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Practical 1

Aim: -Install, configure and run Hadoop and HDFS and explore HDFS on Windows

Code:

Steps to Install Hadoop

1. Install Java JDK 1.8
2. Download Hadoop and extract and place under C drive
3. Set Path in Environment Variables
4. Config files under Hadoop directory
5. Create folder datanode and namenode under data directory
6. Edit HDFS and YARN files
7. Set Java Home environment in Hadoop environment
8. Setup Complete. Test by executing start-all.cmd

There are two ways to install Hadoop, i.e.

9. Single node
10. Multi node

Here, we use multi node cluster.

1. Install Java

11. – Java JDK Link to download
<https://www.oracle.com/java/technologies/javase-jdk8-downloads.html>
12. – extract and install Java in C:\Java
13. – open cmd and type -> javac -version

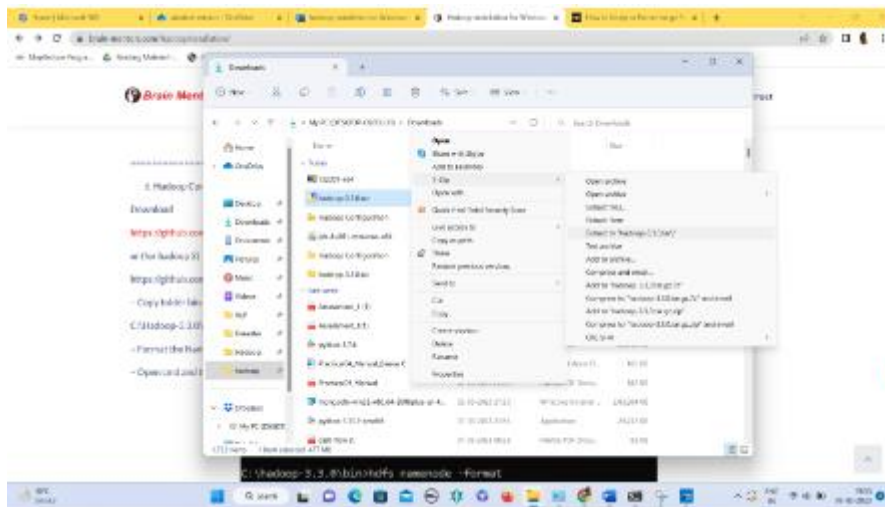
```
C:\Users>cd Beena

C:\Users\Beena>java -version
java version "1.8.0_361"
Java(TM) SE Runtime Environment (build 1.8.0_361-b09)
Java HotSpot(TM) 64-Bit Server VM (build 25.361-b09, mixed mode)
```

2. Download Hadoop

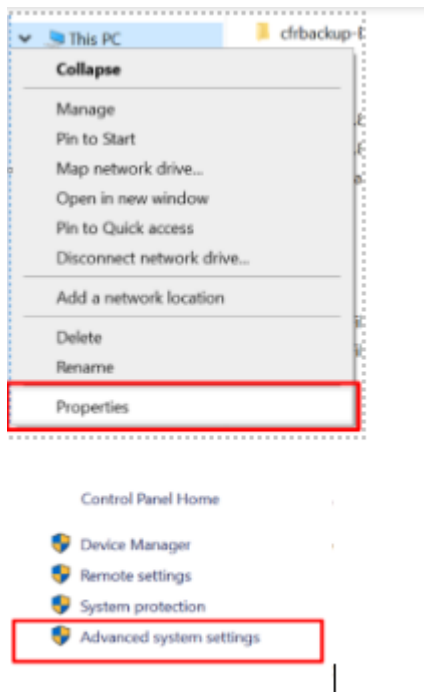
<https://www.apache.org/dyn/closer.cgi/hadoop/common/hadoop-3.3.0/hadoop-3.3.0.tar.gz>

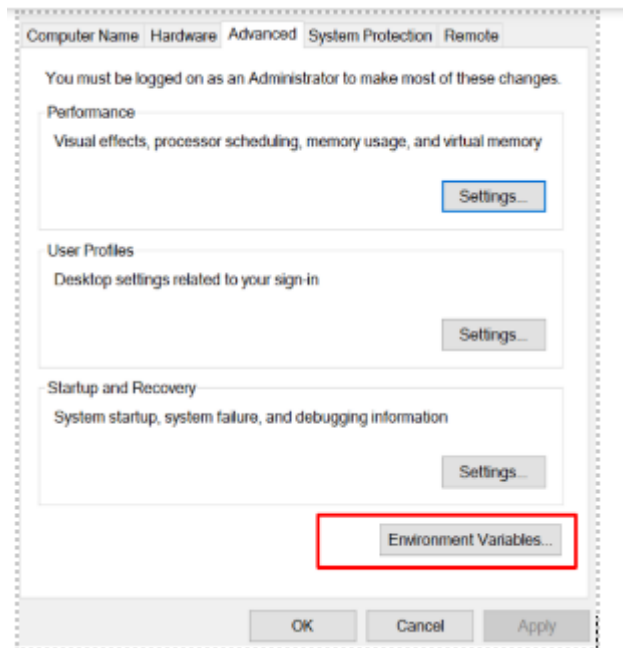
- right click .rar.gz file -> show more options -> 7-zip->and extract to C:\Hadoop-3.3.0\



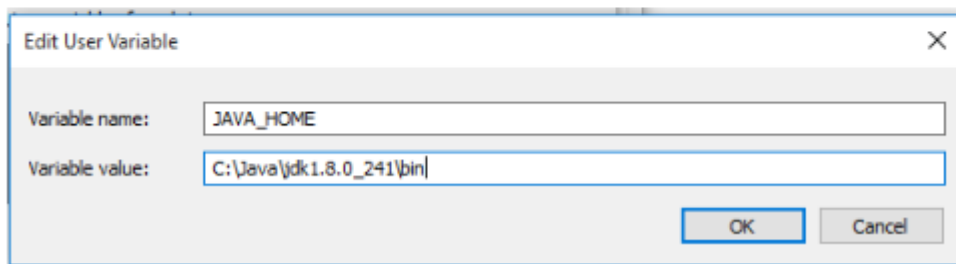
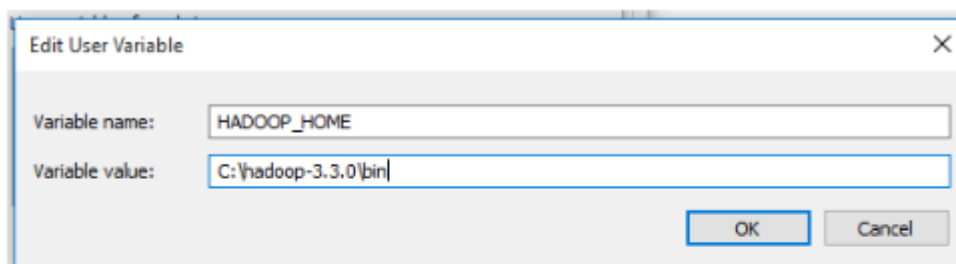
3 Set the path JAVA_HOME Environment variable

4 Set the path HADOOP_HOME Environment variable

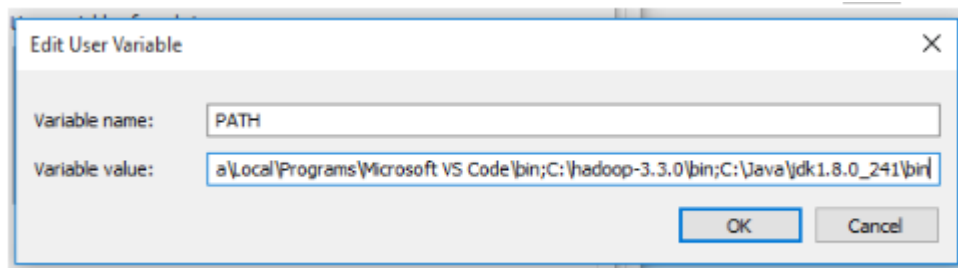




Click on **New** to both user variables and system variables.



Click on user variable -> path -> edit-> add path for Hadoop and java upto 'bin'



Click Ok, Ok, Ok.

5. Configurations

Edit file C:/Hadoop-3.3.0/etc/hadoop/core-site.xml,
paste the xml code in folder and save

=====

```
<configuration>
<property>
  <name>fs.defaultFS</name>
  <value>hdfs://localhost:9000</value>
</property>
</configuration>
```

=====

Rename “mapred-site.xml.template” to “mapred-site.xml” and edit this file C:/Hadoop-3.3.0/etc/hadoop/mapred-site.xml, paste xml code and save this file.

