EXPERIMENT NO:1

AIM: Implement basic commands in R,R Graphics,Indexeing data,loading data,Additional graphical and numerical summaries .

BASIC COMMANDS IN R:

DESCRIPTION: R uses functions to perform operations. To run a function called funcname , we type funcname(input1, input2) , where the inputs (or arguments) input1 and input2 tell R how to run the function. A function can have any number of inputs. For example, to create a vector of numbers, we use the function c() (for concatenate). Any numbers inside the parentheses are joined together.

CODE:

```
x <- c(1,3,2,5)
x
x = c(1,6,2)
x
y = c(1,4,3)
length(x)
length(y)
x+y
ls()
rm(x,y)
ls()
character(0)
rm(list=ls())
?matrix
x=matrix(data=c(1,2,3,4), nrow=2, ncol=2)
x'
```

OUTPUT:

```
R 4.3.0 · ~/
> x <- c(1,3,2,5)
> x
[1] 1 3 2 5
> x = c(1,6,2)
> x
[1] 1 6 2
> y = c(1,4,3)
> length(x)
[1] 3
> length(y)
[1] 3
> x+y
[1]  2 10  5
> ls()
[1] "x" "y"
> rm(x,y)
> ls()
character(0)
> character(0)
character(0)
> rm(list=ls())
> ?matrix
> x=matrix(data=c(1,2,3,4), nrow=2, ncol=2)
> x
     [,1] [,2]
[1,]    1    3
[2,]    2    4
```

CODE:

```
x=matrix(c(1,2,3,4) ,2,2)
matrix(c(1,2,3,4) ,2,2,byrow=TRUE)
sqrt(x)
x^2
x=rnorm(50)
y=x+rnorm(50,mean=50,sd=.1)
cor(x,y)
set.seed(1303)
rnorm(50)
set.seed(3)
y=rnorm(100)
mean(y)
var(y)
sqrt(var(y))
sd(y)
```

OUTPUT:

```
> x=matrix(c(1,2,3,4) ,2,2)
> matrix(c(1,2,3,4) ,2,2,byrow=TRUE)
     [,1] [,2]
[1,]    1    2
[2,]    3    4
> sqrt(x)
         [,1]     [,2]
[1,] 1.000000 1.732051
[2,] 1.414214 2.000000
> x^2
     [,1] [,2]
[1,]    1    9
[2,]    4   16
> x=rnorm(50)
> y=x+rnorm(50,mean=50,sd=.1)
> cor(x,y)
[1] 0.9934096
> set.seed(1303)
> rnorm(50)
 [1] -1.1439763145  1.3421293656  2.1853904757  0.5363925179  0.0631929665  0.5022344825 -0.0004167247  0.5658198405 -0.5725226890
[10] -1.1102250073 -0.0486871234 -0.6956562176  0.8289174803  0.2066528551 -0.2356745091 -0.5563104914 -0.3647543571  0.8623550343
[19] -0.6307715354  0.3136021252 -0.9314953177  0.8238676185  0.5233707021  0.7069214120  0.4202043256 -0.2690521547 -1.5103172999
[28] -0.6902124766 -0.1434719524 -1.0135274099  1.5732737361  0.0127465055  0.8726470499  0.4220661905 -0.0188157917  2.6157489689
[37] -0.6931401748 -0.2663217810 -0.7206364412  1.3677342065  0.2640073322  0.6321868074 -1.3306509858  0.0268888182  1.0406363208
[46]  1.3120237985 -0.0300020767 -0.2500257125  0.0234144857  1.6598706557
> set.seed(3)
> y=rnorm(100)
> mean(y)
[1] 0.01103557
> var(y)
[1] 0.7328675
> sqrt(var(y))
[1] 0.8560768
> sd(y)
[1] 0.8560768
> sd(y)
[1] 0.8560768
```

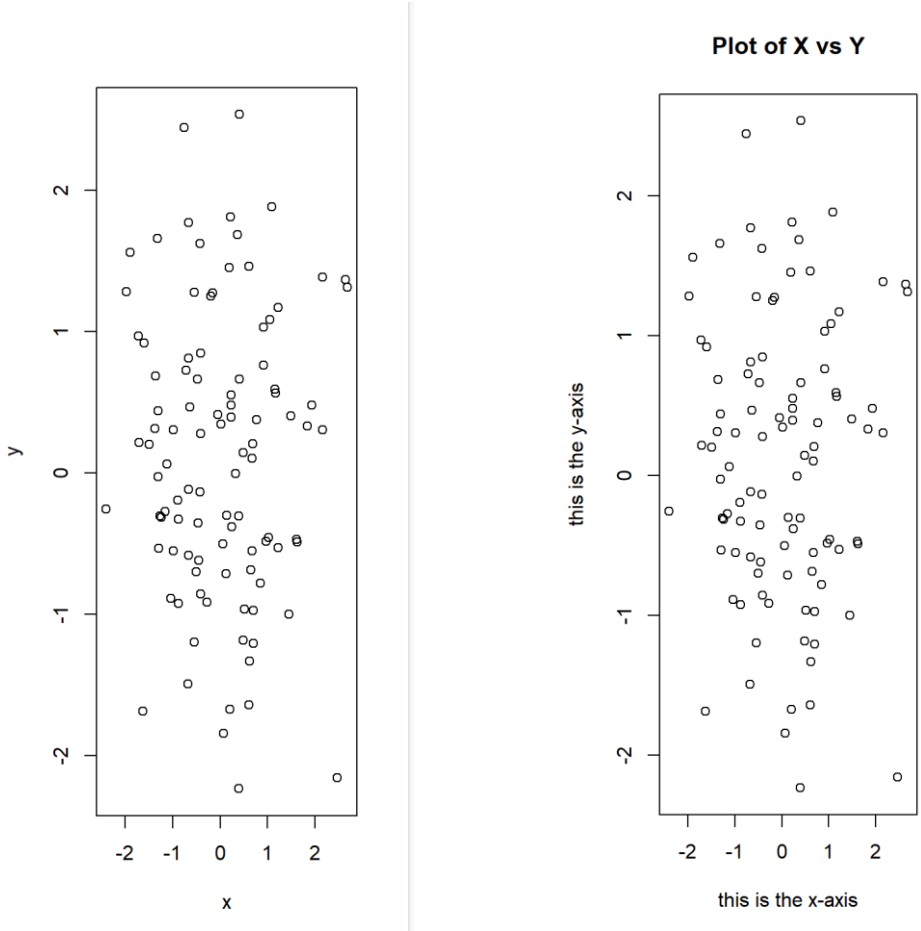
GRAPHICS IN R:

DESCRIPTION: The plot() function is the primary way to plot data in R . For instance, plot(x,y) produces a scatterplot of the numbers in x versus the numbers in y . There are many additional options that can be passed in to the plot() function.

CODE:

```
x=rnorm(100)
y=rnorm(100)
plot(x,y)
plot(x,y,xlab="this is the x-axis",ylab="this is the y-axis", main="Plot of X vs Y")
pdf("Figure.pdf")
plot(x,y,col="green")
dev.off()
x=seq(1,10)
x
x=1:10
x
```

OUTPUT:

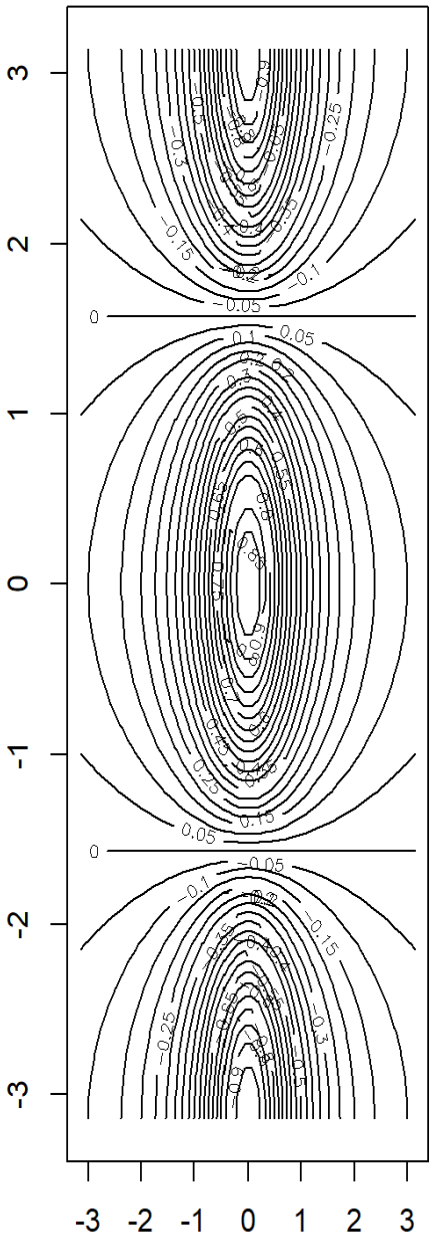


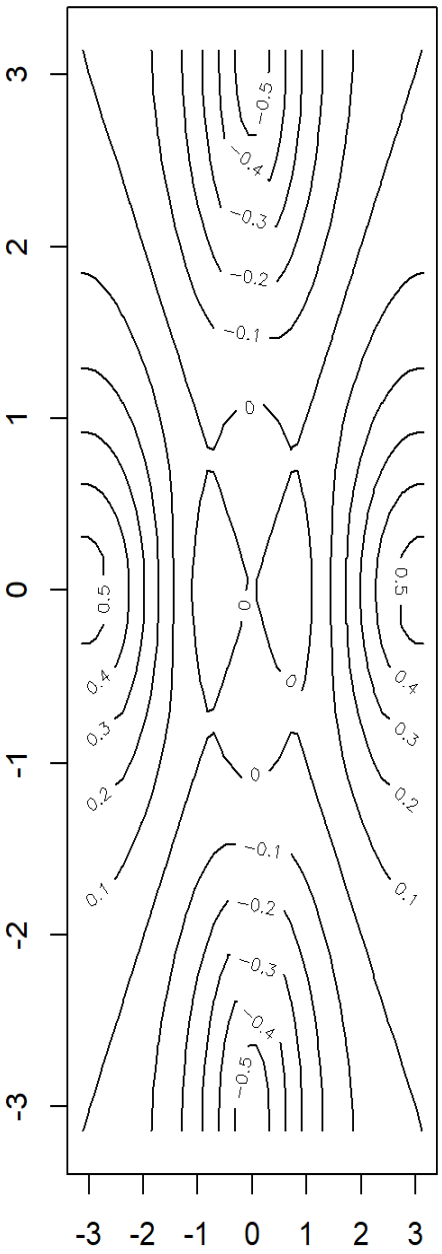

```
> x=seq(1,10)
> x
 [1]  1  2  3  4  5  6  7  8  9 10
> x=1:10
> x
 [1]  1  2  3  4  5  6  7  8  9 10
```

CODE:

```
x=seq(-pi,pi,length =50)
y=x
f=outer(x,y,function(x,y)cos(y)/(1+x^2))
contour(x,y,f)
contour(x,y,f,nlevels=45,add=T)
fa=(f-t(f))/2
contour(x,y,fa,nlevels=15)
```

OUTPUT:

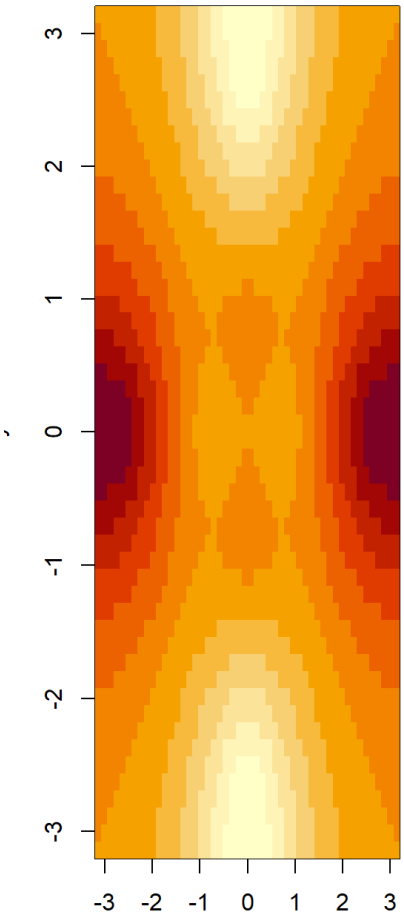


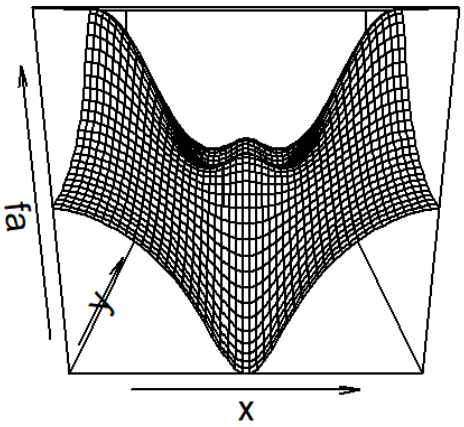


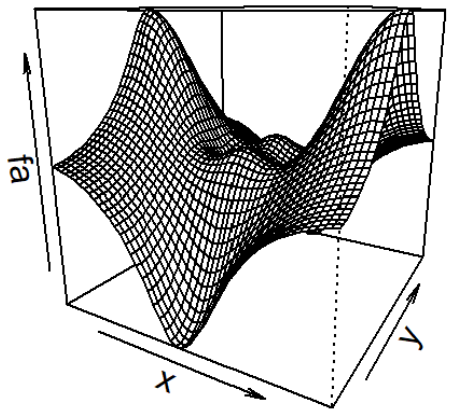
CODE:

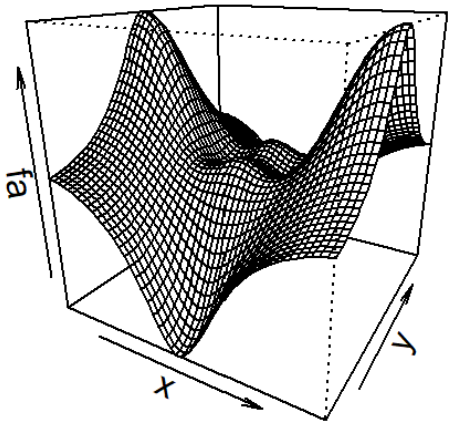
```
image(x,y,fa)
persp(x,y,fa)
persp(x,y,fa,theta =30)
persp(x,y,fa,theta=30,phi=20)
```

OUTPUT:



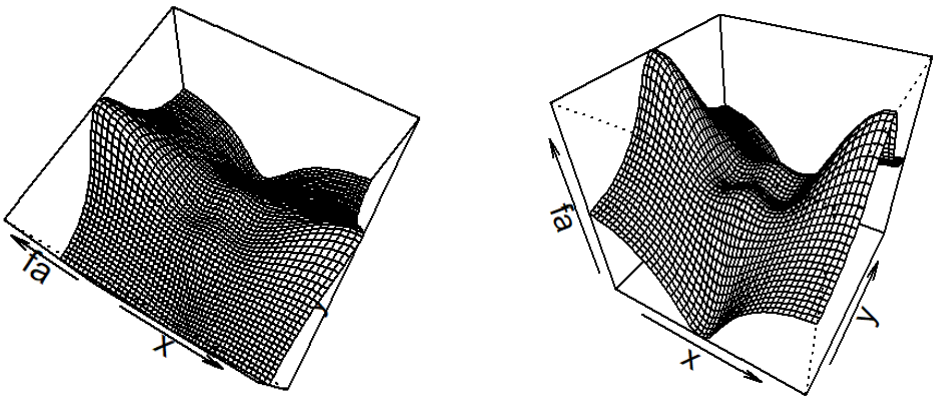






CODE:
persp(x,y,fa,theta=30,phi=70)
persp(x,y,fa,theta=30,phi=40)

OUTPUT:



INDEXING DATA:

DESCRIPTION: We often wish to examine part of a set of data. Suppose that our data is stored in the matrix A .

CODE:
A=matrix(1:16,4,4)
A
A[2,3]
A[c(1,3),c(2,4)]
A[1:3,2:4]
A[1:2,]

OUTPUT:

```
R 4.3.0 · ~/
> A=matrix(1:16,4,4)
> A
     [,1] [,2] [,3] [,4]
[1,]    1    5    9   13
[2,]    2    6   10   14
[3,]    3    7   11   15
[4,]    4    8   12   16
> A[2,3]
[1] 10
> A[c(1,3),c(2,4)]
     [,1] [,2]
[1,]    5   13
[2,]    7   15
> A[1:3,2:4]
     [,1] [,2] [,3]
[1,]    5    9   13
[2,]    6   10   14
[3,]    7   11   15
> A[1:2,]
     [,1] [,2] [,3] [,4]
[1,]    1    5    9   13
[2,]    2    6   10   14
```

CODE:

```
A[,1:2]
A[1,]
A[-c(1,3),]
A[-c(1,3),-c(1,3,4)]
dim(A)
```

OUTPUT:

```
> A[,1:2]
     [,1] [,2]
[1,]    1    5
[2,]    2    6
[3,]    3    7
[4,]    4    8
> A[1,]
[1]  1  5  9 13
> A[-c(1,3),]
     [,1] [,2] [,3] [,4]
[1,]    2    6   10   14
[2,]    4    8   12   16
> A[-c(1,3),-c(1,3,4)]
[1] 6 8
> dim(A)
[1] 4 4
>
```

LOADING DATA:

DESCRIPTION: For most analyses, the first step involves importing a data set into R . The read.table() function is one of the primary ways to do this. The help file read.table() contains details about how to use this function. We can use the function write.table() to export data.

CODE:

```
auto<- read_excel("C:/Users/Hp/OneDrive/Desktop/ML/auto_mpg.csv.xlsx")
str(auto)
auto[1:4,]
auto=na.omit(auto)
dim(auto)
names(auto)
```

OUTPUT:

```
> auto<- read_excel("C:/Users/Hp/OneDrive/Desktop/ML/auto_mpg.csv.xlsx")
> str(auto)
tibble [398 × 9] (S3: tbl_df/tbl/data.frame)
 $ mpg         : num [1:398] 18 15 18 16 17 15 14 14 14 15 ...
 $ cylinders   : num [1:398] 8 8 8 8 8 8 8 8 8 8 ...
 $ displacement: num [1:398] 307 350 318 304 302 429 454 440 455 390 ...
 $ horsepower  : chr [1:398] "130" "165" "150" "150" ...
 $ weight      : num [1:398] 3504 3693 3436 3433 3449 ...
 $ acceleration: num [1:398] 12 11.5 11 12 10.5 10 9 8.5 10 8.5 ...
 $ model year  : num [1:398] 70 70 70 70 70 70 70 70 70 70 ...
 $ origin      : num [1:398] 1 1 1 1 1 1 1 1 1 1 ...
 $ car name    : chr [1:398] "chevrolet chevelle malibu" "buick skylark 320" "plymouth satellite" "amc rebel sst" ...
> auto[1:4,]
# A tibble: 4 × 9
    mpg cylinders displacement horsepower weight acceleration `model year` origin `car name`
  <dbl>     <dbl>        <dbl> <chr>       <dbl>        <dbl>        <dbl>  <dbl> <chr>
1    18         8          307 130          3504         12             70      1 chevrolet chevelle malibu
2    15         8          350 165          3693         11.5           70      1 buick skylark 320
3    18         8          318 150          3436         11             70      1 plymouth satellite
4    16         8          304 150          3433         12             70      1 amc rebel sst
> auto=na.omit(auto)
> dim(auto)
[1] 398   9
> names(auto)
[1] "mpg"          "cylinders"    "displacement" "horsepower"   "weight"       "acceleration" "model year"   "origin"       "car name"
```

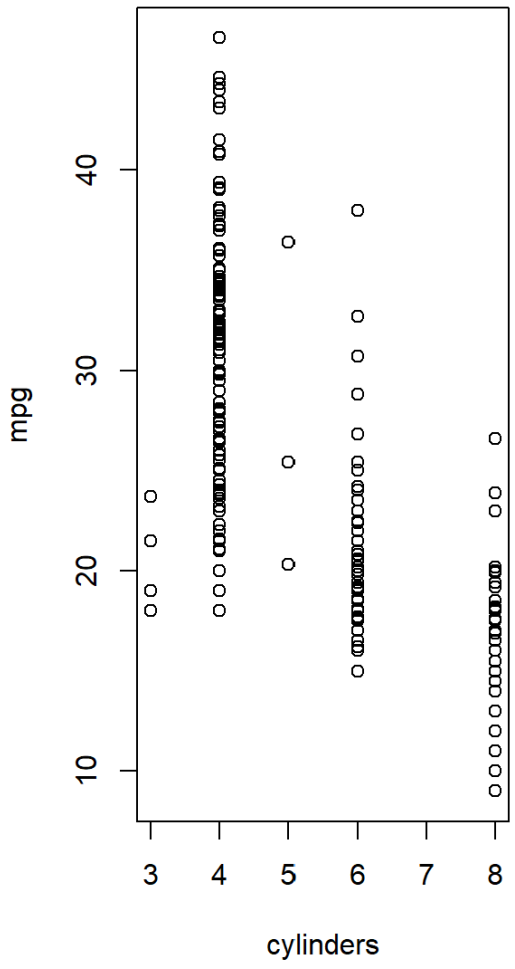
ADDITIONAL GRAPHICAL AND NUMERICAL SUMMARIES :

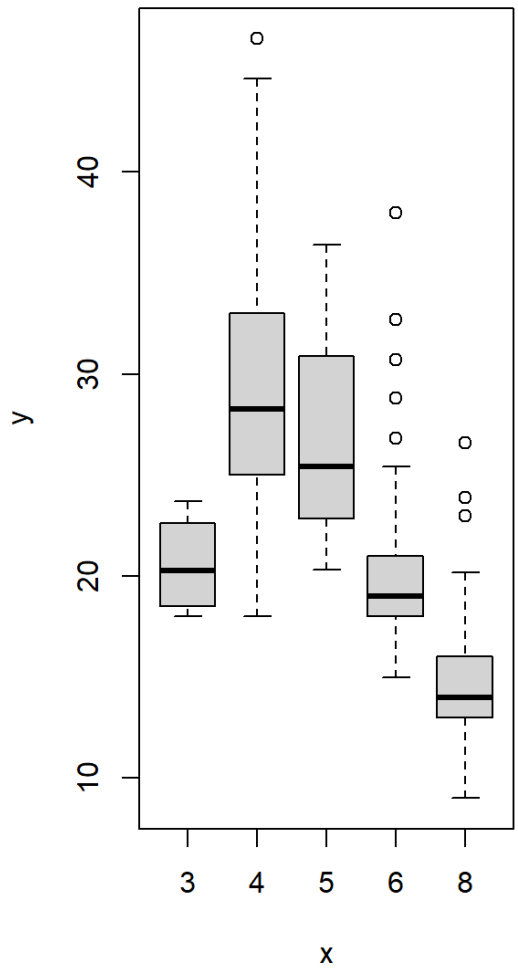
DESCRIPTION: We can use the plot() function to produce scatterplots of the quantitative variables. However, simply typing the variable names will produce an error message, because R does not know to look in the Auto data set for those variables.

