rhdf5 - HDF5 interface for R

Bernd Fischer

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Contents

1 Introduction

The package is an R interface for HDF5. On the one hand it implements *R* interfaces to many of the low level functions from the C interface. On the other hand it provides high level convenience functions on *R* level to make a usage of HDF5 files more easy.

2 Installation of the HDF5 package

To install the package *rhdf5*, you need a current version (>2.15.0) of *R* (www.r-project.org). After installing *R* you can run the following commands from the *R* command shell to install the bioconductor package *rhdf5*.

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("rhdf5")
```

3 High level R -HDF5 functions

3.1 Creating an HDF5 file and group hierarchy

An empty HDF5 file is created by

```
> library(rhdf5)
> h5createFile("myhdf5file.h5")
```

```
[1] TRUE
```

The HDF5 file can contain a group hierarchy. We create a number of groups and list the file content afterwards.

```
> h5createGroup("myhdf5file.h5","foo")
```

```
[1] TRUE
```

```
> h5createGroup("myhdf5file.h5","baa")
```

```
[1] TRUE
```

```
> h5createGroup("myhdf5file.h5","foo/foobaa")
```

```
[1] TRUE
```

```
> h5ls("myhdf5file.h5")
```

```
  group   name     otype dclass dim
0     /    baa H5I_GROUP
1     /    foo H5I_GROUP
2  /foo foobaa H5I_GROUP
```

3.2 Writing and reading objects

Objects can be written to the HDF5 file. Attributes attached to an object are written as well, if `write.attributes=TRUE` is given as argument to `h5write`. Note that not all *R*-attributes can be written as HDF5 attributes.

```
> A = matrix(1:10,nr=5,nc=2)
> h5write(A, "myhdf5file.h5","foo/A")
> B = array(seq(0.1,2.0,by=0.1),dim=c(5,2,2))
> attr(B, "scale") <- "liter"
> h5write(B, "myhdf5file.h5","foo/B")
> C = matrix(paste(LETTERS[1:10],LETTERS[11:20], collapse=""),
+   nr=2,nc=5)
> h5write(C, "myhdf5file.h5","foo/foobaa/C")
> df = data.frame(1L:5L,seq(0,1,length.out=5),
+   c("ab","cde","fghi","a","s"), stringsAsFactors=FALSE)
> h5write(df, "myhdf5file.h5","df")
> h5ls("myhdf5file.h5")
```

```
        group   name       otype   dclass       dim
0           /    baa   H5I_GROUP
1           /     df H5I_DATASET COMPOUND         5
2           /    foo   H5I_GROUP
3        /foo      A H5I_DATASET  INTEGER     5 x 2
4        /foo      B H5I_DATASET    FLOAT 5 x 2 x 2
5        /foo foobaa   H5I_GROUP
6 /foo/foobaa      C H5I_DATASET   STRING     2 x 5
```

```
> D = h5read("myhdf5file.h5","foo/A")
> E = h5read("myhdf5file.h5","foo/B")
> F = h5read("myhdf5file.h5","foo/foobaa/C")
> G = h5read("myhdf5file.h5","df")
```

If a dataset with the given `name` does not yet exist, a dataset is created in the HDF5 file and the object `obj` is written to the HDF5 file. If a dataset with the given `name` already exists and the datatype and the dimensions are the same

as for the object `obj`, the data in the file is overwritten. If the dataset already exists and either the datatype or the dimensions are different, `h5write` fails.

3.3 Writing and reading objects with file, group and dataset handles

File, group and dataset handles are a simpler way to read (and partially to write) HDF5 files. A file is opened by `H5Fopen`.

```
> h5f = H5Fopen("myhdf5file.h5")
> h5f
```

```
HDF5 FILE
        name /
    filename

  name       otype   dclass dim
0  baa H5I_GROUP
1   df  H5I_DATASET COMPOUND   5
2  foo H5I_GROUP
```

The `$` and `&` operators can be used to access the next group level. While the `$` operator reads the object from disk, the `&` operator returns a group or dataset handle.

