Module 1: Introduction and Learning R

Fundamentals of Genomic Prediction and Data-Drive Crop Breeding

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Contents

Section 1 : Overview of R and R Studio

What is R Software

- R is a free open-source software and programming language.
  - Summarize, explore and model the data
- Reproducible research (code +text).
- Huge learning Resources and Community Resource 1; Resource 2; Resource 3; and Resource 4
- Popular graphical capabilities.
- Dominant and useful variety of scientific disciplines.

What is R Studio

RStudio is an integrated development environment (IDE) for R

- Easy to control and manage the R scripts (point and click)
- View and interact with the objects in single environment.
- Easy to set your working directory and access files on your computer
- Graphics more accessible.
- More features see the link: Click here

Installation of R and R Studio

To download **R software** Click here and to download **R Studio** Click here. Go over these resources to know how to download and install R and R Studio; Link 1; Link 2; Link 3

R Package and Installation

What is R package?

- Bundles of codes build by the people to perform certain tasks
- Maintained at Comprehensive R Archive Network (CRAN)/Bioconductor/GitHub

Install from CRAN

install.package("ggplot2")

```
install.packages("ggplot2")
```

Resources CRAN: Link 1; Link 2; and Link 3

Install from Bioconductor Click Here

- Packages for life sciences related data
- BiocManager handles all of the packages hosted on Bioconductor

  install.packages("BiocManager")

  BiocManager::install("GWASTools")

```
# Installs BiocManager if not installed
  if (!require("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
  BiocManager::install(version = "3.20")
# Now Install R Package
  BiocManager::install("GWASTools")
```

Resources Bioconductor: Link 1; Link 2; Link 3; Link 4

Install from GitHub Click Here

install.packages("devtools")

devtools::install_github("tidyr")

```
# First Install Devtools
  install.packages("devtools")
# Then Intsall Package tidyr
  devtools::install_github("tidyr")
```

Resources GitHub: Link 1; Link 2; and Link 3

Section 2: R Essentials

- R works on expression and objects. It is like a big gigantic calculator
- For example, Users enters expression (for example 2+2)
  - Expression involves operators or function calls.
  - Expression work on Objects
- R evaluates it
- And Print the Results , 4

```
# Examples of R Exression
# Add
  2+2
```

```
## [1] 4
```

```
# Subtract
  4-2
```

```
## [1] 2
```

```
# Square
    2^2
```

```
## [1] 4
```

```
# Division
    10/2
```

```
## [1] 5
```

```
# Multiple
    5*5
```

```
## [1] 25
```

```
# Log
    log(10)
```

```
## [1] 2.302585
```

```
# Exponential
    exp(10)
```

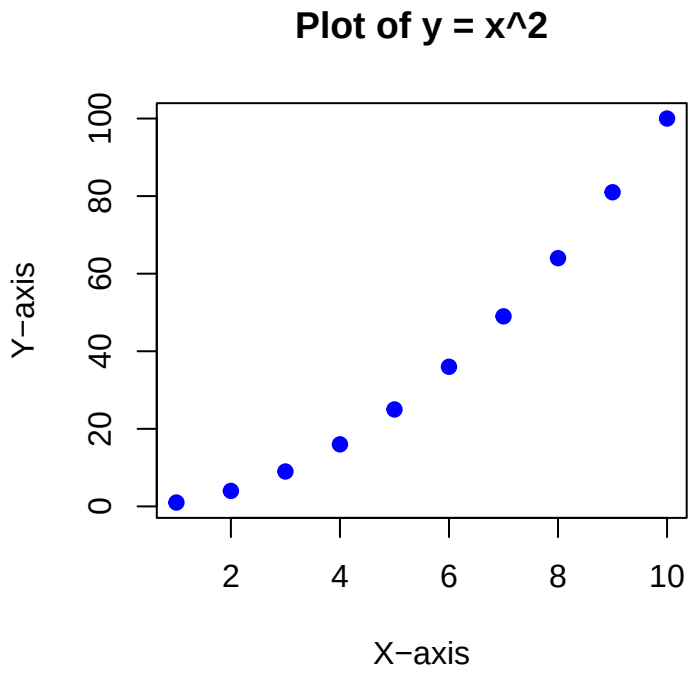
```
## [1] 22026.47
```

Function Calls

- Calling a function which involves one or more variables.
  - For example *sum(x)* or *plot (x)* are function call.
  - It is like expression or object.
- Function format is followed by a set of parentheses containing one or more arguments. *function(argument1, argument2,....)*. For example: *plot (height, weight)* here height and weight are the arguments for the function call *plot()*
- See more details as: *plot(height, weight, pch=2, color="red".....)*
- Positional matching; define the position of arguments *plot(x=height, y=weight, pch=2...)*

```
# Create sample data
  x <- seq(1, 10, by=1)  # x values from 1 to 10
  y <- x^2  # y values are the squares of x
```

```r
# Plot the data
plot(x, y,
     main="Plot of y = x^2",  # Title of the plot
     xlab="X-axis",            # Label for the x-axis
     ylab="Y-axis",            # Label for the y-axis
     col="blue",               # Color of the points
     pch=19)
```




```r
# Question: How many Arguments are in function plot()?
# Can you figure positional matching
```

Operators in R

- Operator is a symbol that tells the compiler to perform specific mathematical or logical manipulations.
- R language is rich in built-in operators and provides following types of operators.
- In R we have **Arithmetic Operators**, **Relational Operators**, and **Logical Operators**. Find more on Operators in R Click Here

Arithmetic Operators in R

Operator	Description
+	Addition
–	Subtraction
*	Multiplication
/	Division
^	Exponent
%%	Modulus (Remainder from division)
%/%	Integer Division

Logical Operators in R

Operator	Description
!	Logical NOT
&	Element-wise logical AND
&&	Logical AND
|	Element-wise logical OR
||	Logical OR

Relational Operators in R

Operator	Description
<	Less than
>	Greater than
<=	Less than or equal to
>=	Greater than or equal to
==	Equal to
!=	Not equal to

```
# RATIONAL OPERATORS (Returns TRUE or FALSE)
# Is 3 > 4
   3>4
```

```
## [1] FALSE
```

```
# Is 5 > 4
  5>4
```

```
## [1] TRUE
```

```
# Is 5==5
  5==5
```

```
## [1] TRUE
```

```
# Is 2 not equal to 3
  2!=3
```

```
## [1] TRUE
```

```
# LOGICAL OPERATORS
  vector <- c(1, 2, 3, 4, 5) # Creating a simple vector
# Check which elements are greater than 2 and less than 5
  result <- vector[vector > 2 & vector < 5]  # result will be c(3, 4)
  result
```

```
## [1] 3 4
```

Data Types in R

- Six data types are in R:

Character: “Block”, “Replication”

Numeric (real or decimal)- 2.4, 2, 10

Integer: 2L, 3L

Logical: TRUE, FALSE

Complex: 1+6i

- In R we use these function call to check type of data

class(): what kind of object is it

length(): how long it is

```
# NUMERIC TYPE
  num1 <- 5      # Integer
  num2 <- 3.14    # Decimal (floating-point)
  num2
```

```
## [1] 3.14
```

```
# INTEGER TYPE
  int_num <- 10L # Integer type
  int_num
```

```
## [1] 10
```

```
# CHARACTER TYPE
  char<- "Hello, R!"  # Character string
  char
```

```
## [1] "Hello, R!"
```

```
# LOGICAL
  True_type <- TRUE
  False_type <- FALSE
  False_type
```

```
## [1] FALSE
```

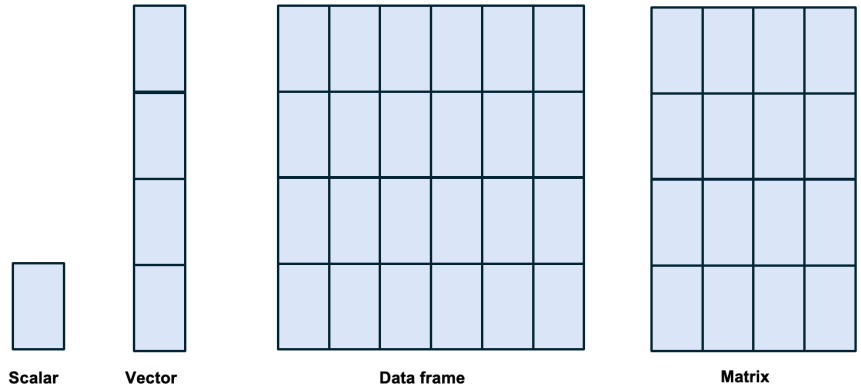
```
# COMPLEX
complex_num <- 3 + 2i  # 3 is the real part, and 2 is the imaginary part
complex_num
```

```
## [1] 3+2i
```

```
#Assignment operator in R is <-, why not Equal sign =
#Question: Could you use class() function to check the type of data
```

Data Structures in R

- In R we have following data structures:



Scalers

- A scalar object is just a single value like a number or a name.
- For example, a <- 100 X<-“name”
- Scalars don’t have to be numeric, they can also be characters (also known as strings)

```
# Examples of numeric scalers
    a <- 100
    a
```

```
## [1] 100
```

```
    b <- 3 / 100
    b
```

```
## [1] 0.03
```

```
    c <- (a + b) / b
    c
```

```
## [1] 3334.333
```

```
# Examples of character scalers
    d <- "ship"
    d
```

```
## [1] "ship"
```

```
    e <- "cannon"
    e
```

```
## [1] "cannon"
```

```
    f <- "Do any modern armies still use cannons?"
    f
```

```
## [1] "Do any modern armies still use cannons?"
```

```
# Could you add two scalers of type character?
```

Vectors

- Vector is a basic data structure in R which contains a list of same elements
- Vectors are created using function *c()*, concatenate the elements

```
# Example of Vector
  X<-c(1,2,3,4,5, 6) # five components
  X
```

```
## [1] 1 2 3 4 5 6
```

```
# Check length
  length(X)
```

```
## [1] 6
```

```
# Creating a vector of 2s eight times
    d<-rep(2, 8)
    d
```

```
## [1] 2 2 2 2 2 2 2 2
```

```
    d<-rep(c(1,2,3,4), 5)
    d
```

```
##  [1] 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4
```

```
    d<-rep(c(1:4), 2)
    d
```

```
## [1] 1 2 3 4 1 2 3 4
```

```
#INDEXING or SUBSETTING

    x[1] # Extract first element
```

```
## [1] 1
```

```
    x[c(1,2, 6)] # Extract first, second and 6 element in vector x (sub vector)
```

```
## [1] 1 2 6
```

```
    x[1:3] # Extracts elemnts from 1 to thrid position
```

```
## [1] 1 2 3
```

```
    x[-6] # Drops last element
```

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

```
    sum(x) # sum function adds all elements
```

```
## [1] 55
```

```
    mean(x) # get mean of x
```

```
## [1] 5.5
```

```
    min(x) # get minimal value
```

```
## [1] 1
```

```
    max(x) # Get maximum value
```

```
## [1] 10
```

Matrices

- Matrices are **numeric** array of rows and columns.
- Think as Stacked version of vectors where each row and column is basically a vector; Combination of n vectors
- We use function *matrix()*, to create a matrix in R

```
# Creat a matrix
## 2.3.1 First approach
    m2<-matrix(1:9, nrow = 3, ncol = 3) # Matrix with 3 rows and columns
    m2 # Matrix filled by rows
```