=====

```
<configuration>
<property>
  <name>mapreduce.framework.name</name>
  <value>yarn</value>
</property>
</configuration>
```

=====

Create folder “data” under “C:\Hadoop-3.3.0”

Create folder “datanode” under “C:\Hadoop-3.3.0\data”

Create folder “namenode” under “C:\Hadoop-3.3.0\data”

=====

Edit file C:\Hadoop-3.3.0/etc/hadoop/hdfs-site.xml,

paste xml code and save this file.

```
<configuration>
<property>
  <name>dfs.replication</name>
```

```

    <value>1</value>
  </property>

  <property>
    <name>dfs.namenode.name.dir</name>
    <value>/hadoop-3.3.0/data/namenode</value>
  </property>
  <property>
    <name>dfs.datanode.data.dir</name>
    <value>/hadoop-3.3.0/data/datanode</value>
  </property>
</configuration>

```

=====
Edit file C:/Hadoop-3.3.0/etc/hadoop/yarn-site.xml,

paste xml code and save this file.

```

<configuration>

</configuration>

```

6. **Edit file C:/Hadoop-3.3.0/etc/hadoop/hadoop-env.cmd**

Find "JAVA_HOME=%JAVA_HOME%" and replace it as
 set JAVA_HOME="C:\Java\jdk1.8.0_361"

7. **Download "redistributable" package**

Download and run VC_redist.x64.exe

This is a "redistributable" package of the Visual C runtime code for 64-bit applications, from Microsoft. It contains certain shared code that every application written with Visual C expects to have available on the Windows computer it runs on.

8. **Hadoop Configurations**

Download **bin** folder from

<https://github.com/s911415/apache-hadoop-3.1.0-winutils>

– Copy the **bin** folder to c:\hadoop-3.3.0. Replace the existing **bin** folder.

9. **copy "hadoop-yarn-server-timelineservice-3.0.3.jar" from ~\hadoop-3.0.3\share\hadoop\yarn\timelineservice to ~\hadoop-3.0.3\share\hadoop\yarn folder.**

10. **Format the NameNode**

– **Open cmd 'Run as Administrator' and type command "hdfs namenode –format"**

```
Microsoft Windows [Version 10.0.22621.1265]
(c) Microsoft Corporation. All rights reserved.

C:\Windows\System32>cd\hadoop-3.3.0\bin

C:\hadoop-3.3.0\bin>hdfs namenode -format
```

```
2023-03-07 21:31:34,685 INFO namenode.FSImageFormatProtobuf: Saving image file C:\hadoop-3.3.0\data\namenode\current\fsi
mage.ckpt_00000000000000000000 using no compression
2023-03-07 21:31:34,844 INFO namenode.FSImageFormatProtobuf: Image file C:\hadoop-3.3.0\data\namenode\current\fsimage.ck
pt_00000000000000000000 of size 400 bytes saved in 0 seconds .
2023-03-07 21:31:34,860 INFO namenode.NNStorageRetentionManager: Going to retain 1 images with txid >= 0
2023-03-07 21:31:34,869 INFO namenode.FSImage: FSImageSaver clean checkpoint: txid=0 when meet shutdown.
2023-03-07 21:31:34,870 INFO namenode.NameNode: SHUTDOWN_MSG:
/*****
SHUTDOWN_MSG: Shutting down NameNode at DESKTOP-OL8FIII\192.168.1.19
*****/
```

11. Testing

– Open cmd ‘Run as Administrator’ and change directory to C:\Hadoop-3.3.0\sbin

– type start-all.cmd

OR

- type start-dfs.cmd

– type start-yarn.cmd

```
C:\hadoop-3.3.0\sbin>start-all.cmd
This script is Deprecated. Instead use start-dfs.cmd and start-yarn.cmd
The filename, directory name, or volume label syntax is incorrect.
The filename, directory name, or volume label syntax is incorrect.
starting yarn daemons
The filename, directory name, or volume label syntax is incorrect.
```

– You will get 4 more running threads for Datanode, namenode, resouce manager and node manager

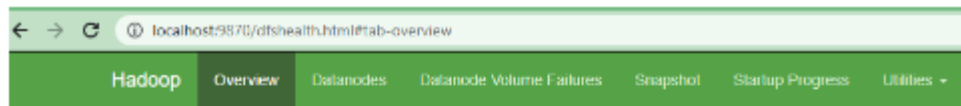
```
Apache Hadoop Distribution - hadoop namenode
2023-03-07 20:33:00,395 INFO ipc.Server: Starting Socket Reader #1 for port 9000
2023-03-07 20:33:00,547 INFO namenode.FSNamesystem: Registered FSNamesystemState, ReplicatedBlocksState and ECBlockGroup
sState MBeans.
2023-03-07 20:33:00,549 INFO common.Util: Assuming 'file' scheme for path /hadoop-3.3.0/data/namenode in configuration.
2023-03-07 20:33:00,554 INFO namenode.LeaseManager: Number of blocks under construction: 0
2023-03-07 20:33:00,563 INFO blockmanagement.DatanodeAdminDefaultMonitor: Initialized the Default Decommission and Maint
enance monitor
2023-03-07 20:33:00,566 INFO blockmanagement.BlockManager: initializing replication queues
2023-03-07 20:33:00,567 INFO hdfs.StateChange: STATE* Leaving safe mode after 0 secs
2023-03-07 20:33:00,567 INFO hdfs.StateChange: STATE* Network topology has 0 racks and 0 datanodes
2023-03-07 20:33:00,569 INFO hdfs.StateChange: STATE* UnderReplicatedBlocks has 0 blocks
2023-03-07 20:33:00,574 INFO blockmanagement.BlockManager: Total number of blocks = 0
2023-03-07 20:33:00,575 INFO blockmanagement.BlockManager: Number of invalid blocks = 0
2023-03-07 20:33:00,575 INFO blockmanagement.BlockManager: Number of under-replicated blocks = 0
2023-03-07 20:33:00,576 INFO blockmanagement.BlockManager: Number of over-replicated blocks = 0
2023-03-07 20:33:00,576 INFO blockmanagement.BlockManager: Number of blocks being written = 0
2023-03-07 20:33:00,576 INFO hdfs.StateChange: STATE* Replication Queue initialization scan for invalid, over- and under
replicated blocks completed in 9 msec
2023-03-07 20:33:00,607 INFO ipc.Server: IPC Server Responder: starting
2023-03-07 20:33:00,607 INFO ipc.Server: IPC Server listener on 9000: starting
2023-03-07 20:33:00,611 INFO namenode.NameNode: NameNode RPC up at: localhost/127.0.0.1:9000
2023-03-07 20:33:00,614 INFO namenode.FSNamesystem: Starting services required for active state
2023-03-07 20:33:00,614 INFO namenode.FSDirectory: Initializing quota with 4 thread(s)
2023-03-07 20:33:00,622 INFO namenode.FSDirectory: Quota initialization completed in 7 milliseconds
name space=1
storage space=0
storage types=RAM_DISK=0, SSD=0, DISK=0, ARCHIVE=0, PROVIDED=0
2023-03-07 20:33:00,626 INFO blockmanagement.CacheReplicationMonitor: Starting CacheReplicationMonitor with interval 300
00 milliseconds
```

Output:

12. Type JPS command to start-all.cmd command prompt, you will get following output.

```
C:\hadoop-3.3.0\sbin>jps
5632 Jps
7572 DataNode
3752 ResourceManager
7992 NameNode
8028 NodeManager
```

13. Run <http://localhost:9870/> from any browser
Or <http://localhost:50070/>



Overview 'localhost:9000' (✓active)

Started:	Wed Mar 15 12:10:54 +0530 2023
Version:	3.3.0, raa96f1871bfc858f9bac59cf2a81ec470da649af
Compiled:	Tue Jul 07 00:14:00 +0530 2020 by brahma from branch-3.3.0
Cluster ID:	CID-1986aba8-0ed3-43a2-9db7-42944ec518b2
Block Pool ID:	BP-1049743432-192.168.56.1-1678862097216