```
> h5f$df
```

```
  X1L.5L seq.0..1..length.out...5. c..ab....cde....fghi....a....s..
1      1                      0.00                                ab
2      2                      0.25                               cde
3      3                      0.50                              fghi
4      4                      0.75                                 a
5      5                      1.00                                 s
```

```
> h5f&'df'
```

```
HDF5 DATASET
        name /df
    filename
        type HST_COMPOUND
        rank 1
        size 5
     maxsize 5
```

Both of the following code lines return the matrix `C`. *warning: However, while first version reads the whole tree `/foo` in memory and then subsets to `/foobaa/C`, the second version only reads the matrix `C`. The first "$" in "h5f$foo$foobaa$C" reads the dataset, the other "$" are accessors of a list. Remind that this can have severe consequences for large datasets and datastructures.*

```
> h5f$foo$foobaa$C
```

```
     [,1]                              [,2]
[1,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
[2,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
     [,3]                              [,4]
[1,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
[2,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
     [,5]
[1,] "A KB LC MD NE OF PG QH RI SJ T"
[2,] "A KB LC MD NE OF PG QH RI SJ T"
```

```
> h5f$"/foo/foobaa/C"
```

```
     [,1]                              [,2]
[1,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
```

```
[2,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
     [,3]                                [,4]
[1,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
[2,] "A KB LC MD NE OF PG QH RI SJ T" "A KB LC MD NE OF PG QH RI SJ T"
     [,5]
[1,] "A KB LC MD NE OF PG QH RI SJ T"
[2,] "A KB LC MD NE OF PG QH RI SJ T"
```

One can as well return a dataset handle for a matrix and then read the matrix in chunks for out-of-memory computations. *warning: Please read the next section on subsetting, chunking and compression for more details*.

```
> h5d = h5f&"/foo/B"
> h5d[]
```

```
, , 1

     [,1] [,2]
[1,]  0.1  0.6
[2,]  0.2  0.7
[3,]  0.3  0.8
[4,]  0.4  0.9
[5,]  0.5  1.0

, , 2

     [,1] [,2]
[1,]  1.1  1.6
[2,]  1.2  1.7
[3,]  1.3  1.8
[4,]  1.4  1.9
[5,]  1.5  2.0
```

```
> h5d[3,,]
```

```
     [,1] [,2]
[1,]  0.3  1.3
[2,]  0.8  1.8
```

The same works as well for writing to datasets. *warning: Remind that it is only guarenteed that the data is written on disk after a call to `H5Fflush` or after closing of the file.*

```
> h5d[3,,] = 1:4
> H5Fflush(h5f)
```

Remind again that in the following code the first version does not change the data on disk, but the second does.

```
> h5f$foo$B = 101:120
> h5f$"/foo/B" = 101:120
```

It is important to close all dataset, group, and file handles when not used anymore

