R/RStudio Introductory Workshop by University of San Diego

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The following link shows what each quadrant in the RStudio IDE represents:
https://www.leonshpaner.com/teaching/post/rstudio/

Let us start with the basics.

General/Console Operations

In R, we can simply type commands in the console window and hit "enter." This is how they are executed. For example, R can be used as a calculator

```
2 + 2
```

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

```
3 * 3
```

```
## [1] 9
```

```
sqrt(9)
```

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

```
log10(100)
```

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

What is a string?

A string is simply any open alpha/alphanumeric text characters surrounded by either single quotation marks or double quotation marks, with no preference assigned for either single or double quotation marks, with a print statement being called prior to the strings. For example,

```
print('This is a string.')
```

```
## [1] "This is a string."
```

```
print( "This is also a string123.")
```

```
## [1] "This is also a string123."
```

Determining and setting the current working directory

The importance of determining and setting the working directory cannot be stressed enough. Obtain the path to the working directory by running the `getwd()` function. Set the working directory by running the `setwd("...")` function, filling the parentheses inside with the correct path.

getwd()
setwd()

Installing Packages

To install a package or library, simply type in `install.packages('package_name).`
For the following exercises, let us ensure that we have installed the following packages:

```
# psychological library as extension for statistical tools
```

install.packages('psych')

```
# for reading rect. data (i.e., 'csv', 'tsv', and 'fwf')
```

install.packages("readr")

```
# additional library for summarizing data
```

install.packages('summarytools')

```
# classification and regression training (modeling)
```

install.packages('caret')

```
# other miscellaneous function
```

install.packages('e1071')

```
# for classification and decision trees
```

install.packages('rpart')

```
# for plotting classification and decision trees
```

install.packages('rpart.plot')

```
# methods for cluster analysis
```

install.packages("cluster")

```
# clustering algorithms & visualization
```

install.packages('factoextra')

To read the documentation for any given library, simply put a "?" before the library name and press "enter." For example,

```
library(summarytools) # load the library first
# ?summarytools # then view the documentation
```

This will open the documentation in the 'Files, Plots, Packages. Help, Viewer' pane.

Source Pane (Workspace) Scripting

Creating objects:

<- : assignment in R. Shortcut: `"Alt + -"` on Windows or `"Option + -"` on Mac.

```
var1 <- c(0, 1, 2, 3)
```

Differences between "=" and "<-"

Whereas `"="` sign can also be used for assignment in R, it is best suited for specifying field equivalents (i.e., number of rows, columns, etc.). For example, let us take the following dataframe with 4 rows and 3 columns. Here, we specify `A=4` and `B=3` as follows:

```
dataframe_1 <- c(A = 4, B = 3)
dataframe_1
```

```
## A B
## 4 3
```

If we specify `A <- 4`, and `B <- 3` instead, `A` and `B` will effectively evaluate to those respective values as opposed to listing them in those respective columns. Let us take a look:

```
dataframe_2 <- c(A <- 4, B <- 3)
dataframe_2
```

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

Import data from flat `.csv` file

Assuming that your file is located in the same working directory that you have specified at the onset of this tutorial/workshop, make an assignment to a new variable (i.e., `ex_csv`) and call read.csv() in the following generalized format

For Windows users:

ex_csv_1 <- read.csv(choose.files(), header = T, quote = "'")

```
# for macOS users
# example1.6 = read.csv(file.choose(), header = T, quote = "'")
```

The `choose.files()`, `file.choose()` function calls, respectively. allow the user to locate the file on their local drive, regardless of the working directory. That being said, there is more than one way to read in a `.csv` file. It does not have to exist on the local machine. If the file exists on the cloud, the path (link) can be parsed into the `read.csv()` function call as a string.

Now, let us print what is contained in `var 1`

```
print(var1)
```

```
## [1] 0 1 2 3
```

or we can simply call var1

```
var1
```

```
## [1] 0 1 2 3
```

Let us assign a variable to our earlier calculation and call the variable.

```
two <- 2+2
two
```

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

Any object (variable, vector, matrix, etc.) that is created is stored in the R workspace. From time to time, it is best practice to clear certain unused elements from the workspace so that it does not congest the memory.

```
rm(two)
```

When we proceed to type in two, we will see that there is an error, confirming that the variable has been removed from the workspace.

There are 4 main data types in R: numeric, character, factor, and logical. There are data classes. Numeric variables includes integers and decimals.

```
num <- 12.6
num
```

```
## [1] 12.6
```

Character (includes characters and strings):

```
char <- "Male"
char
```

```
## [1] "Male"
```

Factor (ordinal/categorical data)"

```
gender <- as.factor(char)
gender
```

```
## [1] Male
## Levels: Male
```

Logical()

```
TRUE
```

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

```
FALSE
```

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

```
T # abbreviation also works for Boolean object
```

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

```
F
```

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

```
TRUE * 7
```

```
## [1] 7
```

```
FALSE * 7
```

```
## [1] 0
```

Data Structures

What is a variable?

A variable is a container for storing a data value, exhibited as a reference to "to an object in memory which means that whenever a variable is assigned # to an instance, it gets mapped to that instance. A variable in R can store a vector, a group of vectors or a combination of many R objects" (GeeksforGeeks, 2020).

There are 3 most important data structures in R: vector, matrix, and dataframe.

Vector: the most basic type of data structure within R; contains a series of values of the same data class. It is a "sequence of data elements" (Thakur, 2018).

Matrix: a 2-dimensional version of a vector. Instead of only having a single row/list of data, we have rows and columns of data of the same data class.

Dataframe: the most important data structure for data science. Think of dataframe as loads of vectors pasted together as columns. Columns in a dataframe can be of different data class, but values within the same column must be the same data class.

The `c()` function is to R what `concatenate()` is to excel. For example,

```
vector_1 <- c(2,3,5)
vector_1
```

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

Similarly, a vector of logical values will contain the following.

```
vector_2 <- c(TRUE, FALSE, TRUE, FALSE, FALSE)
vector_2
```

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

To determine the number of members inside any given vector, we apply the `length()` function call on the vector as follows:

```
length(c(TRUE, FALSE, TRUE, FALSE, FALSE))
```

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

or, since we already assigned this to a data frame named `vector_2`, we can simply call length of `vector_2` as follows:

```
length(vector_2)
```

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

Let's say for example, that we want to access the third element of `vector_1.` We can do so as follows:

```
vector_1[3]
```

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

What if we want to access all elements within the dataframe except for the first one? To this end, we use the `"-"` symbol as follows:

```
vector_1[-1]
```

```
## [1] 3 5
```

Let us create a longer arbitrary vector so we can illustrate some further examples.

```
vector_3 <- c(1,3,5,7,9,20,2,8,10,35,76,89,207)
```

To access the first, fifth, and ninth elements of this dataframe. To this end, we can do the following:

```
vector_3[c(1,5,9)]
```

```
## [1]  1  9 10
```

To access all elements within a specified range, specify the exact range using the `":"` separator as follows:

```
vector_3[3:11]
```

```
## [1]  5  7  9 20  2  8 10 35 76
```

Let us create a mock dataframe for five fictitious individuals representing different ages, and departments at a research facility.

```r
Name <- c('Jack', 'Kathy', 'Latesha', 'Brandon', 'Alexa', 'Jonathan', 'Joshua',
          'Emily', 'Matthew', 'Anthony', 'Margaret', 'Natalie')

Age <- c(47, 41, 23, 55, 36, 54, 48, 23, 22, 27, 37, 43)
Experience <- c(7,5,9,3,11,6,8,9,5,2,1,4)

Position <- c('Economist', 'Director of Operations', 'Human Resources',
              'Admin. Assistant', 'Data Scientist', 'Admin. Assistant',
              'Account Manager', 'Account Manager', 'Attorney', 'Paralegal',
              'Data Analyst', 'Research Assistant')

df <- data.frame(Name, Age, Experience, Position)
df
```

```
##        Name Age Experience               Position
## 1      Jack  47          7              Economist
## 2     Kathy  41          5 Director of Operations
## 3   Latesha  23          9        Human Resources
## 4   Brandon  55          3       Admin. Assistant
## 5     Alexa  36         11         Data Scientist
## 6  Jonathan  54          6       Admin. Assistant
## 7    Joshua  48          8        Account Manager
## 8     Emily  23          9        Account Manager
## 9   Matthew  22          5               Attorney
## 10  Anthony  27          2              Paralegal
## 11 Margaret  37          1           Data Analyst
## 12  Natalie  43          4     Research Assistant
```

Let us examine the structure of the dataframe.

```r
str(df)
```

```
## 'data.frame':    12 obs. of  4 variables:
##  $ Name      : chr  "Jack" "Kathy" "Latesha" "Brandon" ...
##  $ Age       : num  47 41 23 55 36 54 48 23 22 27 ...
##  $ Experience: num  7 5 9 3 11 6 8 9 5 2 ...
##  $ Position  : chr  "Economist" "Director of Operations" "Human Resources" "Admin. Assistant" ...
```

Let us examine the dimensions of the dataframe (number of rows and columns, respectively).

```r
dim(df)
```

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

Sorting Data

Let us say that now we want to sort this dataframe in order of age (youngest to oldest).

```r
df_age <- df[order(Age),]
df_age
```

```
##        Name Age Experience                Position
## 9   Matthew  22          5                Attorney
## 3   Latesha  23          9         Human Resources
## 8     Emily  23          9         Account Manager
## 10  Anthony  27          2               Paralegal
## 5     Alexa  36         11          Data Scientist
## 11 Margaret  37          1            Data Analyst
## 2     Kathy  41          5 Director of Operations
## 12  Natalie  43          4      Research Assistant
## 1      Jack  47          7               Economist
## 7    Joshua  48          8         Account Manager
## 6  Jonathan  54          6        Admin. Assistant
## 4   Brandon  55          3        Admin. Assistant
```

Now, if we want to sort experience by descending order while keeping age sorted according to previous specifications, we can do the following:

```
df_age_exp <- df[order(Age, Experience),]
df_age_exp
```

```
##        Name Age Experience                Position
## 9   Matthew  22          5                Attorney
## 3   Latesha  23          9         Human Resources
## 8     Emily  23          9         Account Manager
## 10  Anthony  27          2               Paralegal
## 5     Alexa  36         11          Data Scientist
## 11 Margaret  37          1            Data Analyst
## 2     Kathy  41          5 Director of Operations
## 12  Natalie  43          4      Research Assistant
## 1      Jack  47          7               Economist
## 7    Joshua  48          8         Account Manager
## 6  Jonathan  54          6        Admin. Assistant
## 4   Brandon  55          3        Admin. Assistant
```