CODE:

```
attach(auto)
plot(cylinders, mpg)
cylinders=as.factor(cylinders)
plot(cylinders,mpg)
```

OUTPUT:

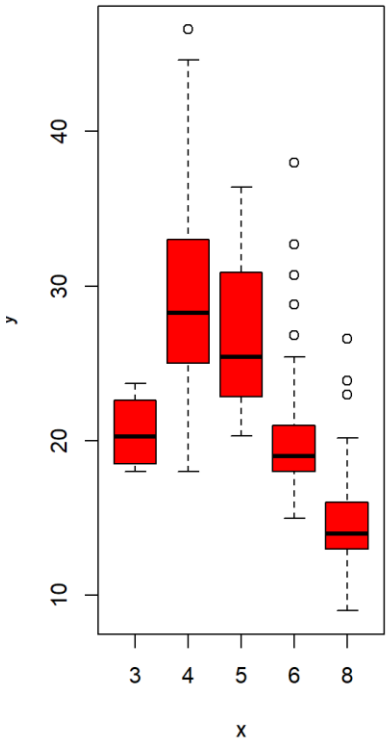


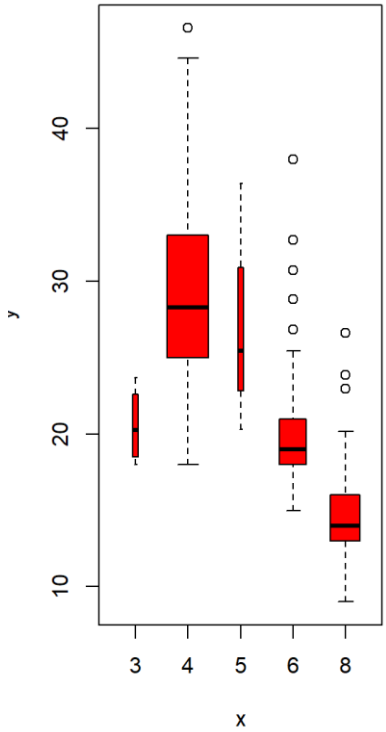


CODE:

```
plot(cylinders,mpg,col="red")
plot(cylinders,mpg,col="red",varwidth=T)
```

OUTPUT:

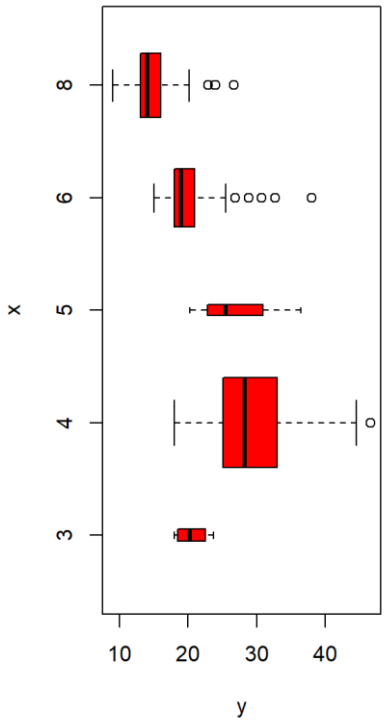


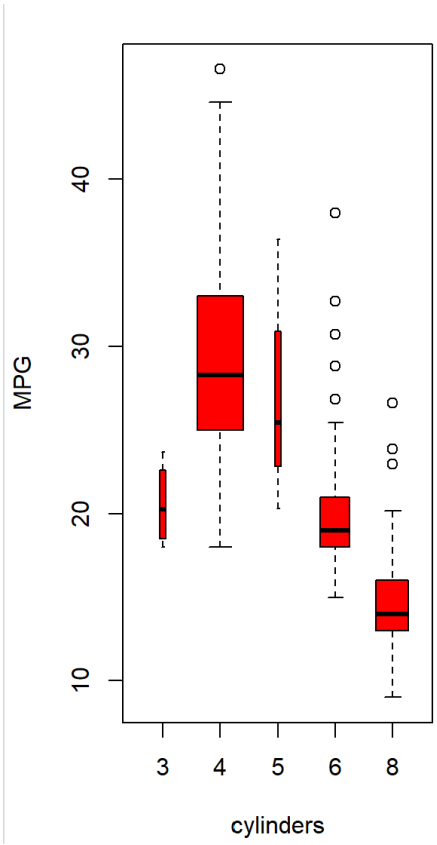


CODE:

```
plot(cylinders,mpg,col="red",varwidth=T,horizontal =T)
plot(cylinders,mpg,col="red",varwidth=T,xlab="cylinders",ylab="MPG")
```

OUTPUT:

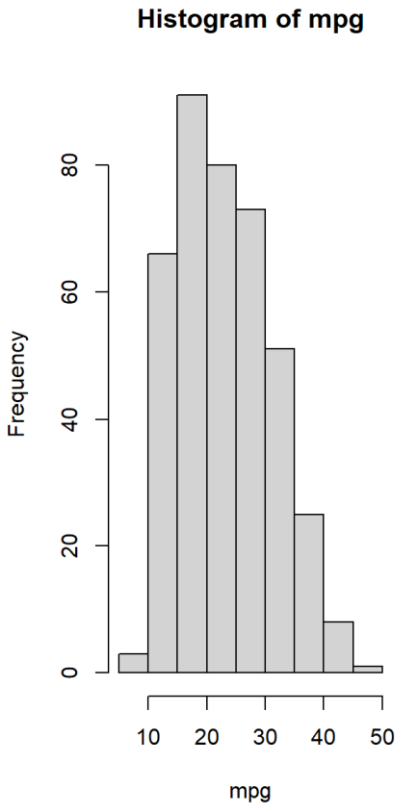


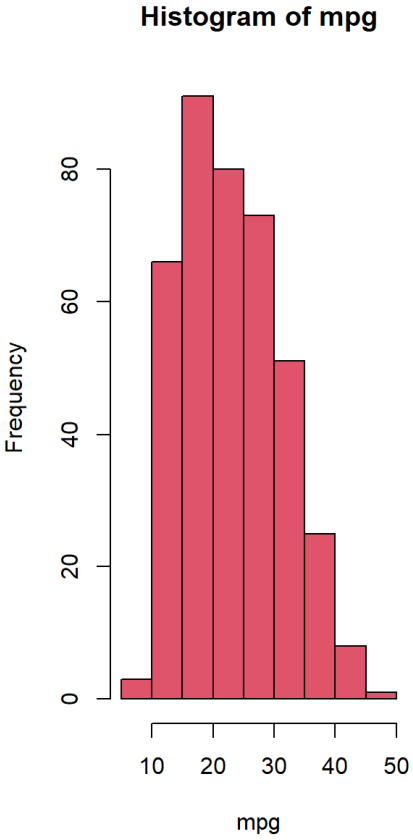


CODE:

```
hist(mpg)
hist(mpg,col=2)
```

OUTPUT:

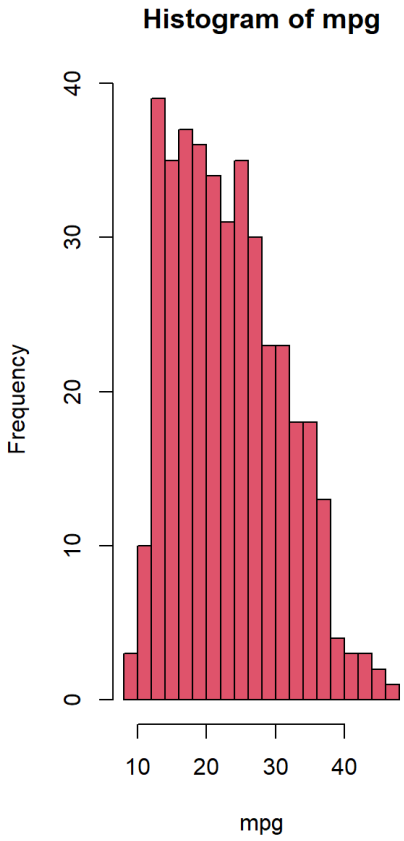


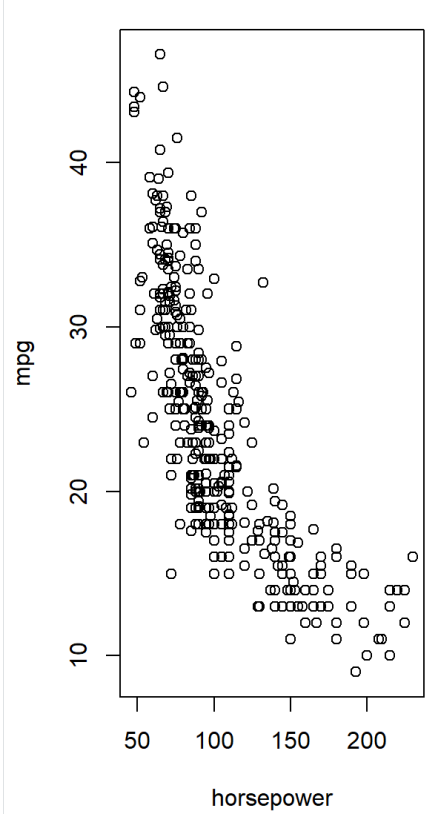


CODE:

```
hist(mpg,col=2,breaks=15)
plot(horsepower,mpg)
```

OUTPUT:

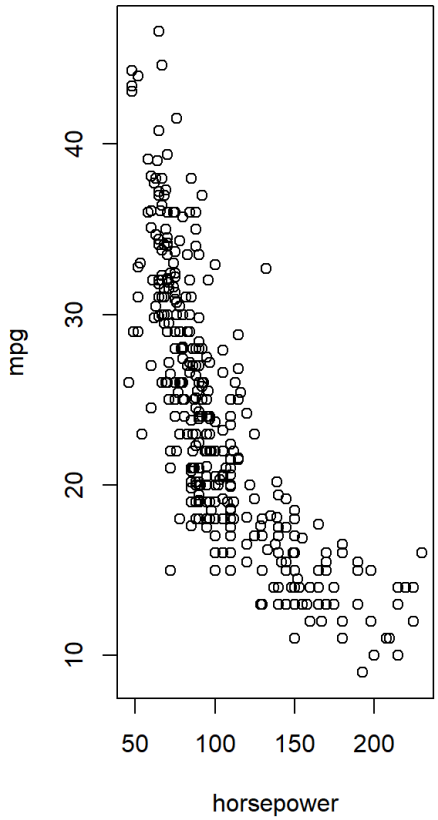




CODE:

```
identify(horsepower,mpg,car.name)
summary(auto)
summary(auto$mpg)
```

OUTPUT:




```
> summary(auto)
      mpg          cylinders      displacement    horsepower          weight      acceleration     model year        origin
 Min.   : 9.00   Min.   :3.000   Min.   : 68.0   Length:398         Min.   :1613   Min.   : 8.00   Min.   :70.00   Min.   :1.000
 1st Qu.:17.50   1st Qu.:4.000   1st Qu.:104.2   Class :character   1st Qu.:2224   1st Qu.:13.82   1st Qu.:73.00   1st Qu.:1.000
 Median :23.00   Median :4.000   Median :148.5   Mode  :character   Median :2804   Median :15.50   Median :76.00   Median :1.000
 Mean   :23.51   Mean   :5.455   Mean   :193.4                      Mean   :2970   Mean   :15.57   Mean   :76.01   Mean   :1.573
 3rd Qu.:29.00   3rd Qu.:8.000   3rd Qu.:262.0                      3rd Qu.:3608   3rd Qu.:17.18   3rd Qu.:79.00   3rd Qu.:2.000
 Max.   :46.60   Max.   :8.000   Max.   :455.0                      Max.   :5140   Max.   :24.80   Max.   :82.00   Max.   :3.000
   car name
 Length:398
 Class :character
 Mode  :character


> summary(auto$mpg)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   9.00   17.50   23.00   23.51   29.00   46.60
```

EXPERIMENT NO.-2

AIM: Implement the code using of simple linear regression on the Auto data set.
a. Use the lm() function to perform a simple linear regression with mpg as the response and horsepower as the predictor.
b. Plot the response and the predictor. Use the abline() function to display the least squares regression line.
c. Use the plot() function to produce diagnostic plots of the least squares regression fit. Comment on any problems you see with the fit.
d. Produce a scatterplot matrix which includes all of the variables in the data set.

(2.a) AIM: Use the lm() function to perform a simple linear regression with mpg as the response and horsepower as the predictor.

DESCRIPTION: The library() function is used to load libraries, or groups of functions and library() data sets that are not included in the base R distribution. Basic functions that perform least squares linear regression and other simple analyses come standard with the base distribution, but more exotic functions require additional libraries. Here we load the MASS package, which is a very large collection of data sets and functions. . Alternatively, this can be done at the R command line via install.packages("ISLR").The lm() function to fit a simple linear regression lm() model, with medv as the response and lstat as the predictor. The basic syntax is lm(y~x,data), where y is the response, x is the predictor, and data is the data set in which these two variables are kept

CODE:

```
library(ISLR)
library(MASS)
data("auto")
head(auto)
lm.fit<-lm(mpg~horsepower,data=Auto)
summary(lm.fit)
```

OUTPUT:

```
  mpg cylinders displacement horsepower weight acceleration year
1  18         8          307        130   3504         12.0   70
2  15         8          350        165   3693         11.5   70
3  18         8          318        150   3436         11.0   70
4  16         8          304        150   3433         12.0   70
5  17         8          302        140   3449         10.5   70
6  15         8          429        198   4341         10.0   70
  origin                       name
1      1 chevrolet chevelle malibu
2      1         buick skylark 320
3      1        plymouth satellite
4      1             amc rebel sst
5      1               ford torino
6      1          ford galaxie 500
```

```
Call:
lm(formula = mpg ~ horsepower, data = Auto)

Residuals:
     Min       1Q   Median       3Q      Max
-13.5710  -3.2592  -0.3435   2.7630  16.9240

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 39.935861   0.717499   55.66   <2e-16 ***
horsepower  -0.157845   0.006446  -24.49   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.906 on 390 degrees of freedom
Multiple R-squared:  0.6059,    Adjusted R-squared:  0.6049
F-statistic: 599.7 on 1 and 390 DF,  p-value: < 2.2e-16
```

CODE:

```
predict(lm.fit,data.frame(horsepower=c(98)),interval="prediction")
predict(lm.fit,data.frame(horsepower=c(98)),interval="confidence")
```

OUTPUT:

```
> predict(lm.fit,data.frame(horsepower=c(98)),interval="prediction")
       fit     lwr      upr
1 24.46708 14.8094 34.12476
> predict(lm.fit,data.frame(horsepower=c(98)),interval="confidence")
       fit      lwr      upr
1 24.46708 23.97308 24.96108
```

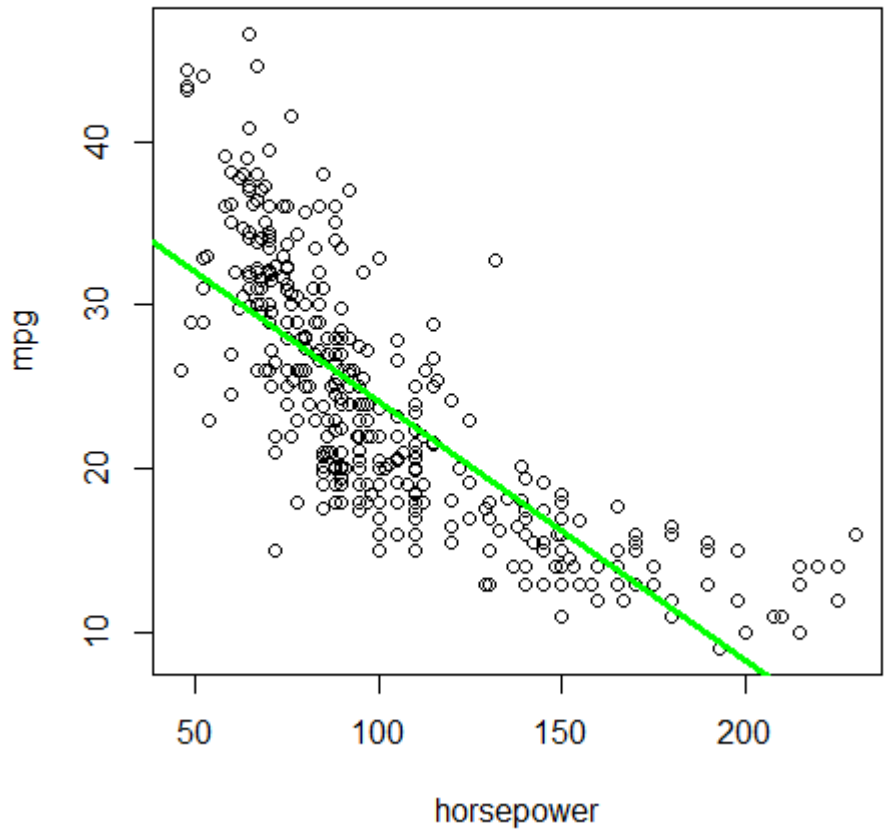
(2.b) AIM : Plot the response and the predictor. Use the abline() function to display the least squares regression line.

DESCRIPTION: The abline() function can be used to draw any line, not just the least squares regression line. To draw a line with intercept a and slope b, we type abline(a,b). Below we experiment with some additional settings for plotting lines and points. The lwd=3 command causes the width of the regression line to be increased by a factor of 3; this works for the plot() and lines() functions also.

CODE:

```
attach(Auto)
plot(horsepower,mpg)
abline(lm.fit,lwd=5,col="blue")
```

OUTPUT:



(2.c) AIM: Use the plot() function to produce diagnostic plots of the least squares regression fit. Comment on any problems you see with the fit.

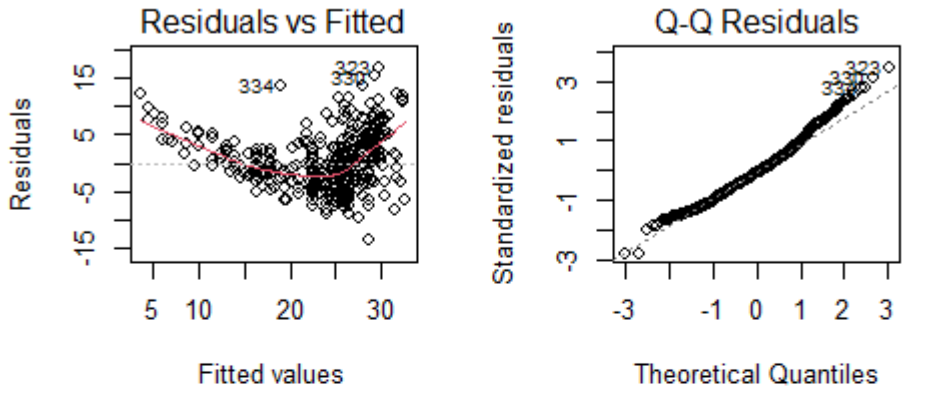
DESCRIPTION: Plot() function in R programming Language is defined as a generic function for plotting. **The plot() function in R is "used to create a plot". It has many options and arguments to control many things, such as the plot type, labels, titles, and colors. For example, plot(x, y) creates a scatter plot of x and y numeric vectors.**

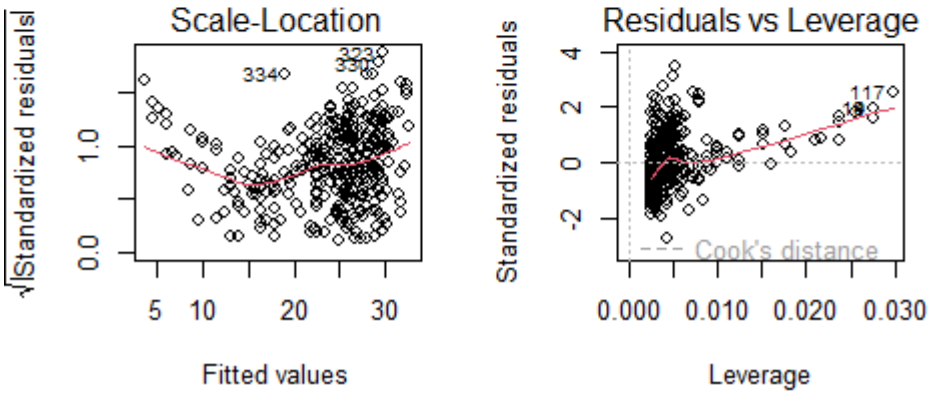
CODE:

```
which.max(hatvalues(lm.fit))
par(mfrow=c(2,2))
plot(lm.fit)
```

OUTPUT:

```
> which.max(hatvalues(lm.fit))
117
116
```



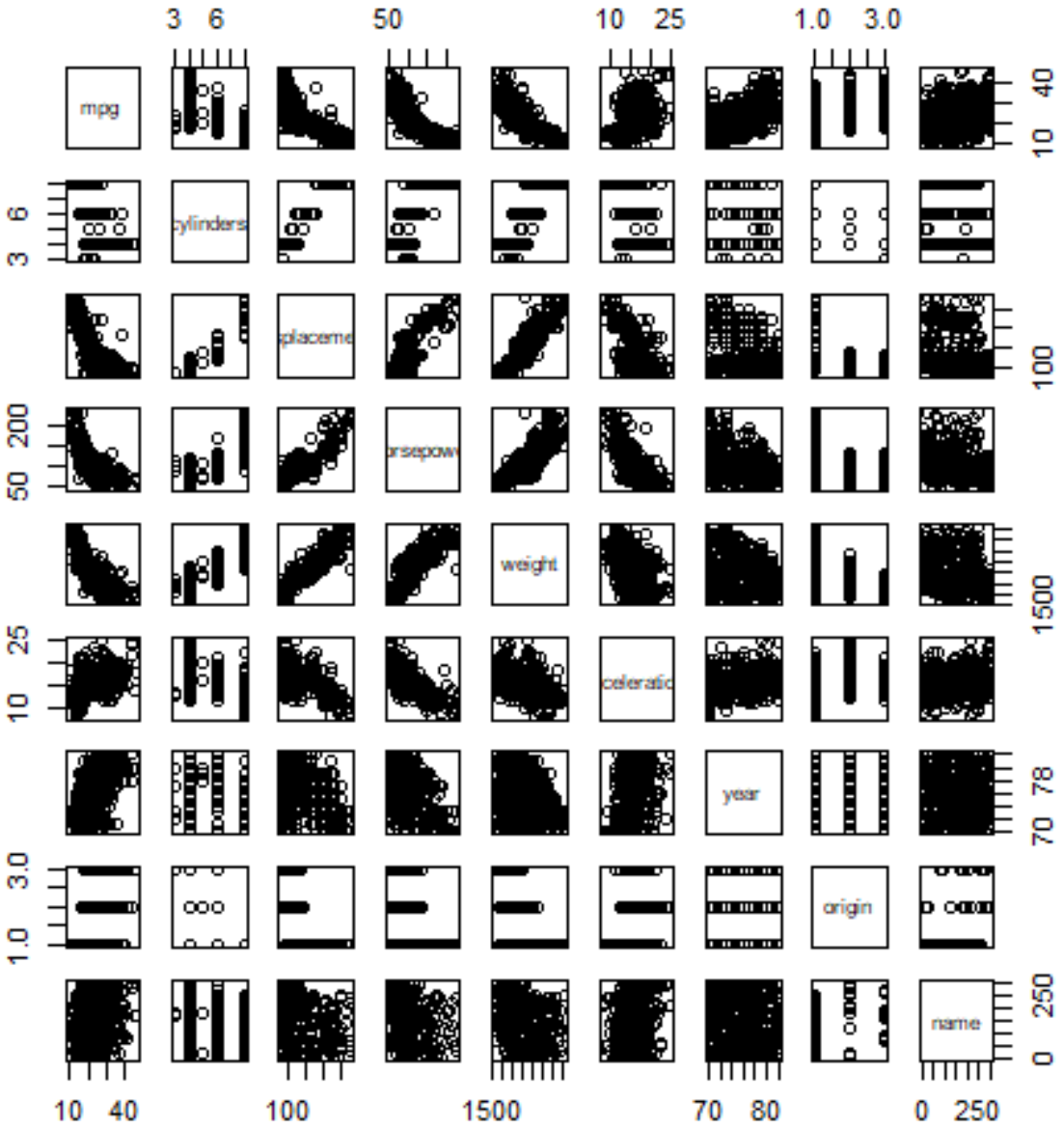


(2.d) AIM: . Produce a scatterplot matrix which includes all of the variables in the data set.

DESCRIPTION: A scatterplot is a set of dotted points representing individual data pieces on the horizontal and vertical axis.In a graph in which the values of two variables are plotted along the axis X and Y,the pattern of the resulting points reveals a correlation between them.We can create a scatter plot in R programming Language using the plot() function.

CODE:
Pairs(Auto)

OUTPUT:



EXPERIMENT NO:- 3

AIM:- Using multiple linear regression perform the following tasks on the Auto data set.

(a) Produce a scatter plot matrix which includes all of the variable sin the data set.

(b) Compute the matrix of correlations between the variables using the function cor() . You will need to exclude the name variable, cor() which is qualitative.

(c) Use the lm() function to perform a multiple linear regression with mpg as the response and all other variables except name as the predictors. Use the summary() function to print the results. Comment on the output, That is

i. **Is there a relationship between the predictors and the response?**
ii. **Which predictors appear to have a statistically significant relationship to the response?**
iii. **What does the coefficient for the year variable suggest?**

(d) Use the plot() function to produce diagnostic plots of the linear regression fit. Comment on any problems you see with the fit. Do the residual plots suggest any unusually large outliers? Does the leverage plot identify any observations with unusually high leverage?

(e) Use the * and : symbols to fit linear regression models with interaction effects. Do any interactions appear to be statistically significant?

(f) Try a few different transformations of the variables, such aslog(X),√ X, X 2 . Comment on your findings.

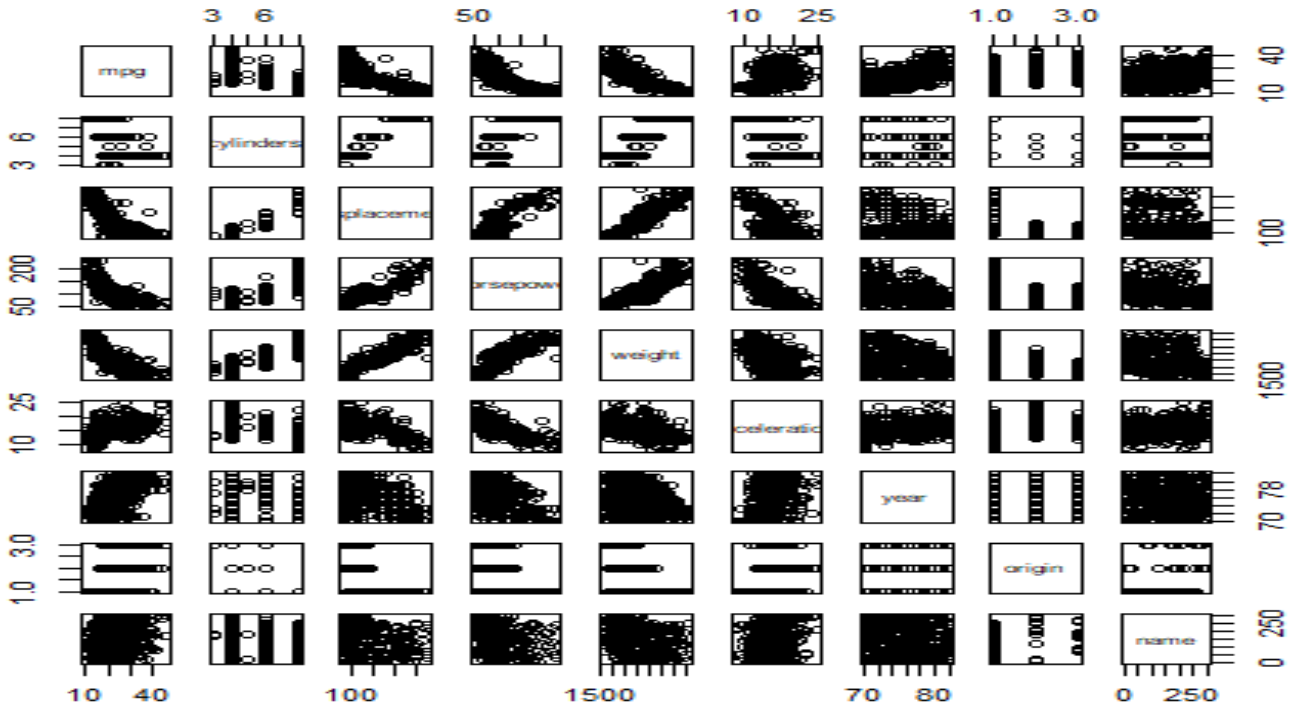
(3a) AIM:- Produce a scatter plot matrix which includes all of the variable sin the data set.

DESCRIPTION: A scatterplot is a set of dotted points representing individual data pieces on the horizontal and vertical axis. In a graph in which the values of two variables are plotted along the axis X and Y, the pattern of the resulting points reveals a correlation between them. We can create a scatter plot in R programming Language using the plot() function.

CODE:

```
data("Auto", package = "ISLR")
pairs(Auto)
```

OUTPUT:



(3b) AIM:- Compute the matrix of correlations between the variables using the function cor() . You will need to exclude the name variable, cor() which is qualitative.

DESCRIPTION: cor() function in R Language is used to measure the correlation coefficient value between two vectors. This returns a simple correlation matrix showing the correlations between pairs of variables (devices). You can choose the correlation coefficient to be computed using the method parameter. The default method is Pearson, but you can also compute Spearman or Kendall coefficients.