```
> H5Dclose(h5d)
> H5Fclose(h5f)
```

or close all open HDF5 handles in the environment by

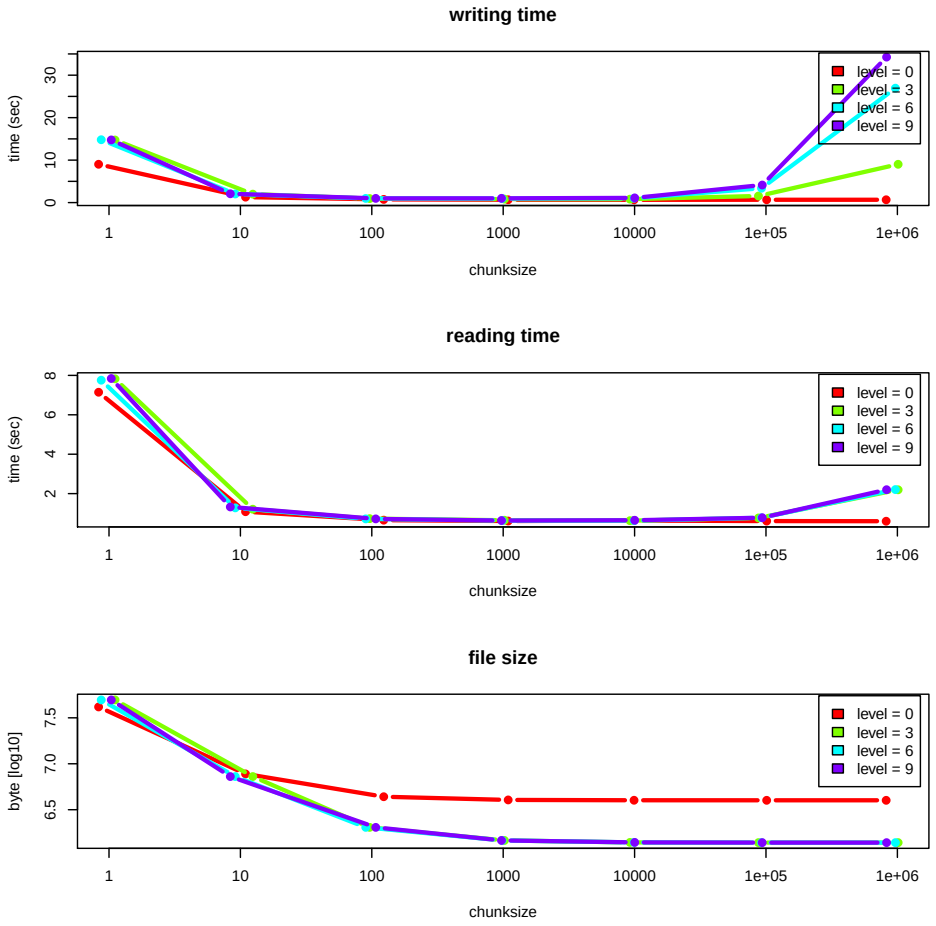
```
> H5close()
```

3.4 Writing and reading with subsetting, chunking and compression

The *rhdf5* package provides two ways of subsetting. One can specify the submatrix with the *R*-style index lists or with the HDF5 style hyperslabs. Note, that the two next examples below show two alternative ways for reading and writing the exact same submatrices. Before writing subsetting or hyperslabbing, the dataset with full dimensions has

to be created in the HDF5 file. This can be achieved by writing once an array with full dimensions as in Section 3.2 or by creating a dataset. Afterwards the dataset can be written sequentially.

Influence of chunk size and compression level The chosen chunk size and compression level have a strong impact on the reading and writing time as well as on the resulting file size. In an example an integer vector of size 10e7is written to an HDF5 file. The file is written in subvectors of size 10'000. The definition of the chunk size influences the reading as well as the writing time. In the chunk size is much smaller or much larger than actually used, the runtime performance decreases dramatically. Furthermore the file size is larger for smaller chunk sizes, because of an overhead. The compression can be much more efficient when the chunk size is very large. The following figure illustrates the runtime and file size behaviour as a function of the chunk size for a small toy dataset.



After the creation of the dataset, the data can be written sequentially to the HDF5 file. Subsetting in *R*-style needs the specification of the argument index to `h5read` and `h5write`.

```
> h5createDataset("myhdf5file.h5", "foo/S", c(5,8),
+                 storage.mode = "integer", chunk=c(5,1), level=7)
```

```
[1] TRUE
```

```
> h5write(matrix(1:5,nr=5,nc=1), file="myhdf5file.h5",
+         name="foo/S", index=list(NULL,1))
> h5read("myhdf5file.h5", "foo/S")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    0    0    0    0    0    0    0
[2,]    2    0    0    0    0    0    0    0
[3,]    3    0    0    0    0    0    0    0
[4,]    4    0    0    0    0    0    0    0
[5,]    5    0    0    0    0    0    0    0
```