Practical 2

Aim: - Implement Decision tree classification techniquesb.

```
install.packages('datasets')
```

```
install.packages('caTools')
```

```
install.packages('party')
```

```
install.packages('dplyr')
```

```
install.packages('magrittr')
```

```
library(datasets)

library(caTools)

library(party)

library(dplyr)

library(magrittr)

data("readingSkills")

head(readingSkills)

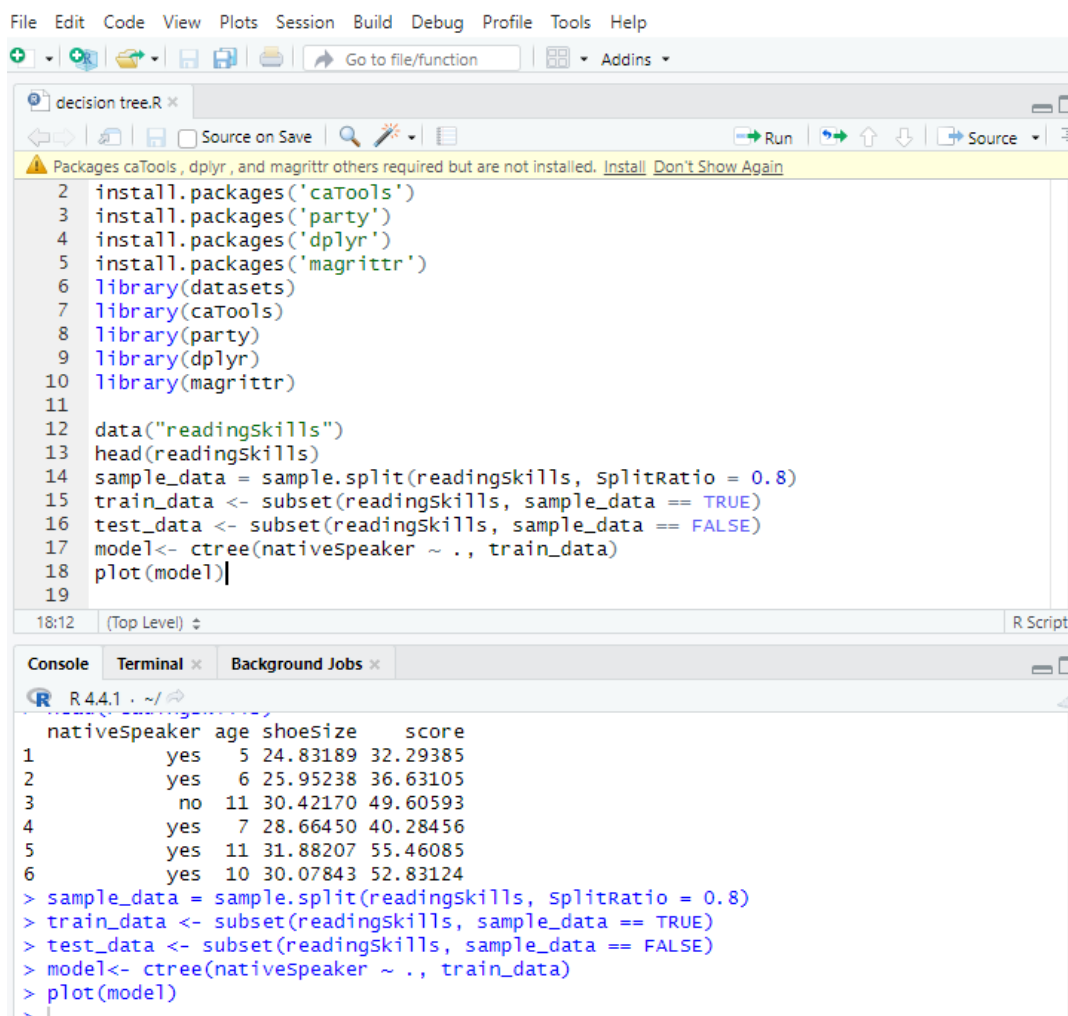
sample_data = sample.split(readingSkills, SplitRatio = 0.8)

train_data <- subset(readingSkills, sample_data == TRUE)

test_data <- subset(readingSkills, sample_data == FALSE)

model<- ctree(nativeSpeaker ~ ., train_data)

plot(model)
```



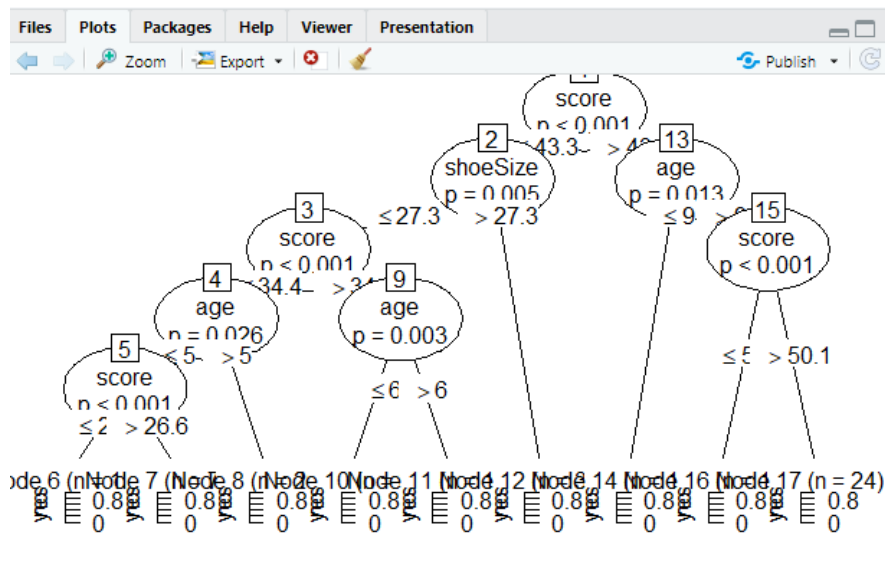
The screenshot shows the RStudio interface. The top menu bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, and Help. Below the menu is a toolbar with icons for file operations and a search bar. The main editor window displays the following R code:

```
2 install.packages('caTools')
3 install.packages('party')
4 install.packages('dplyr')
5 install.packages('magrittr')
6 library(datasets)
7 library(caTools)
8 library(party)
9 library(dplyr)
10 library(magrittr)
11
12 data("readingSkills")
13 head(readingSkills)
14 sample_data = sample.split(readingSkills, splitRatio = 0.8)
15 train_data <- subset(readingSkills, sample_data == TRUE)
16 test_data <- subset(readingSkills, sample_data == FALSE)
17 model<- ctree(nativeSpeaker ~ ., train_data)
18 plot(model)
19
```

A yellow warning banner at the top of the editor window states: "Packages caTools, dplyr, and magrittr others required but are not installed. [Install](#) [Don't Show Again](#)".

The bottom panel shows the Console window with the following output:

```
R 4.4.1 ~ /
> data("readingSkills")
  nativespeaker age shoeSize  score
1         yes   5  24.83189 32.29385
2         yes   6  25.95238 36.63105
3         no   11  30.42170 49.60593
4         yes   7  28.66450 40.28456
5         yes  11  31.88207 55.46085
6         yes  10  30.07843 52.83124
> sample_data = sample.split(readingSkills, splitRatio = 0.8)
> train_data <- subset(readingSkills, sample_data == TRUE)
> test_data <- subset(readingSkills, sample_data == FALSE)
> model<- ctree(nativeSpeaker ~ ., train_data)
> plot(model)
>
```



Practical 3

Aim:- Implement SVM classification techniques

#Code for installation of all necessary packages

```
install.packages("caret")
```

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

```
install.packages("GGally")
```

```
install.packages("psych")
```

```
install.packages("ggpubr")
```

```
install.packages("reshape")
```

Code for importation of all necessary packages

```
library(caret)
```

```
library(ggplot2)
```

```
library(GGally)
```

```
library(psych)
```

```
library(ggpubr)
```

```
library(reshape)
```

Code

```
df <- read.csv("D:\\diabetes.csv")
```

```
head(df)
```

```
> # Code
> df <- read.csv("D:\\diabetes.csv")
> head(df)
  Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  DiabetesPedigreeFunction  Age  Outcome
1          6     148            72           35         0  33.6              0.627    50         1
2          1      85            66           29         0  26.6              0.351    31         0
3          8     183            64           0          0  23.3              0.672    32         1
4          1      89            66           23        94  28.1              0.167    21         0
5          0     137            40           35       168  43.1              2.288    33         1
6          5     116            74           0          0  25.6              0.201    30         0
> |
```

```
# Code
```

```
sum(is.na(df))
```

```
# Code
```

```
dim(df)
```

```
> # Code
> sum(is.na(df))
[1] 0
> # Code
> dim(df)
[1] 768  9
> |
```

```
# Code
```

```
sapply(df, class)
```

```
# Code
```

```
summary(df) # to calculate the summary of our dataset
```

```
> # Code
> sapply(df, class)
      Pregnancies      Glucose      BloodPressure      SkinThickness
      "integer"      "integer"      "integer"      "integer"
      Insulin      BMI  DiabetesPedigreeFunction      Age
      "integer"      "numeric"      "numeric"      "integer"
      Outcome
      "integer"

> # Code
> summary(df) # to calculate the summary of our dataset
      Pregnancies      Glucose      BloodPressure      SkinThickness      Insulin      BMI
Min.   : 0.000  Min.   : 0.0  Min.   : 0.00  Min.   : 0.00  Min.   : 0.0  Min.   : 0.00
1st Qu.: 1.000  1st Qu.: 99.0  1st Qu.: 62.00  1st Qu.: 0.00  1st Qu.: 0.0  1st Qu.:27.30
Median : 3.000  Median :117.0  Median : 72.00  Median :23.00  Median : 30.5  Median :32.00
Mean   : 3.845  Mean   :120.9  Mean   : 69.11  Mean   :20.54  Mean   : 79.8  Mean   :31.99
3rd Qu.: 6.000  3rd Qu.:140.2  3rd Qu.: 80.00  3rd Qu.:32.00  3rd Qu.:127.2  3rd Qu.:36.60
Max.   :17.000  Max.   :199.0  Max.   :122.00  Max.   :99.00  Max.   :846.0  Max.   :67.10
DiabetesPedigreeFunction      Age      Outcome
Min.   :0.0780  Min.   :21.00  Min.   :0.000
1st Qu.:0.2437  1st Qu.:24.00  1st Qu.:0.000
Median :0.3725  Median :29.00  Median :0.000
Mean   :0.4719  Mean   :33.24  Mean   :0.349
3rd Qu.:0.6262  3rd Qu.:41.00  3rd Qu.:1.000
Max.   :2.4200  Max.   :81.00  Max.   :1.000
~ |
```

```
# Code
```

```
a <- ggplot(data = df, aes(x = Pregnancies)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) +  
  geom_density()
```

```
b <- ggplot(data = df, aes(x = Glucose)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) +  
  geom_density()
```

```
c <- ggplot(data = df, aes(x = BloodPressure)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) +  
  geom_density()
```

```
d <- ggplot(data = df, aes(x = SkinThickness)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) +  
  geom_density()
```

