



**RAJALAKSHMI**  
**ENGINEERING COLLEGE**  
An AUTONOMOUS Institution  
Affiliated to ANNA UNIVERSITY, Chennai

## **DEPARTMENT OF ARTIFICIAL INTELLIGENCE AND DATA SCIENCE LAB MANUAL**

**AD23431 - STATISTICAL ANALYSIS AND COMPUTING**

**(REGULATION 2023)**

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**Aim:**

To Implement Simple Programs using R.

**Algorithm:****1. Basic Arithmetic Operations****a. Finding Area of Circle**

- Input: Read radius r.
- Process: Calculate the area using the formula:  
$$\text{Area} = \pi \times r^2$$
- Output: Print the calculated area.

**2. Control Structures (if-else, for loop)****a. Check Whether the Given Year is Leap or Not**

- Input: Read a year ly.
- Process:
  - If ly is divisible by 400, it's a leap year.
  - Else, if divisible by 100 (but not by 400), it's not a leap year.
  - Else, if divisible by 4, it's a leap year.
  - Otherwise, it's not a leap year.
- Output: Print whether the year is a leap year or not.

**b. Reverse a Given Number**

- Input: Read a number num.
- Process:
  - Initialize rev = 0.
  - While num > 0:
    - Extract last digit: ld = num % 10.
    - Update rev = rev \* 10 + ld.
    - Remove last digit: num = num // 10.
- Output: Print the reversed number.

**c. Finding Prime Numbers for the Given Range**

- Input: Read the number n (upper limit).
- Process:
  - For each number i from 1 to n, check if it's prime:
    - If divisible by any number from 2 to  $\sqrt{i}$ , it's not prime.
    - If no divisors found, it is prime.
- Output: Print all prime numbers from 1 to n.

### 3. Functions and Recursive Functions

#### a. Print the Fibonacci Sequence using Functions (Iterative)

- Input: Read n (number of terms in the sequence).
- Process:
  - Initialize first two terms:  $a = 0$ ,  $b = 1$ .
  - Print a and b.
  - Loop (n-2) times:
    - Calculate next term  $c = a + b$ .
    - Update  $a = b$ ,  $b = c$ .
  - Print the sequence of n terms.

#### b. Print the Fibonacci Sequence using Recursive Functions

- Input: Read n (number of terms in the sequence).
- Process:
  - Define a recursive function fibo(n):
    - If  $n == 0$ , return 0 (base case).
    - If  $n == 1$ , return 1 (base case).
    - Else, return  $\text{fibo}(n-1) + \text{fibo}(n-2)$ .
  - Call fibo(i) for each i from 0 to n-1 and print the sequence.

### Programs:

#### 1. Basic Arithmetic Operations

##### a. Finding Area of Circle

```
r=as.integer(readline(("Enter the radius: ")))
area=pi*r*r
print(area)
```

#### Output:

```
> r=as.integer(readline(("Enter the radius: ")))
Enter the radius: 10
> area=pi*r*r
> print(area)
[1] 314.1593
```

#### 2. Control Structure (if-else, for loop)

##### a. To Check Whether the Given Year is Leap or Not

```
ly=as.integer(readline(("Enter a Number: ")))
if(ly%%400==0){
  print("Leap Year")
}else if(ly%%100==0){
  print("Not a Leap Year")
}else if(ly%%4==0){
  print("Leap Year")
}else{
  print("Not a Leap Year")
}
```

```
}
```

**Output:**

```
> ly=as.integer(readline("Enter a Number: "))
Enter a Number: 2000
> if(ly%%400==0){
+   print("Leap Year")
+ }else if(ly%%100==0){
+   print("Not a Leap Year")
+ }else if(ly%%4==0){
+   print("Leap Year")
+ }else{
+   print("Not a Leap Year")
+ }
[1] "Leap Year"
> ly=as.integer(readline("Enter a Number: "))
Enter a Number: 1300
> if(ly%%400==0){
+   print("Leap Year")
+ }else if(ly%%100==0){
+   print("Not a Leap Year")
+ }else if(ly%%4==0){
+   print("Leap Year")
+ }else{
+   print("Not a Leap Year")
+ }
[1] "Not a Leap Year"
```

**b. Reverse a Given Number**

```
num=as.integer(readline("Enter a number: "))
rev=0
while(num>0){
  ld=num%%10
  rev=rev*10+ld
  num=num%/10
}
cat("Reversed NUmber",rev)
```