```
> h5write(6:10, file="myhdf5file.h5",
+         name="foo/S", index=list(1,2:6))
> h5read("myhdf5file.h5", "foo/S")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6    7    8    9   10    0    0
[2,]    2    0    0    0    0    0    0    0
[3,]    3    0    0    0    0    0    0    0
[4,]    4    0    0    0    0    0    0    0
[5,]    5    0    0    0    0    0    0    0
```

```
> h5write(matrix(11:40,nr=5,nc=6), file="myhdf5file.h5",
+         name="foo/S", index=list(1:5,3:8))
> h5read("myhdf5file.h5", "foo/S")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6   11   16   21   26   31   36
[2,]    2    0   12   17   22   27   32   37
[3,]    3    0   13   18   23   28   33   38
[4,]    4    0   14   19   24   29   34   39
[5,]    5    0   15   20   25   30   35   40
```

```
> h5write(matrix(141:144,nr=2,nc=2), file="myhdf5file.h5",
+         name="foo/S", index=list(3:4,1:2))
> h5read("myhdf5file.h5", "foo/S")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6   11   16   21   26   31   36
[2,]    2    0   12   17   22   27   32   37
[3,]  141  143   13   18   23   28   33   38
[4,]  142  144   14   19   24   29   34   39
[5,]    5    0   15   20   25   30   35   40
```

```
> h5write(matrix(151:154,nr=2,nc=2), file="myhdf5file.h5",
+         name="foo/S", index=list(2:3,c(3,6)))
> h5read("myhdf5file.h5", "foo/S")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6   11   16   21   26   31   36
[2,]    2    0  151   17   22  153   32   37
[3,]  141  143  152   18   23  154   33   38
[4,]  142  144   14   19   24   29   34   39
[5,]    5    0   15   20   25   30   35   40
```

```
> h5read("myhdf5file.h5", "foo/S", index=list(2:3,2:3))
```

```
     [,1] [,2]
[1,]    0  151
[2,]  143  152
```

```
> h5read("myhdf5file.h5", "foo/S", index=list(2:3,c(2,4)))
```

```
     [,1] [,2]
[1,]    0   17
[2,]  143   18
```

```
> h5read("myhdf5file.h5", "foo/S", index=list(2:3,c(1,2,4,5)))
```

```
     [,1] [,2] [,3] [,4]
[1,]    2    0   17   22
[2,]  141  143   18   23
```

The HDF5 hyperslabs are defined by some of the arguments `start`, `stride`, `count`, and `block`. These arguments are not effective, if the argument `index` is specified.

```
> h5createDataset("myhdf5file.h5", "foo/H", c(5,8), storage.mode = "integer",
+                 chunk=c(5,1), level=7)
```

```
[1] TRUE
```

```
> h5write(matrix(1:5,nr=5,nc=1), file="myhdf5file.h5", name="foo/H",
+         start=c(1,1))
> h5read("myhdf5file.h5", "foo/H")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    0    0    0    0    0    0    0
[2,]    2    0    0    0    0    0    0    0
[3,]    3    0    0    0    0    0    0    0
[4,]    4    0    0    0    0    0    0    0
[5,]    5    0    0    0    0    0    0    0
```

```
> h5write(6:10, file="myhdf5file.h5", name="foo/H",
+         start=c(1,2), count=c(1,5))
> h5read("myhdf5file.h5", "foo/H")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6    7    8    9   10    0    0
[2,]    2    0    0    0    0    0    0    0
[3,]    3    0    0    0    0    0    0    0
[4,]    4    0    0    0    0    0    0    0
[5,]    5    0    0    0    0    0    0    0
```

```
> h5write(matrix(11:40,nr=5,nc=6), file="myhdf5file.h5", name="foo/H",
+         start=c(1,3))
> h5read("myhdf5file.h5", "foo/H")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6   11   16   21   26   31   36
[2,]    2    0   12   17   22   27   32   37
[3,]    3    0   13   18   23   28   33   38
[4,]    4    0   14   19   24   29   34   39
[5,]    5    0   15   20   25   30   35   40
```