CODE:

```
cor(subset(Auto, select = -name))
```

OUTPUT:

```
> cor(subset(Auto,select =-name))
                    mpg  cylinders displacement horsepower     weight acceleration       year     origin
mpg           1.0000000 -0.7776175   -0.8051269 -0.7784268 -0.8322442    0.4233285  0.5805410  0.5652088
cylinders    -0.7776175  1.0000000    0.9508233  0.8429834  0.8975273   -0.5046834 -0.3456474 -0.5689316
displacement -0.8051269  0.9508233    1.0000000  0.8972570  0.9329944   -0.5438005 -0.3698552 -0.6145351
horsepower   -0.7784268  0.8429834    0.8972570  1.0000000  0.8645377   -0.6891955 -0.4163615 -0.4551715
weight       -0.8322442  0.8975273    0.9329944  0.8645377  1.0000000   -0.4168392 -0.3091199 -0.5850054
acceleration  0.4233285 -0.5046834   -0.5438005 -0.6891955 -0.4168392    1.0000000  0.2903161  0.2127458
year          0.5805410 -0.3456474   -0.3698552 -0.4163615 -0.3091199    0.2903161  1.0000000  0.1815277
origin        0.5652088 -0.5689316   -0.6145351 -0.4551715 -0.5850054    0.2127458  0.1815277  1.0000000
```

(3c) Use the lm() function to perform a multiple linear regression with mpg as the response and all other variables except name as the predictors. Use the summary() function to print the results. Comment on the output, That is

i. **Is there a relationship between the predictors and the response?**
ii. **Which predictors appear to have a statistically significant relationship to the response?**
iii. **What does the coefficient for the year variable suggest?**

DESCRIPTION: The lm() function to fit a simple linear regression lm() model, with medv as the response and lstat as the predictor. The basic syntax is lm(y~x,data), where y is the response, x is the predictor, and data is the data set in which these two variables are kept.

CODE:

```
lm.fit1 <- lm(mpg ~ . - name, data = Auto)
summary(lm.fit1)
```

OUTPUT:

```
> lm.fit1 <- lm(mpg~.-name,data=Auto)
> summary(lm.fit1)

Call:
lm(formula = mpg ~ . - name, data = Auto)

Residuals:
     Min       1Q   Median       3Q      Max
-9.5903 -2.1565 -0.1169  1.8690 13.0604

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  -17.218435   4.644294  -3.707  0.00024 ***
cylinders     -0.493376   0.323282  -1.526  0.12780
displacement   0.019896   0.007515   2.647  0.00844 **
horsepower    -0.016951   0.013787  -1.230  0.21963
weight        -0.006474   0.000652  -9.929  < 2e-16 ***
acceleration   0.080576   0.098845   0.815  0.41548
year           0.750773   0.050973  14.729  < 2e-16 ***
origin         1.426141   0.278136   5.127 4.67e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.328 on 384 degrees of freedom
Multiple R-squared:  0.8215,    Adjusted R-squared:  0.8182
F-statistic: 252.4 on 7 and 384 DF,  p-value: < 2.2e-16
```

(3.c)
(i). Is there a relationship between the predictors and the response?

Yes, there is a relationship between the predictors and the response by testing the null hypothesis of whether all the regression coefficients are zero. The F-statistic is far from 1 (with a small p-value), indicating evidence against the null hypothesis.

(3.c)
(ii). Which predictors appear to have a statistically significant relationship to the response?

Looking at the p-values associated with each predictor's t-statistic, we see that displacement, weight, year, and origin have a statistically significant relationship , while cylinders, horsepower, and acceleration do not.

(3.c)
(iii). What does the coefficient for the `year` variable suggest?

The regression coefficient for year, 0.7507727, suggests that for every one year, mpg increases by the coefficient. In other words, cars become more fuel efficient every year by almost 1 mpg / year.

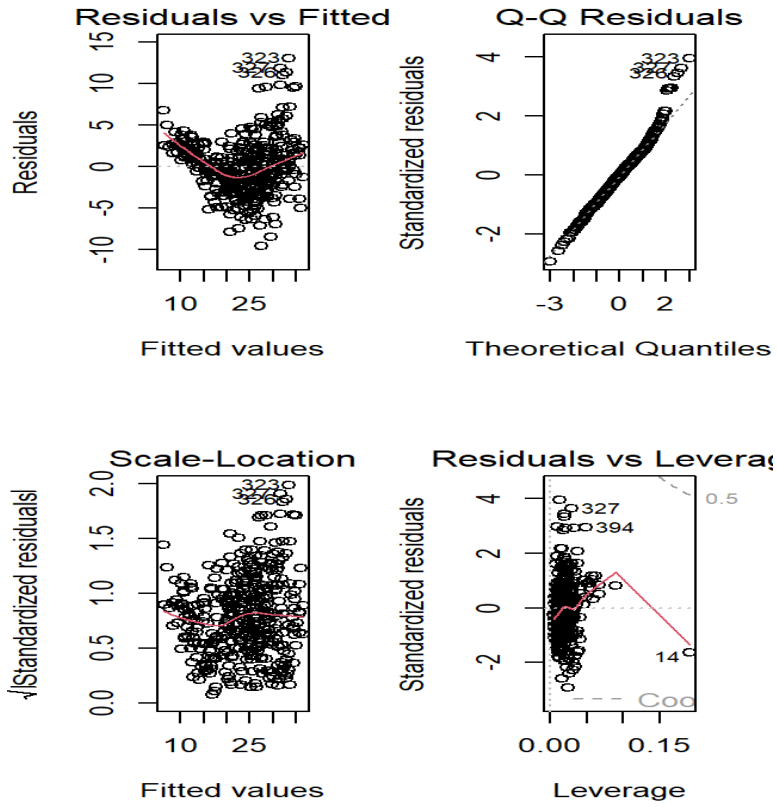
(3d) AIM:- Use the plot() function to produce diagnostic plots of the linear regression fit. Comment on any problems you see with the fit. Do the residual plots suggest any unusually large outliers? Does the leverage plot identify any observations with unusually high leverage?

DESCRIPTION: Based on the plot of Residuals versus fitted values there appears to be non linearity in the data and based on the Residuals vs Leverage plot below, there does appear to be outliers due to the fact that there are data points outside of the -2 and 2 standardized residuals. And there does appear to be high leverage observations greater then 0.05.

CODE:

```
par(mfrow = c(2, 2))
plot(lm.fit1)
```

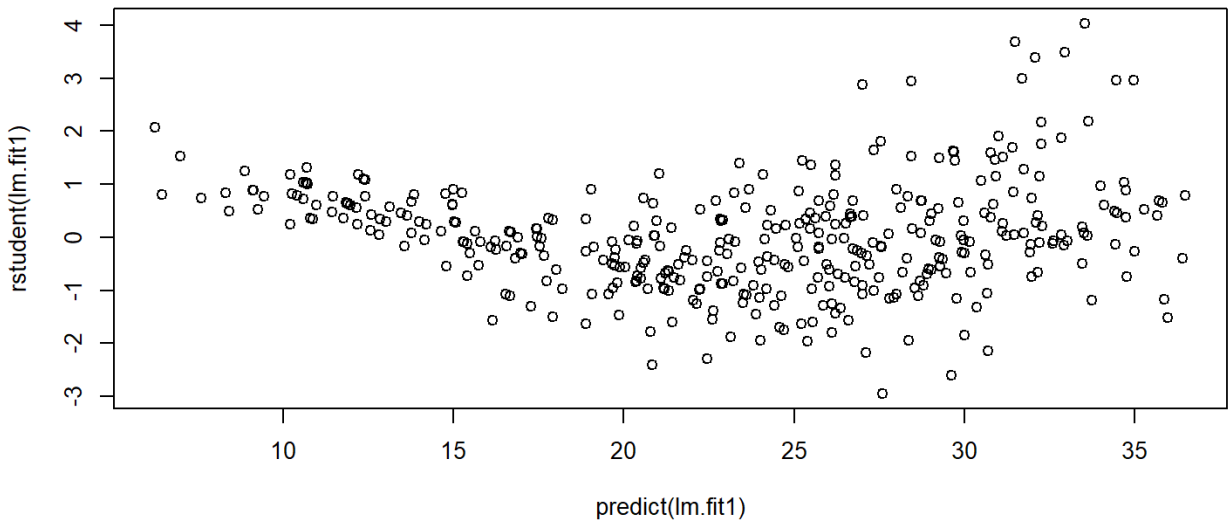
OUTPUT:



CODE:

```
plot(predict(lm.fit1),rstudent(lm.fit1))
```

OUTPUT:



(3e) AIM:- Use the * and : symbols to fit linear regression models with interaction effects. Do any interactions appear to be statistically significant?

DESCRIPTION: Based on here it appears that the interactions between 'cylinders' and 'displacement are not statistically significant but the interactions between 'horsepower' and 'weight' is significant and the interaction between 'acceleration' and 'year' is significant.

CODE:

```
lm.fit2 <- lm(mpg ~ cylinders * displacement + displacement * weight, data = Auto)
summary(lm.fit2)
```

OUTPUT:

```
> lm.fit2<-lm(mpg ~cylinders*displacement+displacement*weight,data=Auto)
> summary(lm.fit2)

Call:
lm(formula = mpg ~ cylinders * displacement + displacement *
    weight, data = Auto)

Residuals:
     Min       1Q   Median       3Q      Max
-13.2934  -2.5184  -0.3476   1.8399  17.7723

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)          5.262e+01  2.237e+00  23.519  < 2e-16 ***
cylinders            7.606e-01  7.669e-01   0.992    0.322
displacement        -7.351e-02  1.669e-02  -4.403 1.38e-05 ***
weight              -9.888e-03  1.329e-03  -7.438 6.69e-13 ***
cylinders:displacement -2.986e-03  3.426e-03  -0.872    0.384
displacement:weight   2.128e-05  5.002e-06   4.254 2.64e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.103 on 386 degrees of freedom
Multiple R-squared:  0.7272,    Adjusted R-squared:  0.7237
F-statistic: 205.8 on 5 and 386 DF,  p-value: < 2.2e-16
```

(3f) AIM:- Try a few different transformations of the variables, such aslog(X),√ X, X 2 . Comment on your findings.

DESCRIPTION: : Applying the log() function on a vector, data frame, or other data set in R results in a log transformation. To avoid applying a logarithm to a 0 number, 1 is added to the base value prior to applying the logarithm.

CODE: summary(lm(mpg ~ . -name + log(acceleration), data=Auto))
summary(lm(mpg ~ . -name + I(horsepower^2), data=Auto))

OUTPUT:

```
> summary(lm(mpg ~ . -name + log(acceleration), data=Auto))

Call:
lm(formula = mpg ~ . - name + log(acceleration), data = Auto)

Residuals:
    Min      1Q  Median      3Q     Max
-9.7931 -2.0052 -0.1279  1.9299 13.1085

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)         4.552e+01  1.479e+01   3.077  0.00224 **
cylinders          -2.796e-01  3.193e-01  -0.876  0.38172
displacement        8.042e-03  7.805e-03   1.030  0.30344
horsepower         -3.434e-02  1.401e-02  -2.450  0.01473 *
weight             -5.343e-03  6.854e-04  -7.795 6.15e-14 ***
acceleration        2.167e+00  4.782e-01   4.532 7.82e-06 ***
year                7.560e-01  4.978e-02  15.186  < 2e-16 ***
origin              1.329e+00  2.724e-01   4.877 1.58e-06 ***
log(acceleration) -3.513e+01  7.886e+00  -4.455 1.10e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.249 on 383 degrees of freedom
Multiple R-squared:  0.8303,    Adjusted R-squared:  0.8267
F-statistic: 234.2 on 8 and 383 DF,  p-value: < 2.2e-16
> summary(lm(mpg ~ . -name + I(horsepower^2), data=Auto))

Call:
lm(formula = mpg ~ . - name + I(horsepower^2), data = Auto)

Residuals:
    Min      1Q  Median      3Q     Max
-8.5497 -1.7311 -0.2236  1.5877 11.9955

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.3236564  4.6247696   0.286 0.774872
cylinders        0.3489063  0.3048310   1.145 0.253094
displacement    -0.0075649  0.0073733  -1.026 0.305550
horsepower      -0.3194633  0.0343447  -9.302  < 2e-16 ***
weight          -0.0032712  0.0006787  -4.820 2.07e-06 ***
acceleration    -0.3305981  0.0991849  -3.333 0.000942 ***
year             0.7353414  0.0459918  15.989  < 2e-16 ***
origin           1.0144130  0.2545545   3.985 8.08e-05 ***
I(horsepower^2)  0.0010060  0.0001065   9.449  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.001 on 383 degrees of freedom
Multiple R-squared:  0.8552,    Adjusted R-squared:  0.8522
F-statistic: 282.8 on 8 and 383 DF,  p-value: < 2.2e-16
```

EXPERIMENT-4

AIM: Implementation of KNN on the German Credit Data set.

DESCRIPTION: To minimize loss from the bank's perspective, the bank needs a decision rule regarding who to give approval of the loan and who not to. An applicant's demographic and socio-economic profiles are considered by loan managers before a decision is taken regarding his/her loan application. The German Credit Data contains data on 20 variables and the classification whether an applicant is considered a Good or a Bad credit risk for 1000 loan applicants. A predictive model developed on this data is expected to provide bank manager guidance for making a decision whether to approve a loan to a prospective applicant based on his/her profiles

DESCRIPTION:

The K-NN working can be explained on the bias of the below algorithm:

o Step-1: Select the number K of the neighbours

o Step-2: Calculate the Euclidean distance of K number of neighbours

o Step-3: Take the K nearest neighbours as per the calculated Euclidean distance.

o Step-4: Among these k neighbours, count the number of the data points in each category.

o Step-5: Assign the new data points to that category for which the number of the neighbour is maximum.

o Step-6: Our model is ready.2

Steps Involved in performing KNN algorithm:

1. Data Collection.
2. Preparing and exploring the data.
   - Understanding data structure.
   - Feature selection (if required)
   - Data normalization.
   - Creating Training and Test data set.
3. Training a model on data.
4. Evaluate the model performance.
5. Improve the performance of model.

1.DATA COLLECTION:

CODE:

```
gc <- read.csv("C:/Users/Hp/OneDrive/Desktop/ML-LAB/german_credit.csv")
gc.bkup <- gc
head (gc)
```

OUTPUT:

```
> gc <- read.csv("C:/Users/Hp/OneDrive/Desktop/ML-LAB/german_credit.csv")
> gc.bkup <- gc
> head (gc)
  Creditability Account.Balance Duration.of.Credit..month. Payment.Status.of.Previous.Credit Purpose
1             1               1                         18                                 4       2
2             1               1                          9                                 4       0
3             1               2                         12                                 2       9
4             1               1                         12                                 4       0
5             1               1                         12                                 4       0
6             1               1                         10                                 4       0
  Credit.Amount Value.Savings.Stocks Length.of.current.employment Instalment.per.cent Sex...Marital.Status
1          1049                    1                            2                   4                    2
2          2799                    1                            3                   2                    3
3           841                    2                            4                   2                    2
4          2122                    1                            3                   3                    3
5          2171                    1                            3                   4                    3
6          2241                    1                            2                   1                    3
  Guarantors Duration.in.Current.address Most.valuable.available.asset Age..years. Concurrent.Credits
1          1                           4                             2          21                  3
2          1                           2                             1          36                  3
3          1                           4                             1          23                  3
4          1                           2                             1          39                  3
5          1                           4                             2          38                  1
6          1                           3                             1          48                  3
  Type.of.apartment No.of.Credits.at.this.Bank Occupation No.of.dependents Telephone Foreign.Worker
1                 1                          1          3                 1         1              1
2                 1                          2          3                 2         1              1
3                 1                          1          2                 1         1              1
4                 1                          2          2                 2         1              2
5                 2                          2          2                 1         1              2
6                 1                          2          2                 2         1              2
```

2.**PREPARING AND EXPLORING THE DATA:**

CODE:

```
str(gc)
gc.subset <-
gc[c('Creditability','Age..years.','Sex...Marital.Status','Occupation','Account.Balance','Credit.Amount','Length.of.current.employment','Purpose')]
head(gc.subset)
normalize <- function(x) {  return ((x - min(x)) / (max(x) - min(x))) }
gc.subset.n<- as.data.frame(lapply(gc.subset[,2:8], normalize))
head(gc.subset.n)
set.seed(123)
dat.d <- sample(1:nrow(gc.subset.n),size=nrow(gc.subset.n)*0.7,replace = FALSE)
train.gc <- gc.subset[dat.d,]
test.gc <- gc.subset[-dat.d,]
train.gc_labels <- gc.subset[dat.d,1]
test.gc_labels <- gc.subset[-dat.d,1]
```

OUTPUT:

```
> str(gc)
'data.frame':   1000 obs. of  21 variables:
 $ Creditability                  : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Account.Balance                : int  1 1 2 1 1 1 1 1 4 2 ...
 $ Duration.of.Credit..month.     : int  18 9 12 12 12 10 8 6 18 24 ...
 $ Payment.Status.of.Previous.Credit: int  4 4 2 4 4 4 4 4 4 2 ...
 $ Purpose                        : int  2 0 9 0 0 0 0 0 3 3 ...
 $ Credit.Amount                  : int  1049 2799 841 2122 2171 2241 3398 1361 1098 3758 ...
 $ Value.Savings.Stocks           : int  1 1 2 1 1 1 1 1 1 3 ...
 $ Length.of.current.employment   : int  2 3 4 3 3 2 4 2 1 1 ...
 $ Instalment.per.cent            : int  4 2 2 3 4 1 1 2 4 1 ...
 $ Sex...Marital.Status           : int  2 3 2 3 3 3 3 3 2 2 ...
 $ Guarantors                     : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Duration.in.Current.address    : int  4 2 4 2 4 3 4 4 4 4 ...
 $ Most.valuable.available.asset  : int  2 1 1 1 2 1 1 1 3 4 ...
 $ Age..years.                    : int  21 36 23 39 38 48 39 40 65 23 ...
 $ Concurrent.Credits             : int  3 3 3 3 1 3 3 3 3 3 ...
 $ Type.of.apartment              : int  1 1 1 1 2 1 2 2 2 1 ...
 $ No.of.Credits.at.this.Bank     : int  1 2 1 2 2 2 2 1 2 1 ...
 $ Occupation                     : int  3 3 2 2 2 2 2 2 1 1 ...
 $ No.of.dependents               : int  1 2 1 2 1 2 1 2 1 1 ...
 $ Telephone                      : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Foreign.Worker                 : int  1 1 1 2 2 2 2 2 1 1 ...
> gc.subset <- gc[c('Creditability','Age..years.','Sex...Marital.Status','Occupation','Account.Balance','Credit.Amount','Length.of.current.employment','Purpose')]
> head(gc.subset)
  Creditability Age..years. Sex...Marital.Status Occupation Account.Balance Credit.Amount
1             1          21                    2          3               1          1049
2             1          36                    3          3               1          2799
3             1          23                    2          2               2           841
4             1          39                    3          2               1          2122
5             1          38                    3          2               1          2171
6             1          48                    3          2               1          2241
  Length.of.current.employment Purpose
1                            2       2
2                            3       0
3                            4       9
4                            3       0
5                            3       0
6                            2       0
> normalize <- function(x) {  return ((x - min(x)) / (max(x) - min(x))) }
> gc.subset.n<- as.data.frame(lapply(gc.subset[,2:8], normalize))
> head(gc.subset.n)
  Age..years. Sex...Marital.Status Occupation Account.Balance Credit.Amount Length.of.current.employment Purpose
1  0.03571429            0.3333333  0.6666667       0.0000000    0.04396390                          0.25     0.2
2  0.30357143            0.6666667  0.6666667       0.0000000    0.14025531                          0.50     0.0
3  0.07142857            0.3333333  0.3333333       0.3333333    0.03251898                          0.75     0.9
4  0.35714286            0.6666667  0.3333333       0.0000000    0.10300429                          0.50     0.0
5  0.33928571            0.6666667  0.3333333       0.0000000    0.10570045                          0.50     0.0
6  0.51785714            0.6666667  0.3333333       0.0000000    0.10955211                          0.25     0.0
> set.seed(123)
> dat.d <- sample(1:nrow(gc.subset.n),size=nrow(gc.subset.n)*0.7,replace = FALSE)
> train.gc <- gc.subset[dat.d,]
> test.gc <- gc.subset[-dat.d,]
> train.gc_labels <- gc.subset[dat.d,1]
> test.gc_labels <- gc.subset[-dat.d,1]
```

3.TRAINING A MODEL ON DATA:

CODE:

```
library(class)
NROW(train.gc_labels)
knn.26 <- knn(train=train.gc, test=test.gc, cl=train.gc_labels, k=26)
knn.27 <- knn(train=train.gc, test=test.gc, cl=train.gc_labels, k=27)
```

OUTPUT:

```
> library(class)
> NROW(train.gc_labels)
[1] 700
> knn.26 <- knn(train=train.gc, test=test.gc, cl=train.gc_labels, k=26)
> knn.27 <- knn(train=train.gc, test=test.gc, cl=train.gc_labels, k=27)
```

4.EVALUATE THE MODEL PERFORMANCE:

CODE:

```
ACC.26 <- 100 * sum(test.gc_labels == knn.26)/NROW(test.gc_labels)
ACC.27 <- 100 * sum(test.gc_labels == knn.27)/NROW(test.gc_labels)
ACC.26
ACC.27
table(knn.26 ,test.gc_labels)
table(knn.27 ,test.gc_labels)
install.packages('caret')
library(caret)
test.gc_labels=as.factor(test.gc_labels)
confusionMatrix(knn.26 ,test.gc_labels)
```

OUPUT:

```
> ACC.26 <- 100 * sum(test.gc_labels == knn.26)/NROW(test.gc_labels)
> ACC.27 <- 100 * sum(test.gc_labels == knn.27)/NROW(test.gc_labels)
> ACC.26
[1] 69
> ACC.27
[1] 69
> table(knn.26 ,test.gc_labels)
      test.gc_labels
knn.26   0   1
     0   8   6
     1  87 199
> table(knn.27 ,test.gc_labels)
      test.gc_labels
knn.27   0   1
     0   8   6
     1  87 199
> install.packages('caret')
Error in install.packages : Updating loaded packages
> library(caret)
> test.gc_labels=as.factor(test.gc_labels)
> confusionMatrix(knn.26 ,test.gc_labels)
Confusion Matrix and Statistics

          Reference
Prediction   0   1
         0   8   6
         1  87 199

               Accuracy : 0.69
                 95% CI : (0.6343, 0.7419)
    No Information Rate : 0.6833
    P-Value [Acc > NIR] : 0.4291

                  Kappa : 0.0712

 Mcnemar's Test P-Value : <2e-16

            Sensitivity : 0.08421
            Specificity : 0.97073
         Pos Pred Value : 0.57143
         Neg Pred Value : 0.69580
             Prevalence : 0.31667
         Detection Rate : 0.02667
   Detection Prevalence : 0.04667
      Balanced Accuracy : 0.52747

       'Positive' Class : 0
```

CODE:

```
confusionMatrix(knn.27 ,test.gc_labels)
```

OUTPUT:

```
> confusionMatrix(knn.27 ,test.gc_labels)
Confusion Matrix and Statistics

          Reference
Prediction   0   1
         0   8   6
         1  87 199

               Accuracy : 0.69
                 95% CI : (0.6343, 0.7419)
    No Information Rate : 0.6833
    P-Value [Acc > NIR] : 0.4291

                  Kappa : 0.0712

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            Sensitivity : 0.08421
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         Neg Pred Value : 0.69580
             Prevalence : 0.31667
         Detection Rate : 0.02667
   Detection Prevalence : 0.04667
      Balanced Accuracy : 0.52747

       'Positive' Class : 0
```

5.IMPROVE THE PERFORMANCE OF MODEL:

CODE:

```
i=1
k.optm=1
for (i in 1:28){
 knn.mod <- knn(train=train.gc, test=test.gc, cl=train.gc_labels, k=i)
 k.optm[i] <- 100 * sum(test.gc_labels == knn.mod)/NROW(test.gc_labels)
 k=i
 cat(k,'=',k.optm[i],'\n')
 }
```

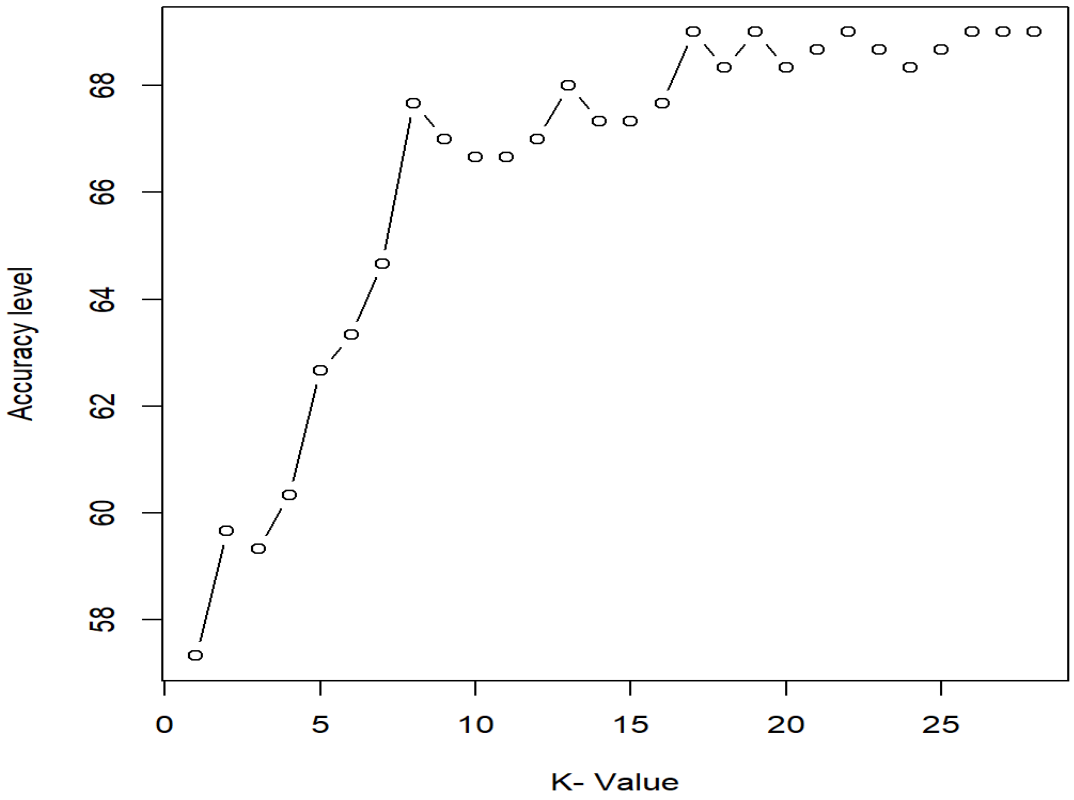
OUTPUT:

```
> i=1
> k.optm=1
> for (i in 1:28){
+    knn.mod <- knn(train=train.gc, test=test.gc, cl=train.gc_labels, k=i)
+    k.optm[i] <- 100 * sum(test.gc_labels == knn.mod)/NROW(test.gc_labels)
+    k=i
+    cat(k,'=',k.optm[i],'\n')
+    }
1 = 57.33333
2 = 59.66667
3 = 59.33333
4 = 60.33333
5 = 62.66667
6 = 63.33333
7 = 64.66667
8 = 67.66667
9 = 67
10 = 66.66667
11 = 66.66667
12 = 67
13 = 68
14 = 67.33333
15 = 67.33333
16 = 67.66667
17 = 69
18 = 68.33333
19 = 69
20 = 68.33333
21 = 68.66667
22 = 69
23 = 68.66667
24 = 68.33333
25 = 68.66667
26 = 69
27 = 69
28 = 69
> plot(k.optm, type="b", xlab="K- Value",ylab="Accuracy level")
```

CODE:

```
plot(k.optm, type="b", xlab="K- Value",ylab="Accuracy level")
```

OUTPUT:



EXPERIMENT NO: 5

AIM: To implement Linear Discriminant Analysis, Quadratic Discriminant Analysis and Naive Bayes algorithms on Stock market Dataset. `

DESCRIPTION:

- **Linear Discriminant Analysis (LDA)** is a supervised learning algorithm used for classification tasks in machine learning. It is a technique used to find a linear combination of features that best separates the classes in a dataset. Quadratic Discriminant Analysis (QDA) is a supervised learning algorithm and extension of linear discriminant analysis. QDA models are designed to be used for classification problems .i.e. when the response variable can be placed into classes or categories. Naive Bayes classifiers (NB) are a collection of classification algorithms based on Bayes Theorem. It is not a single algorithm but a family of algorithms where all of them share a common principle ,i.e. every pair of features being classified is independent of each other.

