ENTMLGY 6707 Entomological Techniques and Data Analysis

Introduction to R

The goal of this activity is to practice working within R. First, we will review some basic commands in R. Then, we will practice loading different types of data into R.

Create a data frame and graph the data

Create a vector called `my_vector` with integer values from 1 to 10.

```
my_vector <- 1:10
my_vector_option2 <- seq(from = 1, to = 10, by = 1)
```

Use `log()` to log-transform `my_vector` and store (using `<-`) the transformed values as `my_vector_ln`. You should complete this step entirely in R - I am not asking you to store or save a new file. Note that in R, `log()` is the natural logarithm (log_e) and not log_{10}.

```
my_vector_ln <- log(my_vector)
```

Create a vector called `my_vector_new` by adding 2 to all values of `my_vector_ln`.

```
my_vector_new <- my_vector_ln + 2
```

Create a data frame called `my_df` using the following code.

```
my_df <- data.frame(variable1 = my_vector, variable2 = my_vector_new)
```

Run the `summary()` command on your data frame. Your output should look exactly the same as the below summary.

```r
summary(my_df)
```

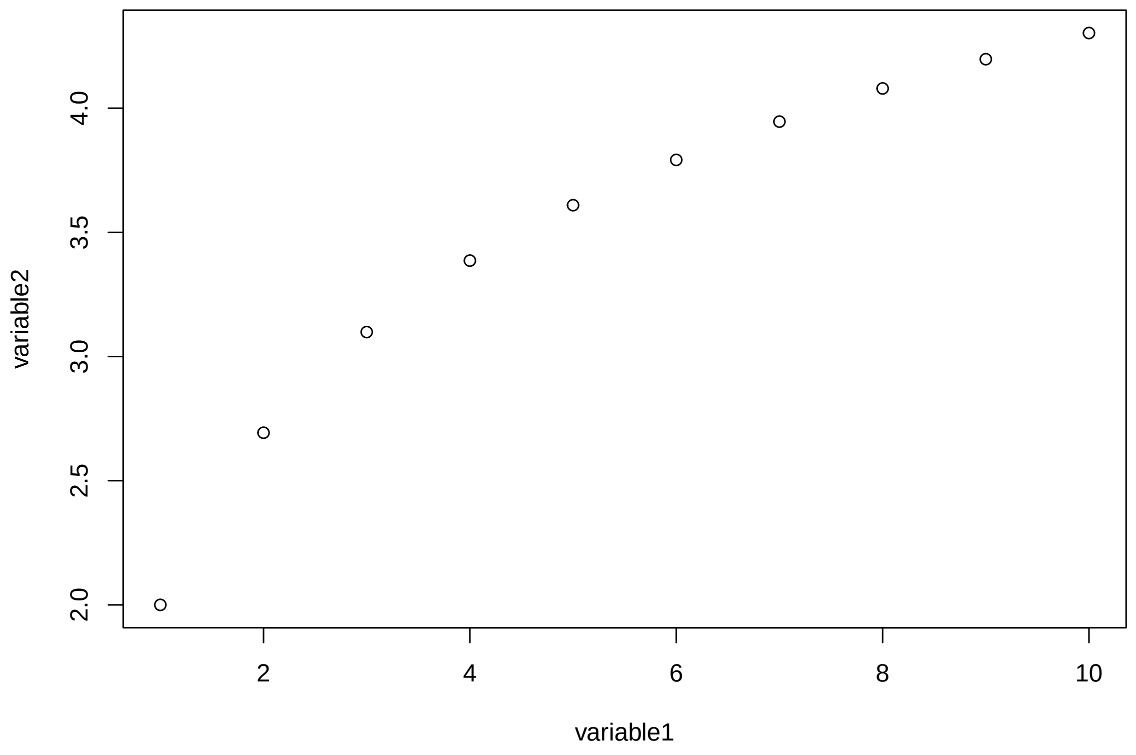
```
   variable1       variable2    
 Min.   : 1.00   Min.   :2.000  
 1st Qu.: 3.25   1st Qu.:3.171  
 Median : 5.50   Median :3.701  
 Mean   : 5.50   Mean   :3.510  
 3rd Qu.: 7.75   3rd Qu.:4.046  
 Max.   :10.00   Max.   :4.303  
```

Use `plot()` to create a scatterplot of `variable2` as a function of `variable1` from the `my_df` data frame.

We will use this phrasing - "Y as a function of X" - a lot this semester. So, in this case, `variable2` would be your response variable and displayed on the y-axis and `variable1` would be your predictor and displayed on the x-axis.

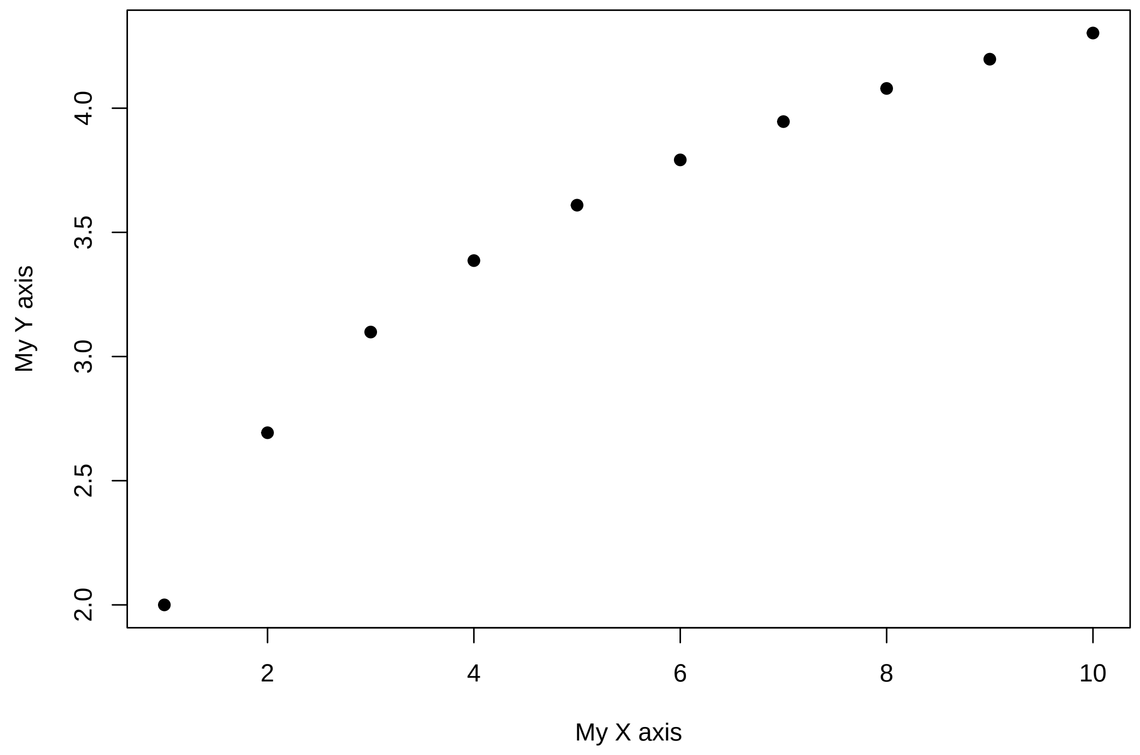
Within R, you can search for information about a function by including a question mark before the function. `?plot()` `?seq()` `?summary()`

```r
plot(variable2 ~ variable1, data = my_df)
```



Reproduce the graph from the previous step, but change the x-axis and y-axis titles to, respectively, “My X axis” and “My Y axis”. Also, fill in the circles so they are easier to see.

```r
plot(variable2 ~ variable1, data = my_df, pch = 19,
     xlab = "My X axis", ylab = "My Y axis")
```