Handling *#NA* values

NA (not available) refers to missing values. What if our dataset has missing values? How should we handle this scenario? For example, age has some missing values.

```
Name_2 <- c('Jack', 'Kathy', 'Latesha', 'Brandon', 'Alexa', 'Jonathan', 'Joshua',
            'Emily', 'Matthew', 'Anthony', 'Margaret', 'Natalie')

Age_2 <- c(47, NA, 23, 55, 36, 54, 48, NA, 22, 27, 37, 43)
Experience_2 <- c(7,5,9,3,11,6,8,9,5,2,1,4)

Position_2 <- c('Economist', 'Director of Operations', 'Human Resources',
                'Admin. Assistant', 'Data Scientist', 'Admin. Assistant',
                'Account Manager', 'Account Manager', 'Attorney', 'Paralegal',
                'Data Analyst', 'Research Assistant')

df_2 <- data.frame(Name_2, Age_2, Experience_2, Position_2)
df_2
```

```
##      Name_2 Age_2 Experience_2             Position_2
## 1      Jack    47            7              Economist
## 2     Kathy    NA            5 Director of Operations
## 3   Latesha    23            9        Human Resources
## 4   Brandon    55            3       Admin. Assistant
## 5     Alexa    36           11         Data Scientist
## 6  Jonathan    54            6       Admin. Assistant
## 7    Joshua    48            8        Account Manager
## 8     Emily    NA            9        Account Manager
## 9   Matthew    22            5               Attorney
## 10  Anthony    27            2              Paralegal
## 11 Margaret    37            1           Data Analyst
## 12  Natalie    43            4     Research Assistant
```

Inspecting *#NA* values

```r
is.na(df_2) # returns a Boolean matrix (True or False)
```

```
##       Name_2 Age_2 Experience_2 Position_2
##  [1,]  FALSE FALSE        FALSE      FALSE
##  [2,]  FALSE  TRUE        FALSE      FALSE
##  [3,]  FALSE FALSE        FALSE      FALSE
##  [4,]  FALSE FALSE        FALSE      FALSE
##  [5,]  FALSE FALSE        FALSE      FALSE
##  [6,]  FALSE FALSE        FALSE      FALSE
##  [7,]  FALSE FALSE        FALSE      FALSE
##  [8,]  FALSE  TRUE        FALSE      FALSE
##  [9,]  FALSE FALSE        FALSE      FALSE
## [10,]  FALSE FALSE        FALSE      FALSE
## [11,]  FALSE FALSE        FALSE      FALSE
## [12,]  FALSE FALSE        FALSE      FALSE
```

```r
sum(is.na(df_2)) # sums up all of the NA values in the dataframe
```

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

```r
df_2[!complete.cases(df_2),] # we can provide a list of rows with missing data
```

```
##   Name_2 Age_2 Experience_2             Position_2
## 2  Kathy    NA            5 Director of Operations
## 8  Emily    NA            9        Account Manager
```

We can delete the rows with missing values by making an `na.omit()` function call in the following manner:

```r
df_2_na_omit <- na.omit(df_2)
df_2_na_omit
```

```
##      Name_2 Age_2 Experience_2         Position_2
## 1      Jack    47            7          Economist
```

```
## 3   Latesha    23             9    Human Resources
## 4   Brandon    55             3   Admin. Assistant
## 5     Alexa    36            11     Data Scientist
## 6  Jonathan    54             6   Admin. Assistant
## 7    Joshua    48             8    Account Manager
## 9   Matthew    22             5           Attorney
## 10  Anthony    27             2          Paralegal
## 11 Margaret    37             1       Data Analyst
## 12  Natalie    43             4 Research Assistant
```

Or we can use `complete.cases()` to subset only those rows that do not have missing values:

```
df_2[complete.cases(df_2), ]
```

```
##      Name_2 Age_2 Experience_2         Position_2
## 1      Jack    47            7          Economist
## 3   Latesha    23            9    Human Resources
## 4   Brandon    55            3   Admin. Assistant
## 5     Alexa    36           11     Data Scientist
## 6  Jonathan    54            6   Admin. Assistant
## 7    Joshua    48            8    Account Manager
## 9   Matthew    22            5           Attorney
## 10  Anthony    27            2          Paralegal
## 11 Margaret    37            1       Data Analyst
## 12  Natalie    43            4 Research Assistant
```

What if we receive a dataframe that, at a cursory glance, warehouses numerical values where we see numbers, but when running additional operations on the dataframe, we discover that we cannot conduct numerical exercises with columns that appear to have numbers. This is exactly why it is of utmost importance for us to always inspect the structure of the dataframe using the `str()` function call. Here is an example of the same dataframe with altered data types.

```
Name_3 <- c('Jack', 'Kathy', 'Latesha', 'Brandon', 'Alexa', 'Jonathan', 'Joshua',
            'Emily', 'Matthew', 'Anthony', 'Margaret', 'Natalie')

Age_3 <- c('47', '41', '23', '55', '36', '54', '48', '23', '22', '27', '37', '43')

Experience_3 <- c(7,5,9,3,11,6,8,9,5,2,1,4)

Position_3 <- c('Economist', 'Director of Operations', 'Human Resources',
                'Admin. Assistant', 'Data Scientist', 'Admin. Assistant',
                'Account Manager', 'Account Manager', 'Attorney', 'Paralegal',
                'Data Analyst', 'Research Assistant')

df_3 <- data.frame(Name_3, Age_3, Experience_3, Position_3)
```

Notice how Age is now expressed as a character data type, whereas Experience still shows as a numeric datatype.

```
str(df_3,
    strict.width = 'wrap')
```

```
## 'data.frame':    12 obs. of  4 variables:
## $ Name_3 : chr "Jack" "Kathy" "Latesha" "Brandon" ...
## $ Age_3 : chr "47" "41" "23" "55" ...
## $ Experience_3: num 7 5 9 3 11 6 8 9 5 2 ...
## $ Position_3 : chr "Economist" "Director of Operations" "Human Resources"
##    "Admin. Assistant" ...
```

Let us convert Age back to numeric using the `as.numeric()` function, and re-examine the dataframe.

```
df_3$Age_3 <- as.numeric(df_3$Age_3)
str(df_3, strict.width = 'wrap')
```

```
## 'data.frame':    12 obs. of  4 variables:
## $ Name_3 : chr "Jack" "Kathy" "Latesha" "Brandon" ...
## $ Age_3 : num 47 41 23 55 36 54 48 23 22 27 ...
## $ Experience_3: num 7 5 9 3 11 6 8 9 5 2 ...
## $ Position_3 : chr "Economist" "Director of Operations" "Human Resources"
##    "Admin. Assistant" ...
```

We can also convert experience from numeric to character/categorical data as follows:

```
options(width = 60)
df_3$Experience_3 <- as.character(df_3$Experience_3)
str(df_3, width = 60, strict.width = 'wrap')
```

```
## 'data.frame':    12 obs. of  4 variables:
## $ Name_3 : chr "Jack" "Kathy" "Latesha" "Brandon" ...
## $ Age_3 : num 47 41 23 55 36 54 48 23 22 27 ...
## $ Experience_3: chr "7" "5" "9" "3" ...
## $ Position_3 : chr "Economist" "Director of Operations"
##    "Human Resources" "Admin. Assistant" ...
```

Basic Statistics

Setting the seed

First, let us discuss the importance of setting a seed. Setting a seed to a specific yet arbitrary value in R ensures the reproducibility of results. It is always best practice to use the same assigned seed throughout the entire experiment. Setting the seed to this arbitrary number (of any length) will guarantee exactly the same output across all R sessions and users, respectively.

Let us create a new data frame of numbers 1 - 100.

```
mystats <- c(1:100)
```

and go over the basic statistical functions

```
mean(mystats) # mean of the vector
```

```
## [1] 50.5
```

```r
median(mystats) # median of the vector
```

```
## [1] 50.5
```

```r
min(mystats) # minimum of the vector
```

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

```r
max(mystats) # maximum of the vector
```

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

```r
range(mystats)  # range of the vector
```

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

```r
sum(mystats) # sum of the vector
```

```
## [1] 5050
```

```r
sd(mystats) # standard deviation of the vector
```

```
## [1] 29.01149
```

```r
class(mystats) # return data class of the vector
```

```
## [1] "integer"
```

```r
length(mystats) # the length of the vector
```

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

```r
# summary of the dataset
summary(mystats)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    1.00   25.75   50.50   50.50   75.25  100.00
```

To use an installed library, we must open that library with the following `library()` function call

```r
library(psych)
```

For example, the psych library uses the `describe()` function call to give us an alternate perspective int the summary statistics of the data.

```r
describe(mystats)
```

```
##    vars   n mean    sd median trimmed   mad min max range
## X1    1 100 50.5 29.01   50.5    50.5 37.06   1 100    99
##    skew kurtosis  se
## X1    0    -1.24 2.9
```

```r
library(summarytools)
dfSummary(mystats, plain.ascii  = FALSE,
          style        = 'grid',
          graph.magnif = 0.85,
          varnumbers = FALSE,
          valid.col    = FALSE,
          tmp.img.dir  = "/tmp",
          method='pandoc')
```

```
## ### Data Frame Summary
## #### mystats
## **Dimensions:** 100 x 1
## **Duplicates:** 0
##
## +-----------+------------------------+----------------------+----------------------+---------+
## | Variable  | Stats / Values         | Freqs (% of Valid)   | Graph                | Missing |
## +===========+========================+======================+======================+=========+
## | mystats\  | Mean (sd) : 50.5 (29)\ | 100 distinct values\ | ![](/tmp/ds0004.png) | 0\      |
## | [integer] | min < med < max:\      | (Integer sequence)   |                      | (0.0%)  |
## |           | 1 < 50.5 < 100\        |                      |                      |         |
## |           | IQR (CV) : 49.5 (0.6)  |                      |                      |         |
## +-----------+------------------------+----------------------+----------------------+---------+
```

Simulating a Normal Distribution

Now, We will use the **rnorm()** function to simulate a vector of 100 random normally distributed data with a mean of 50, and a standard deviation of 10.

```r
set.seed(222) # set.seed() for reproducibility
norm_vals <- rnorm(n = 100, mean = 50, sd = 10)
norm_vals
```

```
##   [1] 64.87757 49.98108 63.81021 46.19786 51.84136 47.53104 37.84439 65.61405
##   [9] 54.27310 37.98976 60.52458 36.94936 43.07392 56.02649 48.02247 38.14125
##  [17] 29.94487 50.07510 55.19490 42.53705 57.26455 57.13657 43.49937 64.98696
##  [25] 35.64172 28.38682 53.95220 46.05166 46.90242 63.30827 41.82571 56.75893
##  [33] 47.84519 48.85350 47.97735 54.06493 56.56772 51.06191 48.15603 59.46034
##  [41] 52.02387 54.95101 44.30645 61.19294 72.09078 53.17183 40.64703 58.13662
##  [49] 46.24635 53.33100 55.94415 55.20868 40.47956 37.72315 47.97593 60.59120
##  [57] 53.81779 62.39694 53.16777 39.56622 38.51764 62.31145 57.89215 57.48845
##  [65] 50.57476 58.42951 51.99859 64.51171 45.39840 22.25533 50.56489 49.38629
##  [73] 38.18032 24.70833 58.13577 52.62389 49.37494 56.71735 50.27176 55.35603
##  [81] 56.89548 38.00871 37.60845 52.13186 35.42848 48.74239 55.44208 57.20830
##  [89] 34.28810 60.97272 46.67537 56.16393 55.08799 66.86555 53.79547 52.35471
##  [97] 54.24988 38.15064 43.56390 50.52614
```

Plots

Stem-and-leaf

Let's make a Simple stem-and-leaf plot. Here, we call the `stem()` function as follows:

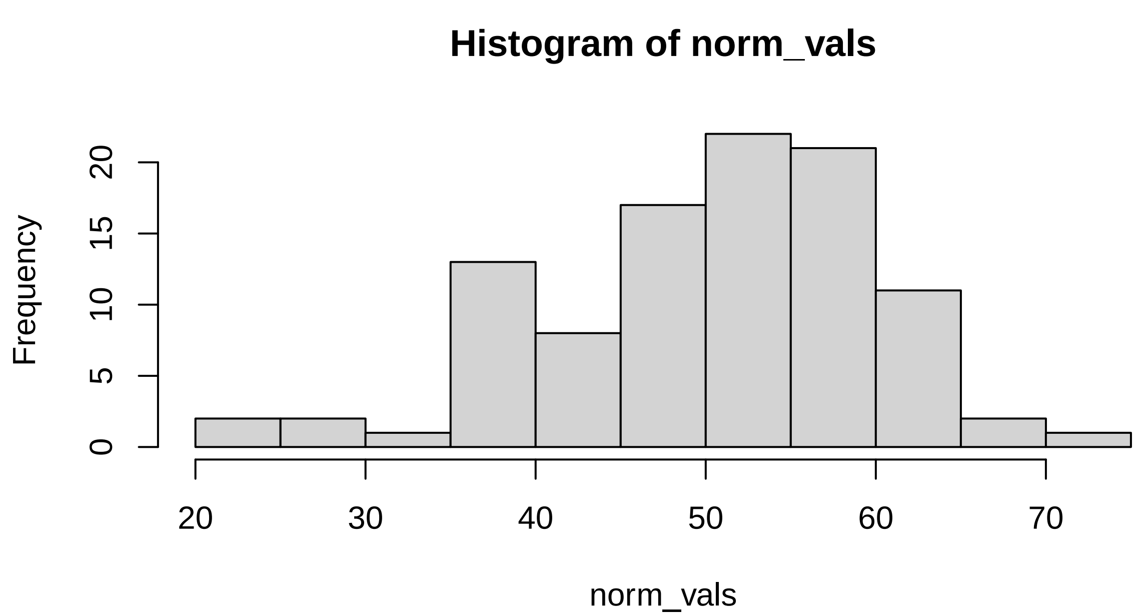
```
stem(norm_vals)
```

```
##
##   The decimal point is 1 digit(s) to the right of the |
##
##   2 | 2
##   2 | 58
##   3 | 04
##   3 | 567888888889
##   4 | 001233344
##   4 | 5666778888889999
##   5 | 0001111222223333444444
##   5 | 5555556667777777788889
##   6 | 11112234
##   6 | 55567
##   7 | 2
```

We can plot a histogram of these `norm_vals` in order to inspect their distribution from a purely graphical standpoint. R uses the built-in `hist()` function to accomplish this task. Let us now plot the histogram.

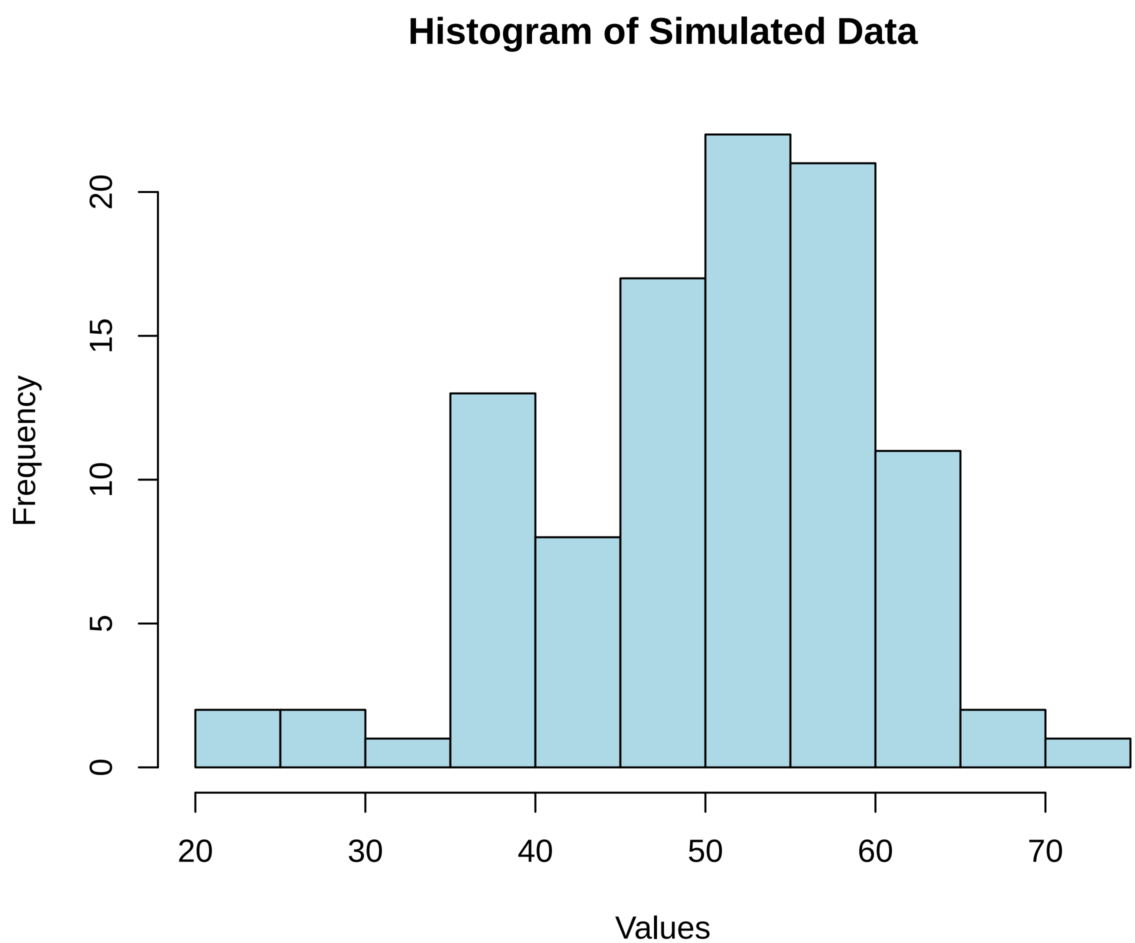
Histograms

```
hist(norm_vals)
```



Our title, x-axis, and y-axis labels are given to us by default. However, let us say that we want to change all of them to our desired specifications. To this end, we can parse in and control the following parameters:

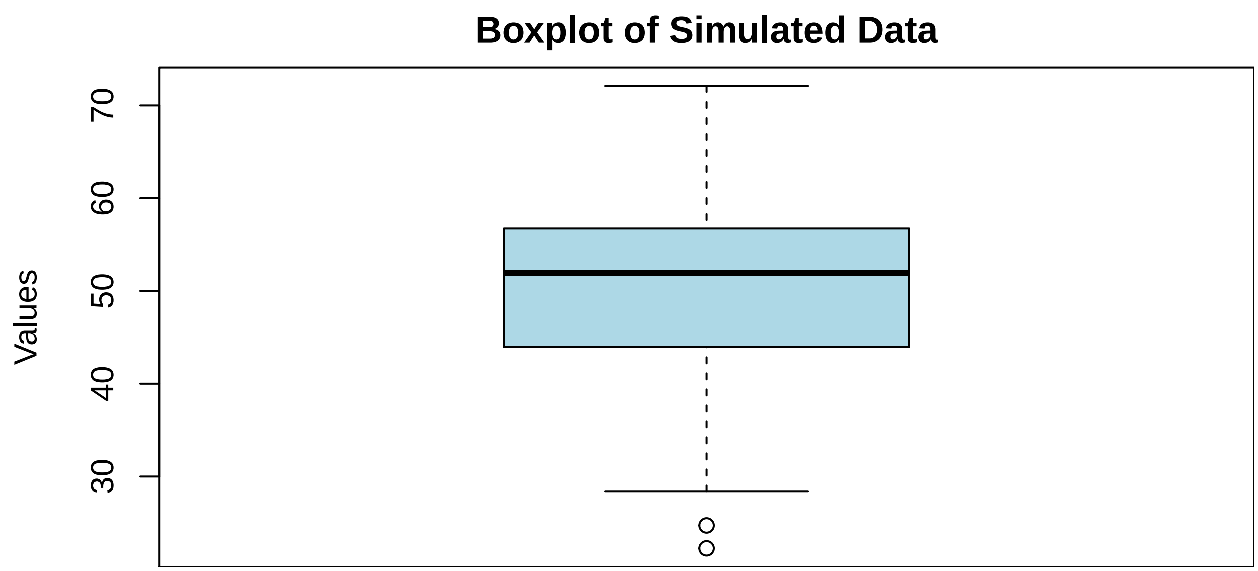
```
hist(norm_vals,
     col = 'lightblue', # specify the color
     xlab = 'Values', # specify the x-axis label
     ylab = 'Frequency', # specify the y-axis label
     main = 'Histogram of Simulated Data', # specify the new title
     )
```



Boxplots

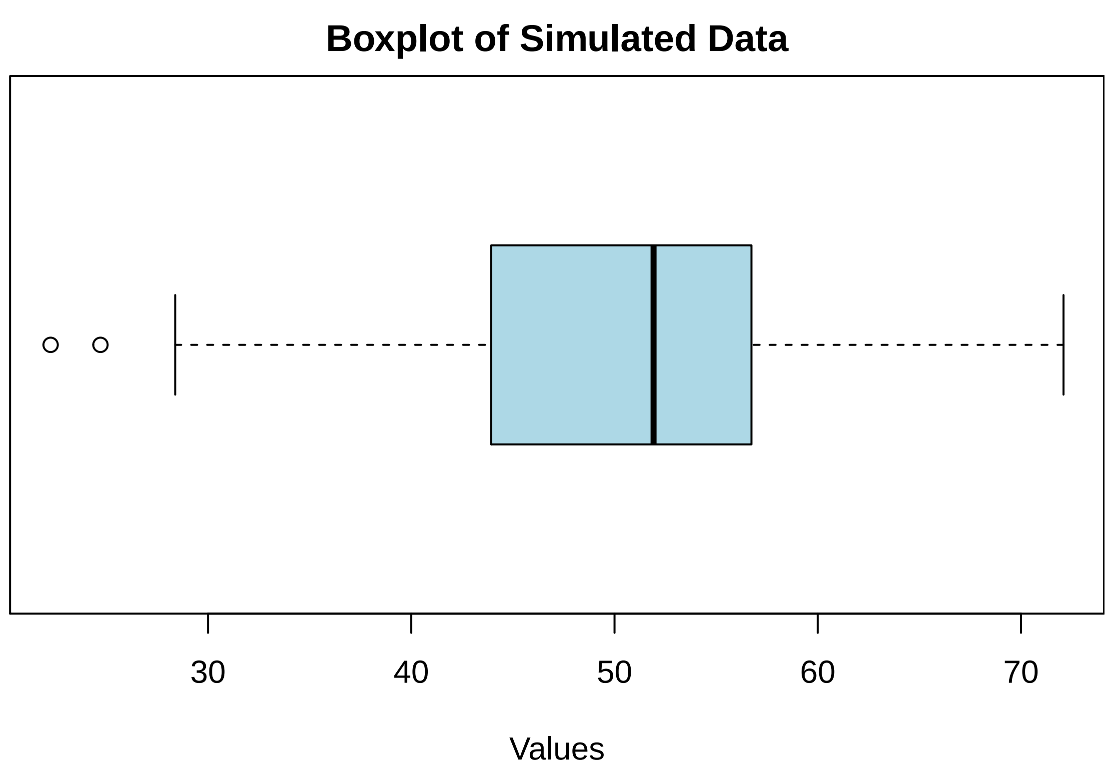
Similarly, we can make a boxplot in base R using the `boxplot()` function call as follows:

```
par(mar = c(0,4,2,0))
boxplot(norm_vals,
        col = 'lightblue', # specify the color
        ylab = 'Values', # specify the y-axis label
        main = 'Boxplot of Simulated Data' # specify the new title
        )
```