  Formula for LDA :-

  For a two-class problem, LDA calculates the discriminant function as follows:

  For Class 1:

  $$D_1(x) = x \cdot \frac{\mu_1}{\sigma^2} - \frac{\mu_1^2}{2\sigma^2} + \log(\pi_1)$$

  For Class 2:

  $$D_2(x) = x \cdot \frac{\mu_2}{\sigma^2} - \frac{\mu_2^2}{2\sigma^2} + \log(\pi_2)$$

  Where:

  - $D_1(x)$ and $D_2(x)$ are the discriminant functions for Class 1 and Class 2.
  - x is the feature vector.
  - μ_1 and μ_2 are the means of the features for Class 1 and Class 2.
  - σ^2 is the common variance of the features.
  - π_1 and π_2 are the prior probabilities of Class 1 and Class 2.

- **Quadratic Discriminant Analysis (QDA)** is a supervised machine learning algorithm used for classification tasks. It is a generative model, meaning that it assumes that the data is generated from a known distribution, in this case a multivariate Gaussian distribution. QDA estimates the mean and covariance matrix for each class, and then uses this information to calculate the probability of a new data point belonging to each class. The data point is then assigned to the class with the highest probability.

  Formula for QDA :-

  $$D_k(x) = -\tfrac{1}{2}(x - \mu_k)^T \Sigma_k^{-1}(x - \mu_k) - \tfrac{1}{2}\log|\Sigma_k| + \log(\pi_k)$$

  Where:

  - $D_k(x)$ is the discriminant function for Class k.
  - x is the feature vector.
  - μ_k is the mean vector of the features for Class k.
  - Σ_k is the covariance matrix for Class k.
  - π_k is the prior probability of Class k.

- **Naive Bayes** is a supervised machine learning algorithm used for classification tasks. It is a probabilistic classifier, which means that it predicts on the basis of the probability of an object. Naive Bayes is based on Bayes' theorem, which is a mathematical formula for calculating the probability of an event occurring, given that another event has already occurred. In the context of Naive Bayes, the event we are trying to predict is the class label of a data point, and the events we have already observed are the values of the data point's features.

Steps for Navie Bayes :-

1. Calculate the prior probabilities $P(C_k)$ for each class.
2. Estimate the likelihood $P(x|C_k)$ for each feature given each class. This is often done using probability density functions.
3. For a new observation with features x, calculate the posterior probabilities $P(C_k|x)$ for each class using Bayes' theorem.
4. Assign the observation to the class with the highest posterior probability.

Formula for Navie Bayes :-

$$P(C_k|x) = \frac{P(x|C_k) \cdot P(C_k)}{P(x)}$$

Where:

- $P(C_k|x)$ is the posterior probability of class C_k given the features x.
- $P(x|C_k)$ is the likelihood of observing features x given class C_k.
- $P(C_k)$ is the prior probability of class C_k.
- $P(x)$ is the probability of observing features x.

CODE:

```
# Load required libraries
library(quantmod)
library(MASS)
library(e1071)
library(caret)
library(ggplot2)
library(pROC)
#Fetch the stock market data
symbols <- c("AAPL","MSFT")
#calculate  daily returns
start_date <- "2020-01-01"
end_date <- "2023-01-01"
getSymbols(symbols, from = start_date, to = end_date)
```

OUTPUT:

```
> getSymbols(symbols, from = start_date, to = end_date)
[1] "AAPL" "MSFT"
```

CODE:

```
stock_data <- merge(Ad(AAPL),Ad(MSFT))
colnames(stock_data) <- symbols
stock_returns <- diff(log(stock_data))
#creating labels based on return  threshold
return_threshold <- 0.01
stock_labels <- ifelse(apply(abs(stock_returns), 1, max) > return_threshold, "High", "Low")
# Combine returns and labels into a data frame
stock_df <- data.frame(stock_returns, stock_labels)
# Split data into training and testing sets
set.seed(123)
train_indices <- sample(1:nrow(stock_df),0.75* nrow(stock_df))
train_data <- stock_df[train_indices, ]
test_data <- stock_df[-train_indices, ]
# When the input data contains missing values, make sure our 'test_data' does not have any missing or NA values. We can use the is.na() function to identify them
any_na <-apply(test_data,2,function(column)
  any(is.na(column)))
```

CODE:

```
print(any_na)
```

OUTPUT:

```
> print(any_na)
        AAPL         MSFT stock_labels
        TRUE         TRUE         TRUE
```

CODE:

```
# If we find missing values, we can clean the data by removing or imputing them before using it for prediction.
# Remove rows with missing values
test_data <- test_data[complete.cases(test_data), ]

#LDA
lda_model <- lda(stock_labels ~ ., data = train_data)
lda_predictions <- predict(lda_model, newdata = test_data)$class

#QDA
qda_model <- qda(stock_labels ~ ., data = train_data)
qda_predictions <- predict(qda_model, newdata = test_data)$class

#NAIVEBAYES Classification
nb_model <- naiveBayes(stock_labels ~ ., data = train_data)
nb_predictions <- predict(nb_model, newdata = test_data)

#calculate accuracies
lda_accuracy <- mean(lda_predictions == test_data$stock_labels)
qda_accuracy <- mean(qda_predictions == test_data$stock_labels)
nb_accuracy <- mean(nb_predictions == test_data$stock_labels)

# Print the accuracy results
cat("LDA ACCURACY:" , lda_accuracy,"\n")
cat("QDA ACCURACY:" , qda_accuracy, "\n")
cat("navive bayes accuracy:",nb_accuracy, "\n")
```

OUTPUT:

```
> cat("LDA ACCURACY:" , lda_accuracy,"\n")
LDA ACCURACY: 0.75
> cat("QDA ACCURACY:" , qda_accuracy, "\n")
QDA ACCURACY: 0.9787234
> cat("navive bayes accuracy:",nb_accuracy, "\n")
navive bayes accuracy: 0.9734043
```

CODE:

```
# Inorder to avoid the error: `data` and `reference` should be factors with the same levels.
test_data$stock_labels=as.factor(test_data$stock_labels)

#Calculate and print confusion matrix
lda_cm <- confusionMatrix(lda_predictions, test_data$stock_labels)
qda_cm <- confusionMatrix(qda_predictions, test_data$stock_labels)
nb_cm <- confusionMatrix(nb_predictions, test_data$stock_labels)
print(lda_cm)
print(qda_cm)
print(nb_cm)
```

OUTPUT:

```
> print(lda_cm)
Confusion Matrix and Statistics

          Reference
Prediction High Low
      High  141  47
      Low     0   0

               Accuracy : 0.75
                 95% CI : (0.6818, 0.8102)
    No Information Rate : 0.75
    P-Value [Acc > NIR] : 0.5391

                  Kappa : 0

 Mcnemar's Test P-Value : 1.949e-11

            Sensitivity : 1.00
            Specificity : 0.00
         Pos Pred Value : 0.75
         Neg Pred Value :  NaN
             Prevalence : 0.75
         Detection Rate : 0.75
   Detection Prevalence : 1.00
      Balanced Accuracy : 0.50

       'Positive' Class : High

> print(qda_cm)
Confusion Matrix and Statistics

          Reference
Prediction High Low
      High  139   2
      Low     2  45

               Accuracy : 0.9787
                 95% CI : (0.9464, 0.9942)
    No Information Rate : 0.75
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.9433

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.9858
            Specificity : 0.9574
         Pos Pred Value : 0.9858
         Neg Pred Value : 0.9574
             Prevalence : 0.7500
         Detection Rate : 0.7394
   Detection Prevalence : 0.7500
      Balanced Accuracy : 0.9716

       'Positive' Class : High

> print(nb_cm)
Confusion Matrix and Statistics

          Reference
Prediction High Low
      High  137   1
      Low     4  46

               Accuracy : 0.9734
                 95% CI : (0.939, 0.9913)
    No Information Rate : 0.75
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.9306

 Mcnemar's Test P-Value : 0.3711

            Sensitivity : 0.9716
            Specificity : 0.9787
         Pos Pred Value : 0.9928
         Neg Pred Value : 0.9200
             Prevalence : 0.7500
         Detection Rate : 0.7287
   Detection Prevalence : 0.7340
      Balanced Accuracy : 0.9752

       'Positive' Class : High
```

CODE:

 # Create data frame for accuracy comparison

```
accuracy_df <- data.frame(Classifier = c("LDA", "QDA", "Naive Bayes"),Accuracy =
c(lda_accuracy,qda_accuracy,nb_accuracy))
```

#create accuracy plot

```
accuracy_plot <- ggplot(accuracy_df, aes(x= Classifier, y= Accuracy, fill = Classifier))+ geom_bar(stat = "identity",
position = "dodge")+labs(y = "Accuracy", title = "Classifier Comparision")+theme_minimal()+theme(legend.position =
"bottom")
print(accuracy_plot)
```

#create ROC curves

```
roc_lda <- roc(test_data$stock_labels, as.numeric(lda_predictions == "high"))
roc_qda <- roc(test_data$stock_labels, as.numeric(qda_predictions == "High"))
roc_nb <- roc(test_data$stock_labels, as.numeric(nb_predictions == "High"))
```

 # Determine the common length of sensitivities

```
min_length <- min(length(roc_lda$sensitivities), length(roc_qda$sensitivities), length(roc_nb$sensitivities))
```

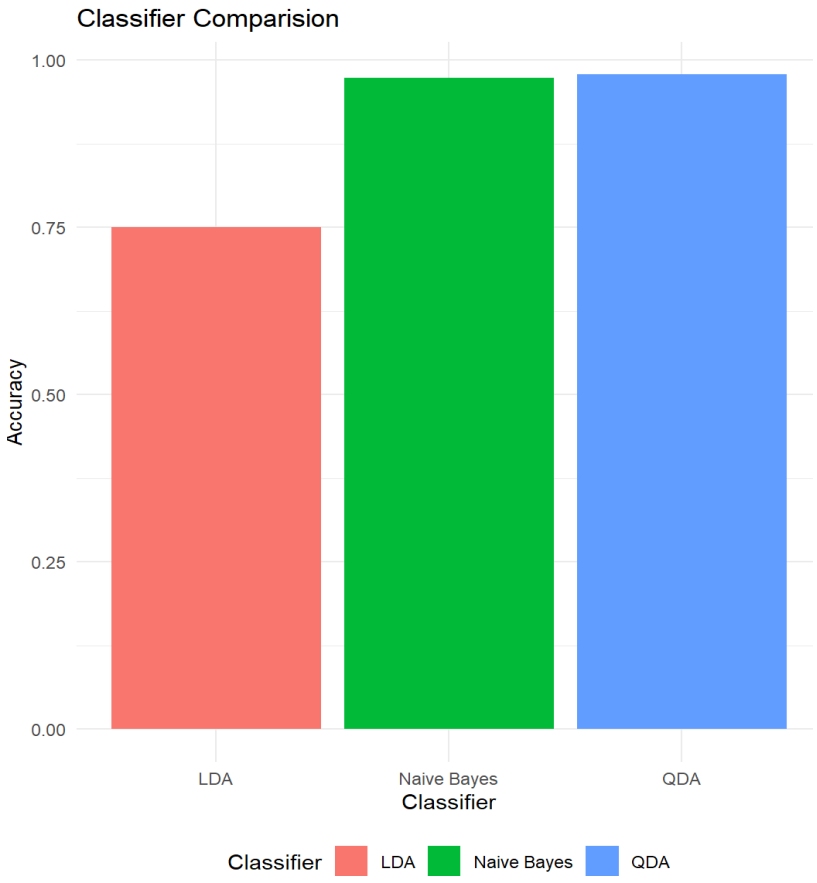
 # Combine ROC curve data into a single data frame

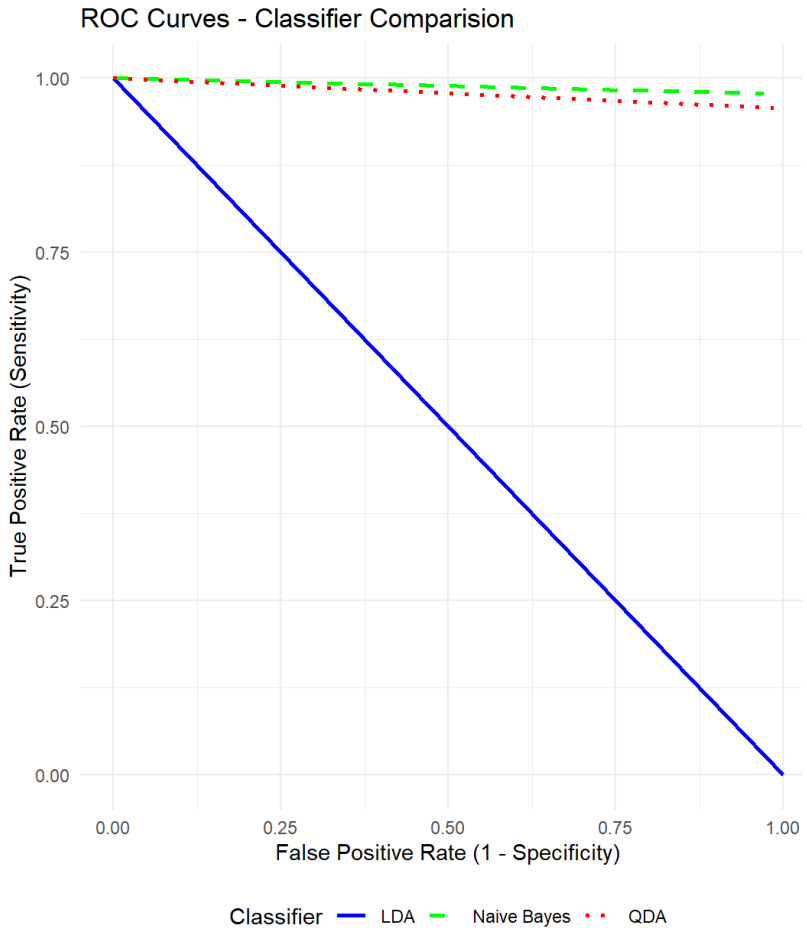
```
roc_data <- data.frame(
  FPR = c(roc_lda$specificities[1:min_length], roc_qda$specificities[1:min_length],
roc_nb$specificities[1:min_length]),
  TPR = c(roc_lda$sensitivities[1:min_length], roc_qda$sensitivities[1:min_length],
roc_nb$sensitivities[1:min_length]),
  Classifier = rep(c("LDA", "QDA", "Naive Bayes"), each = min_length)
)
```

 # Create combined ROC curve plot

```
roc_combined_plot <- ggplot(roc_data, aes(x = FPR, y = TPR, color = Classifier, linetype = Classifier)) +
geom_line(linewidth = 1)+
  labs(x = "False Positive Rate (1 - Specificity)", y = "True Positive Rate (Sensitivity)", title = "ROC Curves - Classifier
Comparision") +
  scale_color_manual(values = c("blue", "green", "red"))+
  scale_linetype_manual(values = c("solid", "dashed", "dotted"))+
  theme_minimal()+
  theme(legend.position = "bottom")
print(roc_combined_plot)
```

OUTPUT:


Classifier Comparision
1.00
0.75
0.50
0.25
0.00
Accuracy
LDA
Naive Bayes
QDA
Classifier
Classifier
LDA
Naive Bayes
QDA


ROC Curves - Classifier Comparision
1.00
0.75
0.50
0.25
0.00
True Positive Rate (Sensitivity)
0.00
0.25
0.50
0.75
1.00
False Positive Rate (1 - Specificity)
Classifier
LDA
Naive Bayes
QDA

Findings:

Quadratic Discriminant Analysis (QDA) is the best algorithm with accuracy rate 97.8% among the Linear Discriminant Analysis(LDA) with accuracy rate 75% ,naive bayes classification with accuracy rate 97.3%.

EXPERIMENT NO:6

AIM:

Write R program to Implement decision trees using mushrooms dataset.

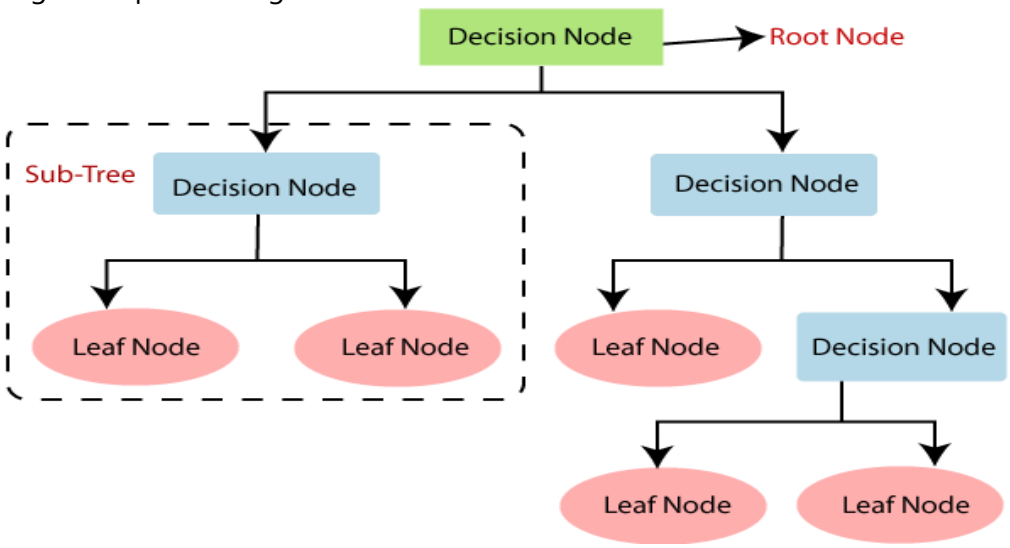
DESCRIPTION:

Decision Tree Classification Algorithm:

Decision Tree is a **Supervised learning technique** that can be used for both classification and Regression problems, but mostly it is preferred for solving Classification problems. It is a tree-structured classifier, where **internal nodes represent the features of a dataset, branches represent the decision rules** and **each leaf node represents the outcome.**

Note: A decision tree can contain categorical data (YES/NO) as well as numeric data.

- Below diagram explains the general structure of a decision tree.



Decision Tree Terminologies:

Root Node: Root node is from where the decision tree starts. It represents the entire dataset, which further gets divided into two or more homogeneous sets.

- **Leaf Node:** Leaf nodes are the final output node, and the tree cannot be segregated further after getting a leaf node.
- **Splitting:** Splitting is the process of dividing the decision node/root node into sub-nodes according to the given conditions.
- **Branch/Sub Tree:** A tree formed by splitting the tree.
- **Pruning:** Pruning is the process of removing the unwanted branches from the tree.
- **Parent/Child node:** The root node of the tree is called the parent node, and other nodes are called the child nodes.

How does the Decision Tree algorithm Work?

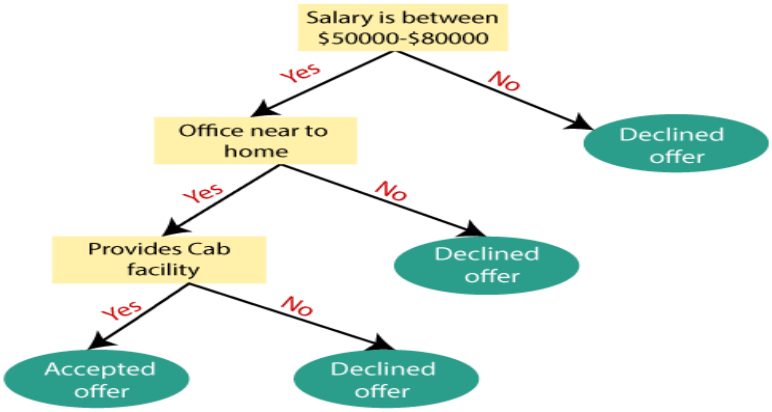
In a decision tree, for predicting the class of the given dataset, the algorithm starts from the root node of the tree. This algorithm compares the values of root attribute with the record (real dataset) attribute and, based on the comparison, follows the branch and jumps to the next node.

For the next node, the algorithm again compares the attribute value with the other sub-nodes and move further. It continues the process until it reaches the leaf node of the tree. The complete process can be better understood using the below algorithm:

- **Step-1:** Begin the tree with the root node, says S, which contains the complete dataset.
- **Step-2:** Find the best attribute in the dataset using **Attribute Selection Measure (ASM).**
- **Step-3:** Divide the S into subsets that contains possible values for the best attributes.
- **Step-4:** Generate the decision tree node, which contains the best attribute.

- **Step-5:** Recursively make new decision trees using the subsets of the dataset created in step -3. Continue this process until a stage is reached where you cannot further classify the nodes and called the final node as a leaf node.

Example: Suppose there is a candidate who has a job offer and wants to decide whether he should accept the offer or Not. So, to solve this problem, the decision tree starts with the root node (Salary attribute by ASM). The root node splits further into the next decision node (distance from the office) and one leaf node based on the corresponding labels. The next decision node further gets split into one decision node (Cab facility) and one leaf node. Finally, the decision node splits into two leaf nodes (Accepted offers and Declined offer). Consider the below diagram:



Attribute Selection Measures:

While implementing a Decision tree, the main issue arises that how to select the best attribute for the root node and for sub-nodes. So, to solve such problems there is a technique which is called as **Attribute selection measure or ASM.** By this measurement, we can easily select the best attribute for the nodes of the tree. There are two popular techniques for ASM, which are:

- **Information Gain**
- **Gini Index**

1. Information Gain:

- Information gain is the measurement of changes in entropy after the segmentation of a dataset based on an attribute.

1. Information Gain= Entropy(S)- [(Weighted Avg) *Entropy(each feature)

Entropy: Entropy is a metric to measure the impurity in a given attribute. It specifies randomness in data. Entropy can be calculated as:

```
Entropy(s)= -P(yes)log2 P(yes)- P(no) log2 P(no)
```

Where,

- **S= Total number of samples**
- **P(yes)= probability of yes**
- **P(no)= probability of no**

2. Gini Index:

- Gini index is a measure of impurity or purity used while creating a decision tree in the CART(Classification and Regression Tree) algorithm.
- Gini index can be calculated using the below formula:

Gini Index= $1- \sum_j P_j^2$

Pruning: Getting an Optimal Decision tree:

Pruning is a process of deleting the unnecessary nodes from a tree in order to get the optimal decision tree.

A too-large tree increases the risk of overfitting, and a small tree may not capture all the important features of the dataset. Therefore, a technique that decreases the size of the learning tree without reducing accuracy is known as Pruning. There are mainly two types of tree **pruning** technology used:

- **Cost Complexity Pruning**
- **Reduced Error Pruning.**

Steps involved in Implementation of Decision Tree:

For this, we will use the dataset "**user_data.csv**," which we have used in previous classification models. By using the same dataset, we can compare the Decision tree classifier with other classification models such as KNN SVM, LogisticRegression, etc.