```
> h5write(matrix(141:144,nr=2,nc=2), file="myhdf5file.h5", name="foo/H",
+         start=c(3,1))
> h5read("myhdf5file.h5", "foo/H")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6   11   16   21   26   31   36
[2,]    2    0   12   17   22   27   32   37
[3,]  141  143   13   18   23   28   33   38
[4,]  142  144   14   19   24   29   34   39
[5,]    5    0   15   20   25   30   35   40
```

```
> h5write(matrix(151:154,nr=2,nc=2), file="myhdf5file.h5", name="foo/H",
+         start=c(2,3), stride=c(1,3))
> h5read("myhdf5file.h5", "foo/H")
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
[1,]    1    6   11   16   21   26   31   36
[2,]    2    0  151   17   22  153   32   37
[3,]  141  143  152   18   23  154   33   38
[4,]  142  144   14   19   24   29   34   39
[5,]    5    0   15   20   25   30   35   40
```

```
> h5read("myhdf5file.h5", "foo/H",
+        start=c(2,2), count=c(2,2))
```

```
     [,1] [,2]
[1,]    0  151
```

```
[2,]  143  152
```

```
> h5read("myhdf5file.h5", "foo/H",
+        start=c(2,2), stride=c(1,2),count=c(2,2))
```

```
     [,1] [,2]
[1,]    0   17
[2,]  143   18
```

```
> h5read("myhdf5file.h5", "foo/H",
+        start=c(2,1), stride=c(1,3),count=c(2,2), block=c(1,2))
```

```
     [,1] [,2] [,3] [,4]
[1,]    2    0   17   22
[2,]  141  143   18   23
```

3.5 Saving multiple objects to an HDF5 file (h5save)

A number of objects can be written to the top level group of an HDF5 file with the function `h5save` (as analogo-nanalogous to the *R* function save).

```
> A = 1:7;  B = 1:18; D = seq(0,1,by=0.1)
> h5save(A, B, D, file="newfile2.h5")
> h5dump("newfile2.h5")
```

```
$A
[1] 1 2 3 4 5 6 7

$B
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18

$D
 [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

3.6 List the content of an HDF5 file

The function `h5ls` provides some ways of viewing the content of an HDF5 file.

```
> h5ls("myhdf5file.h5")
```

```
        group   name       otype   dclass       dim
0           /    baa   H5I_GROUP
1           /     df H5I_DATASET COMPOUND         5
2           /    foo   H5I_GROUP
3        /foo      A H5I_DATASET  INTEGER     5 x 2
4        /foo      B H5I_DATASET    FLOAT 5 x 2 x 2
5        /foo      H H5I_DATASET  INTEGER     5 x 8
6        /foo      S H5I_DATASET  INTEGER     5 x 8
7        /foo foobaa   H5I_GROUP
8 /foo/foobaa      C H5I_DATASET   STRING     2 x 5
```

```
> h5ls("myhdf5file.h5", all=TRUE)
```

```
        group   name         ltype corder_valid corder cset       otype num_attrs
0           /    baa H5L_TYPE_HARD        FALSE      0    0   H5I_GROUP         0
1           /     df H5L_TYPE_HARD        FALSE      0    0 H5I_DATASET         0
2           /    foo H5L_TYPE_HARD        FALSE      0    0   H5I_GROUP         0
3        /foo      A H5L_TYPE_HARD        FALSE      0    0 H5I_DATASET         0
4        /foo      B H5L_TYPE_HARD        FALSE      0    0 H5I_DATASET         0
5        /foo      H H5L_TYPE_HARD        FALSE      0    0 H5I_DATASET         0
6        /foo      S H5L_TYPE_HARD        FALSE      0    0 H5I_DATASET         0
```

```
7        /foo foobaa H5L_TYPE_HARD        FALSE      0    0   H5I_GROUP         0
8 /foo/foobaa      C H5L_TYPE_HARD        FALSE      0    0 H5I_DATASET         0
    dclass          dtype  stype rank       dim    maxdim
0                                  0
1 COMPOUND   HST_COMPOUND SIMPLE    1         5         5
2                                  0
3  INTEGER  H5T_STD_I32LE SIMPLE    2     5 x 2     5 x 2
4    FLOAT H5T_IEEE_F64LE SIMPLE    3 5 x 2 x 2 5 x 2 x 2
5  INTEGER  H5T_STD_I32LE SIMPLE    2     5 x 8     5 x 8
6  INTEGER  H5T_STD_I32LE SIMPLE    2     5 x 8     5 x 8
7                                  0
8   STRING     HST_STRING SIMPLE    2     2 x 5     2 x 5
```

```
> h5ls("myhdf5file.h5", recursive=2)
```

```
  group   name       otype   dclass       dim
0     /    baa   H5I_GROUP
1     /     df H5I_DATASET COMPOUND         5
2     /    foo   H5I_GROUP
3  /foo      A H5I_DATASET  INTEGER     5 x 2
4  /foo      B H5I_DATASET    FLOAT 5 x 2 x 2
5  /foo      H H5I_DATASET  INTEGER     5 x 8
6  /foo      S H5I_DATASET  INTEGER     5 x 8
7  /foo foobaa   H5I_GROUP
```

