

# Self-Study Exercises

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## 1 Introduction

The genotype information for the GWAS study is provided to you in a comma separated file `snpData.csv`. This data has been converted to NetCDF based storage (with byte precision) and stored as a file `snpData.nc`. These files are available in the `extdata` folder of the *AdvancedR2011Data* package.

The exercises that are included in this document are intended to

- Introduce the snp data and explore some of the options in *R* to read data from the `snpData.csv` file.
- Get familiar with the application programming interface provided by the *ncdf* package for accessing NetCDF files and create a script to retrieve horizontal slices of the data from the NetCDF file `snpData.nc`.
- Create a more useful function `getGWAScols` that access vertical slices of data (snps for all samples) from the NetCDF file. This function will be added to the *StudentGWAS* package that is being developed as this course progresses. The function should be general enough to work with NetCDF files of different sizes.
- Create a unit test to verify that the `getGWAScols` function produces the correct output.

### Exercise 1

*The goal of this exercise is to explore some of the functionality available in R to read large text files in an efficient manner by reading in smaller chunks at a time.*

- *The snp data is available as a comma separated file `snpData.csv` located in the `extdata` folder of the *AdvancedR2011Data* package. Make use of the function `system.file` to get a path to the `snpData.csv` file.*
- *Use the function `scan` to read in only the 601th row from the `snpData.csv` file.*

### Solution:

```
> library(AdvancedR2011Data)
> pth <- system.file("extdata", "snpData.csv", package = "AdvancedR2011Data")
> dat <- scan(pth, what = character(0), sep = ",",
+           skip = 600, nlines = 1, quiet = TRUE)
```

### Exercise 2

The goal of this exercise is to create a script to read in all the snps for sample 601 from the NetCDF file `snpData.nc` and verify that the values read from the NetCDF file match those in the file `snpData.csv`. Both files are provided in the `extdata` folder of the `AdvancedR2011Data` package and can be located using the `system.file` function. The `snpData.nc` file contains genotype information for 1000 samples(rows), 113735 snps(columns) per sample.

- Use the function `open.ncdf` to open the NetCDF file `snpData.nc`.
- Use the function `get.var.ncdf` to read in the data for all snps for the sample 601 in the file `snpData.nc`
- Use the `scan` function to read in the snp data for sample 601 from the `snpData.csv` file and compare its performance with that using the `get.var.ncdf` function for the `snpData.nc` file. The `system.time` function can be used to compare the performance of the two functions.
- Check if the results are identical using the `identical` function in R.
- Finally close the NetCDF file using `close.ncdf`

### Solution:

```
> library(ncdf)
> st <- system.time
> ncFile <- system.file("extdata", "snpData.nc", package = "AdvancedR2011Data")
> nc <- open.ncdf(ncFile, write = FALSE)
> st(dat <- get.var.ncdf(nc, varid = "snpData", start= c(601,1), count = c(1, 113735)))

  user  system elapsed
 0.02   0.09   1.02

> csvFile <- system.file("extdata", "snpData.csv", package = "AdvancedR2011Data")
> st(origDat <- scan(csvFile, what = integer(0), sep = ",", skip = 600, nlines = 1,
+   quiet = TRUE))

  user  system elapsed
11.73   0.06  11.81

> identical(as.vector(dat), origDat)
```

```
[1] TRUE  
  
> invisible(close.ncdf(nc))
```

### Exercise 3

For most of the software development in the remainder of the course, we will need to access snp data for all the samples(i.e. along the columns of the NetCDF file) in smaller chunks(couple of columns at a time) for block processing of data. To make it convenient to develop code as we go along, a smaller subset of the data that we have looked at so far has been provided as a NetCDF file in the `extdata` folder of the `StudentGWAS` package. The file `small_snpData.nc` contains genotype information of 50 samples, 25 snips per sample.

Our goal in this exercise is to develop a `getGWAScols` function that retrieves the genotype information for all the samples for the range of snps specified by the user.

The function should take three arguments

- `nc`: An `ncdf` file pointer obtained by a call to the `open.ncdf`
- `first`: A single integer, the start index for the `snpData` (column) to be returned
- `last`: A single integer, the end index for the `snpData` to be returned.

The function should return a `matrix` of data type `raw` having dimensions with number of rows equal to the number of samples in the `small_snpData.nc` file and columns corresponding to the range of input specified by the user. The function `as.raw` can be used to coerce the integer data type returned by `get.var.ncdf` to the `raw` data type.

Since the `getGWAScols` function is going to be included in a package and will likely encounter NetCDF files of varying sizes, the function has to be written with general usability in mind.(rather than hard coding number of rows/columns in the NetCDF file etc.) Additionally, suitable checks need to be put in place for the input arguments to make sure they are of the correct type and are within bounds with regard to the dimensions of the NetCDF file.

To help with the function development, a convenience function `getNcdfVarSummary` has been provided in the file `utils.R` included in the `R` folder of the `StudentGWAS` package. This function takes the NetCDF file pointer returned by the function `open.ncdf` as input and returns a list. Elements `dim1` and `dim2` of this list returned correspond to the number of rows and number of columns in the NetCDF file respectively. The `getNcdfVarSummary` can be pasted into your `R` session or the contents of the file `utils.R` can be sourced into your session using the `source` command for this exercise.

**Solution:**

```

> library(StudentGWAS)
> getNcdfVarSummary <- StudentGWAS::getNcdfVarSummary
> getGWAScols <- function(nc, first, last = first)
+ {
+   if (!is.numeric(first) || length(first) != 1 || is.na(first))
+     stop("'first' must be a single integer")
+   if (!is.numeric(last) || length(last) != 1 || is.na(last))
+     stop("'last' must be a single integer")
+   ncInfo <- getNcdfVarSummary(nc, "snpData")
+   nrows <- ncInfo$dim1
+   ncols <- ncInfo$dim2
+   if (first < 1 || last < first || last > ncols)
+     stop("we need to have 1 <= 'first' <= 'last' <= nb col in NetCDF file")
+   dat <- get.var.ncdf(nc, varid = "snpData", start= c(1,first),
+     count = c(nrows, last - first + 1))
+   structure(as.raw(dat), dim = dim(dat))
+ }
> pth <- system.file("extdata", "small_snpData.nc", package = "StudentGWAS")
> nc <- open.ncdf(pth)
> dat <- getGWAScols(nc, 1, 4)
> invisible(close.ncdf(nc))

```

#### Exercise 4

An important part of the software development process is to include unit tests to verify that the results returned by the functions that we have implemented are correct. This becomes extremely useful as we try to optimize code as the development of the package progresses.

The goal of this exercise is to develop a unit test function `testGWAScols` that checks if the values returned by the `getGWAScols` function are correct. The expected result for a call to the function `getGWAScols` for all columns and samples in the file `small_snpData.nc` has as been provided to you as a file `small_snpData.rda` in the data folder of the StudentGWAS package. This data can be loaded into an R session using the `load` function.

- Create a unit test function `testGWAScols` that takes no inputs
- Retrieve the genotype information for all the snips and samples in the file `small_snpData.nc` using the `getGWAScols` function that we developed in our previous exercise.
- Load the target data from the `extdata` folder of the StudentGWAS package using the `load` function.
- Check if the results match using the `identical` function.

**Solution:**

```

> library(ncdf)
> testGWAScols <- function()
+ {
+   pth <- system.file("extdata", "small_snpData.nc", package = "StudentGWAS")
+   nc <- open.ncdf(pth, write = FALSE)
+   ncols <- getNcdfVarSummary(nc, "snpData")$dim2
+   current <- getGWAScols(nc, 1, ncols)
+   load(system.file("extdata", "small_snpData.rda", package = "StudentGWAS"))
+   identical(current, small_snpData)
+ }
> testGWAScols()

```