Now, let us pivot the boxplot by parsing in the `horizontal = TRUE` parameter:

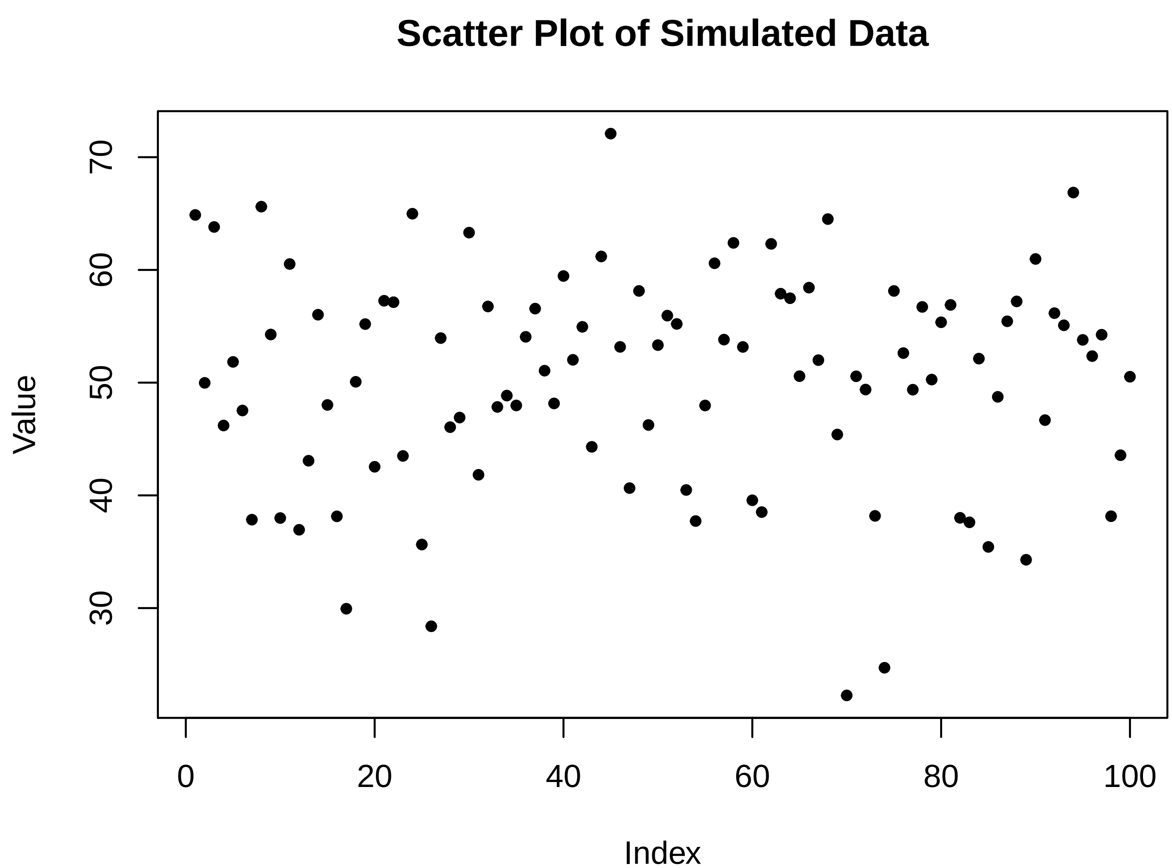
```
par(mar = c(4,4,2,0))
boxplot(norm_vals, horizontal = TRUE,
        col = 'lightblue', # specify the color
        xlab = 'Values', # specify the x-axis label
        main = 'Boxplot of Simulated Data' # specify the new title
        )
```



Scatter Plots

To make a simple scatter plot, we will simply call the `plot()` function on the same dataframe as follows:

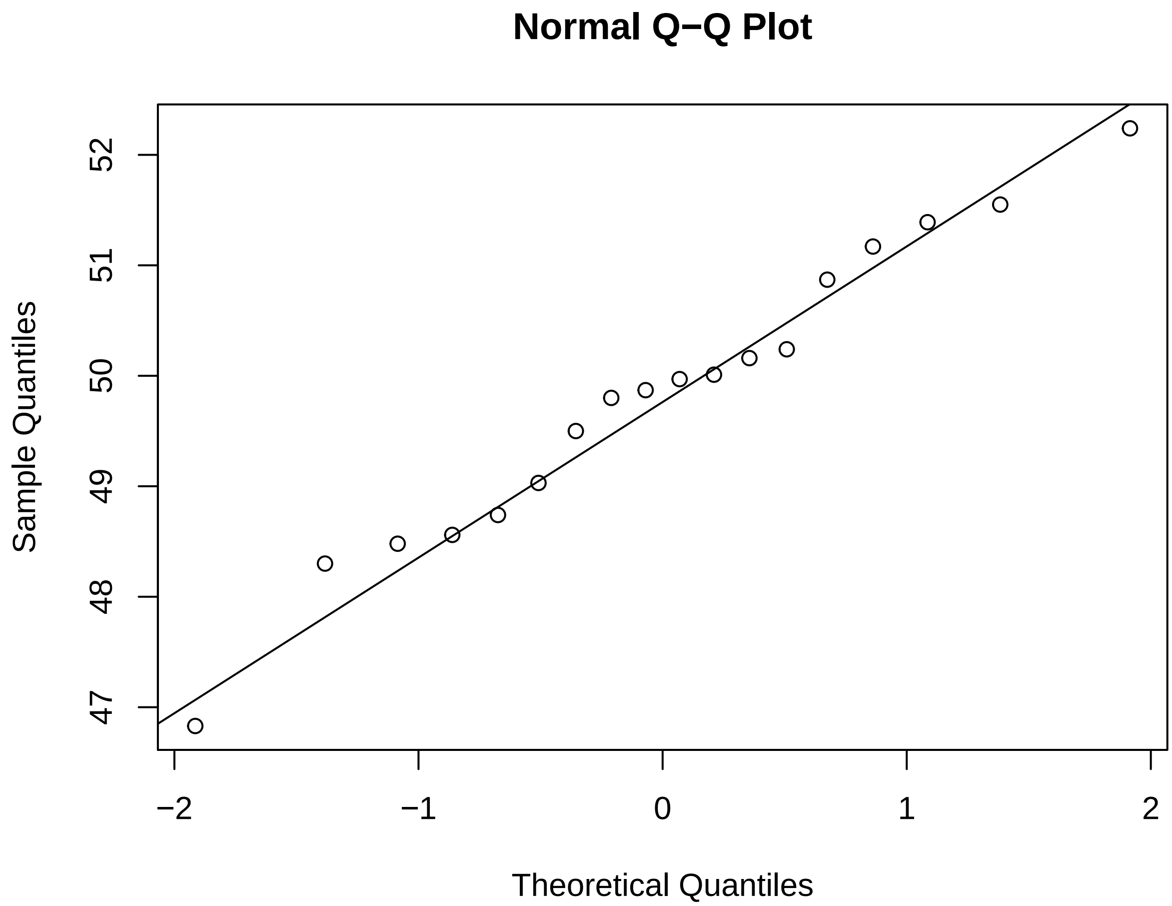
```
plot(norm_vals,
     main = 'Scatter Plot of Simulated Data',
     pch = 20, # plot character - in this case default (circle)
     xlab = 'Index',
     ylab = 'Value')
```



Quantile-Quantile Plot

Let us create a vector for the next example data and generate a normal quantile plot

```
quant_ex <- c(48.30, 49.03, 50.24, 51.39, 48.74, 51.55, 51.17, 49.87, 50.16,
              49.80, 46.83, 48.48, 52.24, 50.01, 49.50, 49.97, 48.56, 50.87)

qqnorm(quant_ex)

qqline(quant_ex) # adding a theoretical Q-Q line
```



Skewness and Box-Cox Transformation

From statistics, let us recall that if the mean is greater than the median, the distribution will be positively skewed. Conversely, if the median is greater than the mean, or the mean is less than the median, the distribution will be negatively skewed. Let us examine the exact skewness of our distribution.

```
# Test skewness by looking at mean and median relationship
mean_norm_vals <- round(mean(norm_vals),0)
median_norm_vals <- round(median(norm_vals),0)
distribution <- data.frame(mean_norm_vals,
                           median_norm_vals)
distribution
```

```
##   mean_norm_vals median_norm_vals
## 1             50               52
```

```
library(e1071)
skewness(norm_vals) # apply `skewness()` function from the e1071 library
```

```
## [1] -0.497993
```

```r
# Applying Box-Cox Transformation on skewed variable
library(caret)
trans <- preProcess(data.frame(norm_vals), method=c("BoxCox"))
trans
```

```
## Created from 100 samples and 1 variables
##
## Pre-processing:
##   - Box-Cox transformation (1)
##   - ignored (0)
##
## Lambda estimates for Box-Cox transformation:
## 1.8
```

Basic Modeling

Linear Regression

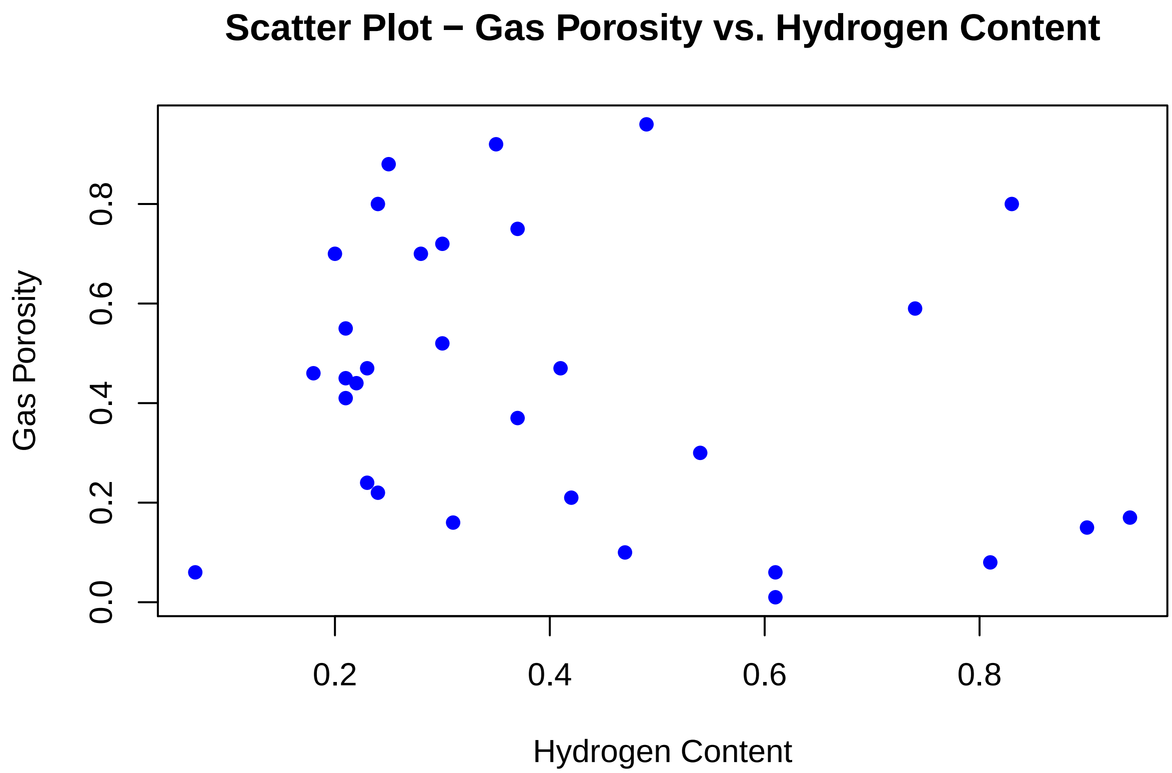
Let us set up an example dataset for the following modeling endeavors.

```r
# independent variables (x's):

# X1
Hydrogen <- c(.18,.20,.21,.21,.21,.22,.23,.23,.24,.24,.25,.28,.30,.37,.31,.90,
              .81,.41,.74,.42,.37,.49,.07,.94,.47,.35,.83,.61,.30,.61,.54)

# X2
Oxygen <- c(.55,.77,.40,.45,.62,.78,.24,.47,.15,.70,.99,.62,.55,.88,.49,.36,.55,
            .42,.39,.74,.50,.17,.18,.94,.97,.29,.85,.17,.33,.29,.85)

# X3
Nitrogen <- c(.35,.48,.31,.75,.32,.56,.06,.46,.79,.88,.66,.04,.44,.61,.15,.48,
              .23,.90,.26,.41,.76,.30,.56,.73,.10,.01,.05,.34,.27,.42,.83)

# there is always one dependent variable (target, response, y)
Gas_Porosity <- c(.46,.70,.41,.45,.55,.44,.24,.47,.22,.80,.88,.70,.72,.75,.16,
                  .15,.08,.47,.59,.21,.37,.96,.06,.17,.10,.92,.80,.06,.52,.01,.3)
```

Simple Linear Regression

Prior to partaking in linear regression, it is best practice to examine correlation from a strictly visual perspective visa vie scatterplot as follows:

```r
plot(Hydrogen,
     Gas_Porosity,
     main = "Scatter Plot - Gas Porosity vs. Hydrogen Content",
     xlab = "Hydrogen Content",
     ylab = "Gas Porosity",
     pch=16,
     col="blue")
```



Now, let's find the correlation coefficient, r

```
r1 <- cor(Hydrogen, Gas_Porosity)
r1
```

```
## [1] -0.2424314
```

Now we can set-up the linear model between one independent variable and one dependent variable.

```
simple_linear_mod <- data.frame(Hydrogen, Gas_Porosity)
```

By the correlation coefficient r you will see that there exists a relatively moderate (positive) relationship. Let us now build a simple linear model from this dataframe.

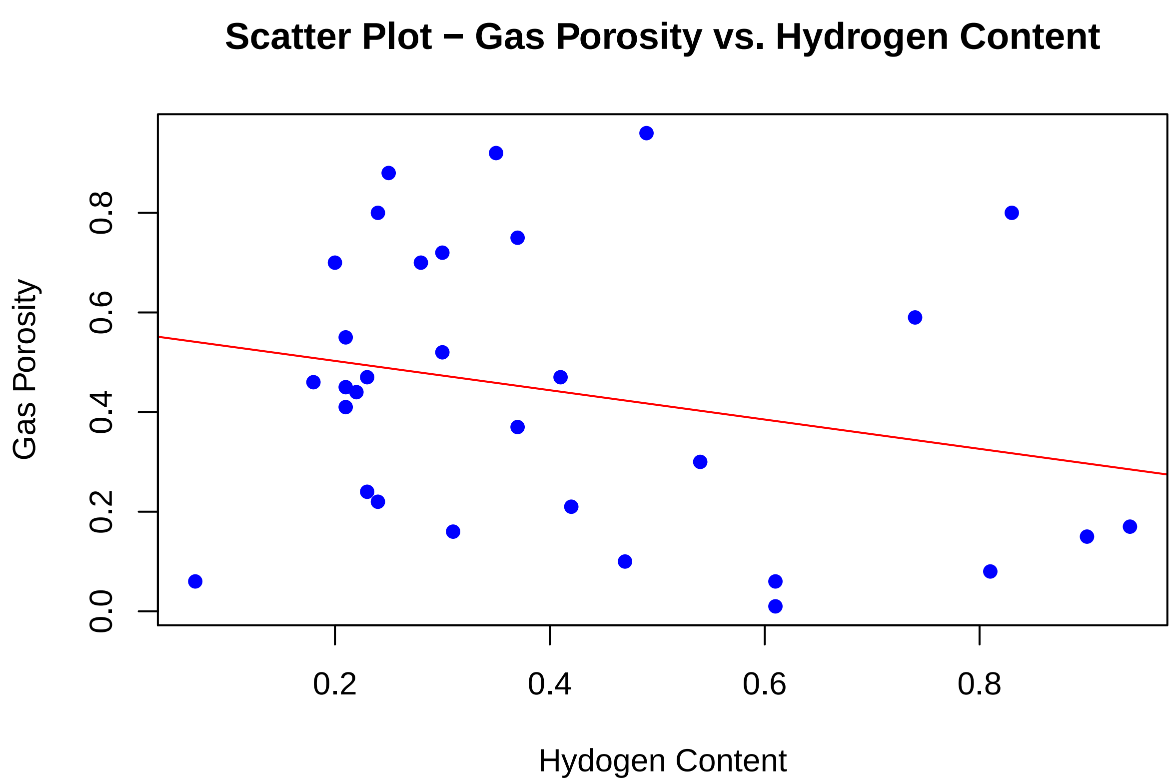
```
lm_model1 <- lm(Gas_Porosity ~ Hydrogen, data = simple_linear_mod)
summary(lm_model1)
```

```
##
## Call:
## lm(formula = Gas_Porosity ~ Hydrogen, data = simple_linear_mod)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.48103 -0.23564 -0.04983  0.23346  0.54258
```

```
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.5616     0.1018   5.516 6.06e-06 ***
## Hydrogen     -0.2943     0.2187  -1.346    0.189
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2807 on 29 degrees of freedom
## Multiple R-squared:  0.05877,    Adjusted R-squared:  0.02632
## F-statistic: 1.811 on 1 and 29 DF,  p-value: 0.1888
```

Notice how the p-value for hydrogen content is 0.189, which lacks statistical significance when compared to the alpha value of 0.05 (at the 95% confidence level). Moreover, the R-Squared value of .05877 suggests that roughly 6% of the variance for gas propensity is explained by hydrogen content.

```
# we can make the same scatter plot, but this time with a best fit line
plot(Hydrogen,
     Gas_Porosity,
     main = "Scatter Plot - Gas Porosity vs. Hydrogen Content",
     xlab = "Hydogen Content",
     ylab = "Gas Porosity",
     pch=16,
     col="blue",
     abline(lm_model1, col="red"))
```



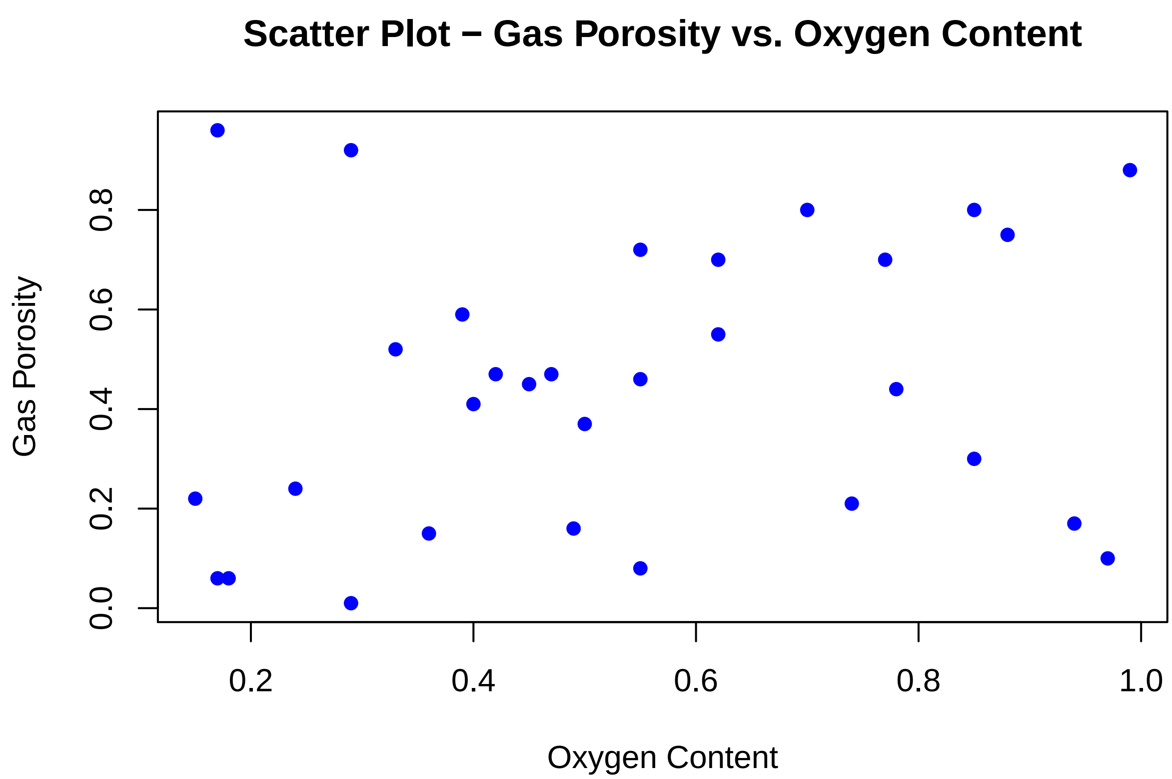
Multiple Linear Regression

To account for all independent (x) variables in the model, let us set up the model in a dataframe:

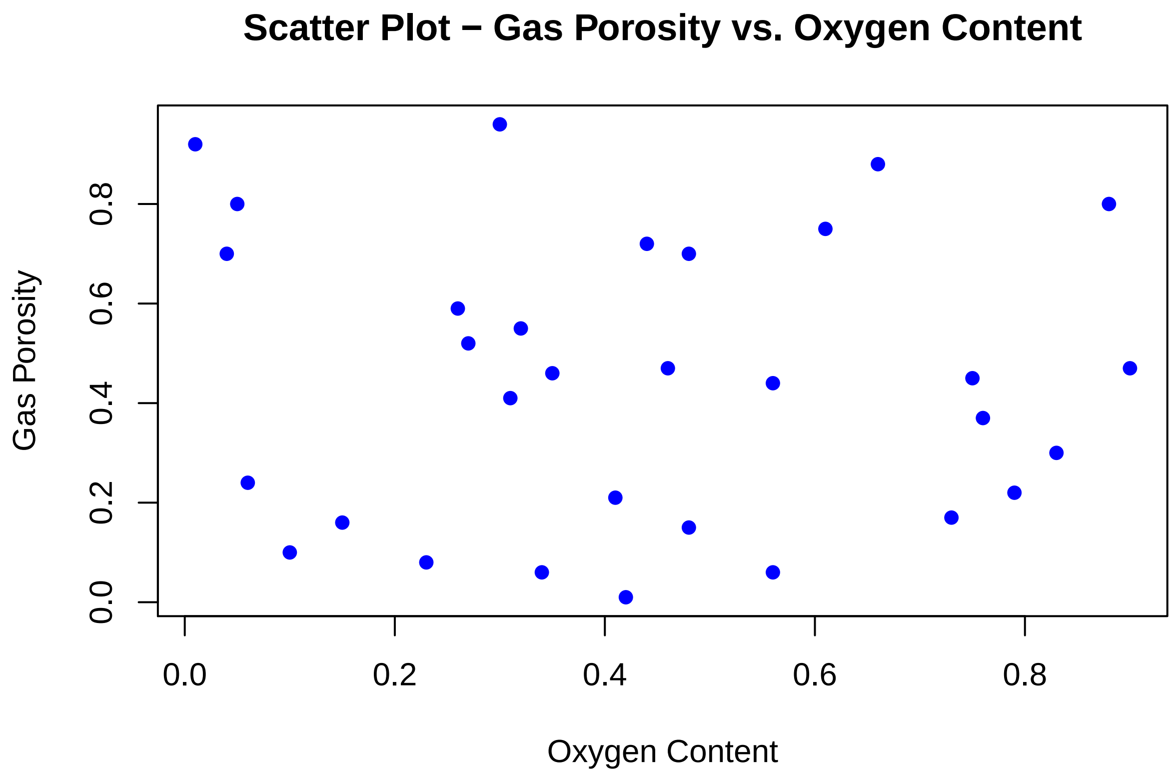
```
multiple_linear_mod <- data.frame(Hydrogen, Oxygen, Nitrogen, Gas_Porosity)
```

We can make additional scatter plots:

```
# gas porosity vs. oxygen
plot(Oxygen,
     Gas_Porosity,
     main = "Scatter Plot - Gas Porosity vs. Oxygen Content",
     xlab = "Oxygen Content",
     ylab = "Gas Porosity",
     pch=16,
     col="blue")
```




```
# gas porosity vs. nitrogen content
plot(Nitrogen,
     Gas_Porosity,
     main = "Scatter Plot - Gas Porosity vs. Oxygen Content",
     xlab = "Oxygen Content",
     ylab = "Gas Porosity",
     pch=16,
     col="blue")
```



and lastly, we can build a multiple linear model from these 3 independent variables:

```
lm_model2 <- lm(Gas_Porosity ~ Hydrogen + Oxygen + Nitrogen,
                data = multiple_linear_mod)
summary(lm_model2)
```

```
##
## Call:
## lm(formula = Gas_Porosity ~ Hydrogen + Oxygen + Nitrogen, data = multiple_linear_mod)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.49593 -0.18800 -0.02835  0.17512  0.63885
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.4853     0.1605   3.024  0.00542 **
## Hydrogen     -0.3536     0.2210  -1.600  0.12122
## Oxygen        0.2998     0.2036   1.473  0.15241
## Nitrogen     -0.1395     0.1970  -0.708  0.48496
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2788 on 27 degrees of freedom
## Multiple R-squared:  0.1352, Adjusted R-squared:  0.03906
## F-statistic: 1.407 on 3 and 27 DF,  p-value: 0.2624
```

Logistic Regression

Whereas in linear regression, it is necessary to have a quantitative and continuous target variable, logistic regression is part of the generalized linear model series that has a categorical (often binary) target (outcome) variable. For example, let us say we want to predict grades for mathematics courses taught at a university.

So, we have the following example dataset:

```
# grades for calculus 1
calculus1 <- c(56,80,10,8,20,90,38,42,57,58,90,2,34,84,19,74,13,67,84,31,82,67,
               99,76,96,59,37,24,3,57,62)

# grades for calculus 2
calculus2 <- c(83,98,50,16,70,31,90,48,67,78,55,75,20,80,74,86,12,100,63,36,91,
               19,69,58,85,77,5,31,57,72,89)

# grades for linear algebra
linear_alg <- c(87,90,85,57,30,78,75,69,83,85,90,85,99,97, 38,95,10,99,62,47,17,
                31,77,92,13,44,3,83,21,38,70)

# students passing/fail
pass_fail <- c('P','F','P','F','P','P','P','P','F','P','P','P','P','P','P','F',
               'P','P','P','F','F','F','P','P','P','P','P','P','P','P','P')
```

At this juncture, we cannot build a model with categorical values until and unless they are binarized using the `ifelse()` function call as follows. A passing score will be designated by a 1, and failing score with a respectively.

```
math_outcome <- ifelse(pass_fail=='P', 1, 0)
math_outcome
```

```
##  [1] 1 0 1 0 1 1 1 1 0 1 1 1 1 1 1 0 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1
```

```
logistic_model <- data.frame(calculus1,
                             calculus2,
                             linear_alg,
                             pass_fail,
                             math_outcome)

# examine data structures of the model
str(logistic_model)
```

```
## 'data.frame':    31 obs. of  5 variables:
##  $ calculus1   : num  56 80 10 8 20 90 38 42 57 58 ...
##  $ calculus2   : num  83 98 50 16 70 31 90 48 67 78 ...
##  $ linear_alg  : num  87 90 85 57 30 78 75 69 83 85 ...
##  $ pass_fail   : chr  "P" "F" "P" "F" ...
##  $ math_outcome: num  1 0 1 0 1 1 1 1 0 1 ...
```

We can also specify `glm` instead of just `lm` as in linear regression example:

```
lm_model3 <- glm(math_outcome ~ calculus1 +
                                calculus2 +
                                linear_alg,
                 family = binomial(),
                 data = logistic_model)

summary(lm_model3)
```

```
##
## Call:
## glm(formula = math_outcome ~ calculus1 + calculus2 + linear_alg,
##     family = binomial(), data = logistic_model)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8114   0.5365   0.6425   0.7439   0.8988
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.132509   1.278396   0.886    0.376
## calculus1   -0.010621   0.016416  -0.647    0.518
## calculus2    0.006131   0.017653   0.347    0.728
## linear_alg   0.004902   0.014960   0.328    0.743
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 33.118  on 30  degrees of freedom
## Residual deviance: 32.589  on 27  degrees of freedom
## AIC: 40.589
##
## Number of Fisher Scoring iterations: 4
```

Decision Trees

Decision trees are valuable supplementary methods for tracing consequential outcomes diagrammatically.

We can plot the trajectory of the outcome using the `rpart()` function of the `library(rpart)` and `library(rpart.plot)`, respectively.

```
library(rpart)
library(rpart.plot)
```

In favor of a larger dataset to illustrate the structure, function, and overall efficacy of decision trees in R, we will rely on the built-in `mtcars` dataset.

```
str(mtcars)
```

```
## 'data.frame':    32 obs. of  11 variables:
##  $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
##  $ disp: num  160 160 108 258 360 ...
##  $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
```

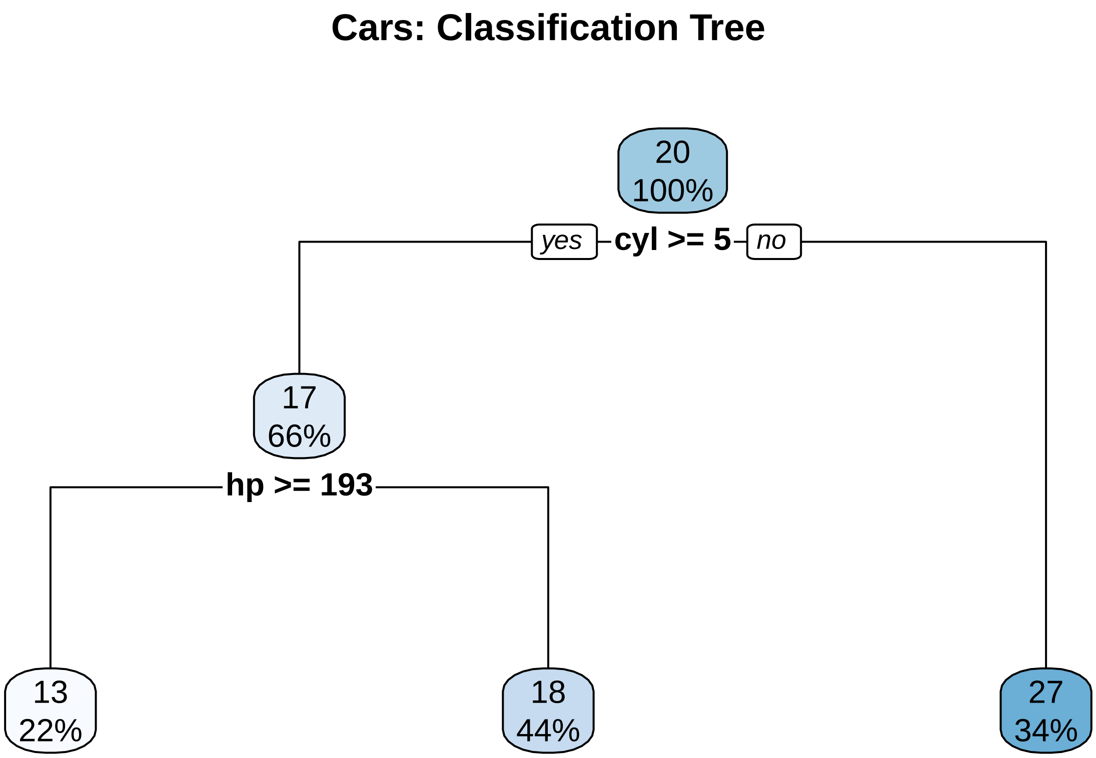
```
##  $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
##  $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
##  $ qsec: num  16.5 17 18.6 19.4 17 ...
##  $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
##  $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
##  $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
##  $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

