Introduction to R
Reading, writing and exploring data

R-peer-group

QUB

February 12, 2013

Session outline

- Review of last weeks exercise
- Introduction to R's read/write system
- Reading data into R
  - Useful functions
  - Common problems
  - Practical using data recorded last week
- Data exploration
  - Data extraction
  - Manipulation
  - Basic analysis (inc. plotting)
  - practical
- Writing data back out of R
  - Useful formats
  - Helpful Packages
  - Practical

Last weeks exercise

Q Record the data and save them as objects in R

A example answer

```
lgths <- c(46.58, 44.25, ..., 46.55)
mean.lgth <- 45.15
sd.lgth <- 1.73
```

Q Check to make sure that the mean and standard deviation given to you corresponds to the mean and standard deviation of the data you've recorded.

A
```
mean(lgths) == mean.lgth    #FALSE
sd(fish.lengths) == sd.lgth     #FALSE
```

Also: `?identical`, `?all.equal`, `?isTRUE`

Last weeks exercise

Q If there is a problem what do you think it is considering the fact that your colleague has told you that all fish were longer than 40 inches? A 4 has been left of the start of one of the lengths in the data. You check with your colleague and they have told you that the problem fish was recorded incorrectly. Its length should be 44.23 inches. How can you fix it?

A example answer

```
lgths[6] <- 44.23
```

Q Using `logical` tests, demonstrate that the mean and standard deviation calculated from the fixed data are the same as those sent to you by your colleague.

A
```
mean(lgths) == mean.lgth    #TRUE
sd(lgths) == sd.lgth     #TRUE
```

Last weeks exercise

Q Convert your vector of lengths from *inches* to *cm*, saving the results in a new vector. [1 inch = 2.54 cm]

A example answer

```
lgths.cm <- lgths * 2.54
# or
lgths.cm <- cm(lgths)
```

Q Calculate the new mean and standard deviation of the converted data.

A
```
new.mean <- mean(lgth.cm)
new.sd <- sd(lgth.cm)
# Alternatives (manual)
# Mean
new.mean <- sum(lgth.cm)/lgth(lgth.cm)
# sd
new.sd <- sqrt(var(lgth.cm))
# or
new.sd <- (sum((lgths.cm-mean(lgths.cm))^2)/(length(lgths.cm)-1))^0.5
```

Last weeks exercise

Q Calculate the variance of both data sets. $[sd = \sqrt{Var(x)}]$.

A example answer

```
var.lgths <- var(lgths)
var.lgth.cm <- var(lgth.cm)
# or
var.lgths <- new.sd^2
```

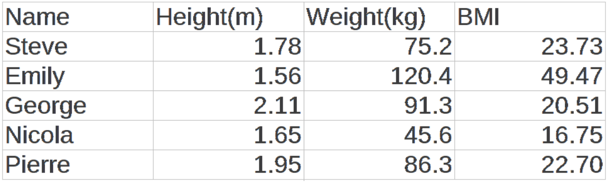
Getting data into R

Reading data

- Initially, one of the most challenging aspects of learning `R` is how to access your data so you can analyse them
- There are many `functions` which make this easy, you just have to make sure your data are in the correct format
  - File type
  - Field delimiter
  - Headers
- The most commonly used function is `read.table()`
- There are many other similar functions with very similar behaviour and arguments
  - `read.csv()`, `read.delim()`, `read.fwf()`, `read.DIF()`
- For more complex data files you can use `scan()` directly, which is the backbone of most other read functions

Reading data

- Imagine we have a data set in a spreadsheet that looks like this:



Name	Height(m)	Weight(kg)	BMI
Steve	1.78	75.2	23.73
Emily	1.56	120.4	49.47
George	2.11	91.3	20.51
Nicola	1.65	45.6	16.75
Pierre	1.95	86.3	22.70

- The simplest way read this data into R would be:
  - -> Save the data to .txt or .csv format (lets say we name it 'mydata.txt')
  - -> Use `read.table()` or `read.csv()` respectively, to read the data

```
> myData <- read.table("mydata.txt", header = TRUE)
```

- This command will load the data set into R so that you can carry out your analyses

Reading data

- After reading data into R, it is important to check that it has maintained the correct format
- We can inspect the data in a number of different ways
  - -> In RStudio we can click on the variable name in the workspace
  - -> Type `fix(myData)` into the console (Usually reserved for editing cells)
  - -> In RStudio, type `View(myData)` (limited to 100 columns and 1000 rows)
  - -> Print to the console (only for small data sets)

```
> myData

    Name Height.m. Weight.kg.   BMI
1  Steve      1.78       75.2 23.73
2  Emily      1.56      120.4 49.47
3 George      2.11       91.3 20.51
4 Nicola      1.65       45.6 16.75
5 Pierre      1.95       86.3 22.70
```

Reading data

- R has done something to the header names of our data set
- Some characters/symbols are not permitted in headers as these are treated as variables in R
  - -> R replaced the characters '()' with '.' automatically in our data
  - -> It will also do this for whitespace characters such as tabs and spaces in headers
- We could look at only the header of myData by typing:

```
> names(myData)
```

```
[1] "Name"       "Height.m."  "Weight.kg." "BMI"
```