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

```
    m2<-matrix(1:9, nrow=3, ncol=3, byrow = TRUE)
# Assign names to rows and columns
    dimnames(m2)<-list(c("X","Y","Z"), c("A","B","C"))
    m2
```

```
##   A B C
## X 1 2 3
## Y 4 5 6
## Z 7 8 9
```

```
# Access and chnage the row and column names
    colnames(m2) # Get column names
```

```
## [1] "A" "B" "C"
```

```
    row.names(m2)
```

```
## [1] "X" "Y" "Z"
```

```
# Change the namaes of columns
    colnames(m2)<-c("A.1", "B.1", "C.1")
    m2
```

```
##   A.1 B.1 C.1
## X   1   2   3
## Y   4   5   6
## Z   7   8   9
```

```
# Change the name of just first column
    colnames(m2)[1]<-"B.B"
    m2
```

```
##   B.B B.1 C.1
## X   1   2   3
## Y   4   5   6
## Z   7   8   9
```

```
## Second approach to create the matrix

# We can use cbind() and rbind() functions, column and row bind
    x<-c(4,2,3,6) # create a vector of x
    y<-c(8,5,6,9) # create a vector of y
    m.col<-cbind(x,y) # now use cbind to bind two vectors column wise
    m.col
```

```
##      x y
## [1,] 4 8
## [2,] 2 5
## [3,] 3 6
## [4,] 6 9
```

```
    m.row<-rbind(x,y) # now use cbind to bind two vectors row wise
    m.row
```

```
##   [,1] [,2] [,3] [,4]
## x    4    2    3    6
## y    8    5    6    9
```

```
### Extract the elements of matrices.
## Square bracket [] indexing method. Elements can be accessed as var[row, column].
```

```r
# First create a new matrix
    m2<-matrix(1:12, nrow=3, ncol=4, byrow = TRUE)
    class(m2)
```

```
## [1] "matrix" "array"
```

```r
    m2[1,] # Extracts first row
```

```
## [1] 1 2 3 4
```

```r
    m2[,4] # Extracts  4th column
```

```
## [1]  4  8 12
```

```r
    m2[1,4] # Extracts first elemnt in row 1 and column 1
```

```
## [1] 4
```

```r
    m2[c(1,3), c(1,2)]
```

```
##      [,1] [,2]
## [1,]    1    2
## [2,]    9   10
```

```r
    m2[-1,] # Leaves first row
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    5    6    7    8
## [2,]    9   10   11   12
```

```r
## Modify the matrix
    m2[1,1]<-10 # Chnages single element in first row and first column
    m2
```

```
##      [,1] [,2] [,3] [,4]
## [1,]   10    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
```

```r
    m2[m2>11]<-20 # Chnage the elements in matrix greater than 12
    m2
```

```
##      [,1] [,2] [,3] [,4]
## [1,]   10    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   20
```

```r
# Add colum or row to existing matrix
    m2<-cbind(m2, c(4,8,12))
    m2
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]   10    2    3    4    4
## [2,]    5    6    7    8    8
## [3,]    9   10   11   20   12
```

```r
    x<-c(4,2,3,6,7) # create a vector of x
    m2<-rbind(m2,x)
    m2
```

```
##   [,1] [,2] [,3] [,4] [,5]
```

```
##     10    2    3    4    4
##      5    6    7    8    8
##      9   10   11   20   12
## x    4    2    3    6    7
```

```
# Note dimensions should be same to add vectors
    m2<-rbind(m2, c(1,2))
```

```
## Warning in rbind(m2, c(1, 2)): number of columns of result is not a multiple of
## vector length (arg 2)
```

```
    m2
```

```
##   [,1] [,2] [,3] [,4] [,5]
##     10    2    3    4    4
##      5    6    7    8    8
##      9   10   11   20   12
## x    4    2    3    6    7
##      1    2    1    2    1
```

```
# Check the dimensions of matrix
    dim(m2)
```

```
## [1] 5 5
```

```
# Transpose the matrix
    t(m2)
```

```
##              x
## [1,] 10 5  9 4 1
## [2,]  2 6 10 2 2
## [3,]  3 7 11 3 1
## [4,]  4 8 20 6 2
## [5,]  4 8 12 7 1
```

Data Frames

- Data Frames are more general than matrix, which has columns with different modes (numeric, character, factor).
- A data frame can be constructed by the *data.frame()*

```
# Create a data.frame
    Genotypes <- c("Genotyp1", "Genotype1", "Genotype2", "Genotype2")
    Replication <- c("1","1","2","2")
    Block<- c("Block1", "Block2", "Block1", "Block2")
    Yield<-c(2500,3500,3200,4500)
    mydata <- data.frame(Genotypes,Replication,Block,Yield)
    class(mydata)
```

```
## [1] "data.frame"
```

```
# Check the structure
    str(mydata)
```

```
## 'data.frame':    4 obs. of  4 variables:
##  $ Genotypes  : chr  "Genotyp1" "Genotype1" "Genotype2" "Genotype2"
##  $ Replication: chr  "1" "1" "2" "2"
##  $ Block      : chr  "Block1" "Block2" "Block1" "Block2"
##  $ Yield      : num  2500 3500 3200 4500
```

```r
# Change the varaibales
    mydata$Block<-as.factor(mydata$Block)
    mydata$Replication<-as.factor(mydata$Replication)
# Check the structure again
    str(mydata)
```

```
## 'data.frame':    4 obs. of  4 variables:
##  $ Genotypes  : chr  "Genotyp1" "Genotype1" "Genotype2" "Genotype2"
##  $ Replication: Factor w/ 2 levels "1","2": 1 1 2 2
##  $ Block      : Factor w/ 2 levels "Block1","Block2": 1 2 1 2
##  $ Yield      : num  2500 3500 3200 4500
```

```r
    levels(mydata$Replication) # Determine the number of levels for replication.
```

```
## [1] "1" "2"
```

```r
# Check column names
    names(mydata)
```

```
## [1] "Genotypes"   "Replication" "Block"       "Yield"
```

```r
# Subsetting or Indexing
    mydata[1:2,]
```

Genotypes	Replication	Block	Yield
Genotyp1	1	Block1	2500
Genotype1	1	Block2	3500

```r
    mydata[c(1,3),]
```

	Genotypes	Replication	Block	Yield
1	Genotyp1	1	Block1	2500
3	Genotype2	2	Block1	3200

```r
# Select columns using $ sign
    mydata$Yield # select Yield column
```

```
## [1] 2500 3500 3200 4500
```

```r
    mydata[mydata$Yield>3500,] # Extract row that has yield greater than 3500
```

	Genotypes	Replication	Block	Yield
4	Genotype2	2	Block2	4500

```r
# Subset based on factor levels
    help("subset")
    mydata2<-subset(mydata,Block=="Block1") # select just Block1
    mydata2
```

	Genotypes	Replication	Block	Yield
1	Genotyp1	1	Block1	2500
3	Genotype2	2	Block1	3200

```
    mydata2<-subset(mydata,Block=="Block1" & Replication=="1") # select just Block1
    mydata2
```

Genotypes	Replication	Block	Yield
Genotyp1	1	Block1	2500

Lists

- List is a data structure having components of mixed data types.
- To create a list we use *function list()*

```
# Creating a simple list
  my_list <- list(name = "Waseem", age = 39, height = 5.5, is_student = FALSE)
  my_list
```

```
## $name
## [1] "Waseem"
##
## $age
## [1] 39
##
## $height
## [1] 5.5
##
## $is_student
## [1] FALSE
```

```
# Mixed List: Creating a list with different types of elements
  mixed_list <- list(vector = c(1, 2, 3),
                     matrix = matrix(1:4, nrow = 2),
                     char = "Hello",
                     logical = c(TRUE, FALSE))
  mixed_list
```

```
## $vector
## [1] 1 2 3
##
## $matrix
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
##
## $char
## [1] "Hello"
##
## $logical
## [1]  TRUE FALSE
```

```r
# Creating a nested list
  nested_list <- list(person1 = list(name = "Alice", age = 25),
                      person2 = list(name = "Bob", age = 30))
# Extracting using $
# Accessing elements in the nested list
  person1_name <- nested_list$person1$name
  person2_age <- nested_list[["person2"]][["age"]]
```

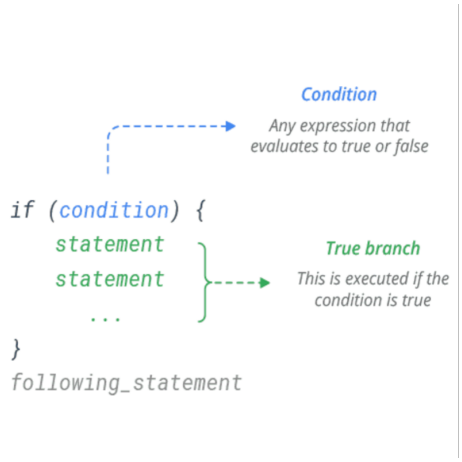
Section 3: Control Structures in R

Allow users to control the flow of execution of a series of R expressions

- Commonly used control structures are:
  - *if and else*: testing a condition and acting on it
  - *for*: execute a loop a fixed number of times
  - *while*: execute a loop while a condition is true
  - *repeat*: execute an infinite loop (must break out of it to stop)
  - *break*: break the execution of a loop
  - *next*: skip an interation of a loop

If statement

- Execute a block of code, if a specified condition is true



Adopted from: https://www.learnbyexample.org/r-if-else-elseif-statement/

```r
# Example 1
    x <- 10
    y <- 12
    if(x < y) {
      print("x is less than 12!")
    }
```

```
## [1] "x is less than 12!"
```

```r
# Example 2
    data("iris")
    if(mean(iris$Sepal.Length)!=mean(iris$Petal.Length)){
```

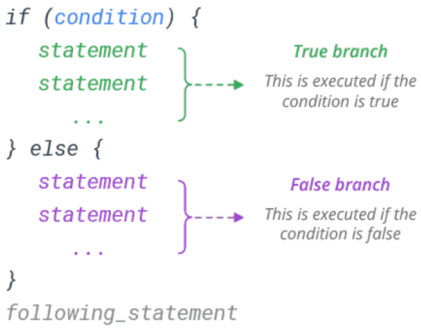
```
  print("It is true")
}
```

```
## [1] "It is true"
```

If and else statement

- Execute a block of code, if the condition is false

Syntax



Adopted from: https://www.learnbyexample.org/r-if-else-elseif-statement/

```
# Example 1
    x <- 10
    y <- 12
    if(x > y) {
      print("x is greater than y")
    } else {
      print("y is greater than x")
    }
```

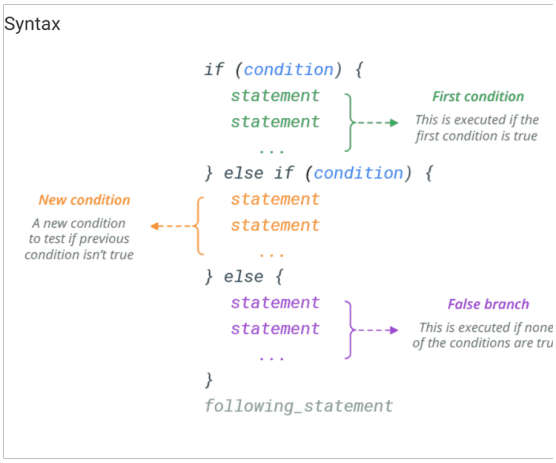
```
## [1] "y is greater than x"
```

```
# Example 2
    if(mean(iris$Sepal.Length)<mean(iris$Petal.Length)) {
      print("This is true and mean of sepal length is less than petal length")
    } else {
      print("This is false and mean of petal length is less than sepal length")
    }
```

```
## [1] "This is false and mean of petal length is less than sepal length"
```

Else If statement

- Specify a new condition to test, if the first condition is false.



Adopted from: https://www.learnbyexample.org/r-if-else-elseif-statement/

```
# Example 1
    x <- 12
    y <- 13
    if(x > y) {
      print("x is greater")
    } else if(x < y) {
      print("y is greater")
    } else {
      print("x and y are equal")
    }
```

```
## [1] "y is greater"
```

```
# Example 2
    x <- 12
    y <- 12
    if(x > y) {
      print("x is greater")
    } else if(x < y) {
      print("y is greater")
    } else {
      print("x and y are equal")
    }
```

```
## [1] "x and y are equal"
```

Multiple Condition Statements

- Join two or more conditions into a single if statement
- Logical operators: && (and), ||(or) and ! (not). && (and) expression is True, if all the conditions are true
- For more details Click Here

```
# Example of Multiple conditions
# First let us check means
    mean(iris$Sepal.Length)
```

```
## [1] 5.843333
```

```
    mean(iris$Petal.Length)
```

```
## [1] 3.758
```

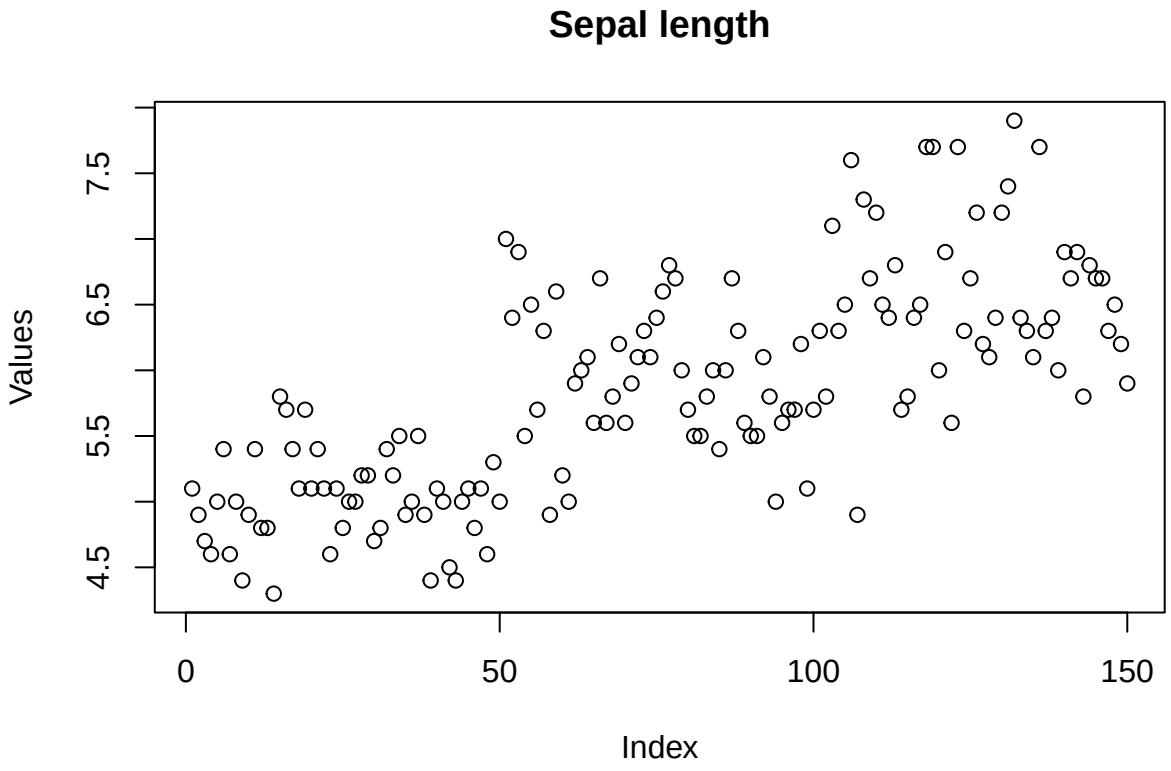
```
    mean(iris$Sepal.Width)
```

```
## [1] 3.057333
```

```
    mean(iris$Petal.Width)
```

```
## [1] 1.199333
```

```
# Test the multiple conditions using operators
    if(mean(iris$Sepal.Length)>mean(iris$Petal.Length) &&
       mean(iris$Sepal.Width)>mean(iris$Petal.Width) ) {
      plot(iris$Sepal.Length, main="Sepal length",
           ylab="Values")
    } else {
      plot(iris$Petal.Length, main="Petal length",
           ylab="Values")
    }
```



ifelse Function

- Function checks the condition for every element of a vector and selects elements from the specified vector depending upon the result.

Syntax

```
ifelse (condition, TrueVector, FalseVector)
```

Condition	True branch	False branch
Condition is checked for every element of a vector	Select element from this if the condition is true	Select element from this if the condition is false

```
# IFELSE Examlple
# Example for ifelse function
    iris$mycolumn<-ifelse(iris$Sepal.Length>iris$Petal.Length,
                          "TRUE", "FALSE")
    iris$mycolumn<-ifelse(iris$Sepal.Length<iris$Petal.Length,
                          iris$Sepal.Length/iris$Petal.Length, NA)
# Let us change the values of sepal length
    iris$Sepal.Length<-iris$Sepal.Length/3
    iris$mycolumn2<-ifelse(iris$Sepal.Length>iris$Petal.Length,
                           iris$Sepal.Length/iris$Petal.Length, NA)
```

Apply Function

- Repetitively perform an action on multiple chunks of data.
- Runs faster than loop and requires less coding

Basic function: *apply(X, MARGIN, FUN)*

- X is an array or matrix.
- Margin specifies whether you want to apply the function across rows (1) or columns (2)
- FUN is the function you want to use

```
### Apply funtion

# First create a matrix
    my.matrx <- matrix(c(1:10, 11:20, 21:30), nrow = 10, ncol = 3)
    my.matrx
```

```
##       [,1] [,2] [,3]
##  [1,]    1   11   21
##  [2,]    2   12   22
##  [3,]    3   13   23
##  [4,]    4   14   24
##  [5,]    5   15   25
##  [6,]    6   16   26
##  [7,]    7   17   27
##  [8,]    8   18   28
##  [9,]    9   19   29
## [10,]   10   20   30
```

```
    colnames(my.matrx)<-c("Length", "Breadth", "Width")
#Get sum across rows by using apply function
    sumrow<-apply(my.matrx, 2, mean)
    sumrow
```

```
##  Length Breadth   Width
##     5.5    15.5    25.5
```

```
# Creating own function
    sumrow<-apply(my.matrx, 1, function (x) sum(x)*2)
    sumrow
```

```
##  [1]  66  72  78  84  90  96 102 108 114 120
```

```
# Creating function outside and then apply
# Creating a function to calculate Cofficient of variation
    my.cofvar<- function(x){
      (sd(x)/mean(x))*100
    }
# Now apply it it dataframe or matrix
    cv<-apply(my.matrx,1, my.cofvar)
    cv
```

```
##  [1] 90.90909 83.33333 76.92308 71.42857 66.66667 62.50000 58.82353 55.55556
##  [9] 52.63158 50.00000
```

lapply function

- *lapply()* operates on list and always returns a list, 'l' in *lapply()* refers to 'list'
- Syntex: *lapply(X, FUN, ...)*
  - X is a list
  - Fun, function to be applied
- …. Additional arguments passed to function
- *lapply()* always returns a list whereas *apply()* can return a vector, list, matrix or array.
- No scope of MARGIN in *lapply()*, always to columns

```
## lapply Function
# Create a list first
    list.1<-list(Length=c(6,4,8,6.5),breadth=c(7,8,6,8),width=c(6.8,7.2,6.6,8))
    list.1
```

```
## $Length
## [1] 6.0 4.0 8.0 6.5
##
## $breadth
## [1] 7 8 6 8
##
## $width
## [1] 6.8 7.2 6.6 8.0
```

```
# Get mean of all lists using lapply function
    mean.all <- lapply(list.1,mean)
    mean.all # Mean for all the lists
```

```
## $Length
## [1] 6.125
##
## $breadth
## [1] 7.25
##
## $width
## [1] 7.15
```

sapply Function

- *syntax for* sapply()*is as follows:* sapply(x, fun,…..)*
- *sapply()* and *lapply()* work basically the same.
- The only difference is that *lapply()* always returns a list, whereas *sapply()* tries to simplify the result into a vector or matrix.
- Additional argument if simplify = F then *sapply()* returns a list similar to *lapply()*

```
## sapply Function
# Create a vector first
    vec<-c(1,2,3,4,5,6,7,8)
    mean.vec <- sapply(vec,mean)
    mean.vec
```

```
## [1] 1 2 3 4 5 6 7 8
```

```
# Additional argument simplify
    vec<-c(1,2,3,4,5,6,7,8)
    mean.vec <- sapply(vec,mean, simplify = FALSE) # RETURNS REULTS AS LAPPLY
    mean.vec
```

```
## [[1]]
## [1] 1
##
## [[2]]
## [1] 2
##
## [[3]]
## [1] 3
##
## [[4]]
## [1] 4
##
## [[5]]
## [1] 5
##
## [[6]]
## [1] 6
##
## [[7]]
## [1] 7
##
## [[8]]
## [1] 8
```

tapply Function

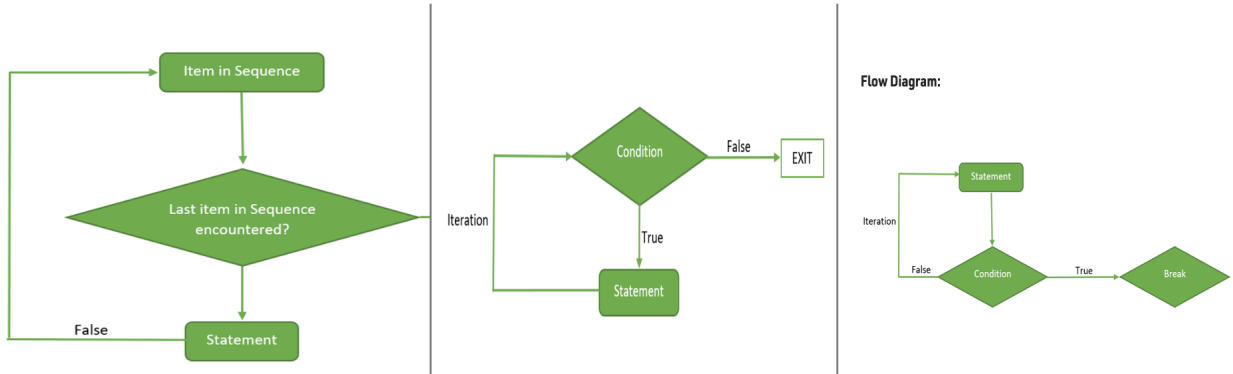
- *tapply()* function breaks the data set up into groups and applies a function to each group.
- The syntax: *tapply(x,INDEX,FUN,…,simplify)*
- x is required vector
- A grouping factor or a list of factors
- The function to be applied
- ….. Additional arguments
- Simplify return simplified results

```
# tapply Function
# First creating a simple data frame
    sample.data <- data.frame(Genotypes=c("Geno1","Geno2","Geno3","Geno4",
                                          "Geno5","Geno6","Geno7"),
    Yield=c(240, 220, 211, 230, 203, 241, 212),
    Type=factor(c("LR","LR","LR","CV", "CV","CV","LR")))
# Now apply tapply function to get mean for various factor levels
    mean<-tapply(sample.data$Yield, sample.data$Type, sum)
    mean
```

```
##  CV  LR
## 674 883
```

Loops in R

- Loops run in cycling or iterating manner. They control statement that allows multiple executions of a statement or a set of statements.



For loop **while loop** **repeat loop**

Adopted from https://www.geeksforgeeks.org/loops-in-r-for-while-repeat/

for loop

- For loop, loops our texts, data frames etc.
- Loops repeatedly depending upon the number of elements

Syntex

for (var in vector) {

statement(s)

}

while loop

- Runs a statement or a set of statements repeatedly unless the given condition becomes false.
- Entry controlled loop.

repeat loop

- repeat loop run the same statement or a group of statements repeatedly until the stop condition has been encountered
- Iterate infinitely if no condition given