Steps will also remain the same, which are given below:

- **Data Pre-processing step**
- **Fitting a Decision-Tree algorithm to the Training set**
- **Predicting the test result**
- **Test accuracy of the result(Creation of Confusion matrix)**
- **Visualizing the test set result.**

CODE:

```
library(rpart)
library(rpart.plot)
library(partykit)
library(caret)
library(pROC)
library(ROCR)
```

OUTPUT:

```
Console  Terminal  Background Jobs
R 4.2.2 · ~/
> library(rpart)
> library(rpart.plot)
Warning message:
package 'rpart.plot' was built under R version 4.2.3
> library(partykit)
Loading required package: grid
Loading required package: libcoin
Loading required package: mvtnorm
Warning messages:
1: package 'partykit' was built under R version 4.2.3
2: package 'libcoin' was built under R version 4.2.3
3: package 'mvtnorm' was built under R version 4.2.3
> library(caret)
Loading required package: ggplot2
Loading required package: lattice
Warning messages:
1: package 'caret' was built under R version 4.2.3
2: package 'ggplot2' was built under R version 4.2.3
> library(pROC)
Type 'citation("pROC")' for a citation.

Attaching package: 'pROC'

The following objects are masked from 'package:stats':

    cov, smooth, var

Warning message:
package 'pROC' was built under R version 4.2.3
> library(ROCR)
Warning message:
package 'ROCR' was built under R version 4.2.3
>
```

CODE:

```
#Load the mushrooms data set
dataset<-read.csv("D:\VVIT.BTECH\3_1\ML_lab\exp-6\mushrooms.csv")
#Convert class labels to factors
dataset$class<-as.factor(dataset$class)
set.seed(123)
sample_indices<-sample(nrow(dataset),0.8*nrow(dataset))
train_data<-dataset[sample_indices,]
test_data<-dataset[-sample_indices,]
```

OUTPUT:

```
> dataset<-read.csv("C:\\Users\\DELL\\Downloads\\mushrooms.csv")
> #Convert class labels to factors
> dataset$class<-as.factor(dataset$class)
> set.seed(123)
> sample_indices<-sample(nrow(dataset),0.8*nrow(dataset))
> train_data<-dataset[sample_indices,]
>
```

CODE:

```
#Build the model
tree_model<-rpart(class~.,data=train_data,method="class")
print(tree_model)
#Make predictions on test set
predictions=predict(tree_model,test_data,type = "class")
#Accuracy score
accuracy=sum(predictions == test_data$class)/nrow(test_data)
cat("Accuracy:",accuracy,"\n")
```

OUTPUT:

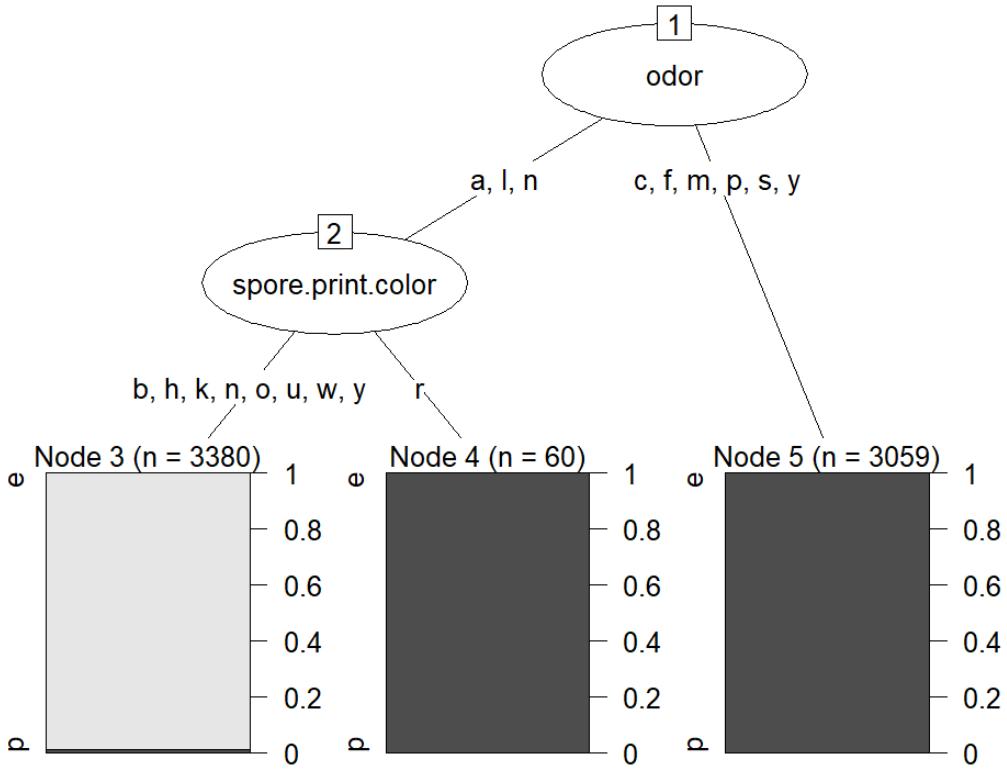
```
> #Build the model
> tree_model<-rpart(class~.,data=train_data,method="class")
> print(tree_model)
n= 6499

node), split, n, loss, yval, (yprob)
      * denotes terminal node

1) root 6499 3155 e (0.51454070 0.48545930)
  2) odor=a,l,n 3440   96 e (0.97209302 0.02790698)
    4) spore.print.color=b,h,k,n,o,u,w,y 3380   36 e (0.98934911 0.01065089) *
    5) spore.print.color=r 60    0 p (0.00000000 1.00000000) *
  3) odor=c,f,m,p,s,y 3059    0 p (0.00000000 1.00000000) *
> #Make predictions on test set
> predictions=predict(tree_model,test_data,type = "class")
> #Accuracy score
> accuracy=sum(predictions == test_data$class)/nrow(test_data)
> cat("Accuracy:",accuracy,"\n")
Accuracy: 0.9926154
>
```

CODE:

```
#Visualize the tree
party_tree<-as.party(tree_model)
plot(party_tree)
```

OUTPUT:

```
> #Visualize the tree
> party_tree<-as.party(tree_model)
> plot(party_tree)
>
```



CODE:

#Display the few predictions

```
predictions=predict(tree_model,newdata=test_data,type = "class")
head(predictions)
```

#Calculate the precision,recall and F1-score.

```
actual_labels<-test_data$class
confusion_matrix<-table(actual_labels,predictions)
print(confusion_matrix)
```

OUTPUT:

```
> #Display the few predictions
> predictions=predict(tree_model,newdata=test_data,type = "class")
> head(predictions)
 3  8 10 12 14 15
 e  e  e  e  p  e
Levels: e p
> actual_labels<-test_data$class
> confusion_matrix<-table(actual_labels,predictions)
> print(confusion_matrix)
             predictions
actual_labels   e   p
            e 864   0
            p  12 749
>
```

CODE:

```
precision<-diag(confusion_matrix)/rowSums(confusion_matrix)

recall<-diag(confusion_matrix)/colSums(confusion_matrix)

f1_score<-2*(precision*recall)/(precision+recall)
```

```
result_df<-data.frame(Precision=precision,Recall=recall,F1_Score=f1_score)
rownames(result_df)<-levels(predictions)
print(result_df)
```

OUTPUT:

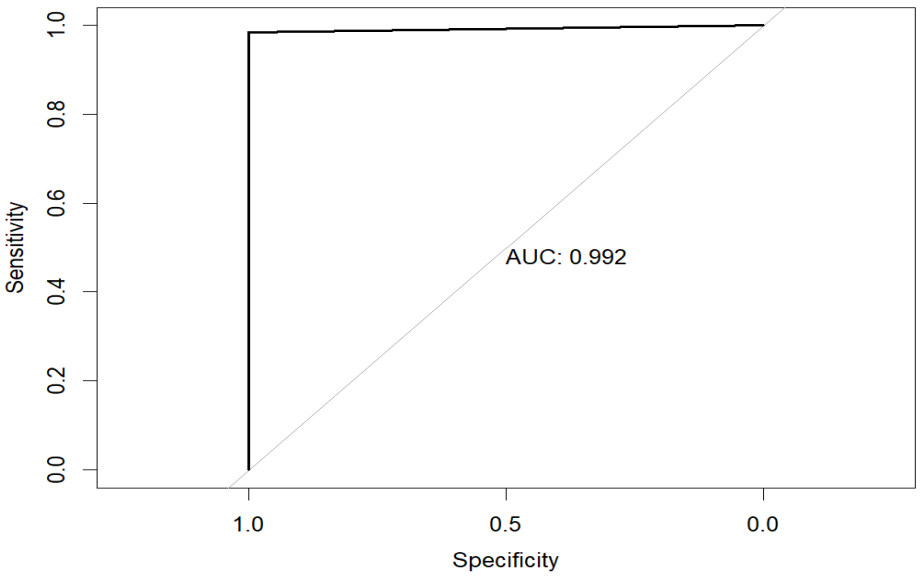
```
> precision<-diag(confusion_matrix)/rowSums(confusion_matrix)
> recall<-diag(confusion_matrix)/colSums(confusion_matrix)
> f1_score<-2*(precision*recall)/(precision+recall)
> result_df<-data.frame(Precision=precision,Recall=recall,F1_Score=f1_score)
> rownames(result_df)<-levels(predictions)
> print(result_df)
  Precision    Recall  F1_Score
e 1.0000000 0.9863014 0.9931034
p 0.9842313 1.0000000 0.9920530
```

CODE:

```
binary_predictions<-ifelse(predictions=="p",1,0)
roc_obj<-roc(as.numeric(test_data$class == "p"),binary_predictions)
plot(roc_obj,print.auc=TRUE)
```

OUTPUT:

```
> binary_predictions<-ifelse(predictions=="p",1,0)
> roc_obj<-roc(as.numeric(test_data$class == "p"),binary_predictions)
Setting levels: control = 0, case = 1
Setting direction: controls < cases
> plot(roc_obj,print.auc=TRUE)
>
```



CODE:

```
auc_score<-auc(roc_obj)
cat("AUC-ROC:",auc_score,"\n")
summary(tree_model)
```

OUTPUT:

```
> auc_score<-auc(roc_obj)
> cat("AUC-ROC:",auc_score,"\n")
AUC-ROC: 0.9921156
> summary(tree_model)
Call:
rpart(formula = class ~ ., data = train_data, method = "class")
  n= 6499

          CP nsplit  rel error     xerror        xstd
1 0.96957211      0 1.00000000 1.00000000 0.012770567
2 0.01901743      1 0.03042789 0.03042789 0.003082512
3 0.01000000      2 0.01141046 0.01141046 0.001896469

Variable importance
                  odor        spore.print.color                gill.color
                    25                       19                       15
stalk.surface.above.ring                ring.type stalk.surface.below.ring
                    14                       13                       13

Node number 1: 6499 observations,    complexity param=0.9695721
  predicted class=e  expected loss=0.4854593  P(node) =1
    class counts:  3344  3155
   probabilities: 0.515 0.485
  left son=2 (3440 obs) right son=3 (3059 obs)
  Primary splits:
      odor                     splits as  LRRLRLRRR,    improve=3060.110, (0 missing)
      spore.print.color        splits as  LRLLLRLRL,    improve=1757.867, (0 missing)
      gill.color               splits as  RLRRLLLLRLLL, improve=1247.353, (0 missing)
      stalk.surface.above.ring splits as  LRLL,         improve=1120.376, (0 missing)
      stalk.surface.below.ring splits as  LRLL,         improve=1054.844, (0 missing)
  Surrogate splits:
      spore.print.color         splits as  LRLLLLLRL,    agree=0.862, adj=0.707, (0 split)
      gill.color                splits as  RLRRLLLLLLLL, agree=0.812, adj=0.600, (0 split)
      stalk.surface.above.ring splits as  LRLL,         agree=0.781, adj=0.535, (0 split)
      ring.type                 splits as  RLRRL,        agree=0.780, adj=0.533, (0 split)
      stalk.surface.below.ring splits as  LRLL,         agree=0.779, adj=0.530, (0 split)

Node number 2: 3440 observations,    complexity param=0.01901743
  predicted class=e  expected loss=0.02790698  P(node) =0.5293122
    class counts:  3344    96
   probabilities: 0.972 0.028
  left son=4 (3380 obs) right son=5 (60 obs)
  Primary splits:
      spore.print.color       splits as  LLLLLRLLL,    improve=115.40870, (0 missing)
      gill.color              splits as  -LLLLLLLRLLL, improve= 38.01964, (0 missing)
      stalk.color.below.ring splits as  --LLLLLLR,    improve= 34.19768, (0 missing)
      cap.color               splits as  RLLLLRLLLL,   improve= 21.94909, (0 missing)
      ring.number             splits as  -LR,          improve= 10.39475, (0 missing)
  Surrogate splits:
      gill.color splits as  -LLLLLLLRLLL, agree=0.988, adj=0.333, (0 split)

Node number 3: 3059 observations
  predicted class=p  expected loss=0  P(node) =0.4706878
    class counts:     0  3059
   probabilities: 0.000 1.000

Node number 4: 3380 observations
  predicted class=e  expected loss=0.01065089  P(node) =0.52008
    class counts:  3344    36
   probabilities: 0.989 0.011

Node number 5: 60 observations
  predicted class=p  expected loss=0  P(node) =0.00923219
    class counts:     0    60
   probabilities: 0.000 1.000
```

CODE:

```
pruned_tree<-prune(tree_model,cp=0.01)
summary(pruned_tree)
```

OUTPUT:

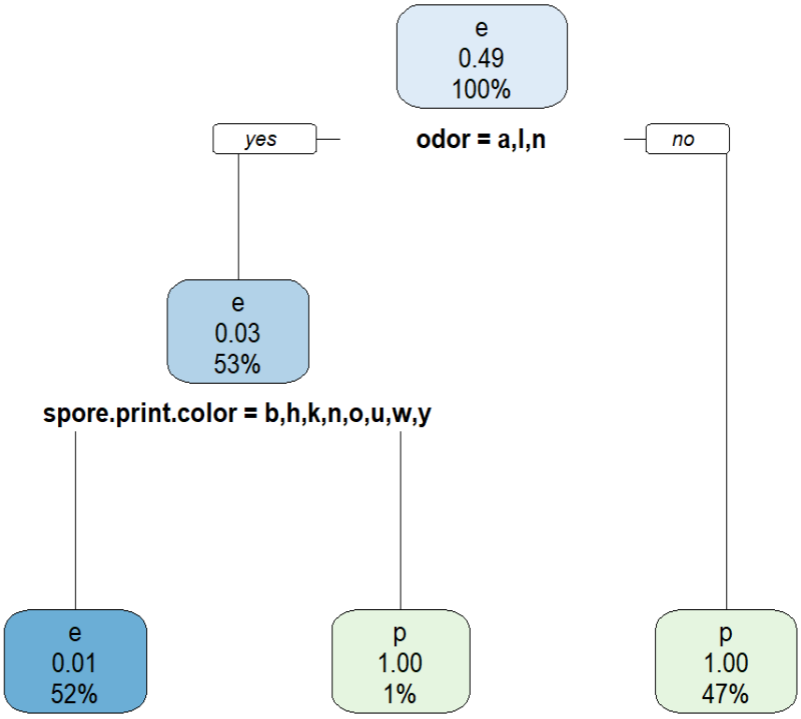
```
> pruned_tree<-prune(tree_model,cp=0.01)
> summary(pruned_tree)
Call:
rpart(formula = class ~ ., data = train_data, method = "class")
  n= 6499

          CP nsplit  rel error     xerror        xstd
1 0.96957211      0 1.00000000 1.00000000 0.012770567
2 0.01901743      1 0.03042789 0.03042789 0.003082512
3 0.01000000      2 0.01141046 0.01141046 0.001896469

Variable importance
                     odor        spore.print.color                gill.color
                       25                       19                       15
stalk.surface.above.ring                ring.type stalk.surface.below.ring
                       14                       13                       13

Node number 1: 6499 observations,    complexity param=0.9695721
  predicted class=e  expected loss=0.4854593  P(node) =1
    class counts:  3344  3155
   probabilities: 0.515 0.485
  left son=2 (3440 obs) right son=3 (3059 obs)
  Primary splits:
      odor                     splits as  LRRLRLRRR,    improve=3060.110, (0 missing)
      spore.print.color        splits as  LRLLLRLRL,    improve=1757.867, (0 missing)
      gill.color               splits as  RLRRLLLLRLLL, improve=1247.353, (0 missing)
      stalk.surface.above.ring splits as  LRLL,         improve=1120.376, (0 missing)
      stalk.surface.below.ring splits as  LRLL,         improve=1054.844, (0 missing)
  Surrogate splits:
      spore.print.color        splits as  LRLLLLLRL,    agree=0.862, adj=0.707, (0 split)
      gill.color               splits as  RLRRLLLLLLLL, agree=0.812, adj=0.600, (0 split)
      stalk.surface.above.ring splits as  LRLL,         agree=0.781, adj=0.535, (0 split)
      ring.type                splits as  RLRRL,        agree=0.780, adj=0.533, (0 split)
      stalk.surface.below.ring splits as  LRLL,         agree=0.779, adj=0.530, (0 split)

Node number 2: 3440 observations,    complexity param=0.01901743
  predicted class=e  expected loss=0.02790698  P(node) =0.5293122
    class counts:  3344    96
   probabilities: 0.972 0.028
  left son=4 (3380 obs) right son=5 (60 obs)
  Primary splits:
      spore.print.color      splits as  LLLLLRLLL,    improve=115.40870, (0 missing)
      gill.color             splits as  -LLLLLLLRLLL, improve= 38.01964, (0 missing)
      stalk.color.below.ring splits as  --LLLLLLR,    improve= 34.19768, (0 missing)
      cap.color              splits as  RLLLLRLLLL,   improve= 21.94909, (0 missing)
      ring.number            splits as  -LR,          improve= 10.39475, (0 missing)
  Surrogate splits:
      gill.color splits as  -LLLLLLLRLLL, agree=0.988, adj=0.333, (0 split)

Node number 3: 3059 observations
  predicted class=p  expected loss=0  P(node) =0.4706878
    class counts:     0  3059
   probabilities: 0.000 1.000

Node number 4: 3380 observations
  predicted class=e  expected loss=0.01065089  P(node) =0.52008
    class counts:  3344    36
   probabilities: 0.989 0.011

Node number 5: 60 observations
  predicted class=p  expected loss=0  P(node) =0.00923219
    class counts:     0    60
   probabilities: 0.000 1.000
```

CODE:

```
rpart.plot(pruned_tree)
```

OUTPUT:

```
> rpart.plot(pruned_tree)
>
```



CODE:

#make predictions on the test set using pruned_tree.

```
pruned_predictions<-predict(pruned_tree,newdata = test_data,type = "class")
pruned_cm<-confusionMatrix(pruned_predictions,test_data$class)
print(pruned_cm)
```

OUTPUT:

```
> pruned_predictions<-predict(pruned_tree,newdata = test_data,type = "class")
> pruned_cm<-confusionMatrix(pruned_predictions,test_data$class)
> print(pruned_cm)
Confusion Matrix and Statistics

          Reference
Prediction   e   p
         e 864  12
         p   0 749

               Accuracy : 0.9926
                 95% CI : (0.9871, 0.9962)
    No Information Rate : 0.5317
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.9852

 Mcnemar's Test P-Value : 0.001496

            Sensitivity : 1.0000
            Specificity : 0.9842
         Pos Pred Value : 0.9863
         Neg Pred Value : 1.0000
             Prevalence : 0.5317
         Detection Rate : 0.5317
   Detection Prevalence : 0.5391
      Balanced Accuracy : 0.9921

       'Positive' Class : e
```

CODE:

```
pruned_accuracy<-sum(pruned_predictions==test_data$class)/length(test_data$class)
cat("Pruned Model Accuracy : ",pruned_accuracy,"\n")
pruned_cm<-confusionMatrix(pruned_predictions,test_data$class)
pruned_precision<-pruned_cm$byClass["Positive predictive value"]
pruned_recall<-pruned_cm$byClass["Sensitivity"]
pruned_f1_score<-pruned_cm$byClass["F1"]
cat("Pruned model precision: ",pruned_precision,"\n")
```

```
cat("Pruned model recall: ",pruned_recall,"\n")
cat("Pruned model f1-score: ",pruned_f1_score,"\n")
```

OUTPUT:

```
> pruned_accuracy<-sum(pruned_predictions==test_data$class)/length(test_data$class)
> cat("Pruned Model Accuracy : ",pruned_accuracy,"\n")
Pruned Model Accuracy :  0.9926154
> pruned_cm<-confusionMatrix(pruned_predictions,test_data$class)
> pruned_precision<-pruned_cm$byClass["Positive predictive value"]
> pruned_recall<-pruned_cm$byClass["Sensitivity"]
> pruned_f1_score<-pruned_cm$byClass["F1"]
> cat("Pruned model precision: ",pruned_precision,"\n")
Pruned model precision:  NA
> cat("Pruned model recall: ",pruned_recall,"\n")
Pruned model recall:  1
> cat("Pruned model f1-score: ",pruned_f1_score,"\n")
Pruned model f1-score:  0.9931034
```

Findings:

Pruned model accuracy: 0.9926154

Pruned model precision: NA

Pruned model recall: 1

Pruned model f1-score: 0.9931034

EXPERIMENT NO:7

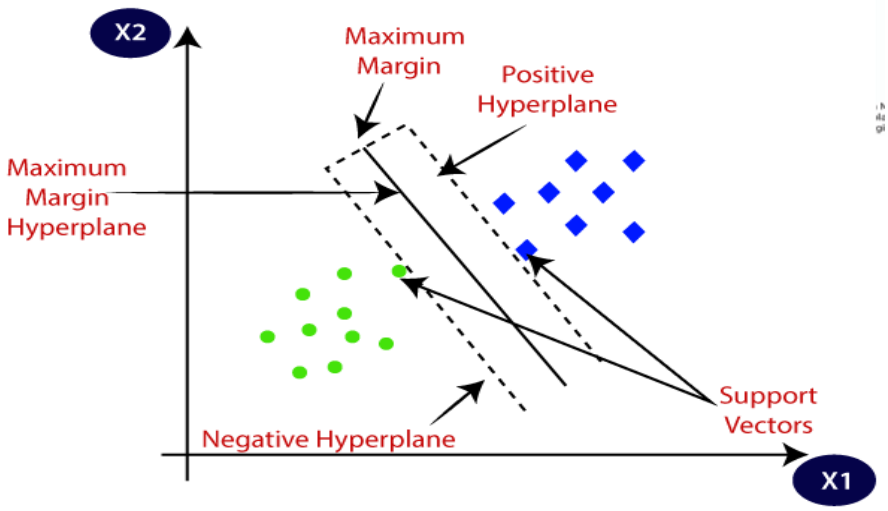
AIM:

Write R program to implement Support Vector Machine(SVM) for Gene Expression Data.

DESCRIPTION:

Support Vector Machine:

Support Vector Machine (SVM) is a supervised machine learning algorithm used for both classification and regression. Though we say regression problems as well it's best suited for classification. The main objective of the SVM algorithm is to find the optimal hyperplane in an N-dimensional space that can separate the data points in different classes in the feature space. The hyperplane tries that the margin between the closest points of different classes should be as maximum as possible. The dimension of the hyperplane depends upon the number of features. If the number of input features is two, then the hyperplane is just a line. If the number of input features is three, then the hyperplane becomes a 2-D plane. It becomes difficult to imagine when the number of features exceeds three.



Support Vector Machine Terminology:

1. **Hyperplane:** Hyperplane is the decision boundary that is used to separate the data points of different classes in a feature space. In the case of linear classifications, it will be a linear equation i.e., wx+b = 0.
2. **Support Vectors:** Support vectors are the closest data points to the hyperplane, which makes a critical role in deciding the hyperplane and margin.
3. **Margin**: Margin is the distance between the support vector and hyperplane. The main objective of the support vector machine algorithm is to maximize the margin. The wider margin indicates better classification performance.
4. **Kernel**: Kernel is the mathematical function, which is used in SVM to map the original input data points into high-dimensional feature spaces, so, that the hyperplane can be easily found out even if the data points are not linearly separable in the original input space. Some of the common kernel functions are linear, polynomial, radial basis function (RBF), and sigmoid.

Hard Margin: The maximum-margin hyperplane or the hard margin hyperplane is a hyperplane that properly separates the data points of different categories without any misclassifications.

5. **Soft Margin:** When the data is not perfectly separable or contains outliers, SVM permits a soft margin technique. Each data point has a slack variable introduced by the soft-margin SVM formulation, which softens the strict margin requirement and permits certain

misclassifications or violations. It discovers a compromise between increasing the margin and reducing violations.

6. **C:** Margin maximisation and misclassification fines are balanced by the regularisation parameter C in SVM. The penalty for going over the margin or misclassifying data items is decided by it. A stricter penalty is imposed with a greater value of C, which results in a smaller margin and perhaps fewer misclassifications.
7. **Hinge Loss:** A typical loss function in SVMs is hinge loss. It punishes incorrect classifications or margin violations. The objective function in SVM is frequently formed by combining it with the regularisation term.
8. **Dual Problem:** A dual Problem of the optimisation problem that requires locating the Lagrange multipliers related to the support vectors can be used to solve SVM. The dual formulation enables the use of kernel tricks and more effective computing.

Mathematical intuition of Support Vector Machine:

Consider a binary classification problem with two classes, labelled as +1 and -1. We have a training dataset consisting of input feature vectors X and their corresponding class labels Y.

The equation for the linear hyperplane can be written as:

$$w^T x + b = 0$$

The vector W represents the normal vector to the hyperplane. i.e the direction perpendicular to the hyperplane. The parameter **b** in the equation represents the offset or distance of the hyperplane from the origin along the normal vector **w**.

The distance between a data point x_i and the decision boundary can be calculated as:

$$d_i = \frac{w^T x_i + b}{||w||}$$

where ||w|| represents the Euclidean norm of the weight vector w. Euclidean norm of the normal vector W

For Linear SVM classifier:

$$\hat{y} = \begin{cases} 1 & : \ w^T x + b \geq 0 \\ 0 & : \ w^T x + b < 0 \end{cases}$$

Optimization:

- **For Hard margin linear SVM classifier:**

$$\underset{w,b}{\text{minimize}} \frac{1}{2} w^T w = \underset{W,b}{\text{minimize}} \frac{1}{2} \|w\|^2$$
$$\text{subject to } y_i(w^T x_i + b) \geq 1 \ for \ i = 1, 2, 3, \cdots, m$$

The target variable or label for the i^{th} training instance is denoted by the symbol t_i in this statement. And t_i=-1 for negative occurrences (when y_i= 0) and t_i=1positive instances (when y_i = 1) respectively. Because we require the decision boundary that satisfy the

constraint: $t_i(w^T x_i + b) \geq 1$

- **For Soft margin linear SVM classifier:**

$$\underset{w,b}{\text{minimize}} \ \frac{1}{2} w^T w + C \sum_{i=1}^{m} \zeta_i$$
$$\text{subject to } y_i(w^T x_i + b) \geq 1 - \zeta_i \ \ and \ \zeta_i \geq 0 \ \ for \ i = 1, 2, 3, \cdots, m$$

- **Dual Problem:** A dual Problem of the optimisation problem that requires locating the Lagrange multipliers related to the support vectors can be used to solve SVM. The optimal Lagrange multipliers α(i) that maximize the following dual objective function

$$\underset{\alpha}{\text{maximize}} : \frac{1}{2} \sum_{i \to m} \sum_{j \to m} \alpha_i \alpha_j t_i t_j K(x_i, x_j) - \sum_{i \to m} \alpha_i$$

where,

- α_i is the Lagrange multiplier associated with the ith training sample.
- $K(x_i, x_j)$ is the kernel function that computes the similarity between two samples x_i and x_j. It allows SVM to handle nonlinear classification problems by implicitly mapping the samples into a higher-dimensional feature space.

- The term $\sum\alpha_i$ represents the sum of all Lagrange multipliers.

The SVM decision boundary can be described in terms of these optimal Lagrange multipliers and the support vectors once the dual issue has been solved and the optimal Lagrange multipliers have been discovered. The training samples that have i > 0 are the support vectors, while the decision boundary is supplied by:

$$w = \sum_{i \to m} \alpha_i t_i K(x_i, x) + b$$
$$t_i(w^T x_i - b) = 1 \iff b = w^T x_i - t_i$$

Types of Support Vector Machine:

Based on the nature of the decision boundary, Support Vector Machines (SVM) can be divided into two main parts:

- **Linear SVM:** Linear SVMs use a linear decision boundary to separate the data points of different classes. When the data can be precisely linearly separated, linear SVMs are very suitable. This means that a single straight line (in 2D) or a hyperplane (in higher dimensions) can entirely divide the data points into their respective classes. A hyperplane that maximizes the margin between the classes is the decision boundary.
- **Non-Linear SVM:** Non-Linear SVM can be used to classify data when it cannot be separated into two classes by a straight line (in the case of 2D). By using kernel functions, nonlinear SVMs can handle nonlinearly separable data. The original input data is transformed by these kernel functions into a higher-dimensional feature space, where the data points can be linearly separated. A linear SVM is used to locate a nonlinear decision boundary in this modified space.