**Output:**

```
> num=as.integer(readline("Enter a number: "))
Enter a number: 79
> rev=0
> while(num>0){
+   ld=num%%10
+   rev=rev*10+ld
+   num=num%/10
+ }
> cat("Reversed NUmber",rev)
Reversed NUmber 97
```

**c. Finding Prime Numbers for the Given Range**

```
prime<-function(n){
  if(n<=1){
    return (FALSE)}
  for (i in 2:sqrt(n)){
```

```

        if(n%%i==0){
            return (FALSE)
        }
    }
    return (TRUE)
}

n=as.integer(readline("Enter a number: "))
for (i in 1:n){
    if(prime(i)){
        print(i)
    }
}

```

### Output:

```

> prime<-function(n){
+   if(n<=1){
+     return (FALSE)}
+   for (i in 2:sqrt(n)){
+     if(n%%i==0){
+       return (FALSE)
+     }
+   }
+   return (TRUE)
+ }
> n=as.integer(readline("Enter a number: "))
Enter a number: 10
> for (i in 1:n){
+   if(prime(i)){
+     print(i)
+   }
+ }
[1] 3
[1] 5
[1] 7
> |

```

## 3. Functions and Recursive Functions

### a. Print the Fibonacci Sequence using Functions

```

fibonacci_iterative <- function(n) {
    fib_series <- numeric(n)
    fib_series[1] <- 0
    if (n > 1) fib_series[2] <- 1

    for (i in 3:n) {
        fib_series[i] <- fib_series[i-1] + fib_series[i-2]
    }

    return(fib_series)
}

n <- as.integer(readline("How many terms? "))
print(fibonacci_iterative(n))

```

**Output:**

```
> fibonacci_iterative <- function(n) {
+   fib_series <- numeric(n)
+   fib_series[1] <- 0
+   if (n > 1) fib_series[2] <- 1
+
+   for (i in 3:n) {
+     fib_series[i] <- fib_series[i-1] + fib_series[i-2]
+   }
+   return(fib_series)
+ }
> n <- as.integer(readline("How many terms? "))
How many terms? 10
> print(fibonacci_iterative(n))
[1] 0 1 1 2 3 5 8 13 21 34
> |
```

**b. Print the Fibonacci Sequence using Recursive Functions**

```
fibonacci_recursive <- function(n) {
  if (n == 1) {
    return(0)
  } else if (n == 2) {
    return(1)
  } else {
    return(fibonacci_recursive(n-1) + fibonacci_recursive(n-2))
  }
}
```

```
n <- as.integer(readline("How many terms? "))
fib_series <- sapply(1:n, fibonacci_recursive)
print(fib_series)
```

**Output:**

```
> fibonacci_recursive <- function(n) {
+   if (n == 1) {
+     return(0)
+   } else if (n == 2) {
+     return(1)
+   } else {
+     return(fibonacci_recursive(n-1) + fibonacci_recursive(n-2))
+   }
+ }
> n <- as.integer(readline("How many terms? "))
How many terms? 10
> fib_series <- sapply(1:n, fibonacci_recursive)
> print(fib_series)
[1] 0 1 1 2 3 5 8 13 21 34
```

**Result:**

The Simple Program using R is Successfully Implemented.



**Aim:**

To Perform Preprocessing of data using R.

**Algorithm:****1. Loading Data / Cleaning the Data:**

- Create emp\_df2 with columns: emp\_id, age, dept, salary, experience.

**2. Storing / Uploading Data to Excel Sheet:**

- Create a workbook wb, add a worksheet "Employee Data Preprocessing", and save emp\_df2 to emp\_df2.xlsx.

**3. Cleaning the Data:**

- Replace missing age and salary with their respective mean values.
- Convert dept to numeric.

**4. Scaling the Data:**

- Scale the age, salary, and experience columns using z-score and update emp\_df2.

**5. Splitting the Data into Train and Test:**

- Set seed, split data into 80% train and 20% test (dataTrain, dataTest).

**6. Correlation Matrix:S**

- Compute the correlation matrix for the scaled features (age, salary, experience) to examine relationships between them.

**Programs:**

```
library(openxlsx)
```

```
emp_df2<-data.frame(  
  emp_id=1:10,  
  age=c(25,30,35,NA,55,65,NA,25,85,78),  
  dept=c("AI&DS","IT","AI&ML","CSE","PHY","FT","BIOTECH","CSBS","CIVIL","MECH"),  
  salary=c(50000,85100,52802,144510,552410,520000,445100,5552410,524160,NA),  
  experience=c(2,5,8,14,4,6,3,2,4,5)  
)
```

```
wb<-createWorkbook()
```

```
addWorksheet(wb,"Employee Data Preprocessing")
```

```
writeData(wb,"Employee Data Preprocessing",emp_df2)
```

```
saveWorkbook(wb,"C:\\Users\\karthick.S\\OneDrive\\Documents\\231801079-  
4\\SAC\\emp_df2.xlsx",overwrite = TRUE)
```

```

emp_df2$age[is.na(emp_df2$age)]<-floor(mean(emp_df2$age,na.rm = TRUE))

emp_df2$salary[is.na(emp_df2$salary)]<-floor(mean(emp_df2$salary,na.rm = TRUE))

emp_df2$dept<-as.numeric(as.factor(emp_df2$dept))

emp_df_scaled<-scale(emp_df2[,c("age","salary","experience")])
emp_df2<-data.frame(emp_df2[,c("emp_id","dept")],emp_df_scaled)

correlation_matrix <- cor(emp_df2[, c("age", "salary", "experience")])
print("Correlation Matrix:")
print(correlation_matrix)

set.seed(42)
trainIndex<-sample(1:nrow(emp_df2),0.8*nrow(emp_df2))
dataTrain<-emp_df2[trainIndex,]
dataTest<-emp_df2[-trainIndex,]

print(dataTrain)
print(dataTest)

```

### Output:

```

> print("First Few Row of Dataset")
[1] "First Few Row of Dataset"
> head(emp_df2)
  emp_id age  dept salary experience
1      1  25 AI&DS  50000           2
2      2  30   IT   85100           5
3      3  35 AI&ML   52802           8
4      4  NA   CSE 144510          14
5      5  55  PHY 552410           4
6      6  65   FT 520000           6

> print("Correlation Matrix:")
[1] "Correlation Matrix:"
> print(correlation_matrix)
              age      salary experience
age          1.0000000 -0.2680396  0.1080326
salary       -0.2680396  1.0000000 -0.3644421
experience    0.1080326 -0.3644421  1.0000000

```

```

> print(dataTrain)
  emp_id dept      age      salary  experience
1      1   1 -1.14775744 -4.991315e-01 -0.92681355
5      5  10  0.25194675 -1.972629e-01 -0.36510837
10     10   9  1.32505330 -1.802523e-07 -0.08425578
8      8   5 -1.14775744  2.806943e+00 -0.92681355
2      2   8 -0.91447341 -4.780420e-01 -0.08425578
4      4   6 -0.02799408 -4.423460e-01  2.44341753
6      6   7  0.71851482 -2.167362e-01  0.19659681
9      9   4  1.65165095 -2.142367e-01 -0.36510837
>
> print(dataTest)
  emp_id dept      age      salary  experience
3      3   2 -0.68118937 -0.4974480   0.758302
7      7   3 -0.02799408 -0.2617392  -0.645961

```

### Result:

Thus, Preprocessing data is cleaned, transformed and formatted dataset ready for analysis or modelling.

**EXP NO: 3**

## **PERFORM STATISTICAL ANALYSIS FOR A GIVEN DATASET**

**Aim:**

To Perform Statistical Analysis for Given Dataset.

**Algorithm:**

**1. Loading Libraries:**

- Load the necessary libraries: dplyr, summarytools, psych.

**2. Loading Data:**

- Create a dataset data with columns Age and Salary.

**3. Statistical Analysis:**

- Mean: Calculate the mean of Age.
- Median: Calculate the median of Age.
- Mode: Calculate the mode of Age using the table function.
- Variance: Calculate the variance of Age.
- Standard Deviation: Calculate the standard deviation of Age.
- Correlation: Calculate the correlation between Age and Salary.

**4. Descriptive Statistics:**

- Use the summary() function to generate summary statistics for the dataset.

**5. Quantile Analysis:**

- Calculate the quantiles for both Age and Salary.

**6. Interquartile Range (IQR):**

- Calculate the IQR for both Age and Salary.

**7. Hypothesis Testing (T-Test):**

- Perform a one-sample t-test on Salary with a hypothesized mean of 70,000.

**8. Visualization:**

- Boxplot: Create a boxplot for Age and Salary to visualize their distributions.

**9. Detailed Descriptive Statistics:**

- Use describe() from the psych package to get detailed statistics for Age and Salary.
- Use descr() from the summarytools package for detailed descriptive statistics.

