```
if(hql_is_loaded()){
  tf = tempfile(fileext = ".h5")
  hql_create_file(tf)

  hql_use_file(tf)
  x = rnorm(10)
  attr(x, "myattribute") = "some information"
  hql_write_dataset(x, "mygroup/mydataset")

  hql_drop_attribute("mygroup/mydataset/myattribute")
  hql_drop_dataset("mygroup/mydataset")
  hql_drop_group("mygroup")

  hql_close_file(tf)
}
```

---

hql_file	<i>Access HDF Files</i>
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**Description**

Open (use) and close HDF files.

**Usage**

```
hql_use_file(file)

hql_close_file(file, all = FALSE)
```

**Arguments**

file	The HDF file path.
all	If TRUE, close all open HDF files.

**Functions**

- hql\_use\_file: Open (use) an HDF file.
- hql\_close\_file: Close an HDF file.

**Examples**

```
if(hql_is_loaded()){
    tf = tempfile(fileext = ".h5")
    hql_create_file(tf)

    hql_use_file(tf)
    hql_flush()

    hql_close_file(tf)
}
```

---

hql_flush	<i>Flush HDF Files</i>
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**Description**

Flush HDF file(s) to write buffered data to the disk.

**Usage**

```
hql_flush(global = TRUE)
```

**Arguments**

global	If TRUE, a global flush is performed and all open HDF files are flushed. If FALSE, a local flush is performed and only the HDF file currently in use is flushed.
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hql_is_loaded	<i>HDFqL Library Status</i>
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**Description**

Check if the HDFqL library loaded.

**Usage**

```
hql_is_loaded()
```

**Value**

Logical TRUE if DLLs are found, FALSE otherwise.

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hql_list	<i>List HDF Groups, Datasets or Attributes</i>
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**Description**

List groups, datasets or attribute in an HDF file.

**Usage**

```
hql_list_groups(path, recursive = FALSE)
```

```
hql_list_datasets(path, recursive = FALSE)
```

```
hql_list_attributes(path)
```

**Arguments**

path	The location of the dataset, attribute, or group within the HDF file.
recursive	Recursively list child groups or datasets.

**Value**

A vector of paths.

**Functions**

- hql\_list\_groups: List groups.
- hql\_list\_datasets: List datasets.
- hql\_list\_attributes: List Attributes

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hql_load	<i>Load HDFql DLLs</i>
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**Description**

Load the HDFql library.

**Usage**

```
hql_load(path)
```

```
hql_unload()
```

**Arguments**

path	The path to the HDFql installation.
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**Functions**

- hql\_unload: Unload HDFqL Library.

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hql_write	<i>Write HDF Dataset or Attribute</i>
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**Description**

Write a dataset or attribute to an HDF file.

**Usage**

```
hql_write_dataset(
  dataset,
  path,
  include.attributes = TRUE,
  overwrite = FALSE,
  parallel = FALSE
)
```

```
hql_write_attribute(attribute, path, overwrite = FALSE, parallel = FALSE)
```

```
hql_write_all_attributes(attributes, path, overwrite = FALSE, parallel = FALSE)
```

**Arguments**

dataset	The dataset to write. The object must be coercible to an array.
path	The location within the HDF file to write the dataset or attribute(s).
include.attributes	If TRUE, write the dataset attributes.
overwrite	If TRUE, overwrite existing dataset or attribute.
parallel	Use parallel processing functionality.
attribute	The attribute to write.
attributes	A list of attributes to write.

**Functions**

- hql\_write\_dataset: Write a dataset to an HDF file.
- hql\_write\_attribute: Write an attribute to an HDF file.
- hql\_write\_all\_attributes: Write multiple attributes to an HDF file.

**Examples**

```
if(hql_is_loaded()){
  tf = tempfile(fileext = ".h5")
  hql_create_file(tf)

  hql_use_file(tf)
  x = matrix(rnorm(100), nrow = 20)
  hql_write_dataset(x, "dataset0")
  hql_write_attribute("normal", "dataset0/dist")

  y = month.name
  attr(y, "abbreviation") = month.abb
  hql_write_dataset(y, "group1/dataset1")

  hql_close_file(tf)
}
```



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