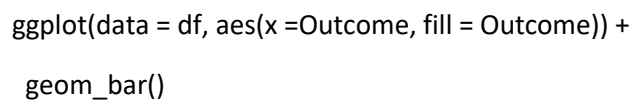
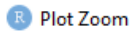
```
e <- ggplot(data = df, aes(x = Insulin)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) +  
  geom_density()
```

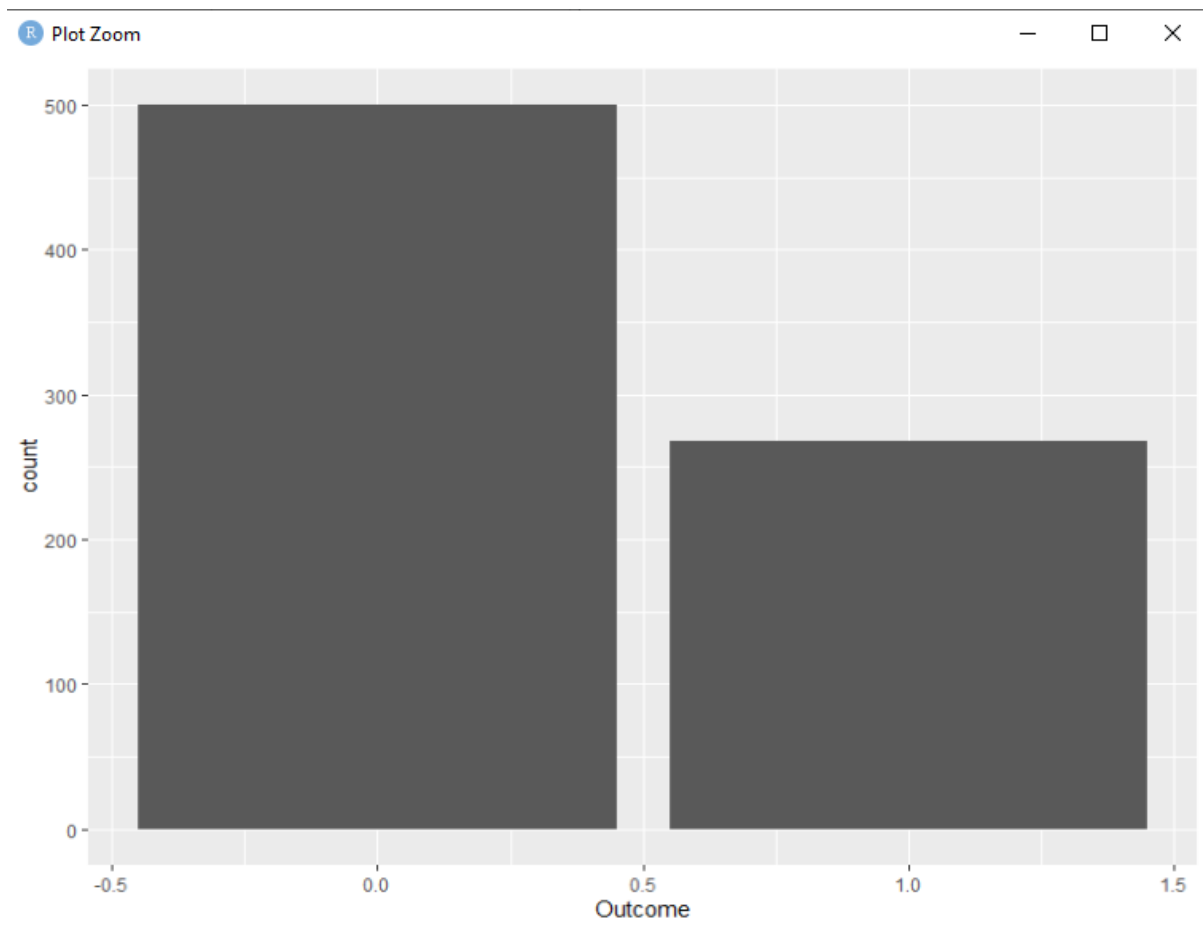
```
f <- ggplot(data = df, aes(x = BMI)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) +  
  geom_density()
```

```
g <- ggplot(data = df, aes(x = DiabetesPedigreeFunction)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) +  
  geom_density()
```

```
h <- ggplot(data = df, aes(x = Age)) +  
  geom_histogram( color = "red", fill = "blue", alpha = 0.1) + geom_density()
```

```
ggarrange(a, b, c, d,e,f,g, h + rremove("x.text"),  
  labels = c("a", "b", "c", "d", "e", "f", "g", "h"),  
  ncol = 3, nrow = 3)
```



