**Test 1**

**(1)** [2 pts] Create (without using function *c*) a sequence of numbers from 34 to 92 with a step size 2 (i.e. 34, 36, 38, ..., 92) and store it into a new variable named *A*. Write here the command you have used:

A <- seq(34,92, by = 2)

**(2)** [1 pt] Determine the length of variable *A* (created above) using the function *length*. Write the command used to accomplish this here:

length(A)

Returned value was:

30

**(3)** [2 pts] Use online help to find how to use function *rnorm* to create 20 random values from a normal distribution, which has average 5.0 and standard deviation 2.0. Store these 20 values into variable *B*. Specify the command here:

B <- rnorm(20, mean = 5.0, sd = 2.0)

In the *data\_mrm.xlsx* data file (available at the top of Moodle page for this course as *Data MRM*), first sheet (*Benlate*) contains 16 observations for two numerical variables (*TotalBio* and *Rhizomes*) and two factor variables (*B* and *P*).

**(4)** [2 pts] Import these data through Clipboard into R program and store them into a data frame called *benlate*. Write the command you have used for import here:

benlate <- read.delim("clipboard", as.is= FALSE)

**(5)** [1 pt] Write here a (single) command that you would use to display values of all four variables present in the sixth (6th) row of the data frame:

benlate[6,]

**(6)** [2 pts] Calculate the average value of the variable *Rhizomes* separately for the two groups of observations differing in the value of the *B* factor (*y* or *n*). Write the command you have used for this here:

with(benlate, tapply(Rhizomes, B, mean))

and the two calculated values here:

when *B* is *n*, average is = 0.2000

when *B* is *y*, average is = 0.5125