Popular kernel functions in SVM:

The SVM kernel is a function that takes low-dimensional input space and transforms it into higher-dimensional space, i.e., it converts non separable problems to separable problems.
It is mostly useful in non-linear separation problems. Simply put the kernel, does some extremely complex data transformations and then finds out the process to separate the data based on the labels or outputs defined.

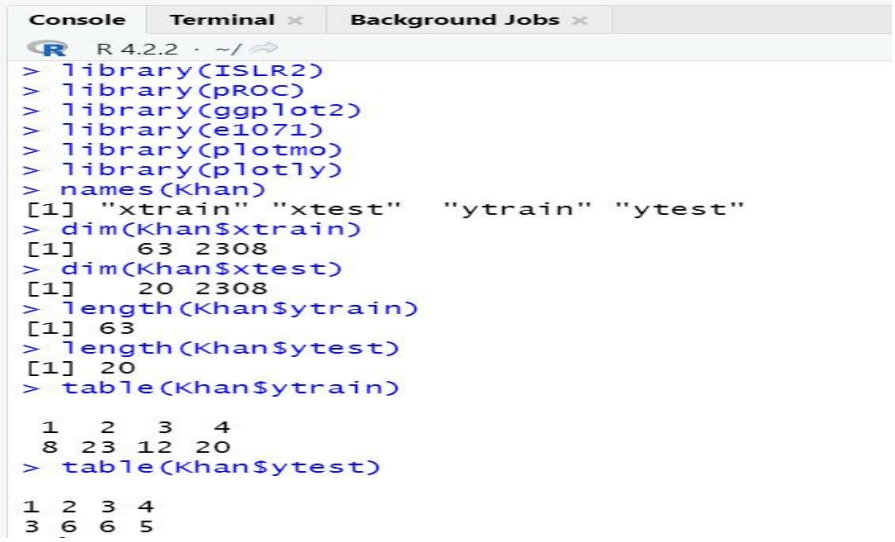
$$\text{Linear}: K(w,b) = w^T x + b$$
$$\text{Polynomial}: K(w,x) = (\gamma w^T x + b)^N$$
$$\text{Gaussian RBF}: K(w,x) = \exp(-\gamma||x_i - x_j||^n$$
$$\text{Sigmoid}: K(x_i, x_j) = \tanh(\alpha x_i^T x_j + b)$$

CODE:

```
# Load necessary packages
library(ISLR2)

 library(pROC)

library(ggplot2)

library(e1071)

library(plotmo)

library(plotly)

# Display column names of the Khan dataset

names(Khan)
```

```
# Check dimensions of training and testing sets

dim(Khan$xtrain)

dim(Khan$xtest)

# Check the length of training and testing labels

length(Khan$ytrain)

length(Khan$ytest)

# Display class distribution in training and testing labels

table(Khan$ytrain)

 table(Khan$ytest)
```

OUTPUT:



CODE:

```
# Create a dataframe 'dat' with training features and labels

dat <- data.frame(x = Khan$xtrain,y = as.factor(Khan$ytrain))

# Train an SVM model with linear kernel

out <- svm(y ~ ., data = dat, kernel = "linear", cost = 10)

# Display summary of the trained SVM model

 summary(out)

# Compare the fitted values with actual labels in the training data

table(out$fitted, dat$y)

# Create a dataframe 'dat.te' with testing features and labels

 dat.te <- data.frame(x = Khan$xtest, y = as.factor(Khan$ytest))

# Predict using the trained SVM model on the testing data
```

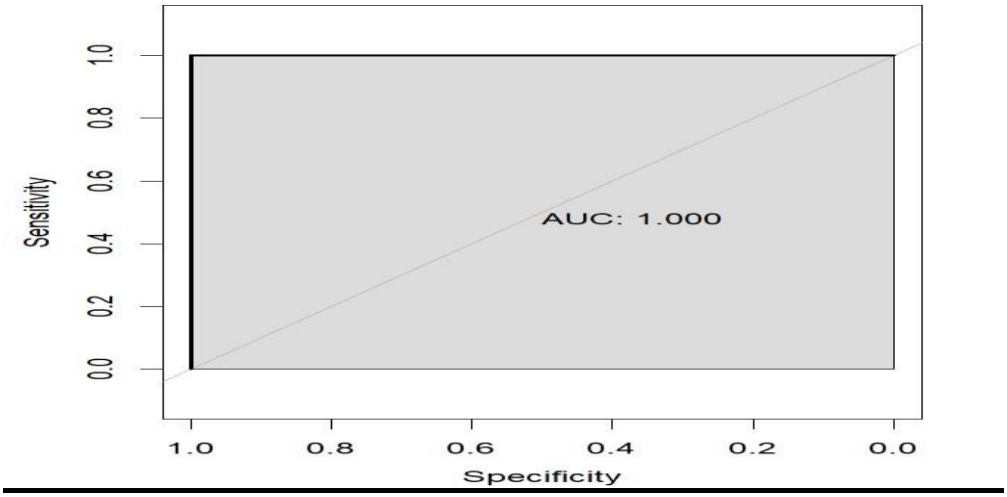
```
pred.te <- predict(out, newdata = dat.te)

# Compare the predicted values with actual labels in the testing data

table(pred.te, dat.te$y)

 # Confusion matrix for training data

train_pred <- predict(out, newdata = dat)

train_conf_matrix <- table(train_pred, dat$y)
```

OUTPUT :

```
Console   Terminal   Background Jobs
R 4.2.2 · ~/
> dat <- data.frame(x = Khan$xtrain,y = as.factor(Khan$ytrain))
> out <- svm(y ~ ., data = dat, kernel = "linear", cost = 10)
> summary(out)

Call:
svm(formula = y ~ ., data = dat, kernel = "linear", cost = 10)


Parameters:
   SVM-Type:  C-classification
 SVM-Kernel:  linear
       cost:  10

Number of Support Vectors:  58

 ( 20 20 11 7 )


Number of Classes:  4

Levels:
 1 2 3 4

> table(out$fitted, dat$y)

    1  2  3  4
1   8  0  0  0
2   0 23  0  0
3   0  0 12  0
4   0  0  0 20
> dat.te <- data.frame(x = Khan$xtest, y = as.factor(Khan$ytest))
> pred.te <- predict(out, newdata = dat.te)
> table(pred.te, dat.te$y)

pred.te 1 2 3 4
       1 3 0 0 0
       2 0 6 2 0
       3 0 0 4 0
       4 0 0 0 5
> train_pred <- predict(out, newdata = dat)
> train_conf_matrix <- table(train_pred, dat$y)
```

CODE:

```
# Convert the confusion matrix to a dataframe

train_conf_df <- as.data.frame(as.table(train_conf_matrix))

# Rename the columns for better readability

colnames(train_conf_df) <- c("Predicted", "Actual", "Frequency")

# Create the heatmap
ggplot(train_conf_df, aes(x = Predicted, y = Actual, fill = Frequency)) +

geom_tile() +

scale_fill_gradient(low = "white", high = "blue") +   l

abs(x = "Predicted Class", y = "Actual Class", fill = "Frequency") +

  theme_minimal()
# Convert factor levels to numeric (1 or 2)

numeric_pred <- as.numeric(train_pred)
```



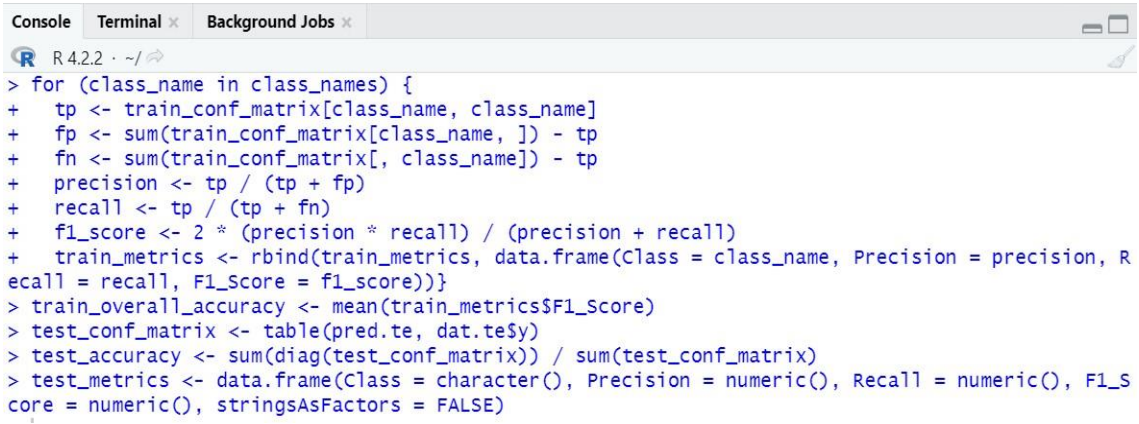
CODE:

```
for (i in 2:length(train_roc$rocs)) { lines(train_roc$rocs[[i]], col = i, print.auc =

TRUE, auc.polygon = TRUE)}

# Add a legend

legend("bottomright", legend = levels(dat$y), col = 1:length(train_roc$rocs), lwd = 2)

# Calculate performance metrics for training data

train_pred <- predict(out, newdata = dat)

train_conf_matrix <- table(train_pred, dat$y)
# Calculate accuracy for training data
train_accuracy <- sum(diag(train_conf_matrix)) / sum(train_conf_matrix)
 # Calculate precision, recall, and F1-score for each class in training data
class_names <- levels(dat$y)
train_metrics <- data.frame(Class = character(), Precision = numeric(), Recall = numeric(),
 F1_Score = numeric(), stringsAsFactors = FALSE)
```

OUTPUT:

```
Console  Terminal  Background Jobs
R 4.2.2 · ~/
> for (i in 2:length(train_roc$rocs)) {
+   lines(train_roc$rocs[[i]], col = i, print.auc = TRUE, auc.polygon = TRUE)
+ }
> legend("bottomright", legend = levels(dat$y), col = 1:length(train_roc$rocs), lwd = 2)
> train_pred <- predict(out, newdata = dat)
There were 20 warnings (use warnings() to see them)
> train_conf_matrix <- table(train_pred, dat$y)
> train_accuracy <- sum(diag(train_conf_matrix)) / sum(train_conf_matrix)
> class_names <- levels(dat$y)
> train_metrics <- data.frame(Class = character(), Precision = numeric(), Recall = numeric(), F1_
Score = numeric(), stringsAsFactors = FALSE)
```

OUTPUT:



CODE:

```
for (class_name in class_names) {

 tp <- test_conf_matrix[class_name, class_name]

fp <- sum(test_conf_matrix[class_name, ]) - tp

 fn <- sum(test_conf_matrix[, class_name]) - tp

 precision <- tp / (tp + fp)

recall <- tp / (tp + fn)

f1_score <- 2 * (precision * recall) / (precision + recall)

  test_metrics <- rbind(test_metrics, data.frame(Class = class_name, Precision = precision, Recall = recall,
F1_Score = f1_score))}
# Calculate overall classification accuracy for testing data

test_overall_accuracy <- mean(test_metrics$F1_Score)

# Print performance metrics for both training and testing data

 cat("Performance Metrics for Training Data:\n")

cat("Overall Accuracy:", train_accuracy, "\n") print(train_metrics)

cat("Overall Classification Accuracy (F1-Score):", train_overall_accuracy, "\n\n")

cat("Performance Metrics for Testing Data:\n")

cat("Overall Accuracy:", test_accuracy, "\n")

print(test_metrics)

cat("Overall Classification Accuracy (F1-Score):", test_overall_accuracy, "\n")
```

OUTPUT:

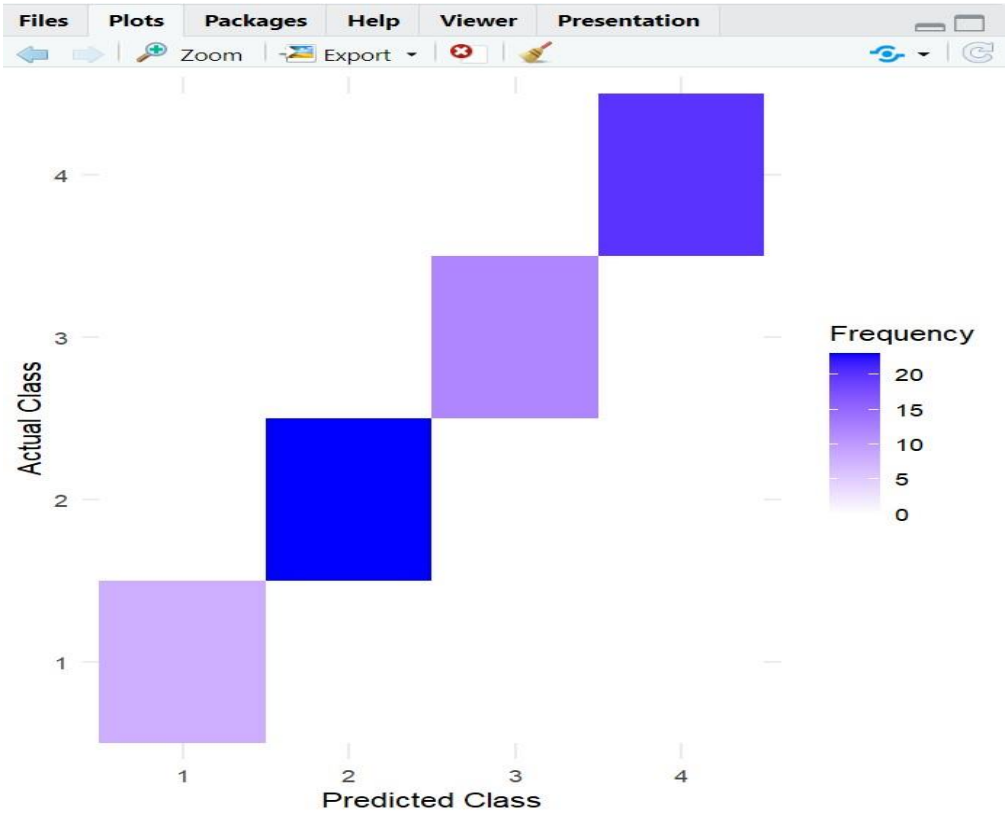
```
Console  Terminal  Background Jobs
R 4.2.2 · ~/
> for (class_name in class_names) {
+   tp <- test_conf_matrix[class_name, class_name]
+   fp <- sum(test_conf_matrix[class_name, ]) - tp
+   fn <- sum(test_conf_matrix[, class_name]) - tp
+   precision <- tp / (tp + fp)
+   recall <- tp / (tp + fn)
+   f1_score <- 2 * (precision * recall) / (precision + recall)
+   test_metrics <- rbind(test_metrics, data.frame(Class = class_name, Precision = precision, R
ecall = recall, F1_Score = f1_score))}
> test_overall_accuracy <- mean(test_metrics$F1_Score)
> cat("Performance Metrics for Training Data:\n")
Performance Metrics for Training Data:
> cat("Overall Accuracy:", train_accuracy, "\n")
Overall Accuracy: 1
> print(train_metrics)
  Class Precision Recall F1_Score
1     1         1      1        1
2     2         1      1        1
3     3         1      1        1
4     4         1      1        1
> cat("Overall Classification Accuracy (F1-Score):", train_overall_accuracy, "\n\n")
Overall Classification Accuracy (F1-Score): 1

> cat("Performance Metrics for Testing Data:\n")
Performance Metrics for Testing Data:

> cat("Overall Accuracy:", test_accuracy, "\n")
Overall Accuracy: 0.9
> print(test_metrics)
  Class Precision    Recall  F1_Score
1     1      1.00 1.0000000 1.0000000
2     2      0.75 1.0000000 0.8571429
3     3      1.00 0.6666667 0.8000000
4     4      1.00 1.0000000 1.0000000
> cat("Overall Classification Accuracy (F1-Score):", test_overall_accuracy, "\n")
Overall Classification Accuracy (F1-Score): 0.9142857
```

CODE:

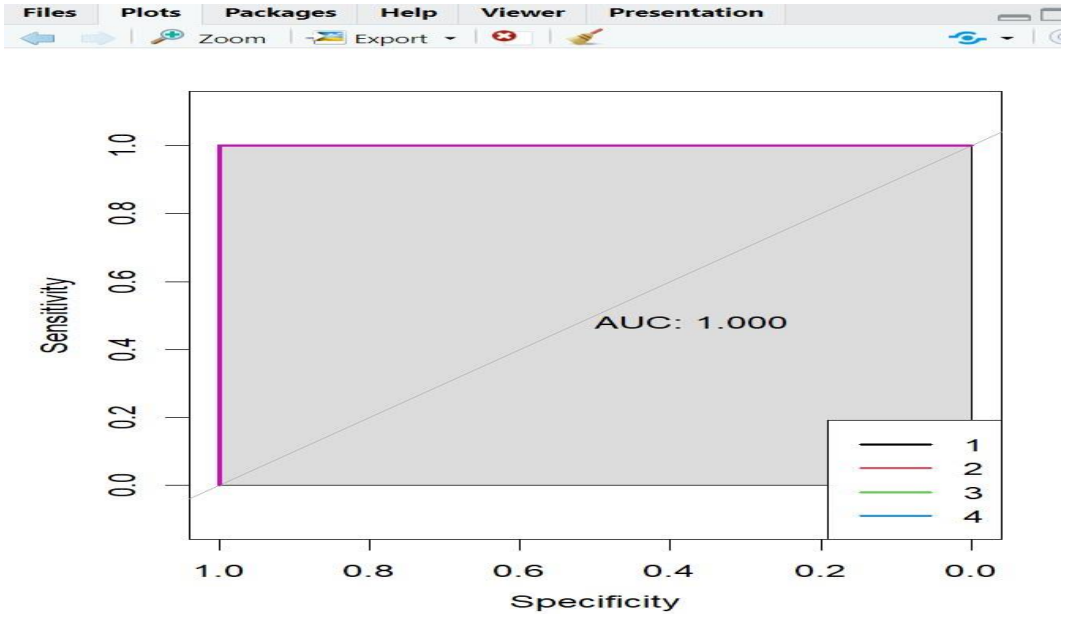
```
# Create a dataframe for training metrics

train_metrics_df <- data.frame(

  Class = train_metrics$Class,
  Precision = train_metrics$Precision,
  Recall = train_metrics$Recall,
  F1_Score = train_metrics$F1_Score)

# Create a bar plot for training metrics

ggplot(train_metrics_df, aes(x = Class, y = F1_Score, fill = Class)) +

geom_bar(stat = "identity", position = "dodge") +

  labs(
    title = "Performance Metrics for Training Data",

 y = "F1-Score",p

    x = "Class" )
  theme_minimal() +

 theme(axis.text.x = element_text(angle = 45, hjust = 1))

# Calculate multiclass ROC curve and AUC for training data

train_roc <- multiclass.roc(dat$y, numeric_pred)

# Plot the multiclass ROC curves for each class

plot(train_roc$rocs[[1]], col = 1, print.auc = TRUE, auc.polygon =

TRUE)
```

OUTPUT:

```
> train_conf_df <- as.data.frame(as.table(train_conf_matrix))
> colnames(train_conf_df) <- c("Predicted", "Actual", "Frequency")
> ggplot(train_conf_df, aes(x = Predicted, y = Actual, fill = Frequency)) +
+   geom_tile() +
+   scale_fill_gradient(low = "white", high = "blue") +
+   labs(x = "Predicted Class", y = "Actual Class", fill = "Frequency") +
+   theme_minimal()
```




```
> numeric_pred <- as.numeric(train_pred)
> train_roc <- multiclass.roc(dat$y, numeric_pred)
Setting direction: controls < cases
Setting direction: controls < cases
Setting direction: controls < cases
Setting direction: controls < cases
Setting direction: controls < cases
Setting direction: controls < cases
> plot(train_roc$rocs[[1]], col = 1, print.auc = TRUE, auc.polygon = TRUE)
```



CODE:

```
for (class_name in class_names) {
  tp <- train_conf_matrix[class_name, class_name]
 fp <- sum(train_conf_matrix[class_name, ]) - tp
  fn <- sum(train_conf_matrix[, class_name]) - tp
  precision <- tp / (tp + fp)   recall <- tp / (tp + fn)
f1_score <- 2 * (precision * recall) / (precision + recall)
  train_metrics <- rbind(train_metrics, data.frame(Class = class_name, Precision = precision, Recall = recall, F1_Score = f1_score))}
# Calculate overall classification accuracy for training data
train_overall_accuracy <- mean(train_metrics$F1_Score)
# Calculate performance metrics for testing data
 test_conf_matrix <- table(pred.te, dat.te$y)
 # Calculate accuracy for testing data
 test_accuracy <- sum(diag(test_conf_matrix)) / sum(test_conf_matrix)
# Calculate precision, recall, and F1-score for each class in testing data
test_metrics <- data.frame(Class = character(), Precision = numeric(), Recall = numeric(), F1_Score = numeric(), stringsAsFactors = FALSE)
```

OUTPUT:

```
Console  Terminal  Background Jobs
R 4.2.2 · ~/
> train_metrics_df <- data.frame(
+   Class = train_metrics$Class,
+   Precision = train_metrics$Precision,
+   Recall = train_metrics$Recall,
+   F1_Score = train_metrics$F1_Score
+ )
> ggplot(train_metrics_df, aes(x = Class, y = F1_Score, fill = Class)) +
+   geom_bar(stat = "identity", position = "dodge") +
+   labs(
+     title = "Performance Metrics for Training Data",
+     y = "F1-Score",
+     x = "Class"
+   ) +
+   theme_minimal() +
+   theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

CODE:

```
# Create a dataframe for testing metrics

test_metrics_df <- data.frame(Class = test_metrics$Class,

 Precision = test_metrics$Precision,
 Recall = test_metrics$Recall,
 F1_Score = test_metrics$F1_Score)

# Create a bar plot for testing metrics

ggplot(test_metrics_df, aes(x = Class, y = F1_Score, fill = Class)) +

geom_bar(stat = "identity", position = "dodge") +

 labs(
   title = "Performance Metrics for Testing Data",

   y = "F1-Score",

    x = "Class"
```

```
) +
 theme_minimal() +

theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

OUTPUT:

```
Console   Terminal ×   Background Jobs ×
R 4.2.2 · ~/
> test_metrics_df <- data.frame(
+   Class = test_metrics$Class,
+   Precision = test_metrics$Precision,
+   Recall = test_metrics$Recall,
+   F1_Score = test_metrics$F1_Score
+ )
> ggplot(test_metrics_df, aes(x = Class, y = F1_Score, fill = Class)) +
+   geom_bar(stat = "identity", position = "dodge") +
+   labs(
+     title = "Performance Metrics for Testing Data",
+     y = "F1-Score",
+     x = "Class"
+   ) +
+   theme_minimal() +
+   theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

EXPERIMENT NO: 8

AIM: To Implement Principal Component Analysis on the US Arrests data set.

DESCRIPTION:

Principal Component Analysis is an unsupervised learning algorithm that is used for the dimensionality reduction in machine learning . It is a statistical process that converts the observations of correlated features into a set of linearly uncorrelated features with the help of orthogonal transformation. These new transformed features are called the **Principal Components**. It is one of the popular tools that is used for exploratory data analysis and predictive modeling. It is a technique to draw strong patterns from the given dataset by reducing the variances.

PCA generally tries to find the lower-dimensional surface to project the high-dimensional data.

PCA works by considering the variance of each attribute because the high attribute shows the good split between the classes, and hence it reduces the dimensionality. Some real-world applications of PCA are ***image processing, movie recommendation system, optimizing the power allocation in various communication channels.*** It is a feature extraction technique, so it contains the important variables and drops the least important variable.

The PCA algorithm is based on some mathematical concepts such as:

- Variance and Covariance
    - Eigenvalues and Eigen factors

Some common terms used in PCA algorithm:

- **Dimensionality:** It is the number of features or variables present in the given dataset. More easily, it is the number of columns present in the dataset.
- **Correlation:** It signifies that how strongly two variables are related to each other. Such as if one changes, the other variable also gets changed. The correlation value ranges from -1 to +1. Here, -1 occurs if variables are inversely proportional to each other, and +1 indicates that variables are directly proportional to each other.
- **Orthogonal:** It defines that variables are not correlated to each other, and hence the correlation between the pair of variables is zero.
- **Eigenvectors:** If there is a square matrix M, and a non-zero vector v is given. Then v will be eigenvector if Av is the scalar multiple of v.
- **Covariance Matrix:** A matrix containing the covariance between the pair of variables is called the Covariance Matrix.

Principal Components in PCA:

- As described above, the transformed new features or the output of PCA are the Principal Components. The number of these PCs are either equal to or less than the original features present in the dataset. Some properties of these principal components are given below:
- The principal component must be the linear combination of the original features.
- These components are orthogonal, i.e., the correlation between a pair of variables is zero.
- The importance of each component decreases when going to 1 to n, it means the 1 PC has the most importance, and n PC will have the least importance.

\

Steps for PCA algorithm:

1. **Getting the dataset**
   Firstly, we need to take the input dataset and divide it into two subparts X and Y, where X is the training set, and Y is the validation set.
2. **Representing data into a structure**
   Now we will represent our dataset into a structure. Such as we will represent the two-dimensional matrix of independent variable X. Here each row corresponds to the data items, and the column corresponds to the Features. The number of columns is the dimensions of the dataset.
3. **Standardizing the data**
   In this step, we will standardize our dataset. Such as in a particular column, the features with high variance are more important compared to the features with lower variance.
   If the importance of features is independent of the variance of the feature, then we will divide each data item in a column with the standard deviation of the column. Here we will name the matrix as Z.
4. **Calculating the Covariance of Z**
   To calculate the covariance of Z, we will take the matrix Z, and will transpose it. After transpose, we will multiply it by Z. The output matrix will be the Covariance matrix of Z.
5. **Calculating the Eigen Values and Eigen Vectors**
   Now we need to calculate the eigenvalues and eigenvectors for the resultant covariance matrix Z. Eigenvectors or the covariance matrix are the directions of the axes with high information. And the coefficients of these eigenvectors are defined as the eigenvalues.
6. **Sorting the Eigen Vectors**
   In this step, we will take all the eigenvalues and will sort them in decreasing order, which means from largest to smallest. And simultaneously sort the eigenvectors accordingly in matrix P of eigenvalues. The resultant matrix will be named as P*.
7. **Calculating the new features Or Principal Components**
   Here we will calculate the new features. To do this, we will multiply the P* matrix to the Z. In the resultant matrix Z*, each observation is the linear combination of original features. Each column of the Z* matrix is independent of each other.
8. **Remove less or unimportant features from the new dataset.**
   The new feature set has occurred, so we will decide here what to keep and what to remove. It means, we will only keep the relevant or important features in the new dataset, and unimportant features will be removed out. library(ggplot2) library(gridExtra) library(caret)