3.7 Dump the content of an HDF5 file

The function `h5dump` is similar to the function `h5ls`. If used with the argument `load=FALSE`, it produces the same result as `h5ls`, but with the group structure resolved as a hierarchy of lists. If the default argument `load=TRUE` is used all datasets from the HDF5 file are read.

```
> h5dump("myhdf5file.h5",load=FALSE)
```

```
$baa
NULL

$df
  group name       otype   dclass dim
1     /   df H5I_DATASET COMPOUND   5

$foo
$foo$A
  group name       otype  dclass   dim
1     /    A H5I_DATASET INTEGER 5 x 2

$foo$B
  group name       otype dclass       dim
1     /    B H5I_DATASET  FLOAT 5 x 2 x 2

$foo$H
  group name       otype  dclass   dim
1     /    H H5I_DATASET INTEGER 5 x 8

$foo$S
  group name       otype  dclass   dim
1     /    S H5I_DATASET INTEGER 5 x 8

$foo$foobaa
$foo$foobaa$C
```

```
  group name       otype dclass   dim
1     /    C H5I_DATASET STRING 2 x 5
```

```
> D <- h5dump("myhdf5file.h5")
```

3.8 Reading HDF5 files with external software

The content of the HDF5 file can be checked with the command line tool *h5dump* (available on linux-like systems with the HDF5 tools package installed) or with the graphical user interface *HDFView* (http://www.hdfgroup.org/hdf-java-html/hdfview/) available for all major platforms.

```
> system("h5dump myhdf5file.h5")
```

warning: Please note, that arrays appear as transposed matrices when opening it with a C-program (h5dump or HDFView). This is due to the fact the fastest changing dimension on C is the last one, but on R it is the first one (as in Fortran).

4 64-bit integers

R does not support a native datatype for 64-bit integers. All integers in *R* are 32-bit integers. When reading 64-bit integers from a HDF5-file, you may run into troubles. *rhdf5* is able to deal with 64-bit integers, but you still should pay attention.

As an example, we create an HDF5 file that contains 64-bit integers.

```
> x = h5createFile("newfile3.h5")
> D = array(1L:30L,dim=c(3,5,2))
> d = h5createDataset(file="newfile3.h5", dataset="D64", dims=c(3,5,2),H5type="H5T_NATIVE_INT64")
> h5write(D,file="newfile3.h5",name="D64")
```

There are three different ways of reading 64-bit integers in *R*. `H5Dread` and `h5read` have the argument `bit64conversion` the specify the conversion method.