When working with data frames in R, we can refer to specific columns using a `$`. Below is an example of how to calculate the mean of `variable1` and the standard deviation of `variable2` in `my_df`.

```
my_df$variable1
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

```
mean(my_df$variable1)
```

```
[1] 5.5
```

```
my_df$variable2
```

```
 [1] 2.000000 2.693147 3.098612 3.386294 3.609438 3.791759 3.945910 4.079442
 [9] 4.197225 4.302585
```

```r
sd(my_df$variable2)
```

```
[1] 0.7330239
```

Loading data into R

We are going to practice loading in different types of data using the `Iris` data from:

Anderson. 1935. The irises of the Gaspe Peninsula. Bulletin of the American Iris Society, (59) 2–5.

Why should I learn how to load in different types of data?

We will learn how to load in a few different types of files because (1) many of you might currently or one day use a program/software that returns data in only one file type, (2) a collaborator might send you data stored in an unfamiliar file type, and/or (3) third party data (e.g., from the USDA) might only be available in certain file types. So, learning to be flexible now, or least knowing there are multiple options, can save you headaches in the future.

Different types of files

A quick way (on a Windows machine) to determine what type of file you have and the directory in which it is located - two pieces of information that are necessary for loading data into R - is to right click on the file and select `Properties`. In the examples below, you will need to replace the file location with the directory in which you saved the file you downloaded from the course GitHub (e.g., "`C:/Users/ENT_6707/Data/Iris_data_csv_file.csv`") AND make sure the file suffix (e.g., .csv vs. .txt) is correct. Note the use of forward slashes, "`/`", and not back slashes "\", to separate levels of a directory.

Delimiters

You need to know which type of file you have because different file types use different characters (most commonly a comma or a tab) to separate the cells of data (= rows and columns of information). You won't actually see the commas, however, in comma separated files, so again looking at the `Properties` of the file can be useful. `R` needs to know the delimiting or separating character to correctly load data.

Example using `read.table()`

Load in the .csv (csv = comma separated values) version of the `Iris` data using the `read.table()` command. This command can handle a few different file types. The `file` argument is where you put your directory and file information. The `header=TRUE` argument tells R the first row of your data contains column names (which is almost always the case) and NOT actual data values. The `sep` argument tells R how values are separated. Again, for R to recognize rows and columns correctly, the `sep` argument needs to be specified correctly. Also note the use of quotation marks to input information for some arguments.

```
iris_df_csv <- read.table(file = "DIRECTORY/FORWARD SLASHES/Iris_data_csv_file.csv",
header = TRUE, sep = ",")
```

Provide a `summary()`, `head()`, `tail()`, and `str()` of the data after loading it into R. This is a useful step to ensure that the data were loaded correctly.

```
iris_df_csv <- read.table(file = "Iris_data_csv_file.csv",
                          header = TRUE, sep = ",")
summary(iris_df_csv)
```

```
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width   
 Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100  
 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300  
 Median :5.800   Median :3.000   Median :4.350   Median :1.300  
 Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199  
 3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800  
 Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500  
   Species         
 Length:150        
 Class :character  
 Mode  :character  
```

```
head(iris_df_csv) # top 6 rows of data
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
```

```
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

```r
tail(iris_df_csv) # bottom 6 rows of data
```

```
    Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
145          6.7         3.3          5.7         2.5 virginica
146          6.7         3.0          5.2         2.3 virginica
147          6.3         2.5          5.0         1.9 virginica
148          6.5         3.0          5.2         2.0 virginica
149          6.2         3.4          5.4         2.3 virginica
150          5.9         3.0          5.1         1.8 virginica
```

```r
str(iris_df_csv) # column type, summary info
```

```
'data.frame':   150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : chr  "setosa" "setosa" "setosa" "setosa" ...
```

If a different number than the default (6) rows is of interest when using `head()` or `tail()` use:

```r
tail(iris_df_csv, n = 2)
```

```
    Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
149          6.2         3.4          5.4         2.3 virginica
150          5.9         3.0          5.1         1.8 virginica
```