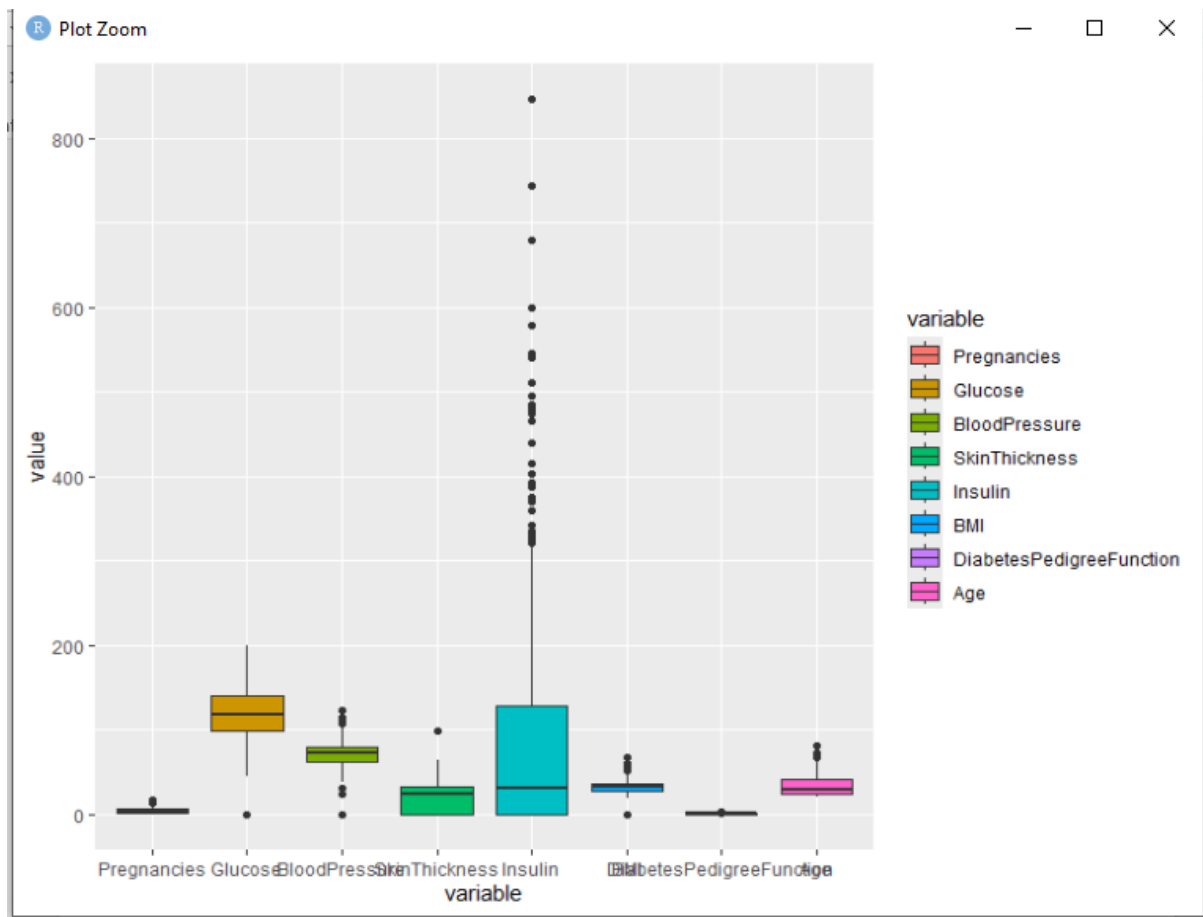


Code to label our categorical variable as a factor

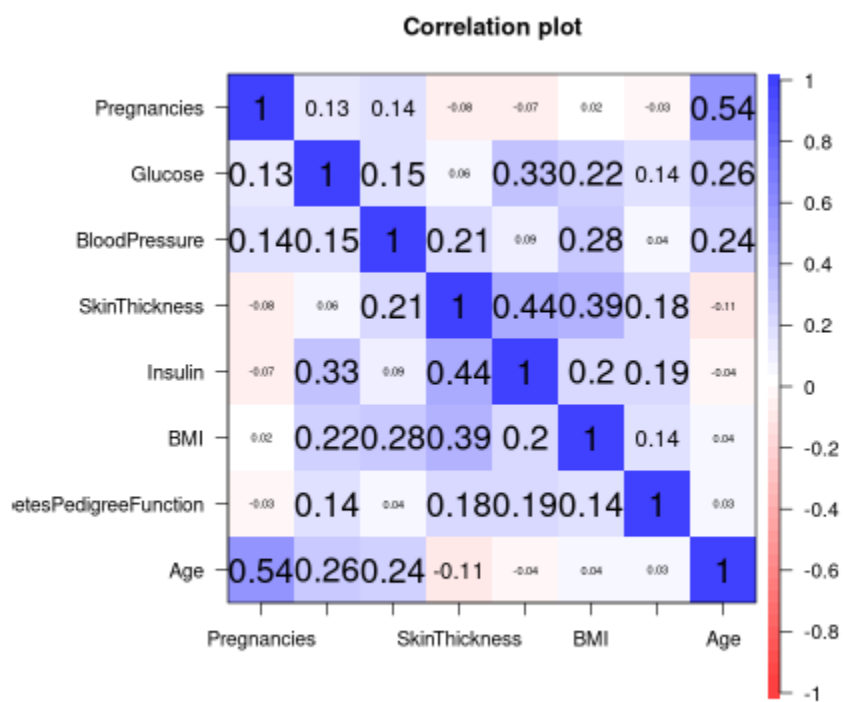
```
df$Outcome<- factor(df$Outcome,  
  levels = c(0, 1),  
  labels = c("Negative", "Positive"))  
out <- subset(df,  
  select = c(Pregnancies,Glucose,  
    BloodPressure,SkinThickness,  
    Insulin,BMI,  
    DiabetesPedigreeFunction,Age))
```

Code for boxplot

```
ggplot(data = melt(out),  
  aes(x=variable, y=value)) +  
  geom_boxplot(aes(fill=variable))
```



```
corPlot(df[, 1:8])
```




```

cutoff <- createDataPartition(df$Outcome, p=0.85, list=FALSE)

# select 15% of the data for validation
testdf <- df[-cutoff,]

# use the remaining 85% of data to training and testing the models
traindf <- df[cutoff,]

# Code to train the SVM
set.seed(1234)

# set the 10 fold crossvalidation with AU
# to pick for us what we call the best model
control <- trainControl(method="cv",number=10, classProbs = TRUE)
metric <- "Accuracy"

model <- train(Outcome ~., data = traindf, method = "svmRadial",
               tuneLength = 8,preProc = c("center","scale"),
               metric=metric, trControl=control)

# Code for model summary

```


Model

Source

Console

Terminal x

Background Jobs x

 R 4.4.1 . ~/


```

> set.seed(1234)
> # set the 10 fold crossvalidation with AU
> # to pick for us what we call the best model
> control <- trainControl(method="cv",number=10, classProbs = TRUE)
> metric <- "Accuracy"
> model <- train(Outcome ~., data = traindf, method = "svmRadial",
+               tuneLength = 8,preProc = c("center","scale"),
+               metric=metric, trControl=control)
> # Code for model summary
> model
Support Vector Machines with Radial Basis Function Kernel

653 samples
 8 predictor
 2 classes: 'Negative', 'Positive'

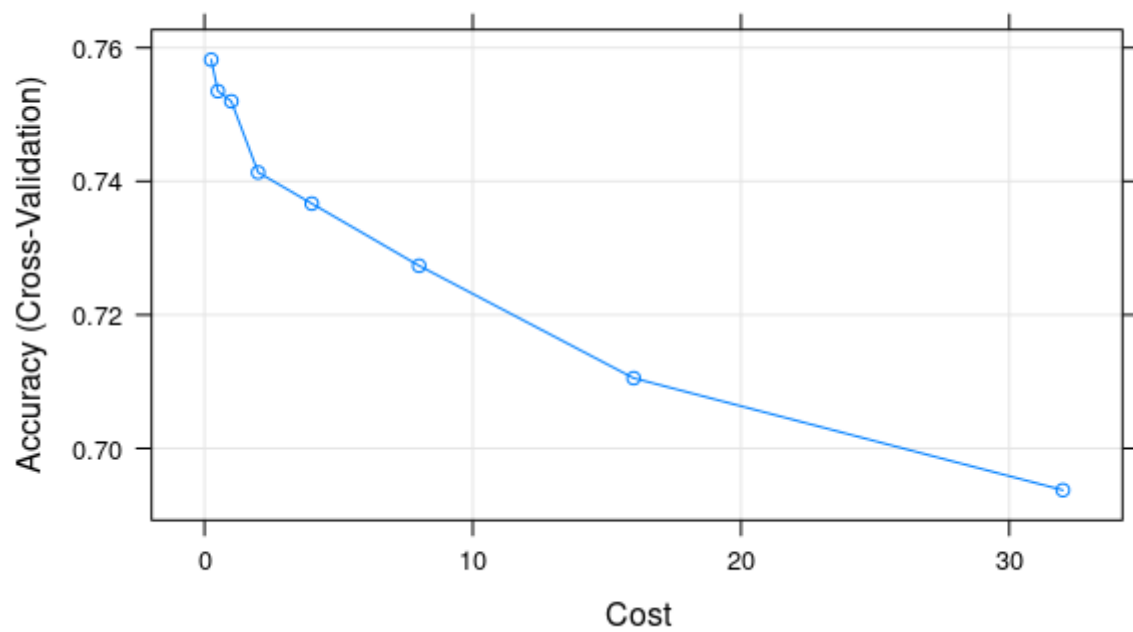
Pre-processing: centered (8), scaled (8)
Resampling: Cross-Validated (10 fold)
Summary of sample sizes: 587, 588, 587, 588, 589, ...
Resampling results across tuning parameters:

  C      Accuracy  Kappa
0.25  0.7578919  0.4410700
0.50  0.7532044  0.4289572
1.00  0.7594063  0.4383532
2.00  0.7564001  0.4380336
4.00  0.7456294  0.4150171
8.00  0.7273317  0.3654897
16.00 0.7227156  0.3481216
32.00 0.7149752  0.3225678

Tuning parameter 'sigma' was held constant at a value of 0.1347287
Accuracy was used to select the optimal model using the largest value.
The final values used for the model were sigma = 0.1347287 and c = 1.
> |
    
```

Code

```
plot(model)
```



Practical 4

Aim: - Implement of REGRESSION MODLE.

```
# Generate random IQ values with mean = 30 and sd =2
IQ <- rnorm(40, 30, 2)

# Sorting IQ level in ascending order
IQ <- sort(IQ)

# Generate vector with pass and fail values of 40 students
result <- c(0, 0, 0, 1, 0, 0, 0, 0, 0, 1,
            1, 0, 0, 0, 1, 1, 0, 0, 1, 0,
            0, 0, 1, 0, 0, 1, 1, 0, 1, 1,
            1, 1, 1, 0, 1, 1, 1, 1, 0, 1)

# Data Frame
df <- as.data.frame(cbind(IQ, result))

# Print data frame
print(df)
```

```
Console Terminal x Background Jobs x
R 4.4.1 . ~/
> df <- as.data.frame(cbind(IQ, result))
>
> # Print data frame
> print(df)
      IQ result
1 26.06677     0
2 26.62661     0
3 27.46988     0
4 27.72373     1
5 27.86435     0
6 27.94799     0
7 28.54222     0
8 28.62629     0
9 28.74992     0
10 28.87905     1
11 28.88832     1
12 29.05442     0
13 29.10868     0
14 29.23906     0
15 29.38807     1
16 29.40986     1
17 29.53965     0
18 29.56405     0
19 29.87618     1
20 30.14102     0
21 30.22137     0
22 30.25858     0
23 30.30675     1
24 30.71963     0
25 30.80154     0
26 30.85293     1
27 30.92183     1
28 30.99570     0
29 31.10784     1
30 31.37728     1
```

