Summer Institute in Statistical Genetics
Module 6: Computing for Statistical Genetics

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Seattle, June 2011

Introduction: Course Aims

- Introducing `R`
  - Manipulating datasets
  - Doing common (genetic) analyses

- Using `R` for sophisticated analyses
  - Doing some popular (genetic) examples
  - Knowing where to start when you need to do more

Introduction: About Prof Lumley

- Prof, University of Auckland
- R Core developer
- Genetic/Genomic research in Cardiovascular Epidemiology
- Sings bass

Introduction: About Prof Rice

- Associate Prof, UW Biostat
- Not an authoR, but a useR (and a teacheR)
- Genetic/Genomic research in Cardiovascular Epidemiology
- Sings bass **this week**

... and you?

Who are you? What's your area of genetics? What are you looking for from the course?

Introduction: Course structure

- 10 sessions over 2.5 days
- Day 1; Basics of `R`
- Day 2; Simple commonly-used genetic examples
- Day 3; More examples, some advanced topics

Introduction: Session structure

- 45 mins teaching (questions welcome)
- 30 mins hands-on
- 15 mins summary, discussion

There will also be one take-home exercise; final session will include in-depth discussion/evaluation

1. Introduction to R:
First steps

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What is R?

R is a ‘programming environment for statistics and graphics’

The base R has fewer prepackaged statistics procedure than SPSS or SAS, but it is much easier to extend with new procedures.

There are about 1500 published extension packages for R, many aimed at genetics and genomics research.

Using R

R is a free implemention of S, for which John Chambers won the ACM Software Systems award.

> For the S system, which has forever altered how people analyze, visualize , and manipulate data.

The downside is that using R effectively may require changing how you analyze, visualize, and manipulate data.

R is a command-line system, not a point-and-click system.

A calculator

```
> 2+2
[1] 4
> 1536/317000
[1] 0.004845426
> exp(pi)-pi
[1] 19.9991
> x <- 3
> y <- 2
> x+y
[1] 5
> ls()
[1] "x" "y"
> round(pi, 6)
[1] 3.141593
> round(pi,
+ 6)
[1] 3.141593
```

Reading data

- Text files
- Other statistics packages datasets
- Web pages

Much more information is in the Data Import/Export manual.

Reading text data

The easiest format has variable names in the first row

```
case    id gender   deg yrdeg field startyr year   rank admin
   1     1      F Other    92 Other      95   95 Assist     0
   2     2      M Other    91 Other      94   94 Assist     0
   3     2      M Other    91 Other      94   95 Assist     0
   4     4      M   PhD    96 Other      95   95 Assist     0
```

and fields separated by spaces. In R, use

```
salary <- read.table("salary.txt", header=TRUE)
```

to read the data from the file `salary.txt` into the data frame `salary`. (Use `dir()` to see which files are in your current directory)

Syntax notes

- Spaces in commands don't matter (except for readability), but Capitalisation Does Matter.
- `TRUE` (and `FALSE`) are logical constants
- Unlike many systems, R does not distinguish between commands that do something and commands that compute a value. Everything is a function: ie returns a value.
- Arguments to functions can be named (`header=TRUE`) or unnamed (`"salary.txt"`)
- A whole data set (called a `data frame` is stored in a variable (`salary`), so more than one dataset can be available at the same time.

Did it work?

The `head()` function shows the first few lines of the data frame

```
> head(salary)
  case id gender   deg yrdeg field startyr year   rank admin salary
1    1  1      F Other    92 Other      95   95 Assist     0   6684
2    2  2      M Other    91 Other      94   94 Assist     0   4743
3    3  2      M Other    91 Other      94   95 Assist     0   4881
4    4  4      M   PhD    96 Other      95   95 Assist     0   4231
5    5  6      M   PhD    66 Other      91   91   Full     1  11182
6    6  6      M   PhD    66 Other      91   92   Full     1  11507
```

It *should* look like this!

Reading text data

Sometimes columns are separated by commas (or tabs)

```
Ozone,Solar.R,Wind,Temp,Month,Day
41,190,7.4,67,5,1
36,118,8,72,5,2
12,149,12.6,74,5,3
18,313,11.5,62,5,4
NA,NA,14.3,56,5,5
```

Use

```
ozone <- read.table("ozone.csv", header=TRUE, sep=",")
```

or

```
ozone <- read.csv("ozone.csv")
```

Syntax notes

- There's more than one way to do it; neither approach is 'best'

- But forgetting `header=TRUE` in `read.table()` *is* bad (try it!)

- Functions can have optional arguments (`sep` wasn't used the first time). Use `help(read.table)` or `?read.table` for a complete description of the function and all the arguments.