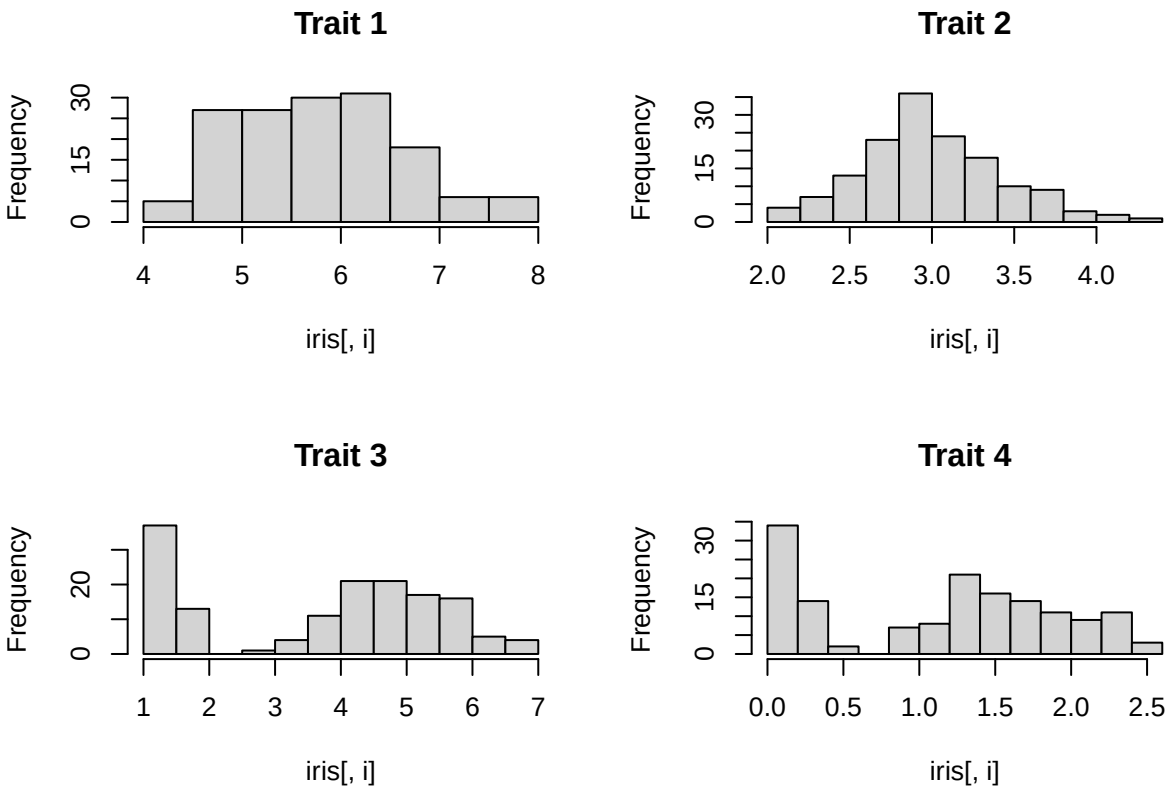
```
#  For loop
# Example 1
    for (i in 1:5) {
      print(i^3)
    }
```

```
## [1] 1
## [1] 8
## [1] 27
## [1] 64
## [1] 125
```

```
# Example 2
    x <- c(-8, 9, 11, 45)
      for (i in x) {
        y<-x/2
        print(y)
      }
```

```
## [1] -4.0  4.5  5.5 22.5
## [1] -4.0  4.5  5.5 22.5
## [1] -4.0  4.5  5.5 22.5
## [1] -4.0  4.5  5.5 22.5
```

```
# Example 3
# Histogram for iris data all columns
# Get iris data
    data(iris)
# Histograms
    par(mfrow = c(2, 2)) # Create 2 x 2 plotting matrix
    for (i in 1:ncol(iris[,c(1:4)])){ # loop over columns
      plot <- hist(iris[,i], main=paste("Trait", i))
      plot
    }
```




```
# Your Assignment to run a simpl example of WHILE AND REPEAT LOOPS
```

Section 4: String Manipulations

- String manipulation refers to operations that modify, analyze, or otherwise work with text data (strings) in programming.
- In R, there are numerous functions for manipulating strings, allowing you to perform actions like concatenation, substring extraction, pattern matching, and more.

Basic String Manipulations

- *nchar()*: number of characters
- *tolower()* :convert to lower case
- *toupper()*: convert to upper case
- *casefold()*: case folding
- *chartr()*: character translation
- *abbreviate()*: abbreviation
- *substr()*: substrings of a character vector
- *paste() or paste0()*: combine strings,*paste0()* removes spaces.

More extensive details can be found in book Handling and Processing Strings

- We will use library stringer to do more manipulations

```
# Load library
   library(stringr)
# First create a string
    x<-c("ICAR", "IRRI", "Training")
# Get number of characters
    nchar(x)
```

```
## [1] 4 4 8
```

```
# Convert to lower case
    y<-tolower(x)
    y
```

```
## [1] "icar"     "irri"     "training"
```

```
# Convert to upper case
    y<-toupper(x)
    y
```

```
## [1] "ICAR"     "IRRI"     "TRAINING"
```

```
# Upper or lower case conversion with casefold()
# upper case folding
    y<-casefold(x, upper = TRUE)
    y
```

```
## [1] "ICAR"     "IRRI"     "TRAINING"
```

```
# Replace 'IRRI' by 'IRRIGO'
    help("chartr")
    z<-"IRRI ICAR TRAINING"
    z2<-chartr("I", "G",z)
    z2
```

```
## [1] "GRRG GCAR TRAGNGNG"
```

```
# abbreviate species name column in iris data set
    iris$Species<- abbreviate(iris$Species, minlength = 3)
    head (iris$Species)
```

```
## [1] "sts" "sts" "sts" "sts" "sts" "sts"
```

```
#with package stringer
    head(abbreviate(iris$Species, minlength = 4, dot = FALSE,
                    strict = FALSE))
```

```
##   sts   sts   sts   sts   sts   sts
## "sts" "sts" "sts" "sts" "sts" "sts"
```

```
# Replace substrings with substr()
    help("substr")
    substr(iris$Species, 1, 3)<-"MY"
# Check similar function in stringr
# Concatenating strings
x<-c("ICAR", "Colloboration", "Genomic")
y<-c("IRR", "Training", "Prediction")
yx<- paste(x, y)
yx
```

```
## [1] "ICAR IRR"               "Colloboration Training" "Genomic Prediction"
```

```
# Without space
yx<- paste0(x, y)  # Output: "HelloWorld"
yx
```

```
## [1] "ICARIRR"                "ColloborationTraining" "GenomicPrediction"
```

Set Operations

- *union()*: set union
- *intersect()*: intersection
- *setdiff()*: set difference
- *setequal()*: equal sets identical() exact equality
- *is.element()*: is element
- *%in%()*: contains
- *sort()*: sorting
- *rep()*: repetition

```
# First create a two character vectors
    set1 = c("ICAR", "IRRI", "TRAINING", "PROGRAM")
    set2 = c("IRRI", "TRAINING", "PROGRAM", "2020")
# union of set1 and set2
    union(set1, set2) #discards any duplicated values in the provided vectors
```

```
## [1] "ICAR"     "IRRI"     "TRAINING" "PROGRAM"  "2020"
```

```
#Set intersection with intersect()
    intersect(set1, set2) # common between two
```

```
## [1] "IRRI"     "TRAINING" "PROGRAM"
```

```
# Set difference with setdiff()
    setdiff(set2, set1)
```

```
## [1] "2020"
```

```
# First create set 3 and set 4
    set3=c("IRRI", "ICAR", "TRAINING", "PROGRAM")
# Set equality with setequal()
    setequal(set1, set3)
```

```
## [1] TRUE
```

```
# Exact equality with identical()
    identical(set1, set3)
```

```
## [1] FALSE
```

```
# Element contained with is.element()
# Create elements
    elem1 = "IRRI"
    elem2 = "2020"
# elem1 in set 1
    is.element(elem1, set1) #if an element is contained in a given set of character strings
```

```
## [1] TRUE
```

```
# elem1 in set10?
    elem1 %in% set1 # alternative
```

```
## [1] TRUE
```

```
# Sorting with sort()
#sort() allows us to sort the elements of a vector, either in increasing order (by
#default) or in decreasing order using the argument decreasing:
# sort (decreasing order)
    set5<-c("boy", "girl", "apple")
    set6<-c("boy", "girl", "apple", "2020")
    sort(set5)
```

```
## [1] "apple" "boy"   "girl"
```

```
    sort(set6)
```

```
## [1] "2020"  "apple" "boy"   "girl"
```

```
#Repetition with rep()
# repeat 'x' 4 times
    help("rep")
    rep("Apple", 4)
```

```
## [1] "Apple" "Apple" "Apple" "Apple"
```

```
    help("paste")
# Check similar  functions in stringr
```

Regular Expressions

Patter matching and substitution

- *grep*: match a pattern
- *grepl*: similar to grep, output as logical
- *regexpr*: similar to grepl, output different and detailed
- *gregexpr*: similar to regexpr, output as list
- *sub()*: replacing one pattern with another one
- *gsub()*: replacing one pattern with another one (all occurrences)

All adopted from the same book given above

```
# Replacing first occurrence with sub()
# string
  help("sub")
  Rstring = c("The r Foundation",
              "for Statistical Computing",
              "R is FREE software",
              "r is a collaborative project")
# substitute 'R' with 'R
  sub("R", "RR", Rstring, ignore.case = TRUE)
```

```
## [1] "The RR Foundation"             "foRR Statistical Computing"
## [3] "RR is FREE software"           "RR is a collaborative project"
```

```
#Replacing all occurrences with gsub()
# substitute
  gsub("R", "RR", Rstring)
```

```
## [1] "The r Foundation"             "for Statistical Computing"
## [3] "RR is FRREE software"         "r is a collaborative project"
```

```r
## Splitting Character Vectors
  sentence = c("R is a collaborative project with many contributors")
# split into words
  strsplit(sentence, " ")
```

```
## [[1]]
## [1] "R"             "is"            "a"             "collaborative"
## [5] "project"       "with"          "many"          "contributors"
```

```r
# telephone numbers
  tels<-c("5_1_0_548_20")
  tels = c("510-548-2238", "707-231-2440", "650-752-1300")
# split each number into its portions
  strsplit(tels, "_")
```

```
## [[1]]
## [1] "510-548-2238"
##
## [[2]]
## [1] "707-231-2440"
##
## [[3]]
## [1] "650-752-1300"
```

```r
# Check similar  functions in stringr: your assignment

## Additional on Regular expressions
# Meta-characters
# string
  money = "$money"
# the naive but wrong way
  sub(pattern = "$", replacement = "", x = money)
```

```
## [1] "$money"
```

```r
# the right way in R
  sub(pattern = "\\$", replacement = "_", x = money)
```

```
## [1] "_money"
```

```r
# Sequences
#replaces the first match, while gsub() replaces all the matches.
# replace digit with '_'
  sub("\\d", "_", "the dandelion war 2010")
```

```
## [1] "the dandelion war _010"
```

```r
  gsub("\\d", "_", "the dandelion war 2010")
```

```
## [1] "the dandelion war ____"
```

```r
  sub("\\D", "_", "the dandelion war 2010")
```

```
## [1] "_he dandelion war 2010"
```

```r
  gsub("\\D", "_", "the dandelion war 2010")
```

```
## [1] "__________________2010"
```

```r
#Spaces and non-spaces
# replace space with '_'
  sub("\\s", "_", "the dandelion war 2010")
```

```
## [1] "the_dandelion war 2010"
```

```r
  gsub("\\s", "_", "the dandelion war 2010")
```

```
## [1] "the_dandelion_war_2010"
```

```r
# replace non-space with '_'
  sub("\\S", "_", "the dandelion war 2010")
```

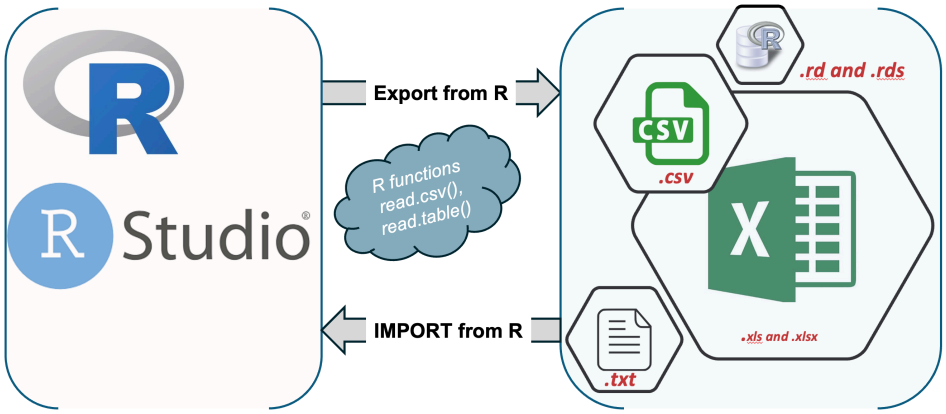
```
## [1] "_he dandelion war 2010"
```

```r
  gsub("\\S", "_", "the dandelion war 2010")
```

```
## [1] "___ _________ ___ ____"
```

Section 5: Importing and Exporting Data

- Data can be in .txt, .csv, .xls or .xlsx etc. In some cases data are also stored in data bases or servers.



In this section we will focus on reading and exporting the data files from the folder. More on data import and export in R can be found here Link 1, and Link 2

First we will know how to set the director and path to the folder

Set Working Directory

Ris always pointed at a directory on your computer

- Check current directory using function *getwd()*
- Set working directory using function *setwd()*
- Create working directory using function *dir.create()*

```r
# Setting a new working directory
  setwd("~/Documents/Research/Workshops/IRRI-IIRR_2024/Module1")
  #setwd("C:Documents/Research/Workshops/") # In windows, replace path
# Get a working directory
  getwd()
```

```
## [1] "/Users/waseemhussain/Documents/Research/Workshops/IRRI-IIRR_2024/Module1"
```

```
# Create a new working directory
  dir.create("Test")
```

```
## Warning in dir.create("Test"): 'Test' already exists
```

Import and Export .csv Files

- The *read.csv()* function is for reading ".csv" files.
- The syntex for reading .csv files is *read.csv(filename or path, header=TRUE, sep=" "...)*

```
# Import .Txt file
# Read .csv file data into R. File in in Data folder
  mydata<-read.csv("./Data/iris.txt", header = TRUE)
#Check this function to know more help("read.table")
# Export the file as .csv file
  write.csv(mydata, "./Data/iris_export.csv",
            row.names=TRUE)
```

Import and Export .txt Files

- The R base function *read.table()* is a general function that can be used to read a file in table format.
- The R base function *write.table()* is used to export the .txt files.
- A simple function is *write.table(x, file, append=FALSE,sep=" ",dec=".",row.names=TRUE,col.names=TRUE)*
- The data will be imported as a data frame. More can be found here Link 1; and Link 2

```
# Import .Txt file
# Read tabular data into R
  mydata<-read.table("./Data/iris.txt", header = TRUE, sep = "\t")
#Check this function to know more help("read.table")
# Export the file as .txt file
  write.table(mydata, "./Data/iris_export.txt",
              append=FALSE,sep="/t",row.names=TRUE,col.names=TRUE)
```

Import and Export .xlsx Files

- For reading excel files or sheets we will use the R package *readxl*, For more details Click here
- For writing the excel sheets or files we will use R package
- We will uplaod the files from the folder **Data**, which is sub-folder of main directory.
- More on reading and exporting excel files can be found here Link 1 and Link 2

```
# IMPORT EXCEL SHEETS
# Load the Library
  library(readxl)
# Read the excel file
# Specify sheet by INDEX
  my_data <- read_excel("./Data/iris.xlsx", sheet = 1)
# Specify sheet by Name
  my_data <- read_excel("./Data/iris.xlsx", sheet = "IRIS_COPY")
# EXPORT EXCEL FILES
```

```
  library(writexl)
# Writing the Existing file
  #write_xlsx(my_data, "./Data/myIrisExoprt.xlsx")
# Check with Library ("xlsx")
```

Import from Web

- Here we will read data directly from web having rice data available at http://ricediversity.org/data/index.cfm.
- The phenotypic data has 34 traits phenotyped for 413 genotypes.

```
# Read from web directly
  rice.pheno <- read.table("http://www.ricediversity.org/data/sets/44kgwas/RiceDiversity_44K_Phenotypes_
    header = TRUE, stringsAsFactors = FALSE, sep = "\t")
# First five rows and columns
  rice.pheno[1:5, 1:5]
```

HybID	NSFTVID	Flowering.time.at.Arkansas	Flowering.time.at.Faridpur	Flowering.time.at.Aberdeen
081215-A05	1	75.08333	64	81
081215-A06	3	89.50000	66	83
081215-A07	4	94.50000	67	93
081215-A08	5	87.50000	70	108
090414-A09	6	89.08333	73	101

Import and Export .rds

- To preserve the data structures, such as column data types (numeric, character or factor), saving or exporting files in *.rds* is best option. .rds is the R data format and can be also used to save big files.
- More on this can be found Click here

```
# Save an .rds object in folder
  saveRDS(my_data, file = "./Data/my_data.rds")
# Restore  or read the same object
  myrds<-readRDS(file = "./Data/my_data.rds")
```

Section 6: Data Wrangling and Manipulations

- There are many ways for data wrangling and manipulation tasks to perform in R. There are handful R packages to do Data wrangling and Manipulations and they fall in **tidyverse** R packages https://www.tidyverse.org/packages/.
- The **dplyr**, **tidyr**, **data.table** in tidyverse R packages provide a powerful and efficient way to work with data in R.
- Some resources on data wrangling and Manipulations are Link 1,Link 2,Link 3, Link 4, Link 5; and Link 6
- Here we will use some examples from dplyr and tidyr R packages

```r
# Install packages and load
  packages = c("dplyr", "tidyr", "reshape", "reshape2")
# Create a function which will install the package if it is not installed
  package.check <- lapply(packages, FUN = function(x) { # apply lapply to list of packages
    if (!require(x, character.only = TRUE)) {
      install.packages(x, dependencies = TRUE) # install dependencies if required'library(x, character.
      }
    })

# Read iris data file
  iris<-read.csv(file="./Data/iris.csv", header = TRUE)
  iris$Species.abr<-abbreviate(iris$Species, minlength = 3)
######################PACKAGEDPLYR#####################################################

# Function FILTER
  iris1<-iris %>% filter(Species == "setosa", Species.abr == "sts")
# same in base R
  iris2<-iris[iris$Species == "setosa" & iris$Species.abr == "sts", ]
# Function ARRANGE
  iris1<- iris1 %>% arrange(Sepal.Length)
# Use desc() to order a column in descending order:
    iris1<-iris1%>% arrange(desc(Sepal.Length))
#Choose rows using their position with slice()
    iris %>% slice(1:5)
```

Lines	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Species.abr
1	5.1	3.5	1.4	0.2	setosa	sts
2	4.9	3.0	1.4	0.2	setosa	sts
3	4.7	3.2	1.3	0.2	setosa	sts
4	4.6	3.1	1.5	0.2	setosa	sts
5	5.0	3.6	1.4	0.2	setosa	sts

```r
# in base R
    test<-iris[c(1,5, 6:10), ]
# Drop
    iris1<-iris %>% slice(-c(1:5))
# Function SELECT
# Select columns by name
    iris1<-iris %>% select(Sepal.Length, Sepal.Width)
# Select all columns between
    iris1<-iris %>% select(Sepal.Length:Petal.Width)
# Select all columns except one
    iris1<- iris %>% select(!Sepal.Length)
    #iris %>% select(!c(Sepal.Length, Petal.Width))
# Select all columns ending with length
    iris1<-iris %>% select(starts_with("Species"))
    iris1<-iris %>% select(ends_with("abr"))
# more: starts_with(), ends_with(), matches() and contains() (Your assignment)
    #select(iris, contains("Length"))
    iris1<-iris %>% select(contains("."))
    #iris1<-select(iris, contains("."))
# Function MUTATE
```

```r
# Add single column
    iris1<-iris %>% mutate(Additional = Sepal.Length/ 100)
# Add several columns
    iris1<-iris%>%mutate(Additional2 = sqrt(Sepal.Length), Check = "vrs")
# What is alternative in R base function (Your Assignment)
# Function SUMMARISE
  summary<-iris %>% summarise(Sepal.Length = mean(Sepal.Length, na.rm = TRUE))
  summary
```

Sepal.Length
5.843333

```r
  iris %>% summarise(Mean=mean(Sepal.Length, na.rm = TRUE), SD=sd(Sepal.Length, na.rm = TRUE))
```

Mean	SD
5.843333	0.8280661

```r
# Summaries with column names
  iris %>% summarise(mean(Sepal.Length, na.rm = TRUE),mean(Petal.Length, na.rm = TRUE))
```

mean(Sepal.Length, na.rm = TRUE)	mean(Petal.Length, na.rm = TRUE)
5.843333	3.758

```r
# Summarise a subset of rows
  iris%>%
    slice(1:10) %>%
    summarise(sum(Sepal.Length))
```

sum(Sepal.Length)
48.6

```r
#Function DISTINCT
  iris%>% distinct(across(Species))
```

Species
setosa
versicolor
virginica

```r
################################PIPE MULTIPLE TASKS##############################
# Pipe to perform multiple tasks
  test<-iris %>%
    filter(Species == "setosa")%>% # filter
    mutate(SePAL.2=Sepal.Length/ 10)%>% # create new column
    select(SePAL.2, Species) # and select the column
# Another pipe example
```

```
    test2<- iris%>%
    group_by(Species) %>%    # Group by these variables
    summarise(  # Summarise data
    length.mean = mean(Sepal.Length),
    width.mean = median(Sepal.Width),
    n = n()
    )
# Assignmet: Check with Tidyr, reshape2, data.table functions
```

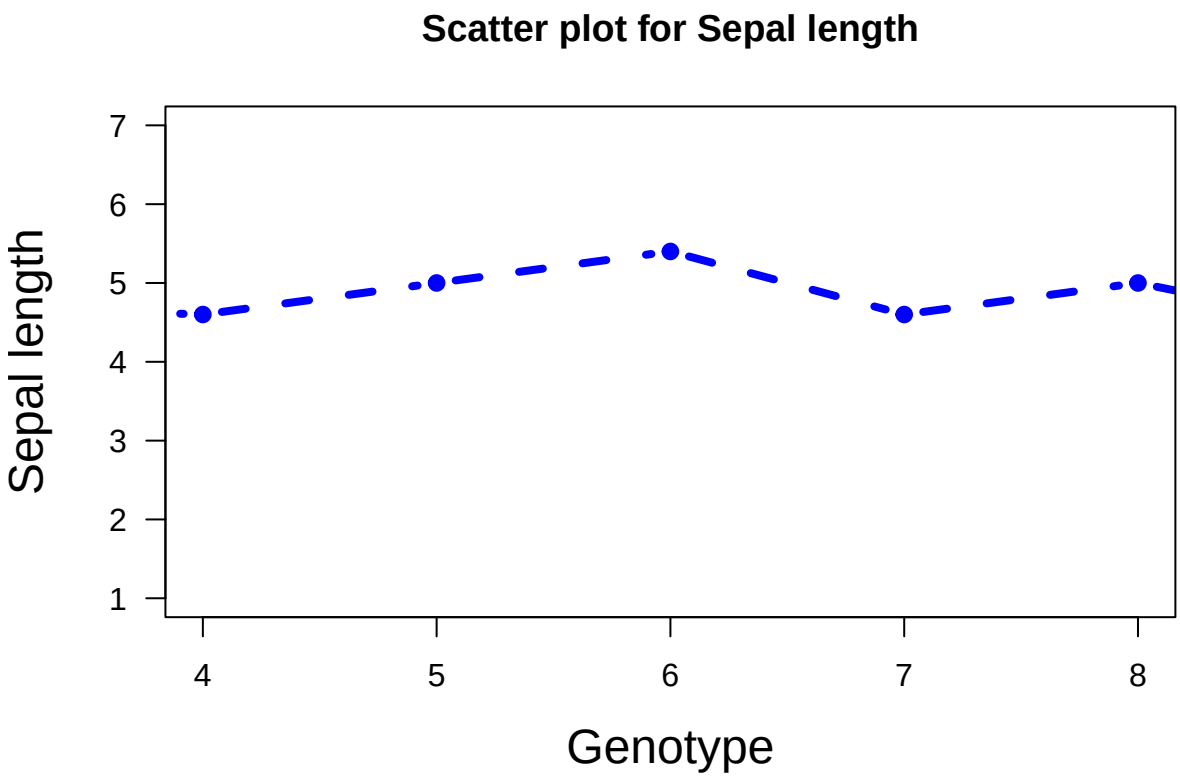
Section 7: Basic and Advanced Graphics

Basic Graphics with R

- In this section we will learn basic data visualization using base function *plot()*.
- More on the basic graphics with inbuilt functions in R can be found Click here.
- Here will will plot various plots like scatter and line plot, bar plot, histograms etc.,

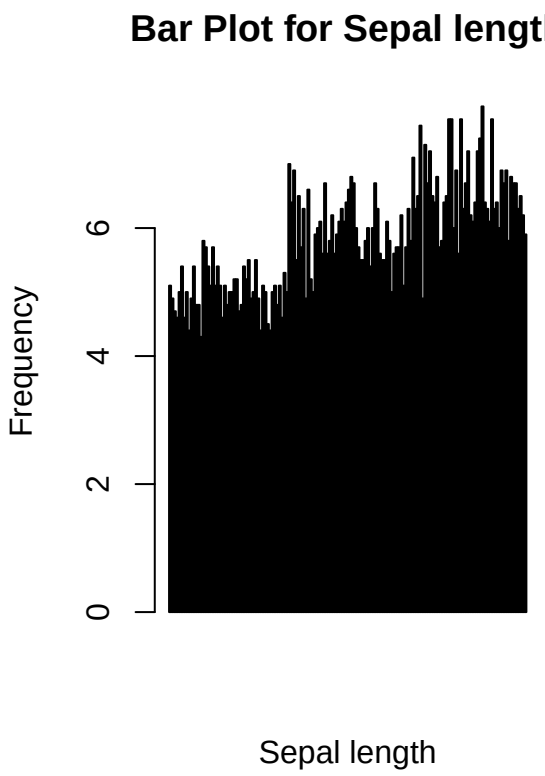
Scatter Plot

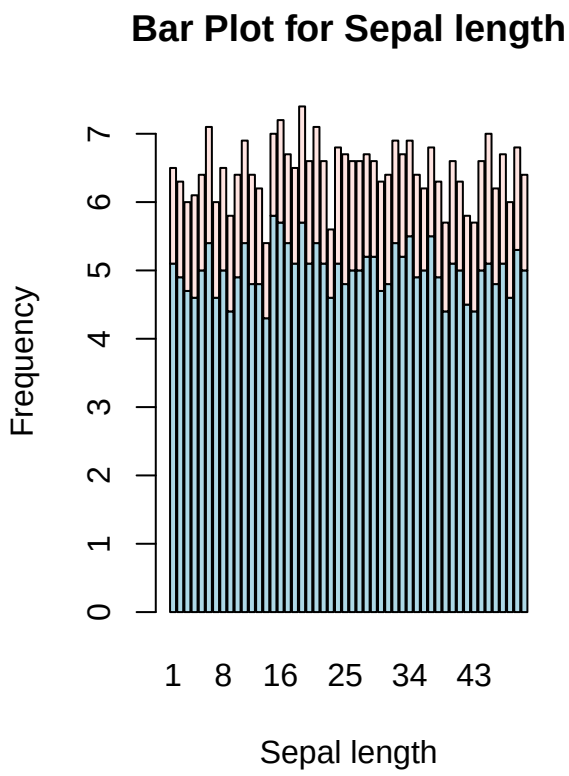
```
#SCATTER PLOT
  plot(iris$Sepal.Length,
# Add features
  xlab="Genotype", # Add x label name
  ylab="Sepal length",  # add y lable name
  main="Scatter plot for Sepal length",# add main title
  type="b",
# Different types of graphsx
  las=1, #0 is the default, with text always parallel to its axis.
  pch=20,
  cex=1,
  col="blue",
  lty=2, # line type
  lwd=4, # line or point width
  font.lab = 1, # font type
  col.lab="black",
  cex.lab = 1.5, # size of axis
  xlim=c(4,8), ylim=c(1,7), # adjust limits of axis
)
```



Barplot

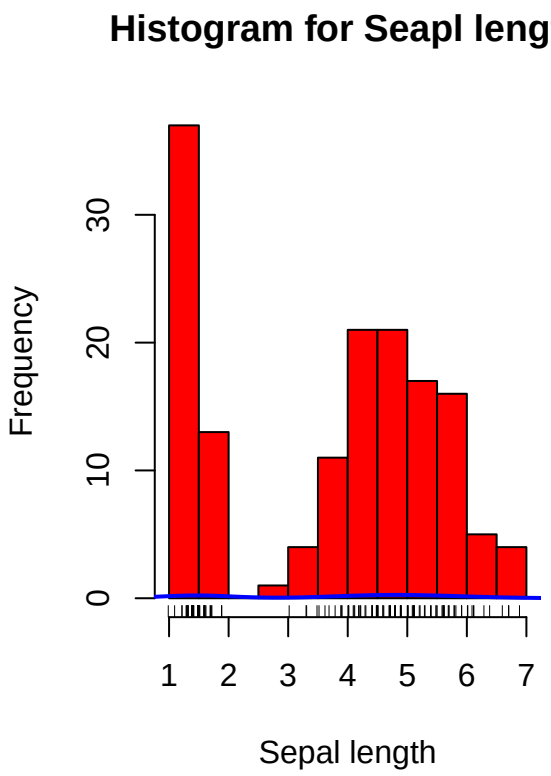
```
# BAR PLOTS
  par(mfrow = c(1,2)) # Plot in One row with two Columns
  barplot(iris$Sepal.Length,
  main="Bar Plot for Sepal length",
  xlab="Sepal length", ylab="Frequency",
  col="blue",
  width = 5,
  horiz = FALSE)
  #?barplot
# do more on bar plots
  barplot(cbind(Sepal.Length, Petal.Length)~Lines, data=iris,
        subset = Species=="setosa",
        col = c("lightblue", "mistyrose"),
        main="Bar Plot for Sepal length",
        xlab="Sepal length", ylab="Frequency")
```

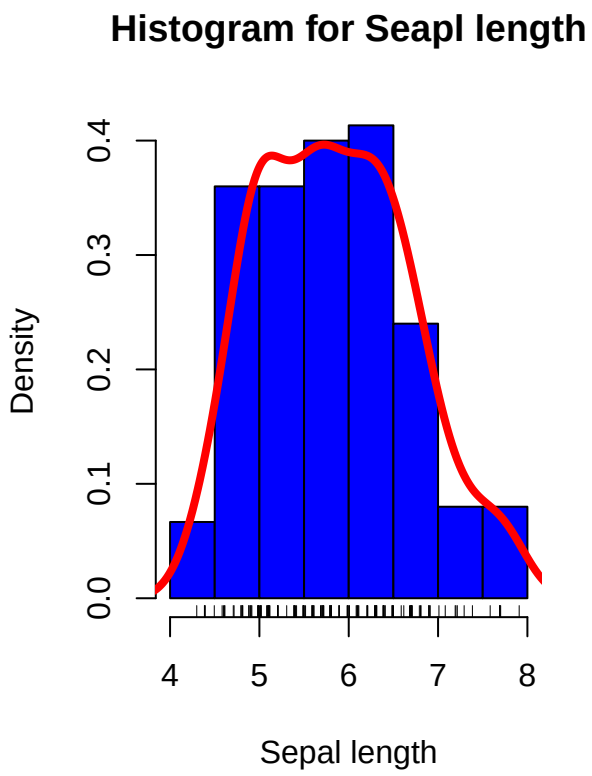




Histograms

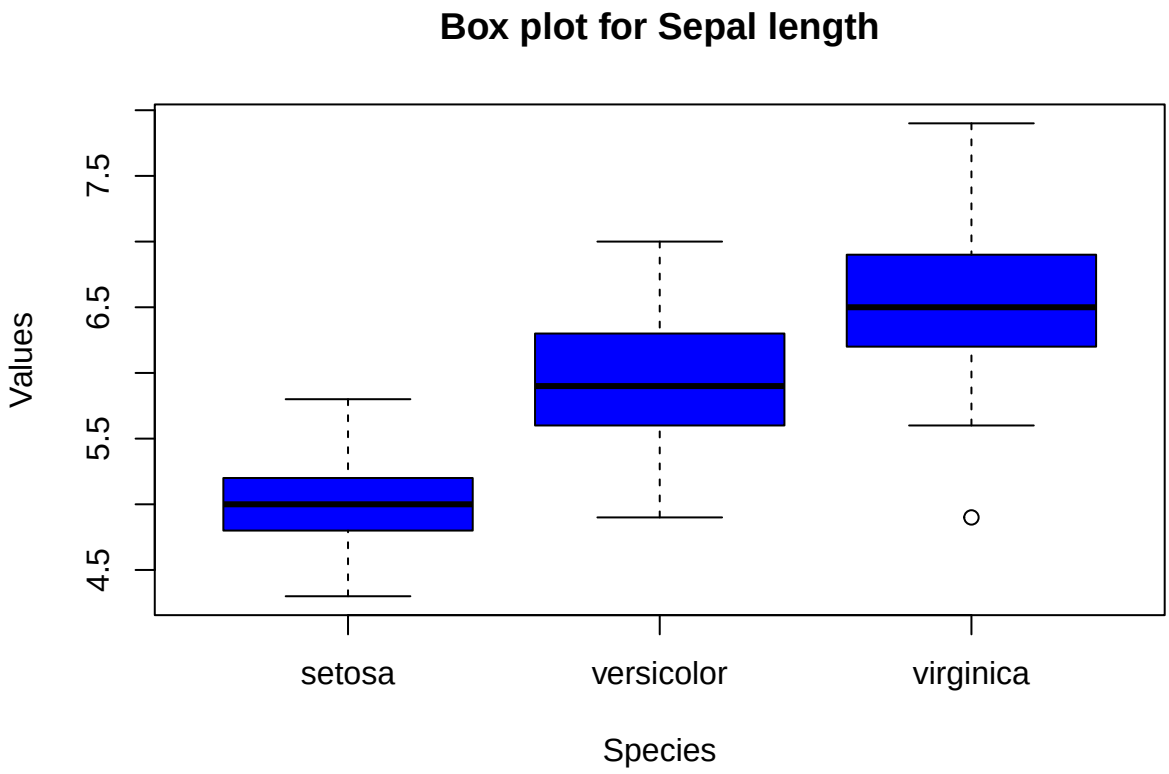
```
  par(mfrow = c(1,2))
  hist(iris$Petal.Length,
     freq=TRUE,
     breaks=12,
     col="red",
     xlab="Sepal length",
     main="Histogram for Seapl length")
  rug(jitter(iris$Petal.Length)) #   add rugs
  lines(density(iris$Petal.Length), col="blue", lwd=2) # add density curve
# Another graph
   hist(iris$Sepal.Length,
     freq=FALSE,
     breaks=8,
     col="blue",
     xlab="Sepal length",
     main="Histogram for Seapl length")
  rug(jitter(iris$Sepal.Length)) #   add rugs
  lines(density(iris$Sepal.Length), col="red", lwd=4) # add density curve
```





Boxplots

```
#BOX PLOTS
boxplot(Sepal.Length ~ Species, data=iris,
        main="Box plot for Sepal length",col="blue",
        xlab="Species",
        ylab="Values")
```



Advanced Graphics with ggplot2

- *ggplot2 ()* is a powerful R package for data visualization (https://ggplot2.tidyverse.org/)
- It uses "Grammar of Graphics" to create customizable and complex plots intuitively, making it ideal for both beginners and advanced users.
- It seamlessly integrates with data frames and extensive community support further enhance its appeal.

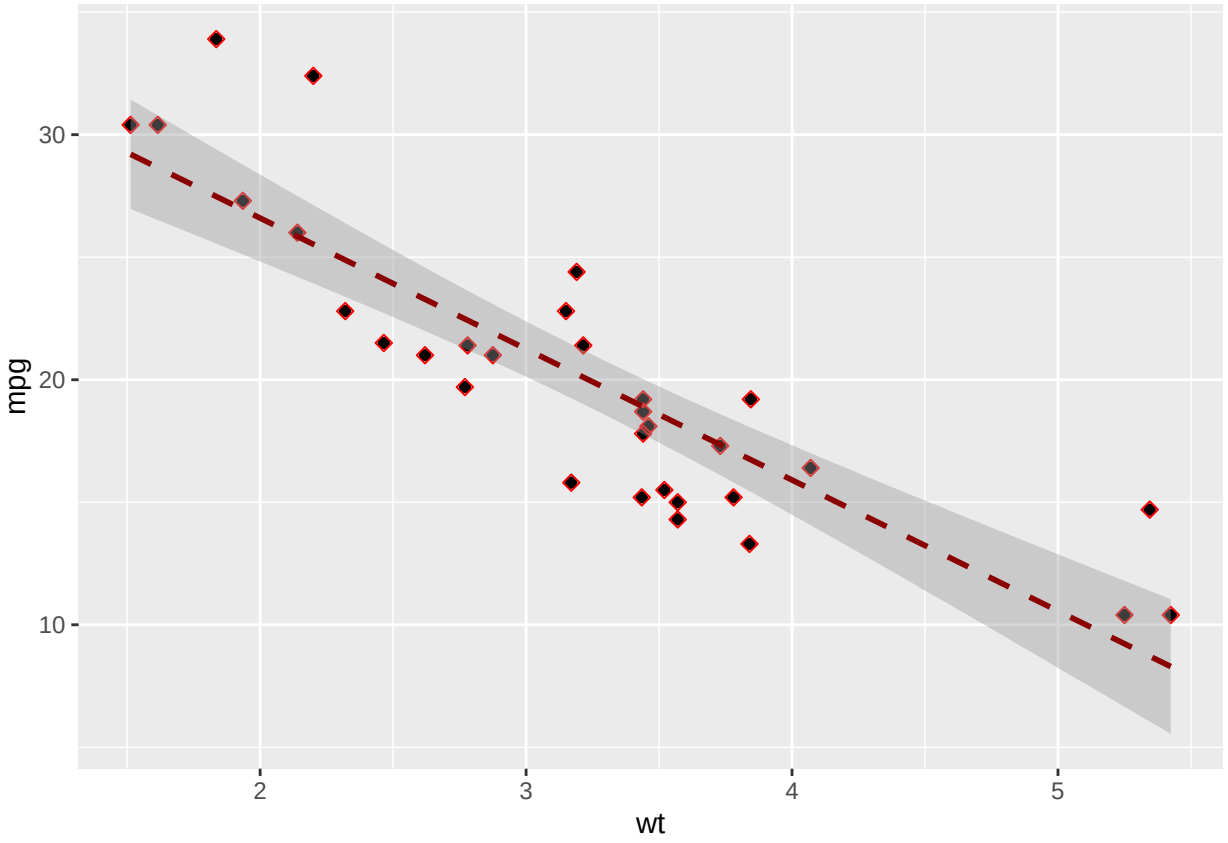
Best ggplot2 Resources: Top 50 GRAPHS in ggplot2, ggplot2 Tutorial, TOP 25 PLOTS in ggplot 2, VISUALIZATION in ggplot2; Cheet Sheet ggplot2; MAKE THIS YOUR FRIEND ##

- Here we will plot some graphs using ggplot 2 and give you flavor how beautiful ggplot2 is in graphics
- We will also learn how to export high resolution figures from R Click here for more

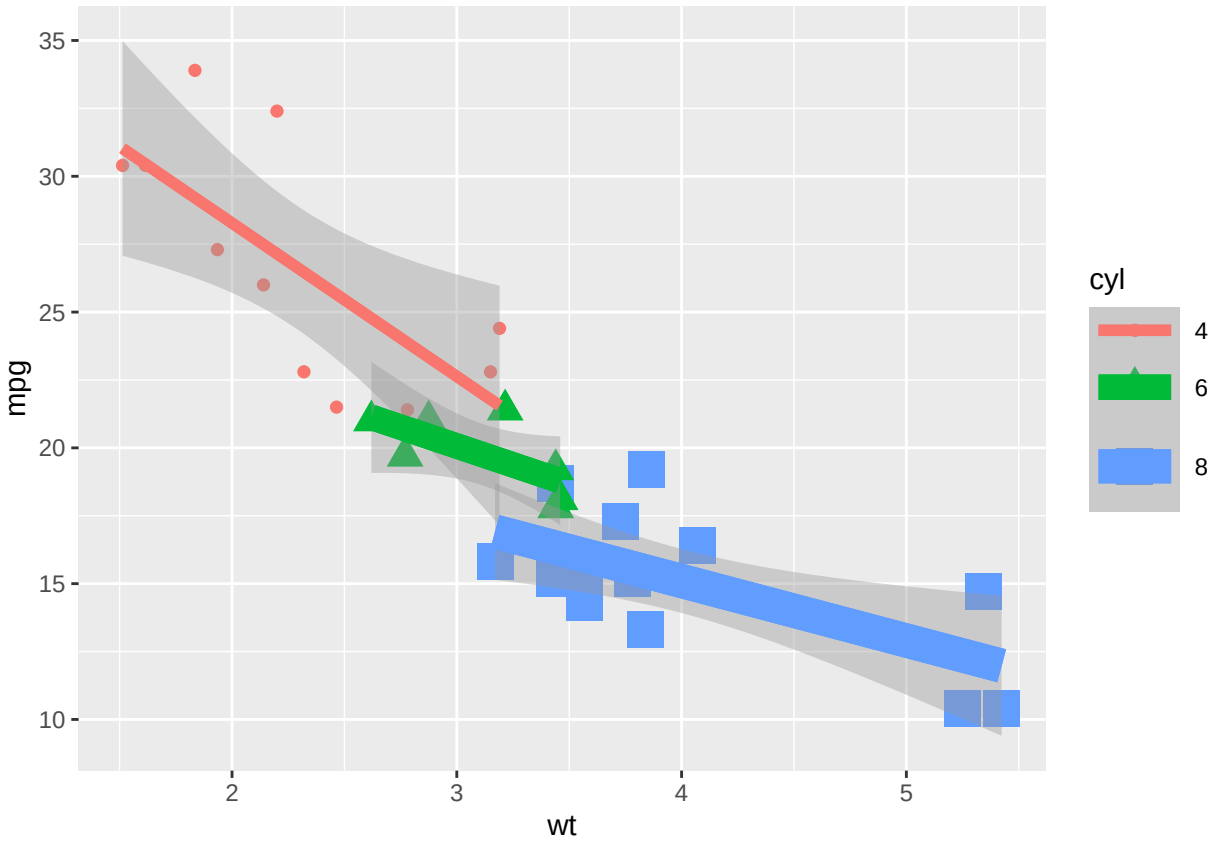
SCATTER PLOT

```
# SCATTER PLOT
# Install and Load the libraries
  packages = c("ggplot2", "grid","ggthemes","plotly")
# Create a function which will install the package if it is not installed
  package.check <- lapply(packages, FUN = function(x) { # apply lapply to list of package
    if (!require(x, character.only = TRUE)) {
      install.packages(x, dependencies = TRUE) # install dependencies if required
      library(x, character.only = TRUE) # Load the package
      }
    })
# Use ggplot Function to plot
  ggplot(mtcars, aes(x=wt, y=mpg))+
```

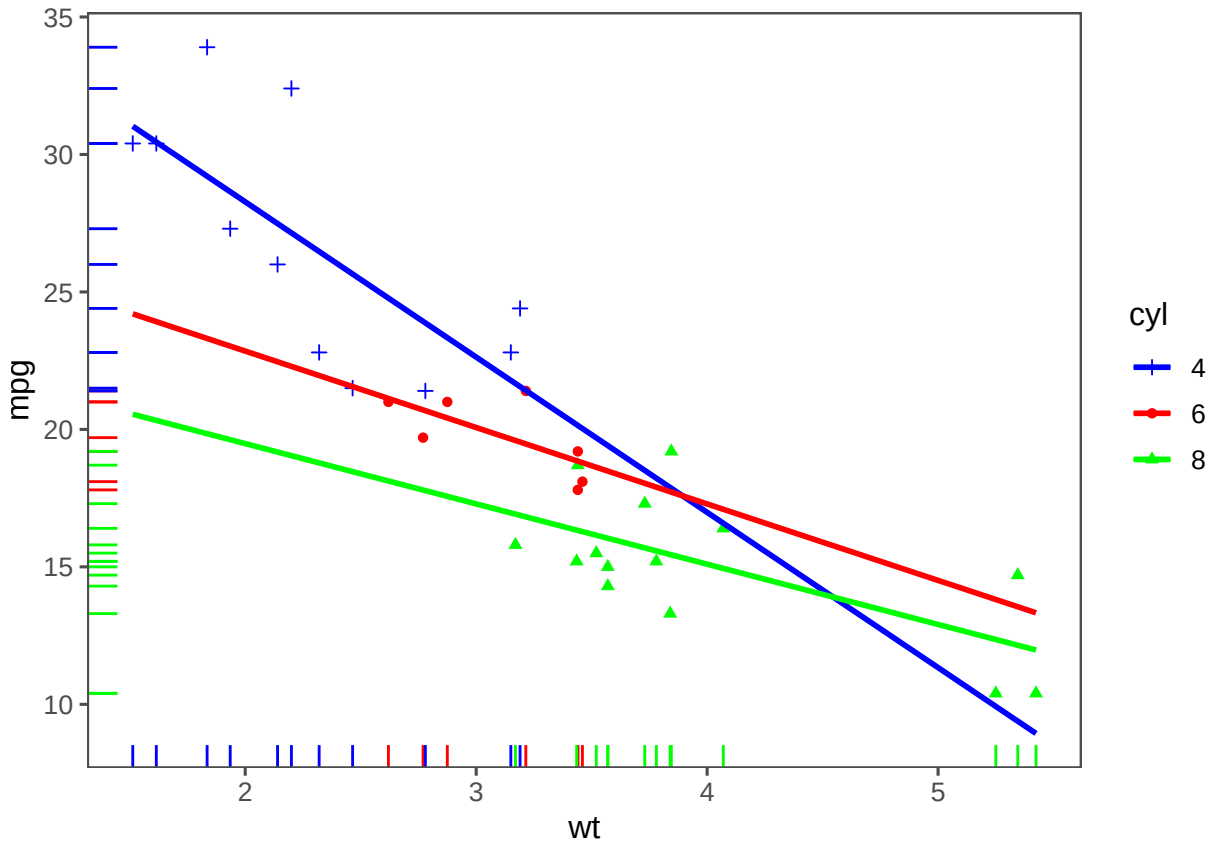
```
  geom_point()+
  geom_point(size=2, shape=23, color="red")+ # Change the point size, and shape
  #geom_smooth(method=lm)+  # Add the regression line
  #geom_smooth(method=lm, se=FALSE)+ # Remove the confidence interval
  geom_smooth(method=lm, se=TRUE, linetype="dashed",
              color="darkred") # Change the line type and color
```



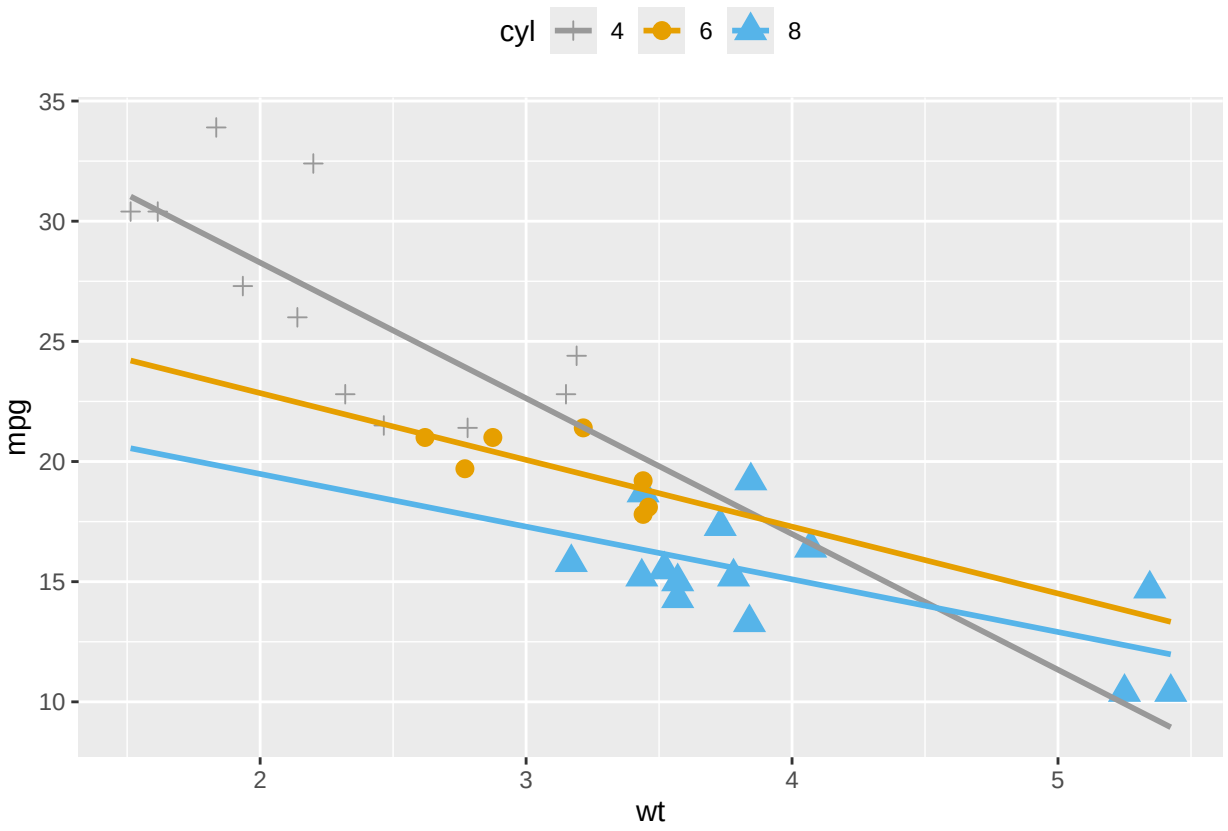

```
# SCATTER PLOT MULTIPLE GROUPS
# Change point shapes by the levels of cyl
  mtcars$cyl<-as.factor(mtcars$cyl)
  ggplot(mtcars, aes(x=wt, y=mpg, shape=cyl, color=cyl, size=cyl)) +
    geom_point()+
    geom_smooth(method=lm)+
    geom_smooth(method=lm, se=FALSE, fullrange=FALSE)
```




```
# Change point shapes and colors manually
  ggplot(mtcars, aes(x=wt, y=mpg, color=cyl, shape=cyl))+
    geom_point()+
    geom_smooth(method=lm, se=FALSE, fullrange=TRUE)+
    scale_shape_manual(values=c(3, 16, 17))+
    scale_color_manual(values=c('blue','red', 'green'))+
    theme(legend.position="top")+
    geom_rug()+
    theme_few()
```




```
# Change the point sizes manually
  ggplot(mtcars, aes(x=wt, y=mpg, color=cyl, shape=cyl))+
    geom_point(aes(size=cyl)) +
    geom_smooth(method=lm, se=FALSE, fullrange=TRUE)+
    scale_shape_manual(values=c(3, 16, 17))+
    scale_color_manual(values=c('#999999','#E69F00', '#56B4E9'))+
    scale_size_manual(values=c(2,3,4))+
    theme(legend.position="top")
```