A word of caution

R will recognize your columns as either categorical (which R calls a `factor` or a `character`) OR numeric. In this case, `Species` is a character and the other columns/variables are numeric. The `str()` command helps you confirm R is doing this step correctly. A single, non-numeric character in a column will make R load in that column as a factor. You can feed data to `as.factor()` to convert, for example, numbers or characters to factors. Make sure you have a good reason for doing so (e.g., you recorded treatments, technically a category, as 1, 2, and 3 in your spreadsheet).

```
iris_df_csv$Species_factor <-  as.factor(iris_df_csv$Species)
iris_df_csv$Sepal.Length_factor <-  as.factor(iris_df_csv$Sepal.Length)
str(iris_df_csv)
```

```
'data.frame':	150 obs. of  7 variables:
 $ Sepal.Length       : num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width        : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length       : num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width        : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species            : chr  "setosa" "setosa" "setosa" "setosa" ...
 $ Species_factor     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ Sepal.Length_factor: Factor w/ 35 levels "4.3","4.4","4.5",..: 9 7 5 4 8 12 4 8 2 7 ...
```

```
summary(iris_df_csv)
```

```
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width   
 Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100  
 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300  
 Median :5.800   Median :3.000   Median :4.350   Median :1.300  
 Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199  
 3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800  
 Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500  
                                                                
   Species             Species_factor Sepal.Length_factor
 Length:150         setosa    :50     5      :10         
 Class :character   versicolor:50     5.1    : 9         
 Mode  :character   virginica :50     6.3    : 9         
                                      5.7    : 8         
                                      6.7    : 8         
                                      5.5    : 7         
                                      (Other):99         
```

Example using `readxl`

Download the `readxl` package to your hard drive using `R`. To achieve this, you can use the `Packages` tab in `RStudio` or using an R function:

`install.packages("readxl")`

After you have downloaded the package to your hard drive, you will not have to complete that step again (each package need only be installed once) unless you get a new computer or update

R. Next, load the package into your current R session. Whenever you close R and start a new session, you will have to repeat this step.

```r
library("readxl")
```

Load the data into R using the `read_excel()` command. This command will require a file type that ends in `.xlsx`. The `sheet` argument tells R which sheet in Excel to look for the data and `range` tells R where the top left and bottom right of your data frame occur in Excel. So, `range=B5:D10` would load in a rectangular data frame and the top left corner would be the cell B5 in Excel and the bottom right corner would be D10 (i.e., a data frame with three columns and 6 rows). Remember: in practice, your data frame will need to be a complete rectangle with no blank cells.

`iris_df_excel <- read_excel(path="DIRECTORY/FILE NAME WITH SUFFIX", sheet = "INSERT CORRECT SHEET NAME", range = "TOP LEFT CELL:BOTTOM RIGHT CELL")`

Provide a summary() of the data after loading it into R.

```r
iris_df_excel <- read_excel(path = "Iris_data_excel.xlsx",
                            sheet = "some_famous_data",
                            range = "A1:E151")

summary(iris_df_excel) # summary of data
```

```
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width   
 Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100  
 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300  
 Median :5.800   Median :3.000   Median :4.350   Median :1.300  
 Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199  
 3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800  
 Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500  
   Species         
 Length:150        
 Class :character  
 Mode  :character  
```

R Activity 1

Load in the .txt version of the `Iris` data using the `read.table()` command. Text files are tab delimited, so you will need to edit the code appropriately. Use `?read.table` and/or a Google search for something like "tab delimitation r read.table." Also, we have replaced some of the values in this .txt version of the data with a ".", which is how we record missing values (i.e., we have created some missing values in the data). You can use different identifiers (e.g., "-", "Missing") in your own work, but whatever you choose, be perfectly consistent across all missing values. Hint: you will need to tell R how to recognize those missing values using an additional argument in the `read.table()`.

1. How many rows are in the data?
2. How many `NA` values are there per column?
3. Provide the first 10 rows of the data.
4. Provide the last 3 rows of the data.