```
mtcars
```

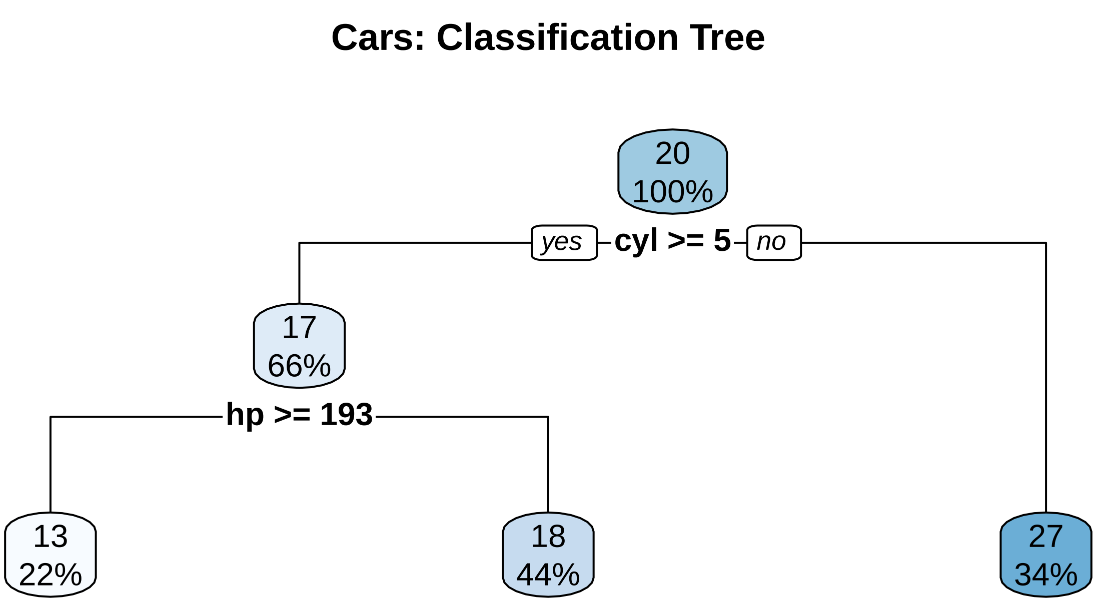
```
##                      mpg cyl  disp  hp drat    wt  qsec vs am gear carb
## Mazda RX4           21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4
## Mazda RX4 Wag       21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
## Datsun 710          22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
## Hornet 4 Drive      21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
## Hornet Sportabout   18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2
## Valiant             18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
## Duster 360          14.3   8 360.0 245 3.21 3.570 15.84  0  0    3    4
## Merc 240D           24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2
## Merc 230            22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2
## Merc 280            19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
## Merc 280C           17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4
## Merc 450SE          16.4   8 275.8 180 3.07 4.070 17.40  0  0    3    3
## Merc 450SL          17.3   8 275.8 180 3.07 3.730 17.60  0  0    3    3
## Merc 450SLC         15.2   8 275.8 180 3.07 3.780 18.00  0  0    3    3
## Cadillac Fleetwood  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
## Lincoln Continental 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4
## Chrysler Imperial   14.7   8 440.0 230 3.23 5.345 17.42  0  0    3    4
## Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
## Honda Civic         30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2
## Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
## Toyota Corona       21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1
## Dodge Challenger    15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2
## AMC Javelin         15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2
## Camaro Z28          13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4
## Pontiac Firebird    19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2
## Fiat X1-9           27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1
## Porsche 914-2       26.0   4 120.3  91 4.43 2.140 16.70  0  1    5    2
## Lotus Europa        30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2
## Ford Pantera L      15.8   8 351.0 264 4.22 3.170 14.50  0  1    5    4
## Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
## Maserati Bora       15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8
## Volvo 142E          21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2
```

So we introduce the model as follows:

```
# the decision tree model
tree_model <- rpart(mpg ~.,
                    data=mtcars)

# plot the decision tree
rpart.plot(tree_model,
           main = 'Cars: Classification Tree')
```




```r
# Passing in a `type=1,2,3,4, or 5` value changes the appearance of the tree
rpart.plot(tree_model, main = 'Cars: Classification Tree', type=2)
```



Basic Modeling with Cross-Validation in R

We use cross-validation as a "a statistical approach for determining how well the results of a statistical investigation generalize to a different data set" (finnstats, 2021). The `library(caret)` will help us in this endeavor.

Train_Test_Split

```
set.seed(222) # for reproducibility
dt <- sort(sample(nrow(mtcars), nrow(mtcars)*.75))
train_cars <-mtcars[dt,]
test_cars <-mtcars[-dt,]

# check size dimensions of respective partions
n_train <- nrow(train_cars)[1]
n_test <- nrow(test_cars)[1]

train_size = n_train/(n_train+n_test)
test_size = n_test/(n_train+n_test)

cat('\n Train Size:', train_size,
    '\n Test Size:', test_size)
```

```
##
##  Train Size: 0.75
##  Test Size: 0.25
```

Let us bring in a generalized linear model for this illustration.

```
cars_model <- glm(mpg ~., data = mtcars)
cars_predictions <- predict(cars_model, test_cars)

# computing model performance metrics
data.frame(R2 = R2(cars_predictions, test_cars$mpg),
           RMSE = RMSE(cars_predictions, test_cars$mpg),
           MAE = MAE(cars_predictions, test_cars$mpg))
```

```
##          R2    RMSE      MAE
## 1 0.9149732 1.72719 1.400446
```

In order to use the `trainControl()` function for cross-validation, we will bring in the `library(caret)`.

```
library(caret)
```

```
# Best model has lowest error(s)
# Now let us train the model with cross-validation
train_control <- trainControl(method = "cv", number = 5, savePredictions=TRUE)
cars_predictions <- train(mpg ~., data=mtcars, # glm model
                          method = 'glm',
                          trControl = train_control) # cross-validation
cars_predictions
```

```
## Generalized Linear Model
##
## 32 samples
## 10 predictors
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 24, 26, 25, 26, 27
## Resampling results:
##
##   RMSE     Rsquared   MAE
##   3.12627  0.8167969  2.587204
```

K-Means Clustering

A cluster is a collection of observations. We want to group these observations based on the most similar attributes. We use distance measures to measure similarity between clusters.

This is one of the most widely-used unsupervised learning techniques that groups "similar data points together and discover underlying patterns. To achieve this objective, K-means looks for a fixed number (k) of clusters in a dataset" (Garbade, 2018).

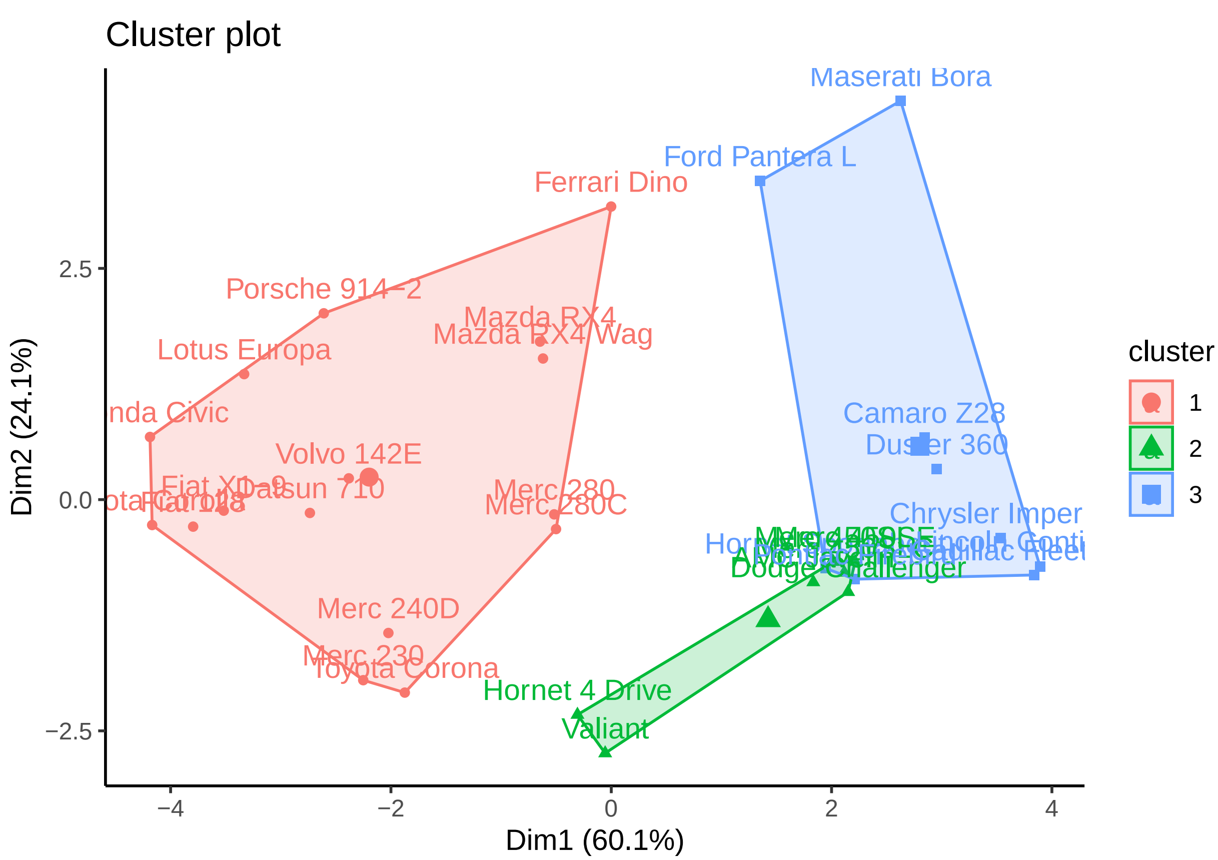
```
# Let us split the mtcars dataset into 3 clusters.
library(cluster)    # clustering algorithms
library(factoextra) # clustering algorithms & visualization

set.seed(222)
kmeans_cars <- kmeans(mtcars,      # dataset
                      centers = 3, # number of centroids
                      nstart = 20) # number of random starts s/b > 1
kmeans_cars
```

```
## K-means clustering with 3 clusters of sizes 16, 7, 9
##
## Cluster means:
##        mpg      cyl     disp       hp     drat       wt     qsec        vs
## 1 24.50000 4.625000 122.2937  96.8750 4.002500 2.518000 18.54312 0.7500000
## 2 17.01429 7.428571 276.0571 150.7143 2.994286 3.601429 18.11857 0.2857143
## 3 14.64444 8.000000 388.2222 232.1111 3.343333 4.161556 16.40444 0.0000000
##          am     gear     carb
## 1 0.6875000 4.125000 2.437500
## 2 0.0000000 3.000000 2.142857
## 3 0.2222222 3.444444 4.000000
##
## Clustering vector:
##           Mazda RX4       Mazda RX4 Wag          Datsun 710      Hornet 4 Drive
##                   1                   1                   1                   2
##   Hornet Sportabout             Valiant          Duster 360           Merc 240D
##                   3                   2                   3                   1
##            Merc 230            Merc 280           Merc 280C          Merc 450SE
##                   1                   1                   1                   2
##          Merc 450SL         Merc 450SLC  Cadillac Fleetwood Lincoln Continental
##                   2                   2                   3                   3
```

```
##   Chrysler Imperial            Fiat 128         Honda Civic      Toyota Corolla
##                   3                   1                   1                   1
##       Toyota Corona    Dodge Challenger         AMC Javelin          Camaro Z28
##                   1                   2                   2                   3
##    Pontiac Firebird           Fiat X1-9       Porsche 914-2        Lotus Europa
##                   3                   1                   1                   1
##      Ford Pantera L        Ferrari Dino       Maserati Bora          Volvo 142E
##                   3                   1                   3                   1
##
## Within cluster sum of squares by cluster:
## [1] 32838.00 11846.09 46659.32
##  (between_SS / total_SS =  85.3 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

Now let's visualize the cluster using the `fviz_cluster()` function from the `factoextra` library.

```
fviz_cluster(kmeans_cars,
             data = mtcars) +
theme_classic()
```



But what is the appropriate number of clusters that we should generate? Can we do better with more clusters?

```
# total sum of squares
kmeans_cars$totss
```

```
## [1] 623387.5
```

```
# between sum of squares
kmeans_cars$betweenss
```

```
## [1] 532044.1
```

```
# within sum of squares
kmeans_cars$withinss
```

```
## [1] 32838.00 11846.09 46659.32
```

```
# ratio for between sum of squares/ total sum of squares
kmeans_cars$betweenss/kmeans_cars$totss
```

```
## [1] 0.8534725
```

Let's create a numeric vector populated with zeroes and ten spots long.

```
wss <- numeric(10)
```

Can we do better? Let's run k-means from 1:10 clusters.