Plotting IQ on x-axis and result on y-axis

```
plot(IQ, result, xlab = "IQ Level",  
     ylab = "Probability of Passing")
```

Create a logistic model

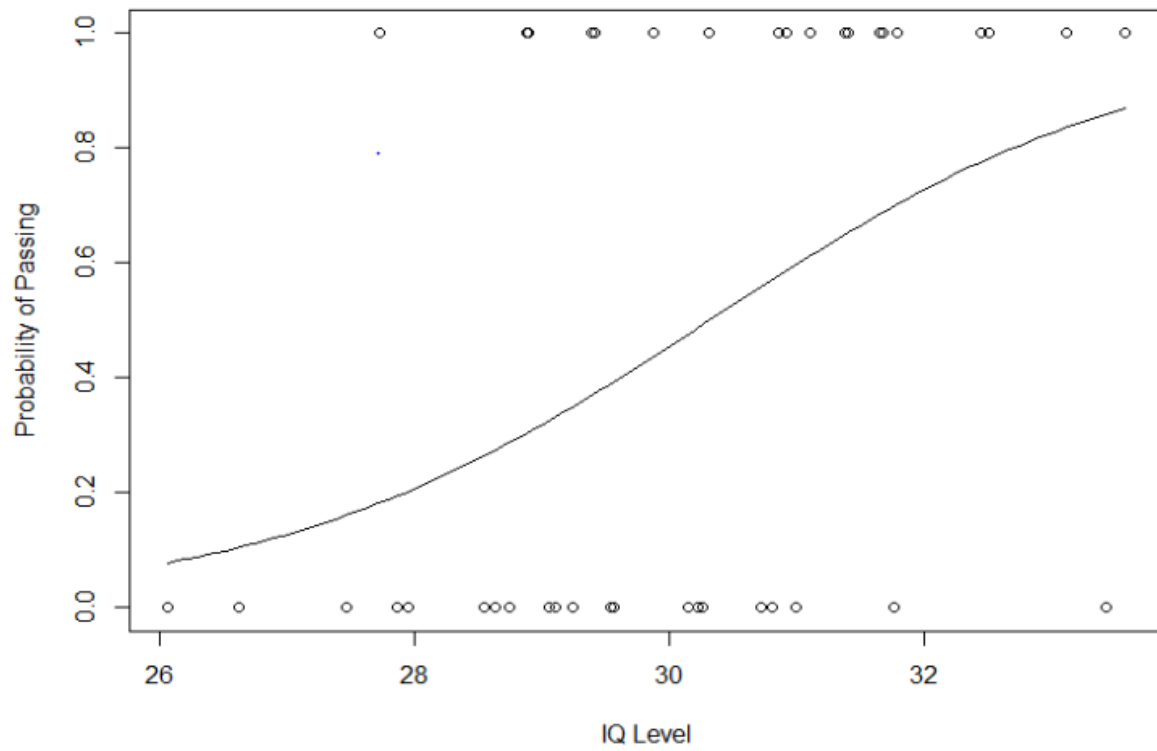
```
g = glm(result~IQ, family=binomial, df)
```

Create a curve based on prediction using the regression model

```
curve(predict(g, data.frame(IQ=x), type="resp"), add=TRUE)
```

Based on fit to the regression model

```
points(IQ, fitted(g), pch=30)
```



Summary of the regression model

summary(g)

```
> # summary of the regression model
> summary(g)

Call:
glm(formula = result ~ IQ, family = binomial, data = df)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -17.6032      7.0531  -2.496   0.0126 *
IQ            0.5808      0.2335   2.488   0.0129 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 55.352  on 39  degrees of freedom
Residual deviance: 47.331  on 38  degrees of freedom
AIC: 51.331

Number of Fisher Scoring iterations: 3
```

Practical 5

Aim :- Implement of Simple Linear Regaression.

```
years_of_exp = c(7,5,1,3)
```

```
salary_in_lakhs = c(21,13,6,8)
```

```
#employee.data = data.frame(satisfaction_score, years_of_exp, salary_in_lakhs)
```

```
employee.data = data.frame(years_of_exp, salary_in_lakhs)
```

```
employee.data
```

Estimation of the salary of an employee, based on his year of experience and satisfaction score in his company.

```
model <- lm(salary_in_lakhs ~ years_of_exp, data = employee.data)
```

```
summary(model)
```

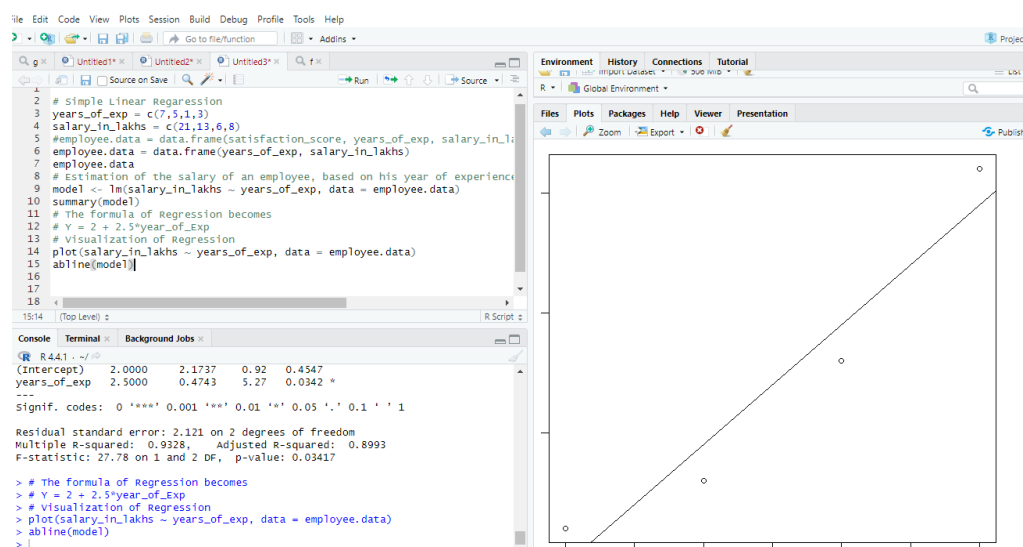
The formula of Regression becomes

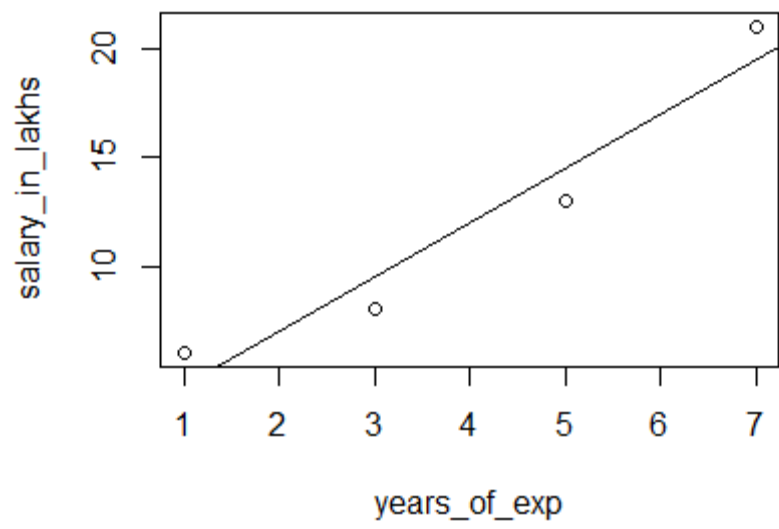
$Y = 2 + 2.5 \times \text{year_of_Exp}$

Visualization of Regression

```
plot(salary_in_lakhs ~ years_of_exp, data = employee.data)
```

```
abline(model)
```





Practical 6

Aim :- Implement of Multiple Linear Regression.

```
# Importing the dataset

dataset = read.csv('D:\\data2.csv')

# Encoding categorical data

dataset$State = factor(dataset$State,
                        levels = c('New York', 'California', 'Florida'),
                        labels = c(1, 2, 3))

dataset$State

# Splitting the dataset into the Training set and Test set

install.packages('caTools')

library(caTools)

set.seed(123)

split = sample.split(dataset$Profit, SplitRatio = 0.8)

training_set = subset(dataset, split == TRUE)

test_set = subset(dataset, split == FALSE)


# Feature Scaling

# training_set = scale(training_set)

# test_set = scale(test_set)


# Fitting Multiple Linear Regression to the Training set

regressor = lm(formula = Profit ~ .,
               data = training_set)


# Predicting the Test set results

y_pred = predict(regressor, newdata = test_set)
```

```
> regressor
```

```
Call:
```

```
lm(formula = Profit ~ ., data = training_set)
```

```
Coefficients:
```

(Intercept)	R.D.Spend	Administration	Marketing.Spend
2.816e+04	8.884e-01	5.670e-02	2.859e-02
State2	State3		
-2.861e+03	9.172e+03		

Practical 7

Aim :- Implement of Logistic regression.