By setting `bit64conversion='int'`, a coercing to 32-bit integers is enforced, with the risc of data loss, but with the insurance that numbers are represented as native integers.

```
> D64a = h5read(file="newfile3.h5",name="D64",bit64conversion="int")
> D64a
```

```
, , 1

              [,1]          [,2]          [,3]          [,4]          [,5]
[1,] 4.940656e-324 1.976263e-323 3.458460e-323 4.940656e-323 6.422853e-323
[2,] 9.881313e-324 2.470328e-323 3.952525e-323 5.434722e-323 6.916919e-323
[3,] 1.482197e-323 2.964394e-323 4.446591e-323 5.928788e-323 7.410985e-323

, , 2

              [,1]          [,2]          [,3]          [,4]          [,5]
[1,] 7.905050e-323 9.387247e-323 1.086944e-322 1.235164e-322 1.383384e-322
[2,] 8.399116e-323 9.881313e-323 1.136351e-322 1.284571e-322 1.432790e-322
[3,] 8.893182e-323 1.037538e-322 1.185758e-322 1.333977e-322 1.482197e-322

attr(,"class")
[1] "integer64"
```

```
> storage.mode(D64a)
```

```
[1] "double"
```

bit64conversion='double' coerces the 64-bit integers to floating point numbers. doubles can represent integers with up to 54-bits, but they are not represented as integer values anymore. For larger numbers there is still a data loss.

```
> D64b = h5read(file="newfile3.h5",name="D64",bit64conversion="double")
> D64b
```

```
, , 1

     [,1] [,2] [,3] [,4] [,5]
[1,]    1    4    7   10   13
[2,]    2    5    8   11   14
[3,]    3    6    9   12   15

, , 2

     [,1] [,2] [,3] [,4] [,5]
[1,]   16   19   22   25   28
[2,]   17   20   23   26   29
[3,]   18   21   24   27   30
```

```
> storage.mode(D64b)
```

```
[1] "double"
```

bit64conversion='bit64' is recommended way of coercing. It represents the 64-bit integers as objects of class *integer64* as defined in the package *bit64*. Make sure that you have installed *bit64*. *warning: The datatype integer64 is not part of base R, but defined in an external package. This can produce unexpected behaviour when working with the data.* When choosing this option the package *bit64* will be loaded.

```
> D64c = h5read(file="newfile3.h5",name="D64",bit64conversion="bit64")
> D64c
```

```
integer64
, , 1

     [,1] [,2] [,3] [,4] [,5]
[1,] 1    4    7    10   13
[2,] 2    5    8    11   14
[3,] 3    6    9    12   15

, , 2

     [,1] [,2] [,3] [,4] [,5]
[1,] 16   19   22   25   28
[2,] 17   20   23   26   29
[3,] 18   21   24   27   30
```

```
> class(D64c)
```

```
[1] "integer64"
```

4.1 Large integer data types

The following table gives an overview of the limits of the different integer representations in R and in HDF5.

value		R-datatype			HDF5 datatype			
		integer	double	integer64	I32	U32	I64	U64
2^{64}	18446744073709551616	-	-	-	-	-	-	-
$2^{64}-1$	18446744073709551615	-	-	-	-	-	-	+
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
2^{63}	9223372036854775808	-	-	-	-	-	-	+
$2^{63}-1$	9223372036854775807	-	-	+	-	-	+	+
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
2^{53}	9007199254740992	-	-	+	-	-	+	+
$2^{53}-1$	9007199254740991	-	+	+	-	-	+	+
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
2^{32}	4294967296	-	+	+	-	-	+	+
$2^{32}-1$	4294967295	-	+	+	-	+	+	+
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
2^{31}	2147483648	-	+	+	-	+	+	+
$2^{31}-1$	2147483647	+	+	+	+	+	+	+
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
2^{0}	1	+	+	+	+	+	+	+
0	0	+	+	+	+	+	+	+
-2^{0}	-1	+	+	+	+	-	+	-
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
$-2^{31}+1$	-2147483647	+	+	+	+	-	+	-
-2^{31}	-2147483648	NA	+	+	+	-	+	-
$-2^{31}-1$	-2147483649	-	+	+	-	-	+	-
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
$-2^{53}+1$	-9007199254740991	-	+	+	-	-	+	-
-2^{53}	-9007199254740992	-	-	+	-	-	+	-
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
$-2^{63}+1$	-9223372036854775807	-	-	+	-	-	+	-
-2^{63}	-9223372036854775808	-	-	NA	-	-	+	-
$-2^{63}-1$	-9223372036854775809	-	-	-	-	-	-	-

