



# Reading HDF5

Jeffrey Leek  
Johns Hopkins Bloomberg School of Public Health

# HDF5

- Used for storing large data sets
- Supports storing a range of data types
- Hierarchical data format
- *groups* containing zero or more data sets and metadata
  - Have a *group header* with group name and list of attributes
  - Have a *group symbol table* with a list of objects in group
- *datasets* multidimensional array of data elements with metadata
  - Have a *header* with name, datatype, dataspace, and storage layout
  - Have a *data array* with the data

<http://www.hdfgroup.org/>

# R HDF5 package

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

```
library(rhdf5)
created = h5createFile("example.h5")
created
```

```
[1] TRUE
```

- This will install packages from Bioconductor <http://bioconductor.org/>, primarily used for genomics but also has good "big data" packages
- Can be used to interface with hdf5 data sets.
- This lecture is modeled very closely on the rhdf5 tutorial that can be found here <http://www.bioconductor.org/packages/release/bioc/vignettes/rhdf5/inst/doc/rhdf5.pdf>

# Create groups

```
created = h5createGroup("example.h5", "foo")
created = h5createGroup("example.h5", "baa")
created = h5createGroup("example.h5", "foo/foobaa")
h5ls("example.h5")
```

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

# Write to groups

```
A = matrix(1:10,nr=5,nc=2)
h5write(A, "example.h5","foo/A")
B = array(seq(0.1,2.0,by=0.1),dim=c(5,2,2))
attr(B, "scale") <- "liter"
h5write(B, "example.h5","foo/foobaa/B")
h5ls("example.h5")
```

	group	name	otype	dclass	dim
0	/	baa	H5I_GROUP		
1	/	foo	H5I_GROUP		
2	/foo	A	H5I_DATASET	INTEGER	5 x 2
3	/foo	foobaa	H5I_GROUP		
4	/foo/foobaa	B	H5I_DATASET	FLOAT	5 x 2 x 2

# Write a data set

```
df = data.frame(1L:5L, seq(0,1,length.out=5),
  c("ab", "cde", "fghi", "a", "s"), stringsAsFactors=FALSE)
h5write(df, "example.h5", "df")
h5ls("example.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	foobaa	H5I_GROUP		
5	/foo/foobaa	B	H5I_DATASET	FLOAT	5 x 2 x 2

# Reading data

```
readA = h5read("example.h5", "foo/A")
readB = h5read("example.h5", "foo/foobaa/B")
readdf= h5read("example.h5", "df")
readA
```

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

# Writing and reading chunks

```
h5write(c(12,13,14),"example.h5","foo/A",index=list(1:3,1))  
h5read("example.h5","foo/A")
```

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



## Notes and further resources

- hdf5 can be used to optimize reading/writing from disc in R
- The rhdf5 tutorial:
  - <http://www.bioconductor.org/packages/release/bioc/vignettes/rhdf5/inst/doc/rhdf5.pdf>
- The HDF group has informaton on HDF5 in general <http://www.hdfgroup.org/HDF5/>