Source code:

```
install.packages("ISLR")

library(ISLR)

#load dataset

data <- ISLR::Default

print (head(ISLR::Default))

#view summary of dataset

summary(data)

#find total observations in dataset

nrow(data)

#Create Training and Test Samples

#split the dataset into a training set to train the model on and a testing set to test the model

set.seed(1)

#Use 70% of dataset as training set and remaining 30% as testing set

sample <- sample(c(TRUE, FALSE), nrow(data), replace=TRUE, prob=c(0.7,0.3))

print (sample)

train <- data[sample, ]

test <- data[!sample, ]

nrow(train)

nrow(test)

# Fit the Logistic Regression Model

# use the glm (general linear model) function and specify family="binomial"

#so that R fits a logistic regression model to the dataset

model <- glm(default~student+balance+income, family="binomial", data=train)

#view model summary

summary(model)

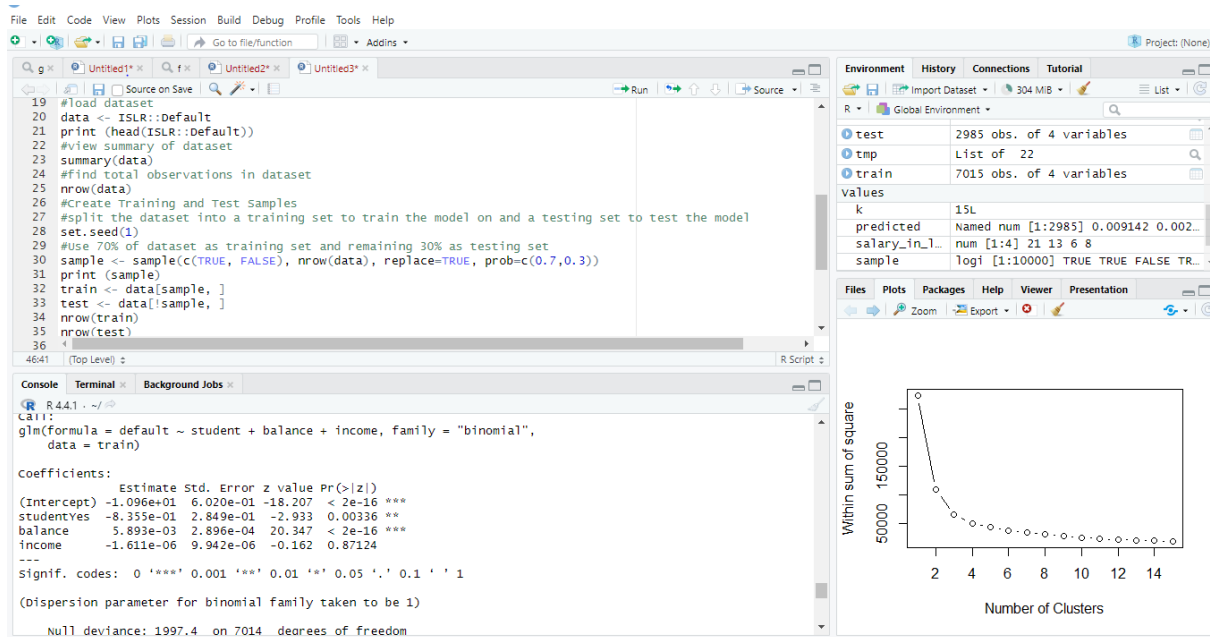
#Model Diagnostics

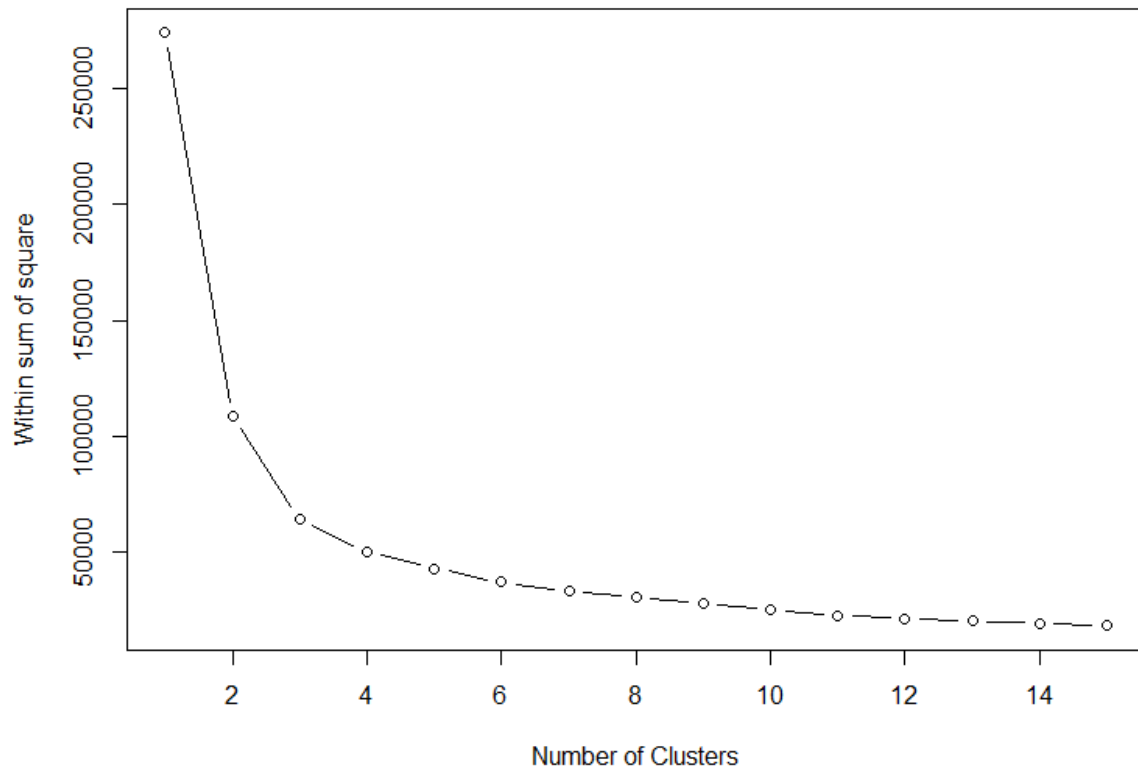
install.packages("InformationValue")
```

```
library(InformationValue)
```

```
predicted <- predict(model, test, type="response")
```

```
confusionMatrix(test$default, predicted)
```





Practical 8

Aim: Read a datafile grades_km_input.csv and apply k-means clustering.

Datafile:

```
# install required packages
```

```
install.packages("plyr")
```

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

```
install.packages("cluster")
```

```
install.packages("lattice")
```

```
install.packages("grid")
```

```
install.packages("gridExtra")
```

```
# Load the package
```

```
library(plyr)
```

```
library(ggplot2)
```

```
library(cluster)
```

```
library(lattice)
```

```
library(grid)
```

```
library(gridExtra)
```

```
# A data frame is a two-dimensional array-like structure in which each column contains values of one variable and each row contains one set of values from each column.
```

```
grade_input=as.data.frame(read.csv("D:\\grades_km_input.csv"))
```

```
kmdata_orig=as.matrix(grade_input[, c ("Student","English","Math","Science")])
```

```
kmdata=kmdata_orig[,2:4]
```

```
kmdata[1:10,]
```

```
# the k-means algorithm is used to identify clusters for k = 1, 2, .. , 15. For each value of k, the WSS is calculated.
```

```
wss=numeric(15)
```

```
# the option n start=25 specifies that the k-means algorithm will be repeated 25 times, each starting with k random initial centroids
```

```
for(k in 1:15)wss[k]=sum(kmeans(kmdata,centers=k,nstart=25)$withinss)
```

```
plot(1:15,wss,type="b",xlab="Number of Clusters",ylab="Within sum of square")
```

#As can be seen, the WSS is greatly reduced when k increases from one to two. Another substantial reduction in WSS occurs at k = 3. However, the improvement in WSS is fairly linear for k > 3.

```
km = kmeans(kmdata,3,nstart=25)
```

```
km
```

```
c( wss[3] , sum(km$withinss))
```

```
df=as.data.frame(kmdata_orig[,2:4])
```

```
df$cluster=factor(km$cluster)
```

```
centers=as.data.frame(km$centers)
```

```
g1=ggplot(data=df, aes(x=English, y=Math, color=cluster )) +
```

```
  geom_point() + theme(legend.position="right") +
```

```
  geom_point(data=centers,aes(x=English,y=Math, color=as.factor(c(1,2,3))),size=10, alpha=.3,  
  show.legend =FALSE)
```

```
g2=ggplot(data=df, aes(x=English, y=Science, color=cluster )) +
```