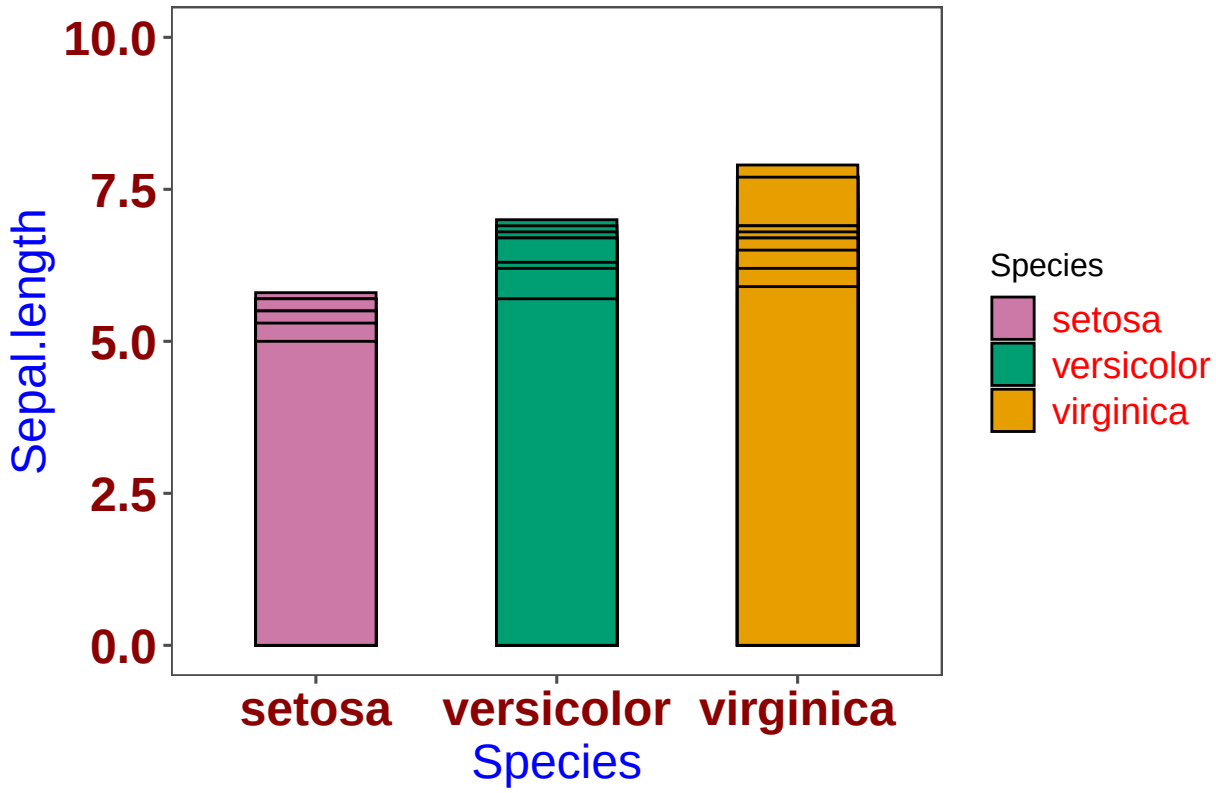


BAR PLOT

- Here will also learn how to export the figures. To export we need to function first. For example, we will export as .png and rest of code followed the function and close it using *dev.off()* function at end.
- In R, the *dev.off()* function is used to close the current graphical device. When you create a plot, R opens a graphical device to display it (such as the R plotting window or a file like a PDF or PNG). Once you are done with your plotting and no longer need that graphical device, you call dev.off() to close it.

```
  #png(file="myBar_plot.png", width=14, height =10,
      #units = 'in',res=700)  # function to Export as .png
  #tiff(""myBar_plot.tiff", units="in", width=5, height=5, res=500) # export as tiff
 # pdf(""myBar_plot.pdf", width = 4, height = 4) # Export as PDF
# ggplot 2 function
  ggplot(mydata, aes(x = Species, y = Sepal.Length, fill=Species))+
    #geom_bar(stat = "identity", width=0.5, color="black")+
    geom_bar(stat = "identity", width=0.5,
             color="black", position=position_dodge())+
    theme_few()+ # Select the theme
    ylim(0, 10)+ # Set Y limit
    labs(title = "", x = "Species", y = "Sepal.length")+ # add titles
    theme (axis.title.x = element_text(color="blue", size=18), # modify axis titles
           axis.title.y = element_text(color="blue", size=18))+
    theme(axis.text= element_text(face = "bold", color = "darkred", size =18))+
    scale_fill_manual(values=c("#CC79A7", "#009E73", "#e79f00"))+ # Manual coloring
    theme(legend.title = element_text(colour="black", size=12),
          legend.position = "right",
```

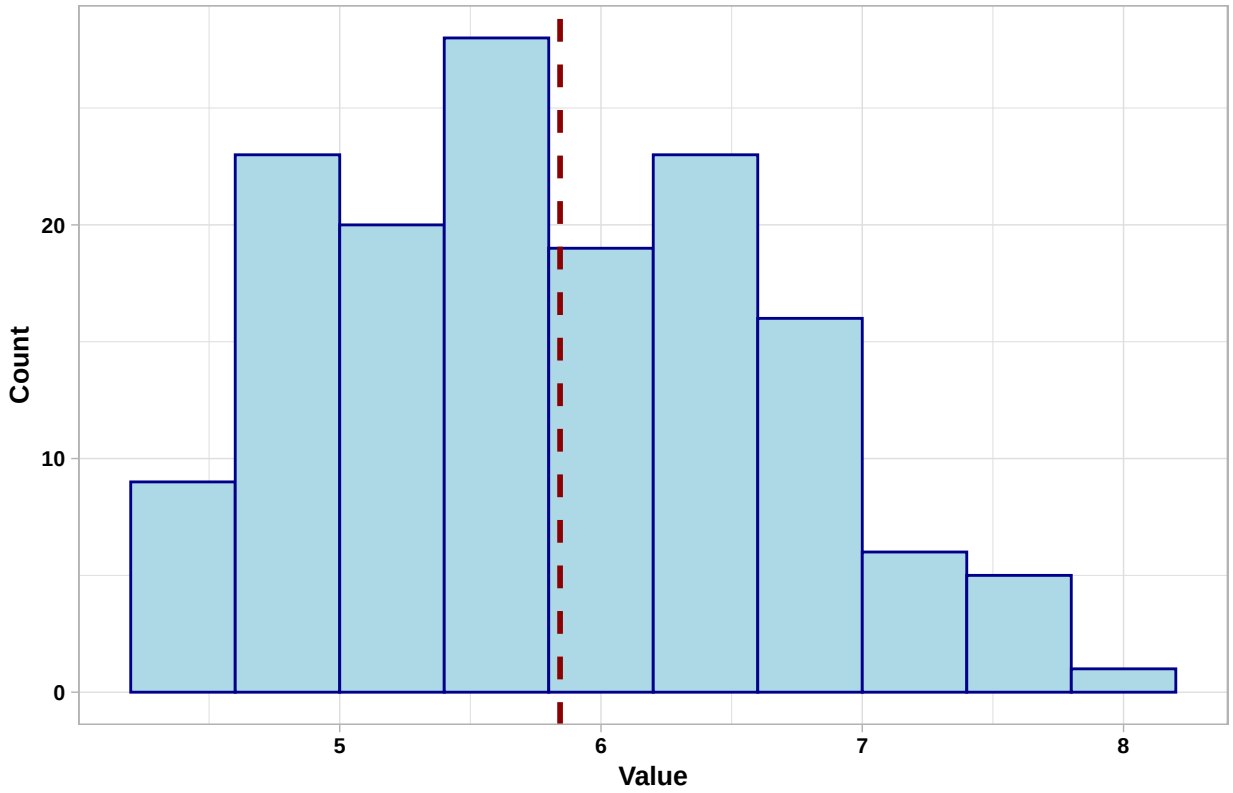
```
        legend.text = element_text(colour="red", size=14))
```




```
  #dev.off()
```

HISTOGRAMS

```
# Hiostograms in ggplot2
ggplot(mydata, aes(Sepal.Length)) +
  geom_histogram(color="darkblue", fill="lightblue", bins = 10)+
  theme_light()+
# adjust x values and breaks
  #geom_histogram(breaks=seq(4, 8, by =0.5), color="darkblue", fill="lightblue")+
  geom_vline(aes(xintercept=mean(Sepal.Length)), # adding the line to represent mean
             color="darkred", linetype="dashed", size=1)+
  labs(title="",x="Value", y = "Count")+
  theme (plot.title = element_text(color="black", size=14, face="bold", hjust=0),
         axis.title.x = element_text(color="black", size=10, face="bold"),
         axis.title.y = element_text(color="black", size=10, face="bold")) +
  theme(axis.text= element_text(face = "bold", color = "black", size = 8))
```



- For more advanced plots check my GitHub Page Additional ggplot2
- For additional Correlation and Heatmap plots in R please check my GitHub Page Correlation Plots**

Section 8: Writting Own Functions

R function is pieces of code that perform a desired operation on given input(s) and return the output back to the user. In this section we will learn how to build own R functions and perform tasks. Building your own functions in R is straightforward. You can define a function using the ***function()*** keyword.

Here's the basic syntax:

Syntax

*functionName <- **function**(argument1, argumen2…) {*

#function Body

***return**(varc)*

}

- **Function Name** − Name of the function.
- **Arguments** − An argument is a placeholder. When a function is invoked, you pass a value to the argument.
- **Function Body** − Collection of statements that defines what the function does.
- **Return Value** − The return value of a function is the last expression in the function body to be evaluated.

```
# Create simple function to calculate coefficient of variation (CV)
# Build function
  my.cofvar<- function(x){
    (sd(x)/mean(x))*100
    }
# Create a data frame
  sample.data2 <- data.frame(Genotypes=c("Geno1","Geno2","Geno3","Geno4",
                                         "Geno5","Geno6","Geno7"),
                             Yield=c(240, 220, 211, 230, 203, 241, 212),
                             Height=c(110, 140, 160, 135, 125, 145, 150),
                             Type=factor(c("LR","LR","LR","CV",
                                           "CV","CV","LR")))

# Now calculate CV for Yield and Height variable
    my.cofvar(sample.data2$Yield)
```

```
## [1] 6.702938
```

```
    my.cofvar(sample.data2$Height)
```

```
## [1] 12.00314
```

For handful resource on writting own R Functions:

1. A tutorial for writing functions in R
2. Write your own R functions
3. Writing Your Own Functions in R: Introduction
4. How to Make a Custom R Package

Section 9: R Markdown

R Markdown is a powerful tool for creating dynamic documents, reports, presentations, and dashboards that can combine text, code, and output. Key Features of R Markdown are:

- Data Analysis Reports
- Interactive Dashboards
- Reproducible Research
- Web Applications

Check our Analytical Pipeline created in R Markdown at https://github.com/whussain2/Analysis-pipeline

For handful resource on R Markdown

1. R Markdown Tutorial 1
2. R Markdown from R Studio
3. R Markdown Tutorial 2

Demo of R Markdown in R

For any suggestions or comments, please feel to reach at waseem.hussain@irri.org; and m.anumalla@irri.org

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