This will effectively measure the homogeneity of the clusters as the number of clusters increases.

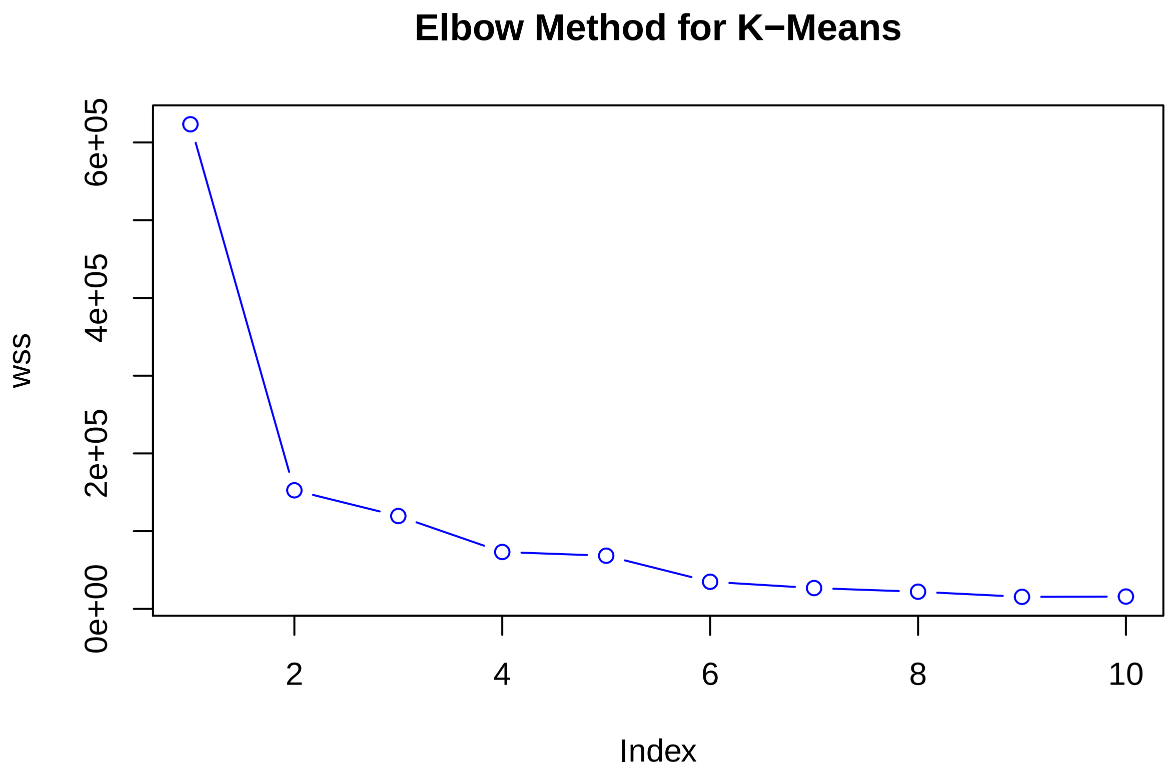
Now let us use a basic for-loop to run through k-means 10 times. K-means is iterated through each of these 10 clusters as follows:

```
# using within sum of squares

for(i in 1:10) {
  wss[i] <- sum(kmeans
               (mtcars,
                centers=i)
                $withinss)
}
```

Basic Elbow Method

Now let's plot these within sum of squares using the elbow method, which is one of the most commonly used approaches for finding the optimal *k*.

```
plot(wss,
     type='b',
     main ='Elbow Method for K-Means',
     col='blue')
```



Once we start to add clusters, the within sum of squares is reduced. Thus, the incremental reduction in within sum of squares is getting progressively smaller. We see that after approximately $k = 3$, each of the new clusters is not separating the data as well.

Hierarchical Clustering

This is another form of unsupervised learning type of cluster analysis, which takes on a more visual method, working particularly well with smaller samples (i.e., $n < 500$), such as this mtcars dataset. We start out with as many clusters as observations, and we go through a procedure of combining observations into clusters, and culminating with combining clusters together as a reduction method for the total number of clusters that are present. Moreover, the premise for combining clusters together is a direct result of:

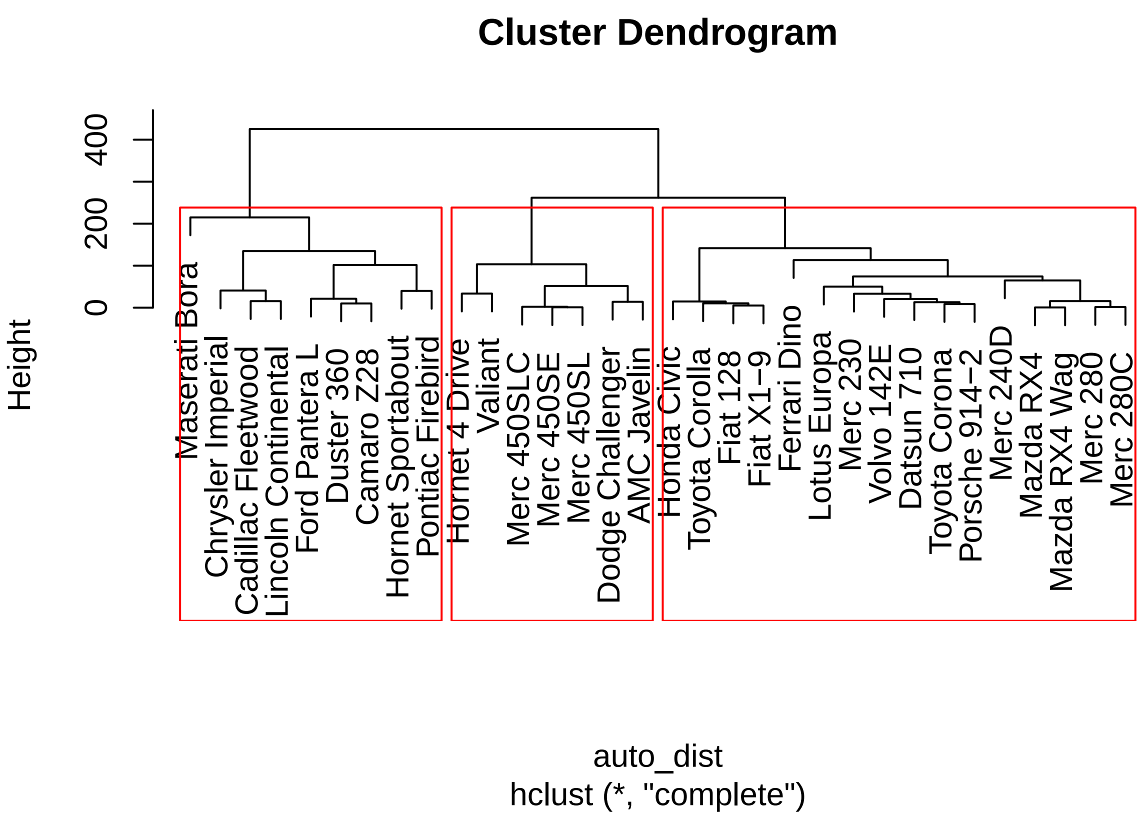
complete linkage - or largest Euclidean distance between clusters.
single linkage - conversely, we look at the observations which are closest together (proximity).
centroid linkage - we can the distance between the centroid of each cluster.
group average (mean) linkage - taking the mean between the pairwise distances of the observations.

Complete linkage is the most traditional approach.

The tree structure that examines this hierarchical structure is called a dendogram.

```
auto_dist <- dist(mtcars,
                  method ='euclidean',
                  diag = FALSE)

auto_cluster <- hclust(auto_dist,
                       method ='complete')
```

```r
# plot the hierarchical cluster
plot(auto_cluster)
rect.hclust(auto_cluster, k = 3, border = 'red') # visualize cluster borders
```



Our dendogram indicates which observation is within which cluster.

We can cut our tree at let's say 3 clusters, segmenting them out as follows:

```r
cut_tree <- cutree(auto_cluster, 3) # each obs. now belongs to cluster 1,2, or 3
mtcars$segment <- cut_tree # segment out the data
```

Now we can view our segmented data in the workspace window as follows:

```r
View(mtcars)
```

Or see it as a dataframe, per usual:

```r
print(mtcars)
```

```
##                      mpg cyl  disp  hp drat    wt  qsec vs am gear carb segment
## Mazda RX4           21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4       1
## Mazda RX4 Wag       21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4       1
## Datsun 710          22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1       1
## Hornet 4 Drive      21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1       2
```

```
## Hornet Sportabout   18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2        3
## Valiant             18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1        2
## Duster 360          14.3   8 360.0 245 3.21 3.570 15.84  0  0    3    4        3
## Merc 240D           24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2        1
## Merc 230            22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2        1
## Merc 280            19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4        1
## Merc 280C           17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4        1
## Merc 450SE          16.4   8 275.8 180 3.07 4.070 17.40  0  0    3    3        2
## Merc 450SL          17.3   8 275.8 180 3.07 3.730 17.60  0  0    3    3        2
## Merc 450SLC         15.2   8 275.8 180 3.07 3.780 18.00  0  0    3    3        2
## Cadillac Fleetwood  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4        3
## Lincoln Continental 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4        3
## Chrysler Imperial   14.7   8 440.0 230 3.23 5.345 17.42  0  0    3    4        3
## Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1        1
## Honda Civic         30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2        1
## Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1        1
## Toyota Corona       21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1        1
## Dodge Challenger    15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2        2
## AMC Javelin         15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2        2
## Camaro Z28          13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4        3
## Pontiac Firebird    19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2        3
## Fiat X1-9           27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1        1
## Porsche 914-2       26.0   4 120.3  91 4.43 2.140 16.70  0  1    5    2        1
## Lotus Europa        30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2        1
## Ford Pantera L      15.8   8 351.0 264 4.22 3.170 14.50  0  1    5    4        3
## Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6        1
## Maserati Bora       15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8        3
## Volvo 142E          21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2        1
```

Sources

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