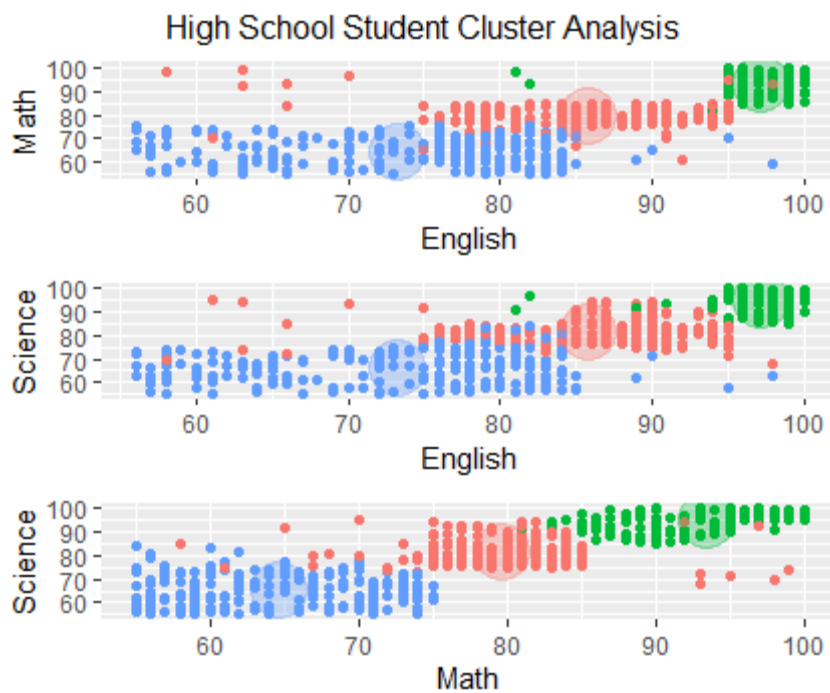
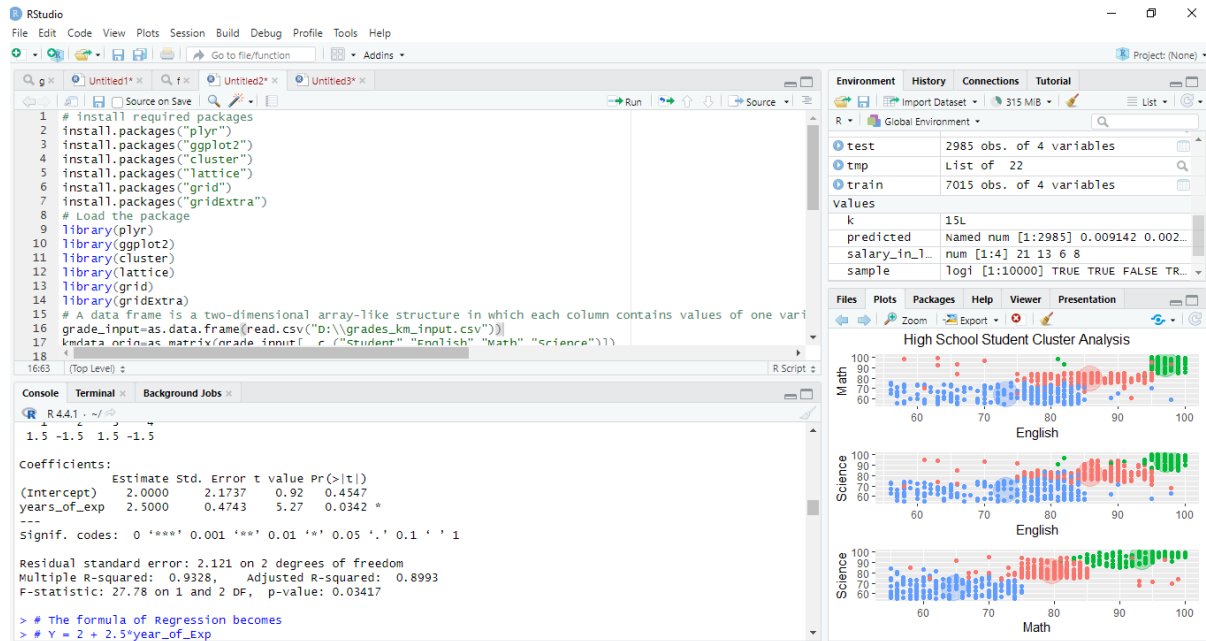
```
  geom_point () +geom_point(data=centers,aes(x=English,y=Science,  
  color=as.factor(c(1,2,3))),size=10, alpha=.3, show.legend=FALSE)
```

```
g3 = ggplot(data=df, aes(x=Math, y=Science, color=cluster )) +
```

```
  geom_point () + geom_point(data=centers,aes(x=Math,y=Science,  
  color=as.factor(c(1,2,3))),size=10, alpha=.3, show.legend=FALSE)
```

```
tmp=ggplot_gtable(ggplot_build(g1))
```

```
grid.arrange(arrangeGrob(g1 + theme(legend.position="none"),g2 +  
  theme(legend.position="none"),g3 + theme(legend.position="none"),top ="High School Student  
  Cluster Analysis" ,ncol=1))
```



Practical 9

Aim: Perform Apriori algorithm using Groceries dataset from the R arules package.

```
install.packages("arules")
install.packages("arulesViz")
install.packages("RColorBrewer")

# Loading Libraries

library(arules)
library(arulesViz)
library(RColorBrewer)

# import dataset

data(Groceries)

Groceries

summary(Groceries)

class(Groceries)

# using apriori() function

rules = apriori(Groceries, parameter = list(supp = 0.02, conf = 0.2))

summary(rules)

# using inspect() function

inspect(rules[1:10])

# using itemFrequencyPlot() function

arules::itemFrequencyPlot(Groceries, topN = 20,
col = brewer.pal(8, 'Pastel2'),
main = 'Relative Item Frequency Plot',
type = "relative",
ylab = "Item Frequency (Relative)")

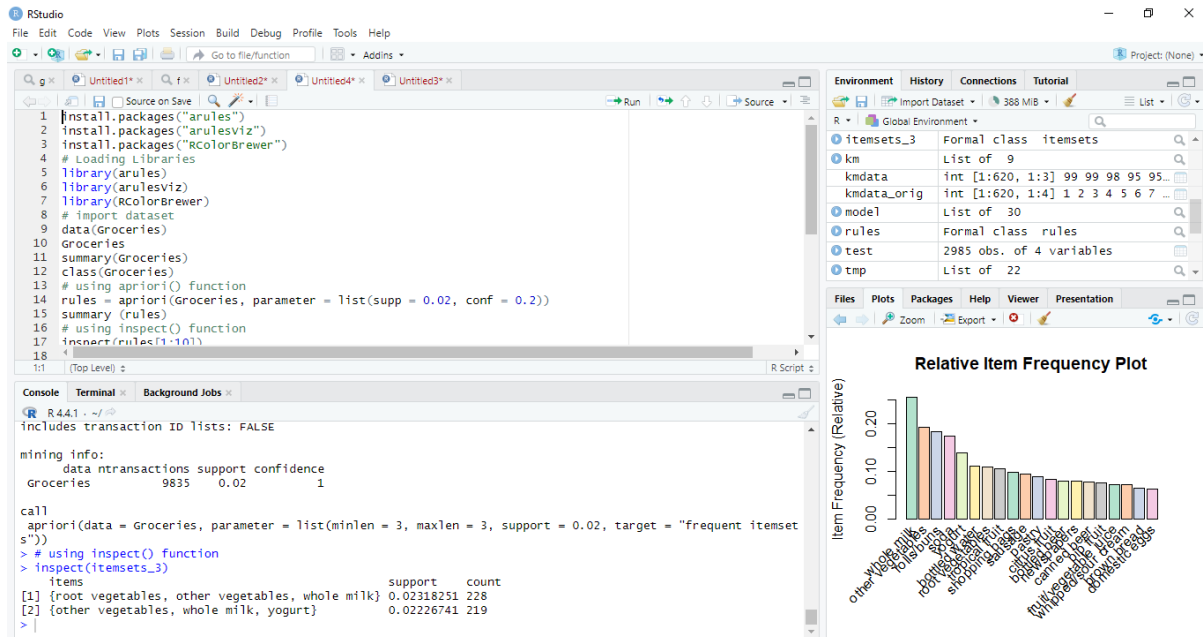
itemsets = apriori(Groceries, parameter = list(minlen=2, maxlen=2,support=0.02, target="frequent
itemsets"))

summary(itemsets)

# using inspect() function

inspect(itemsets[1:10])
```

```
inspect(itemsets_3)
```



Relative Item Frequency Plot