- We could also use:

```
> colnames(myData)
```

```
[1] "Name"       "Height.m."  "Weight.kg." "BMI"
```

Reading data

- Because we will use the headers as variable names for each column in our data set, it is sometimes convenient to change their names to something shorter

```
> names(myData) <- c("nms", "hgt", "wgt", "bmi")
> # or
> colnames(myData) <- c("nms", "hgt", "wgt", "bmi")
```

- Now if we look at `myData`, the header names should have changed

```
> myData

     nms  hgt   wgt   bmi
1  Steve 1.78  75.2 23.73
2  Emily 1.56 120.4 49.47
3 George 2.11  91.3 20.51
4 Nicola 1.65  45.6 16.75
5 Pierre 1.95  86.3 22.70
```

Reading data

- We can also inspect the object (our data) in many different ways
  `typeof()` - Tells you the type/class of an object (e.g. `numeric`, `character`)
  `str()` - Displays the structure of the object
- We can also ask `R` specific question about our data object
  `is.numeric()` - Is my object numeric?
  `is.data.frame()` - Is my object a dataframe?
  `length()` - What length is my data object?
- We could ask `R` how many rows and columns are in `myData` like this:

```
> nrow(myData)
[1] 5
> ncol(myData)
[1] 4
> # or
> dim(myData)
[1] 5 4
```

Reading data

- We can extract useful information from our data in a number of ways
  - Index mapping - remember the `[]` symbols from last week
  - Extraction - done using the `$` symbol

- If we wanted to find out what value was in the 3rd row of the 4th column using index mapping, we would simply type:

```
> myData[3, 4]
```

```
[1] 20.51
```

- To *extract* the BMI column from the data we could type the following:

```
> BMI <- myData$bmi
> BMI
```

```
[1] 23.73 49.47 20.51 16.75 22.70
```

- Let's see if our new object `BMI` is equal to the `bmi` or 4th column of `myData`

```
> identical(BMI, myData[ , 4])
```

```
[1] TRUE
```

Reading data: DIY

1 Create a new project in a convenient directory on your system called 'Session-2'

2 Download this file and save it to the directory you created your R project in.

3 Check what format the data are in (.txt or .csv), and use an appropriate function to read them into R, assigning them to the variable `morph1`.

4 Inspect your data. Notice that on the 31st row there are '?' in two columns. These are missing data. In R missing data are usually recorded as `NA`. Can you think of a way, using `index mapping`, that you could replace these elements with `NA`s?

5 Recode the header names to more convenient header names

Data exploration

Exploring data

- We can inspect the object `morph1` using a few more functions

```
> head(morph1) # displays the first 6 rows
```

```
  sex    col hgt  lrh llf
1   F  Black  73   18  30
2   M  Black  76   21  30
3   M  Brown  68   18  30
4   F Ginger  62 16.2  25
5   F  Brown  67   16  28
6   F Blonde  68   16  25
```

- When R reads data, it treats different variable types in different ways by coercing them to certain classes
- `str()` is the easiest way to inspect how R has treated variables in our dataframe

Exploring data

- We can use this function as follows:

```
> str(morph1)
```

- `morph1$lrh` and `morph1$llf` should be numeric variables, instead R has coerced them to the class `'factor'` because of the original missing data values used (i.e. `?`).
- To coerce them to numeric variables use the following:

```
> morph1$lrh <- as.character(morph1$lrh)
> morph1$lrh <- as.numeric(morph1$lrh)

> morph1$llf <- as.numeric(levels(morph1$llf)[morph1$llf])

# or
morph1$lrh <- as.numeric(as.character(morph1$lrh))
# or
morph1$lrh <- as.numeric(levels(morph1$lrh)[morph1$lrh])
```

Exploring data

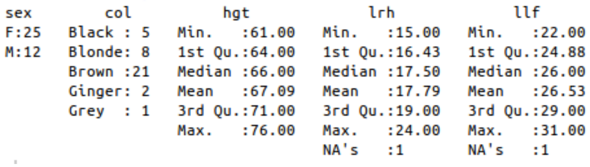
- We can check if our changes worked

  > *is.numeric(morph1$lrh)*

  ```
  [1] TRUE
  ```

- We can also inspect our data using the `summary()` function

  > *summary(morph1)*



```
 sex        col            hgt             lrh             llf
 F:25   Black : 5   Min.   :61.00   Min.   :15.00   Min.   :22.00
 M:12   Blonde: 8   1st Qu.:64.00   1st Qu.:16.43   1st Qu.:24.88
        Brown :21   Median :66.00   Median :17.50   Median :26.00
        Ginger: 2   Mean   :67.09   Mean   :17.79   Mean   :26.53
        Grey  : 1   3rd Qu.:71.00   3rd Qu.:19.00   3rd Qu.:29.00
                    Max.   :76.00   Max.   :24.00   Max.   :31.00
                                    NA's   :1       NA's   :1
```

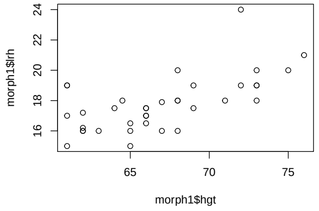
Exploring data graphically

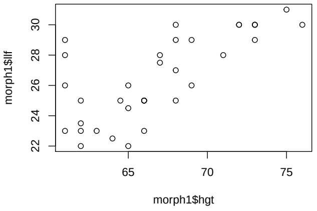
Graphical exploration

Exploring data graphically

- As insightful biologists, we might make the prediction that we should observe a positive relationship between an individual's height and both their right hand length and their left foot length. It is easy to explore this prediction visually in R

```
> plot(x = morph1$hgt, y = morph1$lrh)
> plot(x = morph1$hgt, y = morph1$llf)
```

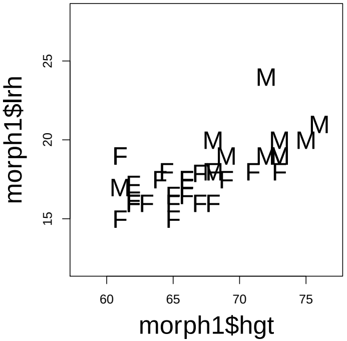




Exploring data graphically

- We can use R's powerful plotting capabilities to explore the data in many ways

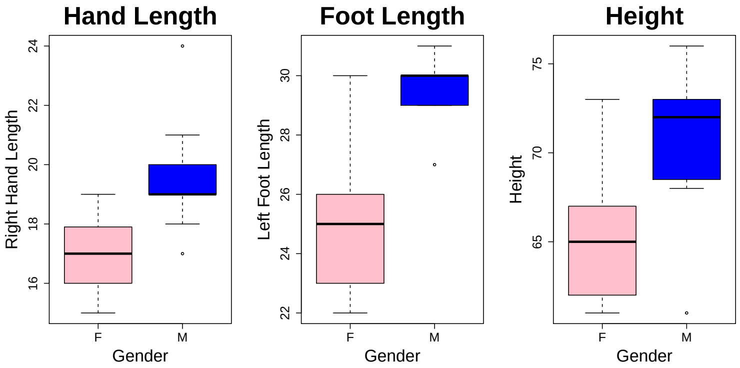
```
> plot(x = morph1$hgt, y = morph1$lrh,
+       pch = as.character(morph1$sex),
+       cex = 2)
```



Exploring data graphically

- We can explore the differences between genders for each of the measurements

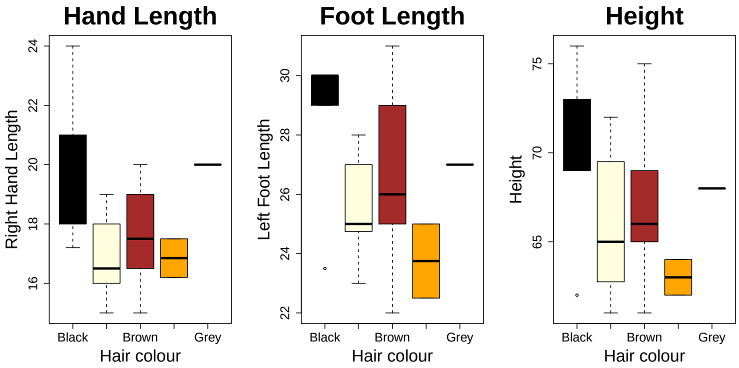
```
> plot(x = morph1$sex, y = morph1$lrh, col = c("pink", "blue"),
+       xlab = "Gender", ylab = "Right Hand Length")
```



Exploring data graphically

- What about hair colour?

```
> plot(x = morph1$col, y = morph1$lrh, xlab = "Hair colour",
+       col = c("black", "lightyellow", "brown", "orange", "lightgrey"),
+       ylab = "Right Hand Length")
```



Exploring data: DIY

Genome size is the amount of DNA contained within a single copy (i.e. a single cell) of a single genome, usually measured in picograms (pg $= 10^{-12}$).

Genome size has been measured for a large number of species on the planet as it was once believed that there was a correlation between genome size and complexity. However, following the discovery of 'non-coding DNA', and observations to the contrary, this idea was understood to be false.

You will be provided with a data set containing genome sizes for various vertebrates grouped into different classes and subclasses. Your task is to follow the instructions to explore the relationship between genome size and taxonomic grouping.

Exploring data: DIY

1. Download the genome size file here and save it to your `session-2` project directory.

2. Inspect the file and read it into `R` using the appropriate function.

3. The data object will have a number of issues. Use the various exploratory functions demonstrated to:
   a. Replace any missing data with `NA`s
   b. Coerce incorrectly classified varibles
   c. Plot the relationship between class and genome size
   d. Plot the relationship between subclass and genome size.
   e. Which class has the most striking difference in genome size among subclasses?

4. Create a new variable in the genome size data frame named `basepairs`. This variable should contain the basepair equivalent to the genome size for each species in the data.
   $1\text{pg} \approx 978,000,000$ basepairs