```
library(ISLR2)

#LOAD THE USARrrests dataset
data("USArrests")

#STANDARDISE THE DATA
scaled_data<-scale(USArrests)

#perform PCA
pca_result<-prcomp(scaled_data,center=TRUE,scale.=TRUE)

#summary the PCA result
summary(pca_result)
```

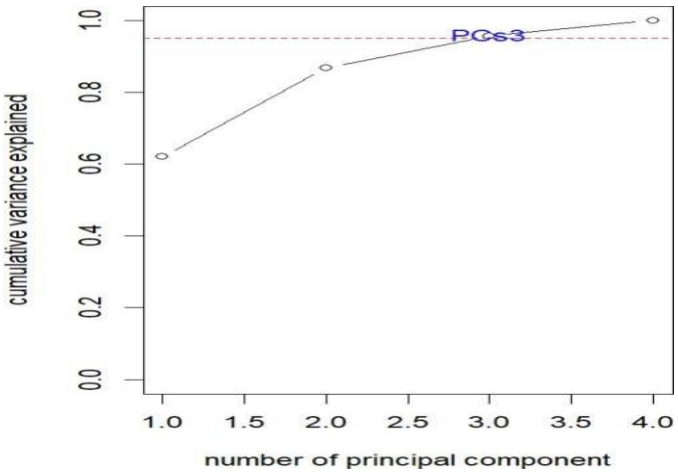
```
#variable explained by each principle component
variance_explained <- pca_result$sdev^2 / sum(pca_result$sdev^2) * 100

#print the variance explained by each pc cat("variance
explained by each principal component:\n")
print(variance_explained)
```

OUTPUT:

```
Importance of components:
                          PC1    PC2     PC3     PC4
Standard deviation     1.5749 0.9949 0.59713 0.41645
Proportion of Variance 0.6201 0.2474 0.08914 0.04336
Cumulative Proportion  0.6201 0.8675 0.95664 1.00000
> #variable explained by each principle component
> variance_explained <- pca_result$sdev^2 / sum(pca_result$sdev^2) * 100
> #print the variance explained by each pc
> cat("variance explained by each principal component:\n")
variance explained by each principal component:
> print(variance_explained)
[1] 62.006039 24.744129  8.914080  4.335752
```

```
#scree plot to visualize the variance explained by each pc
plot(variance_explained,type = "b",xlab="principal component",ylab = "variance explained(%)")

#calculate the cumulative proportion of variance explained
variance_explained <- pca_result$sdev^2 / sum(pca_result$sdev^2)
cumulative_variance_explained <- cumsum(variance_explained)
plot(cumulative_variance_explained, type = "b",
    xlab = "number of principal component",
     ylab = "cumulative variance explained",ylim = c(0,1))

#add a horizontal line at 0.95 to visualize the 95% threshold
abline(h=0.95,col = "red",lty=2)

#find the number of pcs needed to explain atleast 95% of the variance
num_pcs_to_reach_95_percent <- which(cumulative_variance_explained
>=0.95)[1] text(num_pcs_to_reach_95_percent,0.96, labels =
paste0("PCs",num_pcs_to_reach_95_percent), col = "blue")
```

OUTPUT:



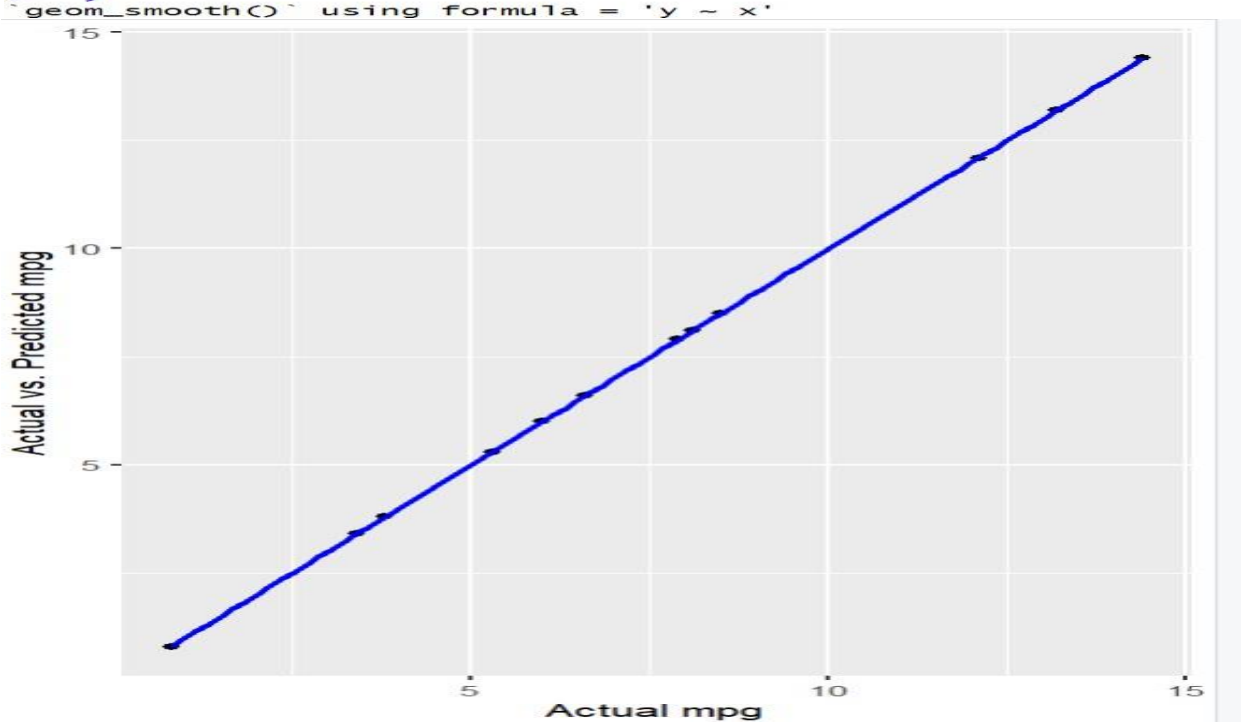
CODE:

```
#define the desired threshold (e.g,90%)
desired_threshold <- 0.90

#find the number of PCs needed to reach or exceed the desired threshold
num_pcs_to_reach_threshold <- which(cumulative_variance_explained >= desired_threshold)[1]

#extract the top "n" principal components
top_n_pcs <- pca_result$x[,1:num_pcs_to_reach_threshold]

#print the result you can now use top_n_pcs
cat("Number if PCs to convert at least",(desired_threshold * 100),
    "% variance:",num_pcs_to_reach_threshold,"\n")

#Retain the first 4 principal components
top_4_pcs <- pca_result$x[, 1:4]

#create a data frame with the top 4 PCs and the mpg variable
data_with_pcs <- data.frame(top_4_pcs,mpg = USArrests$Murder)

#split the data into a training set (75%) nd a testing set(25%)
set.seed(123)
train_index <- createDataPartition(data_with_pcs$mpg, p =0.75, list =
FALSE) train_data <- data_with_pcs[train_index, ] test_data <-
data_with_pcs[-train_index, ] model <- lm(mpg ~ . , data = train_data)
predictions <- predict(model, newdata = test_data) rmse <-
sqrt(mean((test_data$mpg - predictions)^2)) cat("Root Mean Squared Error
(RMSE):", rmse , "\n") result_data <- data.frame(Actual = test_data$mpg,
                    Predicted = predictions)
ggplot(result_data, aes(x = Actual, y = Predicted)) +
geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
  labs(
    x = "Actual mpg",
    y = "Actual vs. Predicted mpg"
```

```
  )
residuals <- test_data$mpg - predictions screen_plot <-
ggplot(NULL,    aes(x    =    1:ncol(top_4_pcs),    y    =
cumulative_variance_explained)) +
  geom_bar(stat = "identity", fill = "blue") +
  labs(
    x = "Principal Component", y =
    "Cumulative Variance Explained",
    title = "Scree Plot (PCA)"
  )
residuals_plot <- ggplot(NULL, aes(x = residuals)) +
  geom_histogram(binwidth = 1, fill = "green", color ="black") +
  labs(
    x = "Residuals", y = "Frequemcy",
    title = "Residual plot
    (Regression)"
  )
actual_vs_predicted_plot <- ggplot(result_data, aes(x= Actual,
                                    y = Predicted)) + geom_point() +
geom_smooth(method = "lm", se = FALSE, color = "blue") + labs(
    x = "Actual mpg", y = "Predicted
    mpg", title = "Actual vs.
    Predicted mpg"
  )
```

OUTPUT:

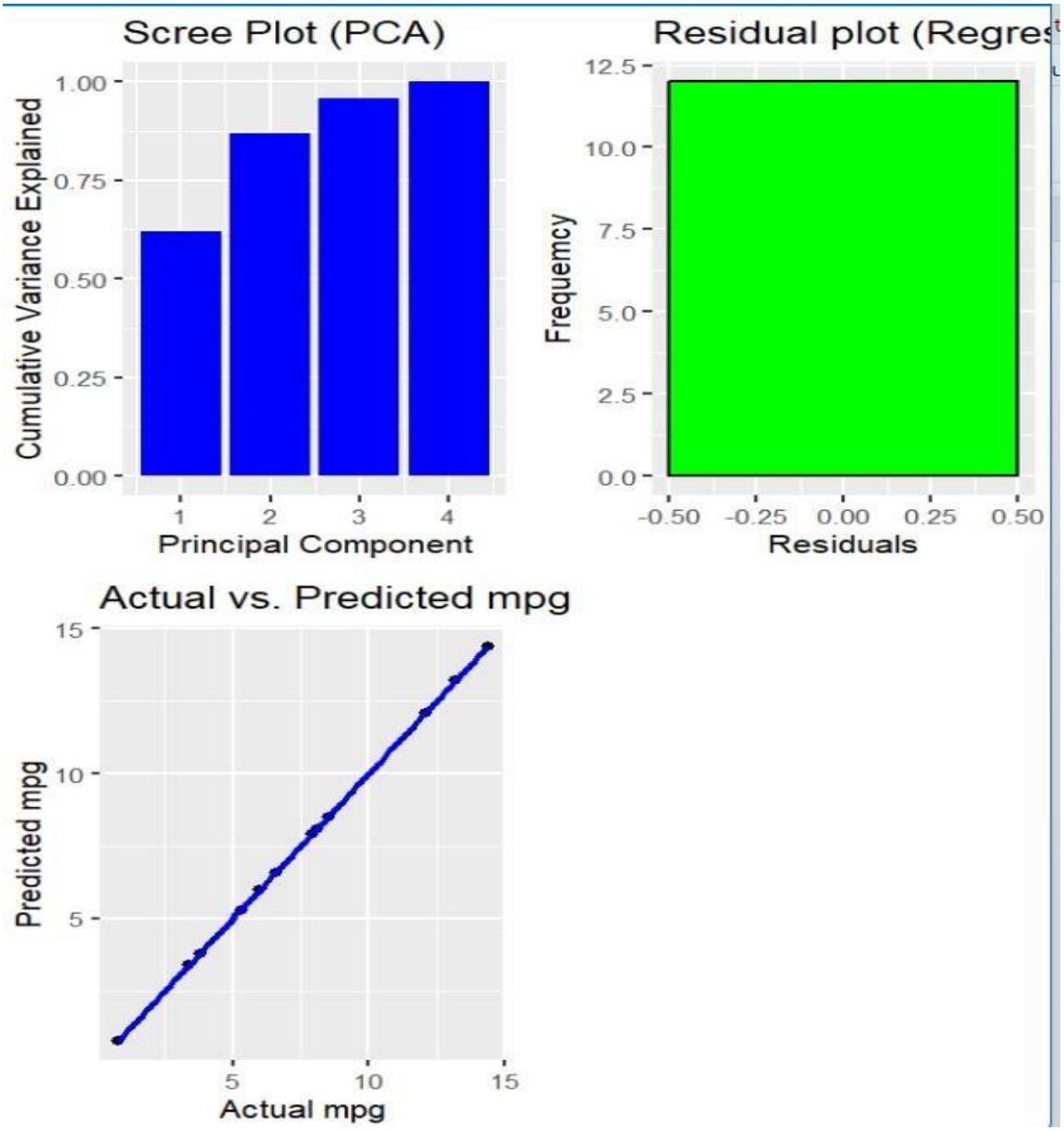
```
> #create a data frame with the top 4 PCs and the mpg variable
> data_with_pcs <- data.frame(top_4_pcs,mpg = USArrests$Murder)
>
> #split the data into a training set (75%) nd a testing set(25%)
> set.seed(123)
> train_index <- createDataPartition(data_with_pcs$mpg, p =0.75,
+                                    list = FALSE)
> train_data <- data_with_pcs[train_index, ]
> test_data <- data_with_pcs[-train_index, ]
> model <- lm(mpg ~ . , data = train_data)
> predictions <- predict(model, newdata = test_data)
> rmse <- sqrt(mean((test_data$mpg - predictions)^2))
> cat("Root Mean Squared Error (RMSE):", rmse , "\n")
Root Mean Squared Error (RMSE): 2.187121e-15
> result_data <- data.frame(Actual = test_data$mpg,
+                           Predicted = predictions)
> ggplot(result_data, aes(x = Actual, y = Predicted)) +
+   geom_point() +
+   geom_smooth(method = "lm", se = FALSE, color = "blue") +
+   labs(
+     x = "Actual mpg",
+     y = "Actual vs. Predicted mpg"
+   )
`geom_smooth()` using formula = 'y ~ x'
```



CODE:

```
summary_plot <- grid.arrange(screen_plot, residuals_plot,
                             actual_vs_predicted_plot, ncol = 2)
print(summary_plot)
```

OUTPUT:


Scree Plot (PCA)
Cumulative Variance Explained
1.00
0.75
0.50
0.25
0.00
1
2
3
4
Principal Component
Residual plot (Regres
Frequemcy
12.5
10.0
7.5
5.0
2.5
0.0
-0.50
-0.25
0.00
0.25
0.50
Residuals
Actual vs. Predicted mpg
Predicted mpg
15
10
5
5
10
15
Actual mpg

EXPERIMENT NO:9
AIM: To Perform K-Means Clustering on NC160 Dataset.

DESCRIPTION: K-means clustering is a technique in which we place each observation in a dataset into one of K clusters. The end goal is to have K clusters in which the observations within each cluster are quite similar to each other while the observations in different clusters are quite different from each other.

In practice, we use the following steps to perform K-means clustering:
1.Choose a value for K.
• First, we must decide how many clusters we'd like to identify in the data. Often we have to simply test several different values for K and analyze the results to see which number of clusters seems to make the most sense for a given problem.
2. Randomly assign each observation to an initial cluster, from 1 to K.
3. Perform the following procedure until the cluster assignments stop changing.
• For each of the K clusters, compute the cluster centroid. This is simply the vector of the p feature means for the observations in the kth cluster.
• Assign each observation to the cluster whose centroid is closest. Here, closest is defined using Euclidean distance.

K-Means Clustering in R.
The following tutorial provides a step-by-step example of how to perform k-means clustering in R.
Step 1: Load the Necessary Packages
First, we'll load two packages that contain several useful functions for k-means clustering in R
Step 2: Load and Prep the Data
For this example we'll use the USArrests dataset built into R, which contains the number of arrests per 100,000 residents in each U.S. state in 1973 for Murder, Assault, and Rape along with the percentage of the population in each state living in urban areas, UrbanPop.
The following code shows how to do the following:
• Load the USArrests dataset
• Remove any rows with missing values
• Scale each variable in the dataset to have a mean of 0 and a standard deviation of 1
Step 3: Find the Optimal Number of Clusters
To perform k-means clustering in R we can use the built-in kmeans() function, which uses the following syntax:

kmeans(data, centers, nstart)

where:
• data: Name of the dataset.
• centers: The number of clusters, denoted k.
• nstart: The number of initial configurations. Because it's possible that different initial starting clusters can lead to different results, it's recommended to use several different initial configurations. The k-means algorithm will find the initial configurations that lead to the smallest within-cluster variation.
Since we don't know beforehand how many clusters is optimal, we'll create two different plots that can help us decide:
1.Number of Clusters vs. the Total Within Sum of Squares
First, we'll use the fviz_nbclust() function to create a plot of the number of clusters vs. the total within sum of squares.
Typically when we create this type of plot we look for an "elbow" where the sum of squares begins to "bend" or level off. This is typically the optimal number of clusters.
For this plot it appears that there is a bit of an elbow or "bend" at k = 4 clusters.
2. Number of Clusters vs. Gap Statistic

Another way to determine the optimal number of clusters is to use a metric known as the gap statistic, which compares the total intra-cluster variation for different values of k with their expected values for a distribution with no clustering.

We can calculate the gap statistic for each number of clusters using the clusGap() function from the cluster package along with a plot of clusters vs. gap statistic using the fviz_gap_stat() function

From the plot we can see that gap statistic is highest at k = 4 clusters, which matches the elbow method we used earlier.

Step 4: Perform K-Means Clustering with Optimal K

Lastly, we can perform k-means clustering on the dataset using the optimal value for k of 4.

From the results we can see that:

- 16 states were assigned to the first cluster
- 13 states were assigned to the second cluster
- 13 states were assigned to the third cluster
- 8 states were assigned to the fourth cluster.

We can visualize the clusters on a scatterplot that displays the first two principal components on the axes using the fivz_cluster() function

We can also use the aggregate() function to find the mean of the variables in each cluster.

We interpret this output is as follows:

- The mean number of murders per 100,000 citizens among the states in cluster 1 is 3.6.
- The mean number of assaults per 100,000 citizens among the states in cluster 1 is 78.5.
- The mean percentage of residents living in an urban area among the states in cluster 1 is 52.1%.
- The mean number of rapes per 100,000 citizens among the states in cluster 1 is 12.2.

And so on.

We can also append the cluster assignments of each state back to the original dataset.

CODE:

```
#Load necessary packages
library(factoextra)
library(cluster)

#load data
df <- USArrests

#remove rows with missing values
df <- na.omit(df)

#scale each variable to have a mean of 0 and sd of 1
df <- scale(df)

#view first six rows of dataset
head(df)

#Number of Clusters vs. the Total Within Sum of Squares
fviz_nbclust(df, kmeans, method = "wss")

#calculate gap statistic based on number of clusters
gap_stat <- clusGap(df,FUN = kmeans,
                    nstart = 25,
                    K.max = 10,
                    B = 50)
```

OUTPUT:

```
> head(df)
               Murder   Assault   UrbanPop         Rape
Alabama    1.24256408 0.7828393 -0.5209066 -0.003416473
Alaska     0.50786248 1.1068225 -1.2117642  2.484202941
Arizona    0.07163341 1.4788032  0.9989801  1.042878388
Arkansas   0.23234938 0.2308680 -1.0735927 -0.184916602
California 0.27826823 1.2628144  1.7589234  2.067820292
Colorado   0.02571456 0.3988593  0.8608085  1.864967207
Clustering k = 1,2,..., K.max (= 10): .. done
Bootstrapping, b = 1,2,..., B (= 50)  [one "." per sample]:
.................................................. 50
```

CODE:

#plot number of clusters vs. gap statistic

fviz_gap_stat(gap_stat)

#make this example reproducible

set.seed(1**)**

#perform k-means clustering with k = 4 clusters

km <- kmeans(df, centers = 4, nstart = 25)

CODE:

#view results

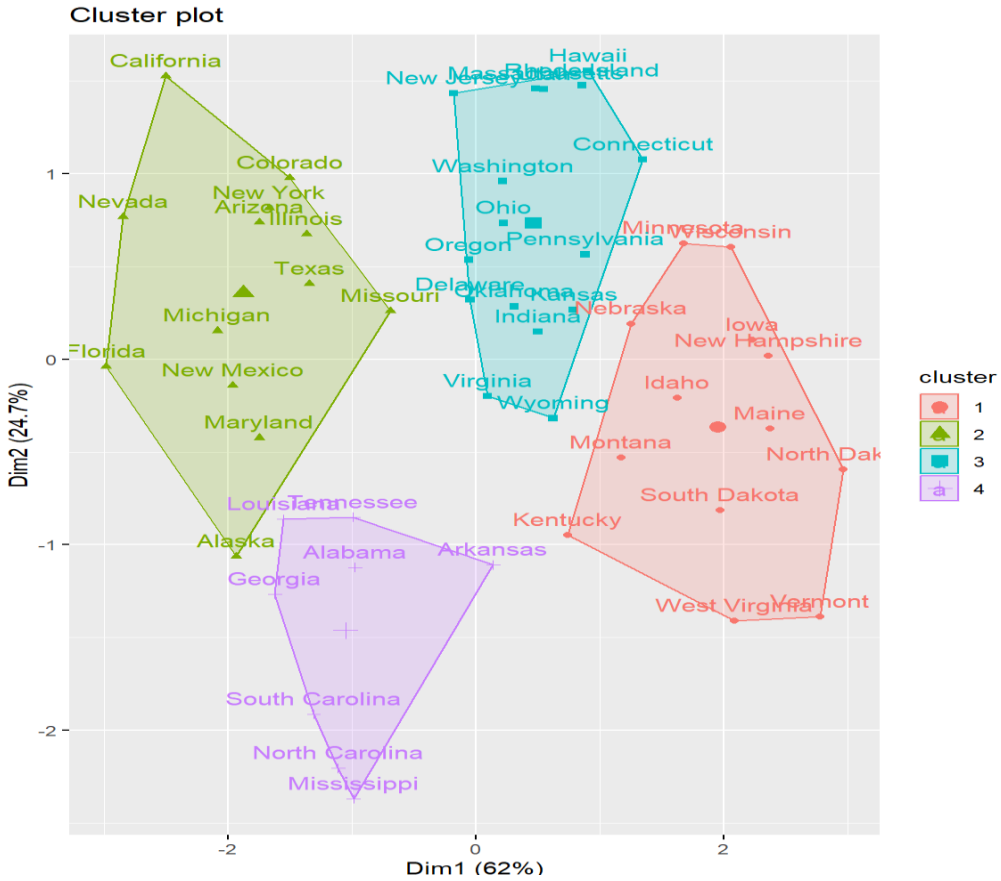
Km

#plot results of final k-means model

fviz_cluster(km, data = df)

OUTPUT:

```
> km
K-means clustering with 4 clusters of sizes 13, 13, 16, 8

Cluster means:
      Murder    Assault   UrbanPop        Rape
1 -0.9615407 -1.1066010 -0.9301069 -0.96676331
2  0.6950701  1.0394414  0.7226370  1.27693964
3 -0.4894375 -0.3826001  0.5758298 -0.26165379
4  1.4118898  0.8743346 -0.8145211  0.01927104

Clustering vector:
       Alabama         Alaska        Arizona       Arkansas     California       Colorado    Connecticut
             4              2              2              4              2              2              3
      Delaware        Florida        Georgia         Hawaii          Idaho       Illinois        Indiana
             3              2              4              3              1              2              3
          Iowa         Kansas       Kentucky      Louisiana          Maine       Maryland  Massachusetts
             1              3              1              4              1              2              3
      Michigan      Minnesota    Mississippi       Missouri        Montana       Nebraska         Nevada
             2              1              4              2              1              1              2
 New Hampshire     New Jersey     New Mexico       New York North Carolina   North Dakota           Ohio
             1              3              2              2              4              1              3
      Oklahoma         Oregon   Pennsylvania   Rhode Island South Carolina   South Dakota      Tennessee
             3              3              3              3              4              1              4
         Texas           Utah        Vermont       Virginia     Washington  West Virginia      Wisconsin
             2              3              1              3              3              1              1
       Wyoming
             3

Within cluster sum of squares by cluster:
[1] 11.952463 19.922437 16.212213  8.316061
 (between_SS / total_SS =  71.2 %)

Available components:

[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss" "betweenss"    "size"
[8] "iter"         "ifault"
```



CODE:

#find means of each cluster

```
aggregate(USArrests, by=list(cluster=km$cluster),mean)
```

#add cluster assigment to original data

```
final_data <- cbind(USArrests, cluster = km$cluster)
```

#view final data

```
head(final_data)
```

OUTPUT:

```
> aggregate(USArrests, by=list(cluster=km$cluster),
+           mean)
  cluster   Murder   Assault UrbanPop     Rape
1       1  3.60000  78.53846 52.07692 12.17692
2       2 10.81538 257.38462 76.00000 33.19231
3       3  5.65625 138.87500 73.87500 18.78125
4       4 13.93750 243.62500 53.75000 21.41250
> head(final_data)
           Murder Assault UrbanPop Rape cluster
Alabama      13.2     236       58 21.2       4
Alaska       10.0     263       48 44.5       2
Arizona       8.1     294       80 31.0       2
Arkansas      8.8     190       50 19.5       4
California    9.0     276       91 40.6       2
Colorado      7.9     204       78 38.7       2
```

Pros & Cons of K-Means Clustering:

K-means clustering offers the following benefits:

- It is a fast algorithm.
- It can handle large datasets well.

However, it comes with the following potential drawbacks:

- It requires us to specify the number of clusters before performing the algorithm.
- It's sensitive to outliers.

Two alternatives to k-means clustering are k-means clustering and hierarchical clustering.

EXPERIMENT NO:10

AIM: Implement R program on Hierarchical Clustering on mtcars Dataset.

DESCRIPTION:

Hierarchical clustering in R Programming Language is an Unsupervised non-linear algorithm in which clusters are created such that they have a hierarchy(or a pre-determined ordering). For example, consider a family of up to three generations. A grandfather and mother have their children that become father and mother of their children. So, they all are grouped together to the same family i.e they form a hierarchy.

Hierarchical clustering is of two types:

- **Agglomerative Hierarchical clustering:** It starts at individual leaves and successfully merges clusters together. Its a Bottom-up approach.
- **Divisive Hierarchical clustering:** It starts at the root and recursively split the clusters. It's a top-down approach.

In hierarchical clustering, Objects are categorized into a hierarchy similar to a tree-shaped structure which is used to interpret hierarchical clustering models. The algorithm is as follows:

1. Make each data point in a single point cluster that forms **N** clusters.
2. Take the two closest data points and make them one cluster that forms **N-1** clusters.
3. Take the two closest clusters and make them one cluster that forms **N-2** clusters.
4. Repeat steps 3 until there is only one cluster.

Dendrogram is a hierarchy of clusters in which distances are converted into heights. It clusters **n** units or objects each with p feature into smaller groups. Units in the same cluster are joined by a horizontal line. The leaves at the bottom represent individual units. It provides a visual representation of clusters.
Thumb Rule: Largest vertical distance which doesn't cut any horizontal line defines the optimal number of clusters.

mtcars(motor trend car road test) comprise fuel consumption, performance, and 10 aspects of automobile design for 32 automobiles. It comes pre-installed with dplyr package in R.

Performing Hierarchical clustering on Dataset
Using Hierarchical Clustering algorithm on the dataset using **hclust()** which is pre-installed in stats package when R is installed.

- The values are shown as per the distance matrix calculation with the method as euclidean.
- In the model, the cluster method is average, distance is euclidean and no. of objects are 32.
- The plot dendrogram is shown with x-axis as distance matrix and y-axis as height.
- So, Tree is cut where k = 3 and each category represents its number of clusters.
- The plot denotes dendrogram after being cut. The green lines show the number of clusters as per the thumb rule.

CODE:

#loading packages