- `NA` is the code for missing data – expect to see it in practice. Think of it as "Don't Know". R handles it sensibly in computations: eg 1+NA, NA & FALSE, NA & TRUE. You cannot test `temp==NA` (Is temperature equal to some number I don't know?), so there is a function `is.na()`.

Reading text data

Sometime the variable names aren't included

```
 1      0.2      115       90     1        3       68    42 yes
 2      0.7      193       90     3        1       61    48 yes
 3      0.2       58       90     1        3       63    40 yes
 4      0.2        5       80     2        3       65    75 yes
 5      0.2      8.5       90     1        2       64    30 yes
```

but you can supply them;

```
psa <- read.table("psa.txt", col.names=c("ptid","nadirpsa",
       "pretxpsa", "ps","bss","grade","age",
       "obstime","inrem"))
```

or another way;

```
psa <- read.table("psa.txt")
names(psa) <- c("ptid","nadirpsa","pretxpsa", "ps",
           "bss","grade","age","obstime","inrem")
```

Syntax notes

- Assigning a single vector (or anything else) to a variable uses the same syntax (`<-`) as assigning a whole data frame.
- `c()` is a function that makes a single vector from its arguments.
- `names` is a function that accesses the variable names of a data frame
- Some functions (such as `names`) can be used on the LHS of an assignment.

Other data formats

We load the foreign package, to enable reading these;

```
library("foreign")
stata <- read.dta("salary.dta")
spss <- read.spss("salary.sav", to.data.frame=TRUE)
sasxport <- read.xport("salary.xpt")
epiinfo <- read.epiinfo("salary.rec")
```

- Many functions in R live in optional packages. The `library()` function lists packages, shows help, or loads packages from the package library.

- The foreign package is in the standard distribution. It handles import and export of data. Hundreds of extra packages are available at `http://cran.r-project.org`.

The web

Files for `read.table()` can live on the web

```
fl2000<-read.table("http://faculty.washington.edu/tlumley/
data/FLvote.dat", header=TRUE)
```

... but only if you don't get forwarded to e.g. a UW NetID login URL.

It's also possible to read from more complex web services (such as the genome databases)

Operating on data

As R can have more than one data frame available, you need to specify where to find a variable.

The syntax `antibiotics$duration` means the variable `duration` in the data frame `antibiotics`.

```
## This is a comment
## Convert temperature to real degrees
antibiotics$tempC <- (antibiotics$temp-32)*5/9
## display mean, quartiles of all variables
summary(antibiotics)
```

Subsets

Everything in R is a vector (but some have only one element).
Use `[]` to extract subsets

```
## First element
antibiotics$temp[1]
## All but first element
antibiotics$temp[-1]
## Elements 5 through 10
antibiotics$temp[5:10]
## Elements 5 and 7
antibiotics$temp[c(5,7)]
## People who received antibiotics (note ==)
antibiotics$temp[ antibiotics$antib==1 ]
## or
with(antibiotics, temp[antib==1])
```

Notes

- Positive indices select elements, negative indices drop elements

- `5:10` is the sequence from 5 to 10

- You need `==` to test equality, not just `=`

- `with()` temporarily sets up a data frame as the default place to look up variables. It can save typing a lot of `$` signs.

More subsets

For data frames you need two indices

```
## First row
antibiotics[1,]
## Second column
antibiotics[,2]
## Some rows and columns
antibiotics[3:7, 2:4]
## Columns by name
antibiotics[, c("id","temp","wbc")]
## People who received antibiotics
antibiotics[antibiotics$antib==1, ]
## Put this subset into a new data frame
yes <- antibiotics[antibiotics$antib==1,]
```

Computations

```
mean(antibiotics$temp)
median(antibiotics$temp)
var(antibiotics$temp)
sd(antibiotics$temp)
mean(yes$temp)
mean(antibiotics$temp[antibiotics$antib==1])
with(antibiotics, mean(temp[sex==2]))
toohot <- with(antibiotics, temp>99)
mean(toohot)
```

Factors

Factors represent categorical variables. You can't do mathematical operations on them (except for `==`)

```
> table(salary$rank,salary$field)

         Arts Other Prof
  Assist  668 2626   754
  Assoc  1229 4229  1071
  Full    942 6285  1984
> antibiotics$antib<-factor(antibiotics$antib,
                             labels=c("Yes","No"))
> antibiotics$agegp<-cut(antibiotics$age, c(0,18,65,100))
> table(antibiotics$agegp)
  (0,18]  (18,65] (65,100]
       2       19        4
```

Help!

- `?fn` or `help(fn)` for help on fn

- `help.search("topic")` for help pages related to ”topic”

- `apropos("tab")` for functions whose names contain ”tab”

- `RSiteSearch("FDR")` to search the R Project website (requires internet access)