

# R: A self-learn tutorial

I.E. WHAT WE NEED  
IN BUSINESS  
ANALYTICS

## 1 Introduction

R is a software language for carrying out complicated (and simple) statistical analyses. It includes routines for data summary and exploration, graphical presentation and data modelling. The aim of this document is to provide you with a basic fluency in the language. It is suggested that you work through this document at the computer, having started an R session. Type in all of the commands that are printed, and check that you understand how they operate. Then try the simple exercises at the end of each section.

= PLEASE DO IT.

When you work in R you create objects that are stored in the current workspace (sometimes called image). Each object created remains in the image unless you explicitly delete it. At the end of the session the workspace will be lost unless you save it. You can save the workspace at any time ~~by clicking on the disc icon at the top of the control panel.~~ USING THE COMMAND SAVE

Commands written in R are saved in memory throughout the session. You can scroll back to previous commands typed by using the 'up' arrow key (and 'down' to scroll back again). You can also 'copy' and 'paste' using standard windows editor techniques (for example, using the 'copy' and 'paste' dialog buttons). If at any point you want to save the transcript of your session, click on 'File' and then 'Save History', which will enable you to save a copy of the commands you have used for later use. As an alternative you might copy and paste commands manually into a notepad editor or something similar.

You finish an R session by typing

```
> q()
```

at which point you will also be prompted as to whether or not you want to save the current workspace. If you do not, it will be lost.

## 2 Objects and Arithmetic

R stores information and operates on *objects*. The simplest objects are *scalars*, *vectors* and *matrices*. But there are many others: *lists* and *dataframes* for example. In advanced use of R it can also be useful to define new types of object, specific for particular application. We will stick with just the most commonly used objects here.

An important feature of R is that it will do different things on different types of objects. For example, type:<sup>1</sup>

```
> 4+6
```

The result should be

```
[1] 10
```

So, R does scalar arithmetic returning the scalar value 10. (In actual fact, R returns a vector of length 1 - hence the [1] denoting first element of the vector.)

We can assign objects values for subsequent use. For example:

```
x<-6  
y<-4  
z<-x+y
```

I know you have already done that, but please PRACTICE AGAIN!

→ SCALAR IS A "FANCY" WAY TO SAY NUMBER (in this case)

Do you remember THE CONCEPT OF VECTOR, RIGHT?

<sup>1</sup>We adopt the convention of using typeface font to denote things typed in R. The > sign is not typed however; it denotes the prompt symbol.

would do the same calculation as above, storing the result in an object called `z`. We can look at the contents of the object by simply typing its name:

```
z
[1] 10
```

At any time we can list the objects which we have created:

```
> ls()
[1] "x"      "y"      "z"
```

← IT'S JUST THE DIRECTORY

Notice that `ls` is actually an object itself. Typing `ls` would result in a display of the contents of this object, in this case, the commands of the function. The use of parentheses, `ls()`, ensures that the function is *executed* and its result - in this case, a list of the objects in the directory - displayed.

More commonly a function will operate on an object, for example

```
> sqrt(16)
[1] 4
```

calculates the square root of 16. Objects can be removed from the current workspace with the `rm` function:

```
> rm(x,y)
```

for example.

There are many standard functions available in **R**, and it is also possible to create new ones.

Vectors can be created in **R** in a number of ways. We can describe all of the elements:

```
> z<-c(5,9,1,0)
```

Note the use of the function `c` to *concatenate* or 'glue together' individual elements. This function can be used much more widely, for example

```
> x<-c(5,9)
> y<-c(1,0)
> z<-c(x,y)
```

would lead to the same result by gluing together two vectors to create a single vector.

Sequences can be generated as follows:

```
> x<-1:10
```

while more general sequences can be generated using the `seq` command. For example:

```
> seq(1,9,by=2)
[1] 1 3 5 7 9
```

and

```
> seq(8,20,length=6)
[1] 8.0 10.4 12.8 15.2 17.6 20.0
```

These examples illustrate that many functions in **R** have optional arguments, in this case, either the step length or the total length of the sequence (it doesn't make sense to use both). If you leave out both of these options, **R** will make its own default choice, in this case assuming a step length of 1. So, for example,

```
> x<-seq(1,10)
```



PLEASE, TRY  
THEM ALL  
yourself -

## Exercises

### 1. Define

```
> x<-c(4,2,6)
> y<-c(1,0,-1)
```

Decide what the result will be of the following:

- (a) `length(x)`
- (b) `sum(x)`
- (c) `sum(x^2)`
- (d) `x+y`
- (e) `x*y`
- (f) `x-2`
- (g) `x^2`

Use **R** to check your answers.

