

rhdf5

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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")

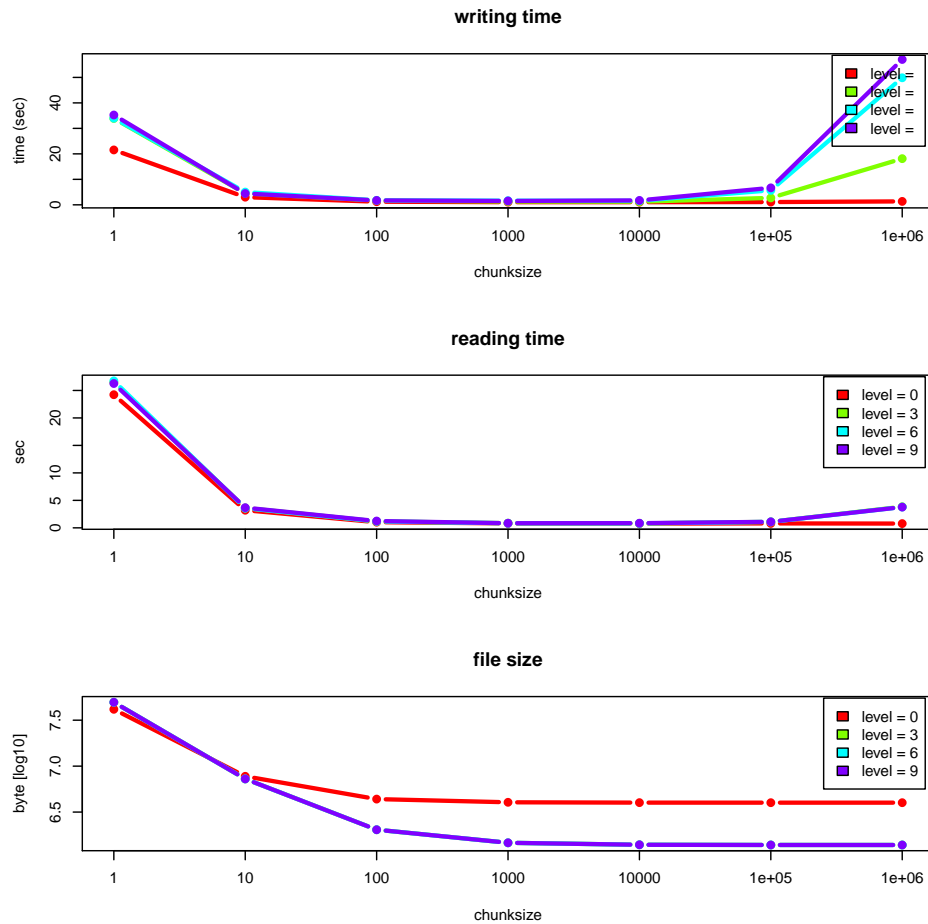
```

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 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 10^7 is written to an hdf5 file. The file is written in subvectors of size 10^4 . 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

```

3.4 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 analogous 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

```

3.5 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
0        /    baa H5L_TYPE_HARD      FALSE      0      0  H5I_GROUP
1        /     df H5L_TYPE_HARD      FALSE      0      0 H5I_DATASET

```

2	/	foo	H5L_TYPE_HARD	FALSE	0	0	H5I_GROUP
3	/foo	A	H5L_TYPE_HARD	FALSE	0	0	H5I_DATASET
4	/foo	B	H5L_TYPE_HARD	FALSE	0	0	H5I_DATASET
5	/foo	H	H5L_TYPE_HARD	FALSE	0	0	H5I_DATASET
6	/foo	S	H5L_TYPE_HARD	FALSE	0	0	H5I_DATASET
7	/foo	foobaa	H5L_TYPE_HARD	FALSE	0	0	H5I_GROUP
8	/foo/foobaa	C	H5L_TYPE_HARD	FALSE	0	0	H5I_DATASET
	num_attrs	dclass	dtype	stype	rank	dim	maxdim
0	0				0		
1	0	COMPOUND	HST_COMPOUND	SIMPLE	1	5	5
2	0				0		
3	0	INTEGER	H5T_STD_I32LE	SIMPLE	2	5 x 2	5 x 2
4	0	FLOAT	H5T_IEEE_F64LE	SIMPLE	3	5 x 2 x 2	5 x 2 x 2
5	0	INTEGER	H5T_STD_I32LE	SIMPLE	2	5 x 8	5 x 8
6	0	INTEGER	H5T_STD_I32LE	SIMPLE	2	5 x 8	5 x 8
7	0				0		
8	0	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		

3.6 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")

```

3.7 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")

```

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 Low level HDF5 functions

4.1 Creating an HDF5 file and a group hierarchy

Create a file.

```

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

```

HDF5 FILE

```

      name /
      filename

```

and a group hierarchy

```

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

```

HDF5 GROUP

```

      name /foo/foobaa
      filename

```

4.2 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 7 x 5
      maxsize 7 x 5

> 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 7 x 5
      maxsize 7 x 5
```

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, dataspace, and the file. There are different functions to close datasets, dataspace, groups, and files.

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

5 Session Info

```
> sessionInfo()
```

```
R version 2.15.0 (2012-03-30)
Platform: i386-apple-darwin9.8.0/i386 (32-bit)
```

```
locale:
[1] C
```

```
attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

```
other attached packages:
```

```
[1] rhdf5_2.0.2
```

```
loaded via a namespace (and not attached):
```

```
[1] tools_2.15.0  zlibbioc_1.2.0
```