From the table it becomes obvious that some integer values in HDF5 files cannot be displayed in R. Note that this can happen for both 64-bit integer as well as for unsigned 32-bit integer. When generating an HDF5 file, it is recommended to use signed 32-bit integers.

5 Low level HDF5 functions

5.1 Creating an HDF5 file and a group hierarchy

Create a file.

```
> library(rhdf5)
> h5file = H5Fcreate("newfile.h5")
> h5file
```

```
HDF5 FILE
        name /
    filename

[1] name   otype  dclass dim
<0 rows> (or 0-length row.names)
```

and a group hierarchy

```
> h5group1 <- H5Gcreate(h5file, "foo")
> h5group2 <- H5Gcreate(h5file, "baa")
> h5group3 <- H5Gcreate(h5group1, "foobaa")
> h5group3
```

```
HDF5 GROUP
        name /foo/foobaa
    filename

[1] name   otype  dclass dim
<0 rows> (or 0-length row.names)
```

5.2 Writing data to an HDF5 file

Create 4 different simple and scalar data spaces. The data space sets the dimensions for the datasets.

```
> d = c(5,7)
> h5space1 = H5Screate_simple(d,d)
> h5space2 = H5Screate_simple(d,NULL)
> h5space3 = H5Scopy(h5space1)
> h5space4 = H5Screate("H5S_SCALAR")
> h5space1
```

```
HDF5 DATASPACE
        rank 2
        size 5 x 7
     maxsize 5 x 7
```

```
> H5Sis_simple(h5space1)
```

```
[1] TRUE
```

Create two datasets, one with integer and one with floating point numbers.

```
> h5dataset1 = H5Dcreate( h5file, "dataset1", "H5T_IEEE_F32LE", h5space1 )
> h5dataset2 = H5Dcreate( h5group2, "dataset2", "H5T_STD_I32LE", h5space1 )
> h5dataset1
```

```
HDF5 DATASET
        name /dataset1
    filename
        type H5T_IEEE_F32LE
        rank 2
        size 5 x 7
     maxsize 5 x 7
```

Now lets write data to the datasets.

```
> A = seq(0.1,3.5,length.out=5*7)
> H5Dwrite(h5dataset1, A)
> B = 1:35
> H5Dwrite(h5dataset2, B)
```

To release resources and to ensure that the data is written on disk, we have to close datasets, dataspaces, and the file. There are different functions to close datasets, dataspaces, groups, and files.

```
> H5Dclose(h5dataset1)
> H5Dclose(h5dataset2)
> H5Sclose(h5space1)
> H5Sclose(h5space2)
> H5Sclose(h5space3)
> H5Sclose(h5space4)
> H5Gclose(h5group1)
> H5Gclose(h5group2)
> H5Gclose(h5group3)
> H5Fclose(h5file)
```

6 Session Info

```
> toLatex(sessionInfo())
```

- R Under development (unstable) (2017-02-13 r72168), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 16.04.2 LTS
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: bit 1.1-12, bit64 0.9-5, rhdf5 2.19.1
- Loaded via a namespace (and not attached): BiocStyle 2.3.31, Rcpp 0.12.9, backports 1.0.5, compiler 3.4.0, digest 0.6.12, evaluate 0.10, htmltools 0.3.5, knitr 1.15.1, magrittr 1.5, rmarkdown 1.3, rprojroot 1.2, stringi 1.1.2, stringr 1.2.0, tools 3.4.0, yaml 2.1.14, zlibbioc 1.21.0