### 2. Decide what the following sequences are and use **R** to check your answers:

- (a) `7:11`
- (b) `seq(2,9)`
- (c) `seq(4,10,by=2)`
- (d) `seq(3,30,length=10)`
- (e) `seq(6,-4,by=-2)`

### 3. Determine what the result will be of the following **R** expressions, and then use **R** to check you are right:

- (a) `rep(2,4)`
- (b) `rep(c(1,2),4)`
- (c) `rep(c(1,2),c(4,4))`
- (d) `rep(1:4,4)`
- (e) `rep(1:4,rep(3,4))`

### 4. Use the `rep` function to define simply the following vectors in R.

- (a) `6,6,6,6,6,6`
- (b) `5,8,5,8,5,8,5,8`
- (c) `5,5,5,5,8,8,8,8`

### 3 Summaries and Subscripting

Let's suppose we've collected some data from an experiment and stored them in an object `x`:

```
> x<-c(7.5,8.2,3.1,5.6,8.2,9.3,6.5,7.0,9.3,1.2,14.5,6.2)
```

Some simple summary statistics of these data can be produced:

```
> mean(x)
[1] 7.216667
> var(x)
[1] 11.00879
> summary(x)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1.200	6.050	7.250	7.217	8.475	14.500

THE QUARTILES! we saw them in this week's lecture

which should all be self explanatory. It may be, however, that we subsequently learn that the first 6 data correspond to measurements made on one machine, and the second six on another machine. This might suggest summarizing the two sets of data separately, so we would need to extract from `x` the two relevant subvectors. This is achieved by subscripting:

```
> x[1:6]
```

and

```
> x[7:12]
```

give the relevant subvectors. Hence,

```
> summary(x[1:6])
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 3.100  6.075   7.850   6.983   8.200   9.300
> summary(x[7:12])
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 1.200  6.275   6.750   7.450   8.725  14.500
```

Other subsets can be created in the obvious way. For example:

```
> x[c(2,4,9)]
[1] 8.2 5.6 9.3
```

Negative integers can be used to *exclude* particular elements. For example

```
x[-(1:6)]
```

has the same effect as `x[7:12]`.

#### Exercises

1. If `x<- c(5,9,2,3,4,6,7,0,8,12,2,9)` decide what each of the following is and use **R** to check your answers:

(a) `x[2]`

(b) `x[2:4]`

(c) `x[c(2,3,6)]`

(d) `x[c(1:5,10:12)]`

(e) `x[-(10:12)]`

2. The data `y<-c(33,44,29,16,25,45,33,19,54,22,21,49,11,24,56)` contain sales of milk in litres for 5 days in three different shops (the first 3 values are for shops 1,2 and 3 on Monday, etc.) Produce a statistical summary of the sales for each day of the week and also for each shop.

## 4 Matrices

⇒ SUPER IMPORTANT!

Matrices can be created in **R** in a variety of ways. Perhaps the simplest is to create the columns and then glue them together with the command `cbind`. For example,

```
> x<-c(5,7,9)
> y<-c(6,3,4)
> z<-cbind(x,y)
> z
```

```
      x y
[1,] 5 6
[2,] 7 3
[3,] 9 4
```

WE CAN EXPRESS OUR DATA SET  
IN THE FORM OF A  
MATRIX!

The dimension of a matrix can be checked with the `dim` command:

```
> dim(z)
[1] 3 2
```

i.e., three rows and two columns. There is a similar command, `rbind`, for building matrices by gluing rows together.

The functions `cbind` and `rbind` can also be applied to matrices themselves (provided the dimensions match) to form larger matrices. For example,

```
> rbind(z,z)
      [,1] [,2]
[1,]    5    6
[2,]    7    3
[3,]    9    4
[4,]    5    6
[5,]    7    3
[6,]    9    4
```

Matrices can also be built by explicit construction via the function `matrix`. For example,

```
z<-matrix(c(5,7,9,6,3,4),nrow=3)
```

results in a matrix `z` identical to `z` above. Notice that the dimension of the matrix is determined by the size of the vector and the requirement that the number of rows is 3, as specified by the argument `nrow=3`. As an alternative we could have specified the number of columns with the argument `ncol=2` (obviously, it is unnecessary to give both). Notice that the matrix is 'filled up' column-wise. If instead you wish to fill up row-wise, add the option `byrow=T`. For example,

```
> z<-matrix(c(5,7,9,6,3,4),nr=3,byrow=T)
```

```
> z
      [,1] [,2]
[1,]    5    7
[2,]    9    6
[3,]    3    4
```

Notice that the argument `nrow` has been abbreviated to `nr`. Such abbreviations are always possible for function arguments provided it induces no ambiguity - if in doubt always use the full argument name.

As usual, **R** will try to interpret operations on matrices in a natural way. For example, with `z` as above, and

```
> y<-matrix(c(1,3,0,9,5,-1),nrow=3,byrow=T)
```

```
> y
      [,1] [,2]
[1,]    1    3
[2,]    0    9
[3,]    5   -1
```

we obtain

```
> y+z
      [,1] [,2]
[1,]    6   10
[2,]    9   15
[3,]    8    3
```

and

```
> y*z
      [,1] [,2]
[1,]    5   21
[2,]    0   54
[3,]   15   -4
```

Notice, multiplication here is componentwise rather than conventional matrix multiplication. Indeed, conventional matrix multiplication is undefined for `y` and `z` as the dimensions fail to match. Let's now define

```
> x<-matrix(c(3,4,-2,6),nrow=2,byrow=T)
```

```
> x
      [,1] [,2]
[1,]    3    4
[2,]   -2    6
```

*STOL*

Matrix multiplication is expressed using notation `%*%:`

```
> y%*%x
      [,1] [,2]
[1,]   -3   22
[2,]  -18   54
[3,]   17   14
```

Other useful functions on matrices are `t` to calculate a matrix transpose and `solve` to calculate inverses:

```
> t(z)
      [,1] [,2] [,3]
[1,]    5    9    3
[2,]    7    6    4

and

> solve(x)
      [,1] [,2]
[1,] 0.23076923 -0.1538462
[2,] 0.07692308  0.1153846
```

As with vectors it is useful to be able to extract sub-components of matrices. In this case, we may wish to pick out individual elements, rows or columns. As before, the `[ ]` notation is used to subscript. The following examples should make things clear:

```
> z[1,1]
[1] 5

> z[c(2,3),2]
[1] 6 4

> z[,2]
[1] 7 6 4

> z[1:2,]
      [,1] [,2]
[1,]    5    7
[2,]    9    6
```

So, in particular, it is necessary to specify which rows and columns are required, whilst omitting the integer for either dimension implies that every element in that dimension is selected.

## Exercises

1. Create in **R** the matrices

$$x = \begin{bmatrix} 3 & 2 \\ -1 & 1 \end{bmatrix}$$

and

$$y = \begin{bmatrix} 1 & 4 & 0 \\ 0 & 1 & -1 \end{bmatrix}$$

Calculate the following and check your answers in R:

- (a) `2*x`
- (b) `x*x`
- (c) `x%*%x`



- (d) `x%%y`
- (e) `t(y)`
- (f) `solve(x)`

2. With `x` and `y` as above, calculate the effect of the following subscript operations and check your answers in R.

- (a) `x[1,]`
- (b) `x[2,]`
- (c) `x[,2]`
- (d) `y[1,2]`
- (e) `y[,2:3]`

## 5 Attaching to objects

R includes a number of datasets that it is convenient to use for examples. You can get a description of what's available by typing

```
> data()
```

To access any of these datasets, you then type `data(dataset)` where `dataset` is the name of the dataset you wish to access. For example,

```
> data(trees)
```

Typing

```
> trees[1:5,]  
  Girth Height Volume  
1   8.3    70   10.3  
2   8.6    65   10.3  
3   8.8    63   10.2  
4  10.5    72   16.4  
5  10.7    81   18.8
```

gives us the first 5 rows of these data, and we can now see that the columns represent measurements of girth, height and volume of trees (actually cherry trees: see `help(trees)`) respectively.

Now, if we want to work on the columns of these data, we can use the subscripting technique explained above: for example, `trees[,2]` gives all of the heights. This is a bit tedious however, and it would be easier if we could refer to the heights more explicitly. We can achieve this by attaching to the `trees` dataset:

```
> attach(trees)
```

Effectively, this makes the contents of `trees` a directory, and if we type the name of an object, **R** will look inside this directory to find it. Since `Height` is the name of one of the columns of `trees`, **R** now recognises this object when we type the name. Hence, for example,

```
> mean(Height)  
[1] 76
```

and

you will find the data  
set on your workspace!

```
> mean(trees[,2])
[1] 76
```

are synonymous, while it is easier to remember exactly what calculation is being performed by the first of these expressions. In actual fact, `trees` is an object called a dataframe, essentially a matrix with named columns (though a dataframe, unlike a matrix, may also include non-numerical variables, such as character names). Because of this, there is another equivalent syntax to extract, for example, the vector of heights:

```
> trees$Height
```

which can also be used without having first attached to the dataset.

## Exercises

1. Attach to the dataset `quakes` and produce a statistical summary of the variables `depth` and `mag`.
2. Attach to the dataset `mtcars` and find the mean weight and mean fuel consumption for vehicles in the dataset (type `help(mtcars)` for a description of the variables available).

## 6 The apply function

It is possible to write loops in R, but they are best avoided whenever possible. A common situation is where we want to apply the same function to every row or column of a matrix. For example, we may want to find the mean value of each variable in the `trees` dataset. Obviously, we could operate on each column separately but this can be tedious, especially if there are many columns. The function `apply` simplifies things. It is easiest understood by example:

```
> apply(trees,2,mean)
      Girth   Height   Volume 
13.24839 76.00000 30.17097
```

has the effect of calculating the mean of each column (dimension 2) of `trees`. We'd have used a 1 instead of a 2 if we wanted the mean of every row.

Any function can be applied in this way, though if optional arguments to the function are required these need to be specified as well - see `help(apply)` for further details.

### Exercise

1. Repeat the analyses of the datasets `quakes` and `mtcars` using the function `apply` to simplify the calculations.
2. If

$$y = \begin{bmatrix} 1 & 4 & 1 \\ 0 & 2 & -1 \end{bmatrix}$$

what is the result of `apply(y[,2:3],1,mean)`? Check your answer in R.