```
library(dplyr)

library(ggplot2)
```

#summary of the dataset in the package

```
head(mtcars)
```

OUTPUT:

```
> #summary of the dataset in the package
> head(mtcars)
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

CODE:

#finding the distance matrix

```
distance_mat<-dist(mtcars,method='euclidean')
distance_mat
```

OUTPUT:

```
                     Merc 280C          227.8813169  64.8898713  39.3868519   1.5231546
Merc 450SE         106.4084264 175.1620073 159.8179555 122.3642489 122.3461050
Merc 450SL         106.4320572 175.1189767 159.7760899 122.3443771 122.3355492   0.9826495
Merc 450SLC        106.4010305 175.2118218 159.8495837 122.3934970 122.3586862   1.3726252   2.1383405
Cadillac Fleetwood 119.0239068 355.6627498 349.2832611 315.3904859 315.3557081 197.8842803 197.9154476
Lincoln Continental 104.5112999 348.9901277 341.3154316 306.6760719 306.6406187 187.5997191 187.6330806
Chrysler Imperial   81.4297699 338.1959373 328.4335161 292.7146896 292.6989332 171.6600758 171.6743028
Fiat 128           333.9792070  68.6105903  69.3127910 106.5053149 106.6829794 228.3247948 228.2592340
Honda Civic        344.0518316  72.0014488  78.5387212 116.7280991 116.8711475 238.0141824 237.9588183
Toyota Corolla     341.0218232  76.2806458  76.7731674 113.6290721 113.8118009 235.5183809 235.4481971
Toyota Corona      282.0508820  44.0850975  21.0962017  54.3641713  54.4258314 176.6020527 176.5727477
Dodge Challenger   103.9023864 192.8617917 185.8331870 152.8929263 152.8722437  51.8008639  51.8242520
AMC Javelin        110.3084921 180.5479760 172.5312555 139.1457974 139.1181977  41.2080044  41.2411618
Camaro Z28          10.0761203 273.8367985 257.7469734 219.5520854 219.5276434  98.7203049  98.7566899
Pontiac Firebird    80.8057339 277.4606884 271.3871978 238.1726099 238.1806292 124.3368538 124.3204160
Fiat X1-9          333.4843231  67.9163981  68.5564864 105.7412910 105.8560373 227.7627676 227.7173075
Porsche 914-2      285.1986201  39.4469276  22.1180967  57.6458160  57.8473863 179.5034108 179.4550855
Lotus Europa       296.4572287  72.8971106  50.1094030  74.1443580  74.3824296 193.3074449 193.2407697
Ford Pantera L      21.2655990 287.5238795 269.9772035 231.4081306 231.4024263 112.8181834 112.8296774
Ferrari Dino       226.2036333 113.3023005  80.6550953  56.8365103  56.8987601 131.0272205 131.0077635
Maserati Bora      107.7224977 313.8633093 288.8755628 250.5874125 250.5774357 157.1633256 157.1768956
Volvo 142E         275.1353516  53.6823481  24.6913548  48.8053450  48.8884618 170.4500681 170.4225164
                   Merc 450SLC Cadillac Fleetwood Lincoln Continental Chrysler Imperial     Fiat 128
Mazda RX4 Wag
Datsun 710
Hornet 4 Drive
Hornet Sportabout
Valiant
Duster 360
Merc 240D
Merc 230
Merc 280
Merc 280C
Merc 450SE
Merc 450SL
Merc 450SLC
Cadillac Fleetwood  197.8526242
Lincoln Continental 187.5671081          15.6224446
Chrysler Imperial   171.6557637          40.8399636          25.3714237
Fiat 128            228.4051825         417.7687579         410.0206984        397.2276375
Honda Civic         238.0828999         425.3271621         417.9679574        405.8152201  14.5590942
Toyota Corolla      235.6024098         425.3446517         417.5429986        404.6335386   7.8324789
Toyota Corona       176.6305359         368.3195488         360.0267515        346.5724649  52.8798281
Dodge Challenger     51.8012606         163.6314881         156.2805020        145.9194779 254.2367888
AMC Javelin          41.1929050         176.8610896         169.0925457        157.8097554 241.1203621
Camaro Z28           98.7035830         128.4587210         114.0932078         91.2880886 325.6636235
Pontiac Firebird    124.3726128          78.5385347          72.6947903         68.2030747 339.5857659
> distance_mat
                    Mazda RX4 Mazda RX4 Wag  Datsun 710 Hornet 4 Drive Hornet Sportabout     Valiant
Mazda RX4 Wag        0.6153251
Datsun 710          54.9086059    54.8915169
Hornet 4 Drive      98.1125212    98.0958939 150.9935191
Hornet Sportabout  210.3374396   210.3358546 265.0831615    121.0297564
Valiant             65.4717710    65.4392224 117.7547018     33.5508692       152.1241352
Duster 360         241.4076490   241.4088680 294.4790230    169.4299647        70.1767262 194.6094525
Merc 240D           50.1532711    50.1146059  49.6584796    121.2739722       241.5069657  89.5911056
Merc 230            25.4683117    25.3284509  33.1803843    118.2433145       233.4924012  85.0079649
Merc 280            15.3641921    15.2956865  66.9363534     91.4224033       199.3344960  60.2909811
Merc 280C           15.6724727    15.5837744  67.0261397     91.4612914       199.3406564  60.2655656
Merc 450SE         135.4307018   135.4254826 189.1954941     72.4964325        84.3888482  90.6970264
Merc 450SL         135.4014424   135.3960351 189.1631745     72.4313532        84.3683999  90.6769728
Merc 450SLC        135.4794674   135.4723157 189.2345426     72.5718466        84.4332423  90.7092989
Cadillac Fleetwood 326.3395903   326.3355070 381.0926242    234.4403876       116.2804201 266.6280942
Lincoln Continental 318.0469808   318.0429333 372.8012090    227.9726091       108.0624299 259.6304391
Chrysler Imperial  304.7203408   304.7169175 359.3014906    218.1548299        97.2049146 248.7713290
Fiat 128            93.2679950    93.2530993  40.9933763    184.9689734       302.0377212 152.1153263
Honda Civic        102.8307567   102.8238713  52.7704607    191.5518700       310.0324645 158.9615769
Toyota Corolla     100.6040368   100.5887588  47.6535017    192.6714187       309.5581776 159.8302995
Toyota Corona       42.3075233    42.2659224  12.9654743    138.5304725       252.3331988 105.2876428
Dodge Challenger   163.1150750   163.1134210 217.7795805     72.4403915        48.9838851 103.4310693
AMC Javelin        149.6047203   149.6014522 204.3188913     61.3601899        61.4274240  91.0444349
Camaro Z28         233.2228758   233.2248748 286.0049209    163.6632641        70.9665308 187.8463771
Pontiac Firebird   248.6780270   248.6762035 303.3583889    156.2240346        40.0052475 188.5272116
Fiat X1-9           92.5048389    92.4940020  39.8815148    184.4471198       301.5669483 151.4379425
Porsche 914-2       44.4033659    44.4073589  13.1357109    139.1579524       254.1452553 106.0585767
Lotus Europa        65.7328377    65.7362635  25.0948550    163.2367437       272.3582423 130.8248192
Ford Pantera L     245.4247064   245.4293785 297.2940489    180.1140339        89.5934049 203.0177926
Ferrari Dino        66.7661029    66.7764167  90.2415509    130.5523007       215.0673853 106.5694802
Maserati Bora      265.6454248   265.6491465 309.7718171    229.3419352       170.7094473 242.4393015
Volvo 142E          39.1894029    39.1626037  20.6939436    137.0363299       248.0063378 104.1863681
                    Duster 360   Merc 240D    Merc 230    Merc 280   Merc 280C  Merc 450SE  Merc 450SL
Mazda RX4 Wag
Datsun 710
Hornet 4 Drive
Hornet Sportabout
Valiant
Duster 360
Merc 240D          281.2962502
Merc 230           265.8823313  33.6873047
Merc 280           227.8998521  64.7754228  39.2994160
```

OUTPUT:

```
Fiat X1-9           227.8176554        417.2490481         409.4998363       396.7597522   5.1473415
Porsche 914-2       179.5720446        370.0956775         362.0145494       348.8466861  49.0644372
Lotus Europa        193.3969216        388.5350012         379.4716659       364.5994326  49.9112509
Ford Pantera L      112.8332602        134.8119464         119.7236456        95.3805385 337.1639236
Ferrari Dino        131.0704490        328.5441628         317.7063117       300.1640703 128.3950054
Maserati Bora       157.1683970        214.9366858         199.3420611       174.2936864 349.5338830
Volvo 142E          170.4843735        364.1000930         355.4009443       341.2896659  61.3301247
                    Honda Civic Toyota Corolla Toyota Corona Dodge Challenger AMC Javelin  Camaro Z28
Mazda RX4 Wag
Datsun 710
Hornet 4 Drive
Hornet Sportabout
Valiant
Duster 360
Merc 240D
Merc 230
Merc 280
Merc 280C
Merc 450SE
Merc 450SL
Merc 450SLC
Cadillac Fleetwood
Lincoln Continental
Chrysler Imperial
Fiat 128
Honda Civic
Toyota Corolla       14.3480626
Toyota Corona        63.8985563     59.8451285
Dodge Challenger    261.8498815    261.8345312   205.0347927
AMC Javelin         248.9636504    248.6917065   191.5580526       14.0154995
Camaro Z28          335.8883188    332.6589699   273.6316895      100.3046106 105.6062618
Pontiac Firebird    347.0655360    347.1667643   290.6240706       85.8075196  99.2836114  86.2665759
Fiat X1-9            14.7807070     10.3922856    51.8411748      253.6624046 240.5266823 325.1490914
Porsche 914-2        59.4588768     56.3243031     8.6535903      206.6452569 193.3080584 276.8924414
Lotus Europa         64.0495153     53.8846563    31.2536926      226.5004836 212.7568765 287.6179004
Ford Pantera L      347.8337714    343.9920962   285.1287911      118.7516779 123.3832044  19.3589023
Ferrari Dino        141.7044478    133.4707617    82.2355734      174.9280395 161.1060307 216.7489910
Maserati Bora       362.1620777    355.2601619   299.1865216      185.9059273 185.1553411 102.5946154
Volvo 142E           73.3766041     67.7189421    12.2505275      201.3682522 187.6978440 266.5277736
                    Pontiac Firebird   Fiat X1-9 Porsche 914-2 Lotus Europa Ford Pantera L Ferrari Dino
Mazda RX4 Wag
Datsun 710
Hornet 4 Drive
Hornet Sportabout
Valiant
Duster 360
Merc 240D
Merc 230
Merc 280
Merc 280C
Merc 450SE
Merc 450SL
Merc 450SLC
Cadillac Fleetwood
Lincoln Continental
Chrysler Imperial
Fiat 128
Honda Civic
Toyota Corolla
Toyota Corona
Dodge Challenger
AMC Javelin
Camaro Z28
Pontiac Firebird
Fiat X1-9               339.1396182
Porsche 914-2           292.1646488  48.3775209
Lotus Europa            311.3862342  49.8406880    33.7678653
Ford Pantera L          101.7389686 336.7018783   288.5852993  297.5376920
Ferrari Dino            255.0570519 127.8210813    87.9105966   80.4553451    224.4587490
Maserati Bora           188.3240020 349.1199576   303.9222549  303.2796468     86.9383253  223.5342175
Volvo 142E              286.7497823  60.4120429    18.7555858   27.8104457    277.4803312   70.4751034
                    Maserati Bora
Mazda RX4 Wag
Datsun 710
Hornet 4 Drive
Hornet Sportabout
Valiant
Duster 360
Merc 240D
Merc 230
Merc 280
Merc 280C
Merc 450SE
Merc 450SL
Merc 450SLC
Cadillac Fleetwood
Lincoln Continental
Chrysler Imperial
Fiat 128
Honda Civic
Toyota Corolla
Toyota Corona
Dodge Challenger
AMC Javelin
```

OUTPUT:

```
Camaro Z28
Pontiac Firebird
Fiat X1-9
Porsche 914-2
Lotus Europa
Ford Pantera L
Ferrari Dino
Maserati Bora
Volvo 142E              289.1157363
```

CODE:

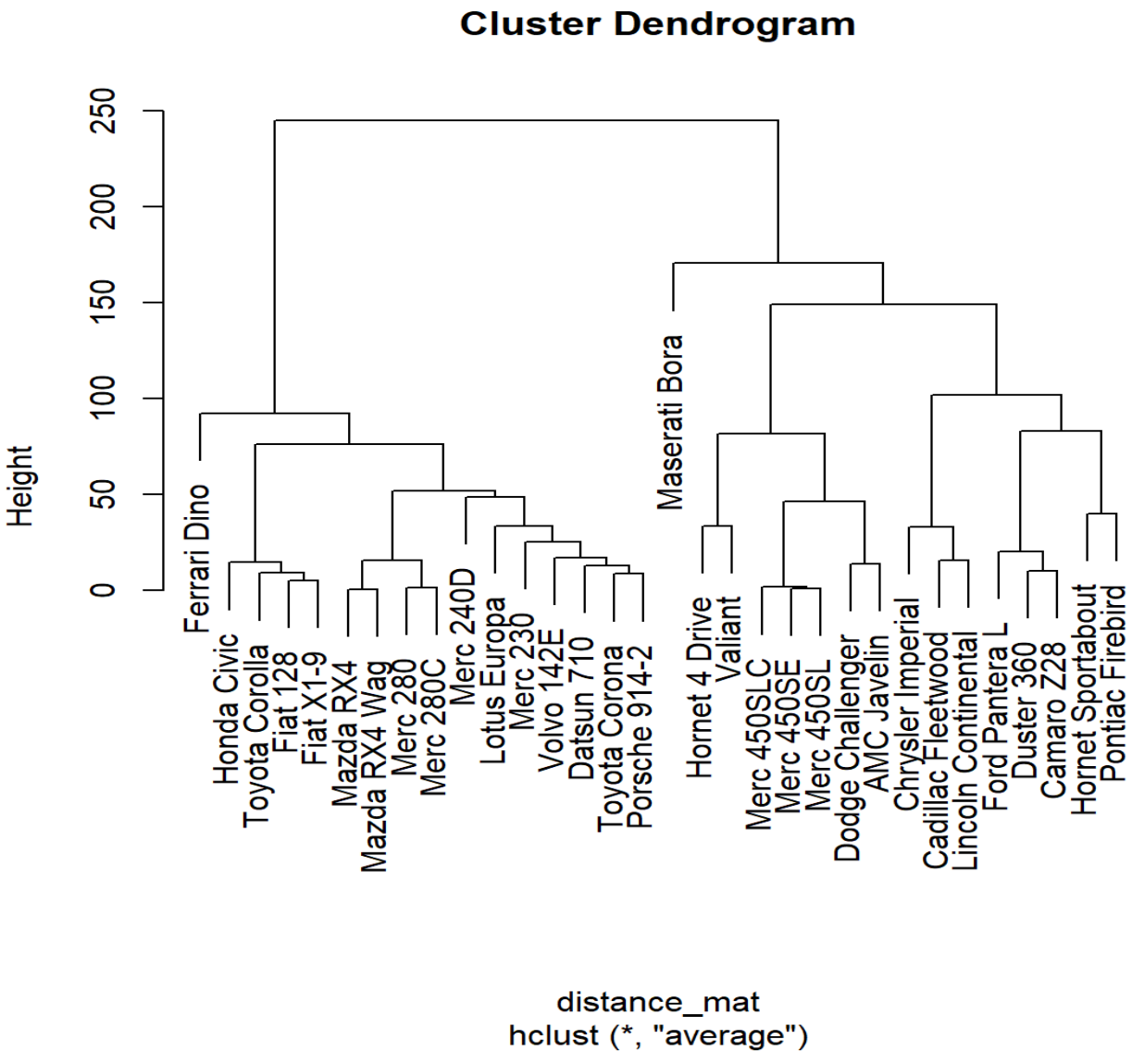
#fitting the hierarchical clustering model to the training data

```
Hierar_cl<-hclust(distance_mat,method="average")
```

#plotting the dendrogram

```
plot(Hierar_cl)
```

OUTPUT:



CODE:

#choosing the number of clusters (cut by the number of clustering)

num_clusters<-3 **#change this to the desired number of clusters**

fit<-cutree(Hierar_cl,k=num_clusters)

fit

#display the count of datapoints in each cluster

table(fit)

OUTPUT:

```
> fit
          Mazda RX4       Mazda RX4 Wag          Datsun 710      Hornet 4 Drive   Hornet Sportabout
                  1                   1                   1                   2                   2
            Valiant          Duster 360           Merc 240D            Merc 230            Merc 280
                  2                   2                   1                   1                   1
          Merc 280C          Merc 450SE          Merc 450SL         Merc 450SLC  Cadillac Fleetwood
                  1                   2                   2                   2                   2
Lincoln Continental   Chrysler Imperial            Fiat 128         Honda Civic      Toyota Corolla
                  2                   2                   1                   1                   1
      Toyota Corona    Dodge Challenger         AMC Javelin          Camaro Z28    Pontiac Firebird
                  1                   2                   2                   2                   2
          Fiat X1-9       Porsche 914-2        Lotus Europa      Ford Pantera L         Ferrari Dino
                  1                   1                   1                   2                   1
      Maserati Bora          Volvo 142E
                  3                   1
>
> #display the count of datapoints in each cluster
> table(fit)
fit
 1  2  3
16 15  1
```

CODE:

#highlight clusters on the dendrogram

rect.hclust(Hierar_cl,k=num_clusters,border="green")

#create a dataframe with cluster assignments

clustered_data<-data.frame(mtcars,Cluster=factor(fit))

#define the custom cluster colors

custom_colors<-c("red","pink","lavender")

#create a scatterplot with custom colors

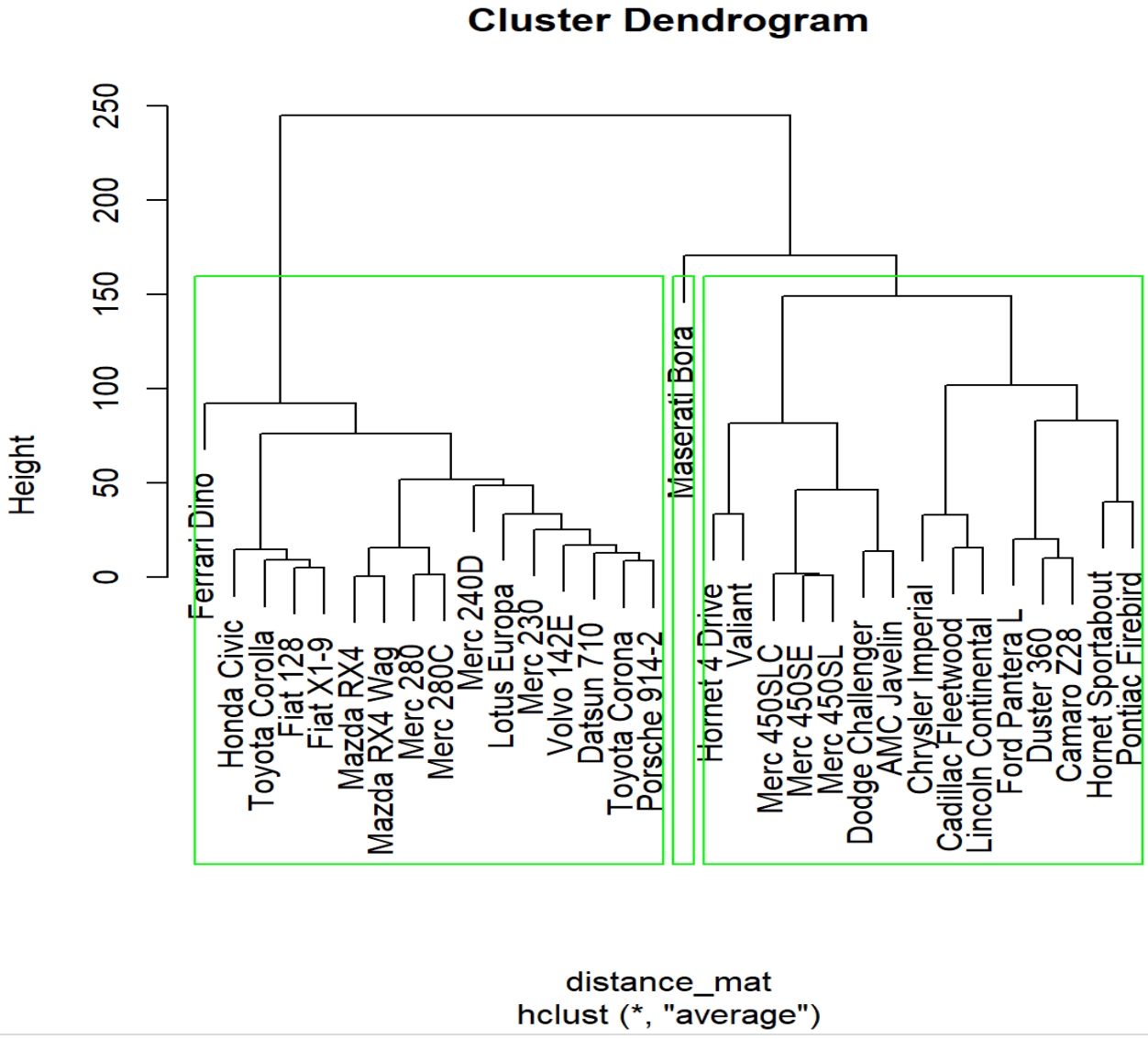
scatterplot<-ggplot(clustered_data,aes(x=mpg,

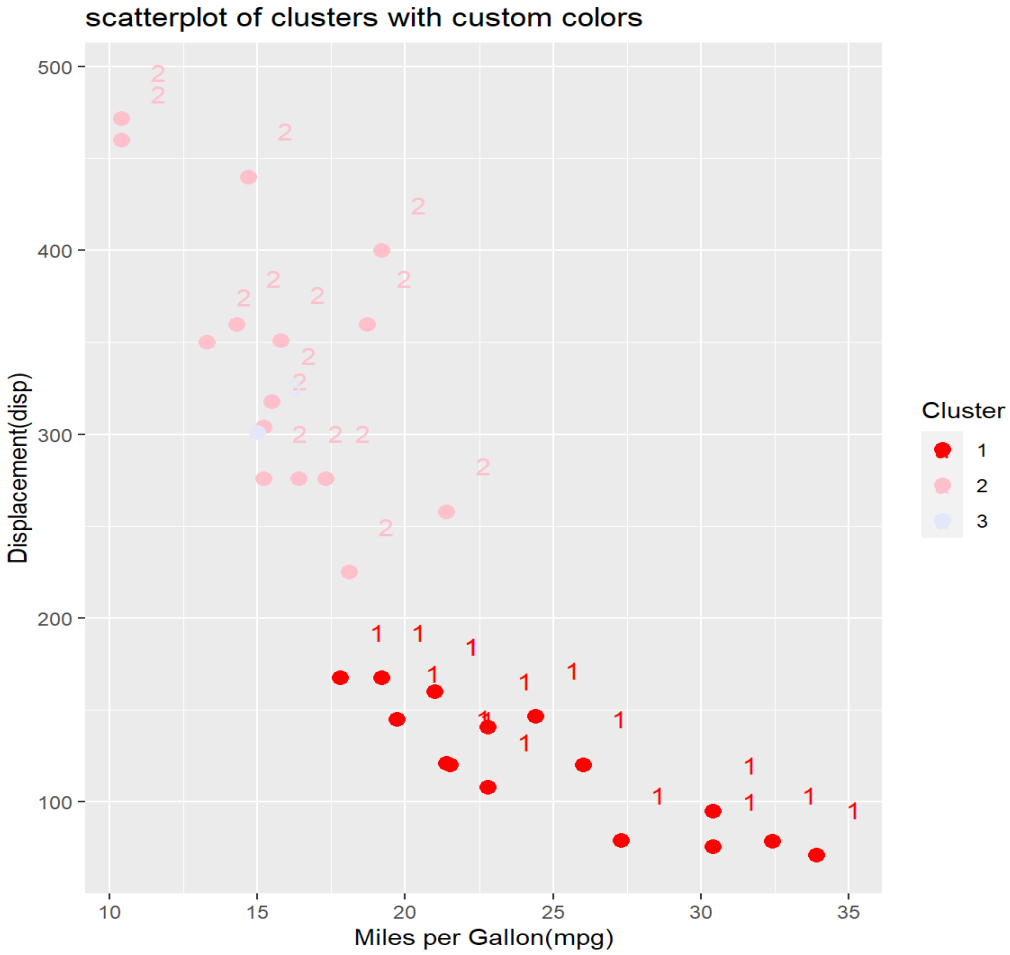
```
                    y=disp,
                    color=Cluster))+
  geom_point(size=3)+
  geom_text(aes(label=Cluster),hjust=0,vjust=0,
            nudge_x=1,nudge_y=20,size=4)+
  labs(x="Miles per Gallon(mpg)",y="Displacement(disp)",
       title="scatterplot of clusters with custom colors")+
  scale_color_manual(values=custom_colors,name='Cluster')
```

#display scatter plot

scatterplot

OUTPUT:





CODE:

 # Calculate the mean mpg for each cluster

```
cluster_means <- clustered_data %>%
  group_by(Cluster) %>%
  summarise(mean_mpg = mean(mpg))
```

 # Create bar graphs for "mpg" variable within each cluster

```
bar_graph <- ggplot(cluster_means, aes(x = Cluster, y = mean_mpg, fill = Cluster)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = round(mean_mpg, 2), y = mean_mpg + 0.5), vjust = -0.5, position = position_dodge(width = 0.9)) +
  labs(x = "Cluster", y = "Miles per Gallon (mpg)", title = "Bar Graphs of miles per gallon (mpg) by Cluster") +
  scale_fill_manual(values = custom_colors, name = "Cluster") +
  theme_minimal()
```

#display barplot

print(bar_graph)

OUTPUT: