R for data analysis ... Or ...
Doing stuff with the R you've learnt today

4

3 steps to
Basic data analysis

1. Reading in data
    - read.table()
    - read.csv(), read.delim()

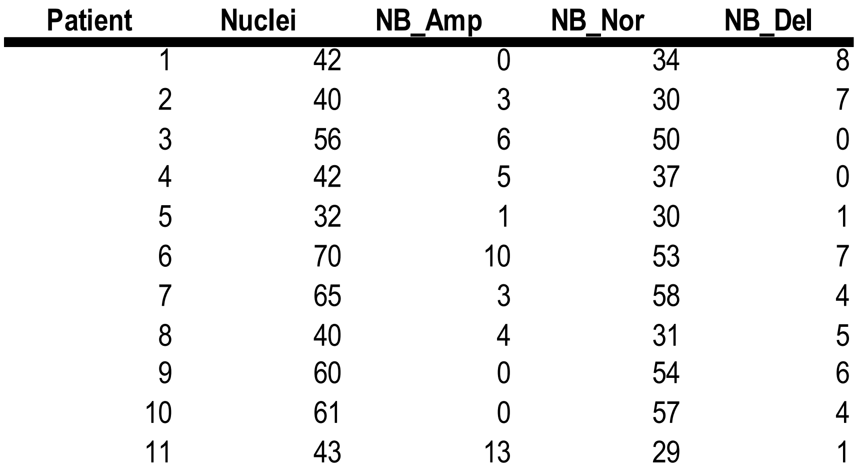
2. Analysis
    - Manipulating & reshaping the data
    - Any maths you like
    - Plotting the outcome
        - High level plotting functions (covered tomorrow)

3. Writing out results
    - write.table()
    - write.csv()

A simple walkthrough
Exemplifies 3 steps to R analysis

- 50 neuroblastoma patients were tested for NMYC gene copy number by interphase nuclei FISH
  - Amplification of NMYC correlates with worse prognosis
  - We have count data
    - Numbers of cells per patient assayed
      - For each we have NMYC copy number relative to base ploidy
- We need to determine which patients have amplifications
  - (i.e >33% of cells show NMYC amplification)

Step 1.
Read in the data



Patient	Nuclei	NB_Amp	NB_Nor	NB_Del
1	42	0	34	8
2	40	3	30	7
3	56	6	50	0
4	42	5	37	0
5	32	1	30	1
6	70	10	53	7
7	65	3	58	4
8	40	4	31	5
9	60	0	54	6
10	61	0	57	4
11	43	13	29	1

This data is a tab delimited text file
Each row is a record, each column is a field
Columns are separated by tabs in the text.

We need to read in the results table and assign it to an object (rawData)

```
rawData <- read.delim("08_NBcountData.txt")
rawData[1:10,]     # View the first 10 rows to ensure import is OK
                   # Note data frame contains a patient index column
```

If the data had been comma separated values, then sep=","

```
read.csv("08_NBcountData.csv")
?read.table
```

for a full list of arguments

08_NBcountData.R
(script commands)

08_NBcountData.txt
(data file)

Step 2.
Analysis (reshaping data & maths)

- Our analysis involves identifying patients with > 33% NB amplification

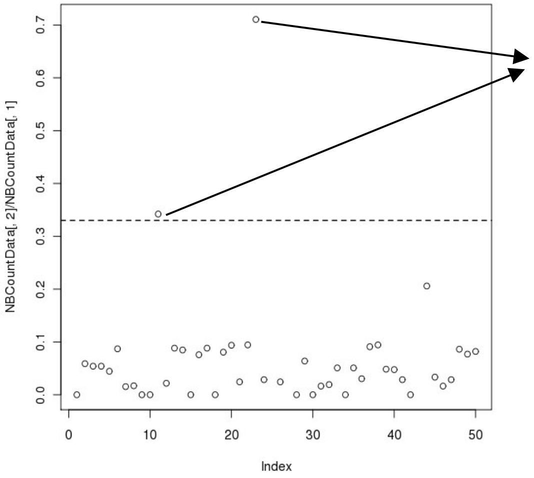
  -
    ```
    prop <- rawData$NB_Amp / rawData$Nuclei # create an index of results
    ```

  -
    ```
    amp <- which(prop > 0.33) # Get sample names of amplified patients
    ```

- We can plot a simple chart of the % NB amplification

  -
    ```
    plot(prop, ylim=c(0,1.2))
    ```

  -
    ```
    abline(h=0.33,lwd=1.5,lty=2)
    ```



These 2 samples are amplified (11 & 23)

Step 3.
Outputting the results

- We write out a data frame of results (patients > 33% NB amplification) as a 'comma separated values' text file
  - `write.csv(rawData[amp,],file="selectedSamples.csv") # Export table↰, file name = selectedSamples.csv`
    - Files are directly readable by Excel and Calc

- Its often helpful to double check where the data has been saved
  - Use get working directory function
    - `getwd()↰ # print working directory`

Data analysis exercise:
Which samples are near normal?

- Patients are near normal if:

(NB_Amp/Nuclei <0.33 & NB_Del ==0)

- Modify the condition in our previous code to find these patients

- Write out a results file of the samples that match these criteria, and open it in a spreadsheet program

08_NBcountData.R
(script commands)

Solution to NB normality test

Basic data analysis

```
> norm <- which( prop < 0.33 & rawData$NB_Del==0)
> norm

[1] 3  4  7 15 20 24 36 37 42 47


> write.csv(rawData[norm,],"My_NB_output.csv")
```