**Program:**

```
library(dplyr)
```

```
library(summarytools)
```

```
library(psych)
```

```
data <- data.frame(Age = c(25, 30, 28, 35, 40, 45, 50, 32, 38, 42),
```

```
Salary = c(50000, 60000, 55000, 75000, 80000, 85000, 90000, 65000, 78000, 82000))
```

```
cat("Dataset:\n")
```

```

print(data)

mean_age <- mean(data$Age)
median_age <- median(data$Age)
mode_age <- as.numeric(names(sort(table(data$Age), decreasing = TRUE))[1])

var_age <- var(data$Age)
sd_age <- sd(data$Age)

corr <- cor(data$Age, data$Salary)

cat("\nStatistical Analysis Results:\n")
print(mean_age)
print(median_age)
print(mode_age)
print(var_age)
print(sd_age)
print(corr)

data_summary <- summary(data)
print(data_summary)

quantile_age <- quantile(data$Age)
quantile_salary <- quantile(data$Salary)

IQR_age <- IQR(data$Age)
IQR_salary <- IQR(data$Salary)

cat("Quantile Age", quantile_age)
cat("\nQuantile Salary", quantile_salary)

cat("\nIQR Age", IQR_age)
cat("\nIQR Salary", IQR_salary)

t_test_result <- t.test(data$Salary, mu = 70000)
print(t_test_result)

boxplot(data$Age, main = "Boxplot of Age", ylab = "Age", col = "lightblue")
boxplot(data$Salary, main = "Boxplot of Salary", ylab = "Salary", col = "lightgreen")

cat("\nDescribe Method From Describe of psych")
descr_stats <- describe(data[, c("Age", "Salary")])
print("Detailed Descriptive Statistics:")
print(descr_stats)
cat("\nDescribe Method From Descr of SummaryTools")
print(descr(data))

```

### Output:

```
> cat("Dataset:\n")
Dataset:
> print(data)
  Age Salary
1   25  50000
2   30  60000
3   28  55000
4   35  75000
5   40  80000
6   45  85000
7   50  90000
8   32  65000
9   38  78000
10  42  82000
>

> cat("\nStatistical Analysis Results:\n")

Statistical Analysis Results:
> print(mean_age)
[1] 36.5
> print(median_age)
[1] 36.5
> print(mode_age)
[1] 25
> print(var_age)
[1] 63.16667
> print(sd_age)
[1] 7.947746
> print(corr)
[1] 0.9735205

> print(data_summary)
      Age      Salary
Min.   :25.0   Min.   :50000
1st Qu.:30.5   1st Qu.:61250
Median :36.5   Median :76500
Mean   :36.5   Mean   :72000
3rd Qu.:41.5   3rd Qu.:81500
Max.   :50.0   Max.   :90000

> cat("Quantile Age\n", quantile_age)
Quantile Age
 25 30.5 36.5 41.5 50> cat("Quantile Salary\n", quantile_salary)
Quantile Salary
50000 61250 76500 81500 90000>
> cat("IQR Age\n", IQR_age)
IQR Age
11> cat("IQR Salary\n", IQR_salary)
IQR Salary
20250>
```

```

> print(t_test_result)

One Sample t-test

data: data$Salary
t = 0.46457, df = 9, p-value = 0.6533
alternative hypothesis: true mean is not equal to 70000
95 percent confidence interval:
 62261.33 81738.67
sample estimates:
mean of x
 72000

> cat("\nDescribe Method From Describe of psych")

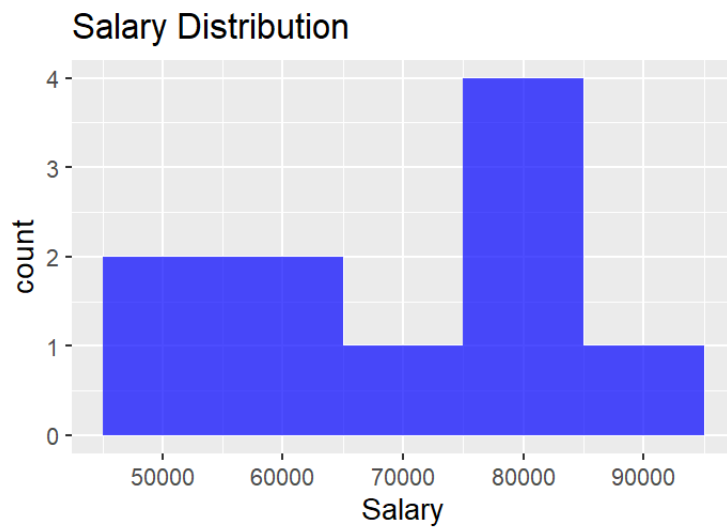
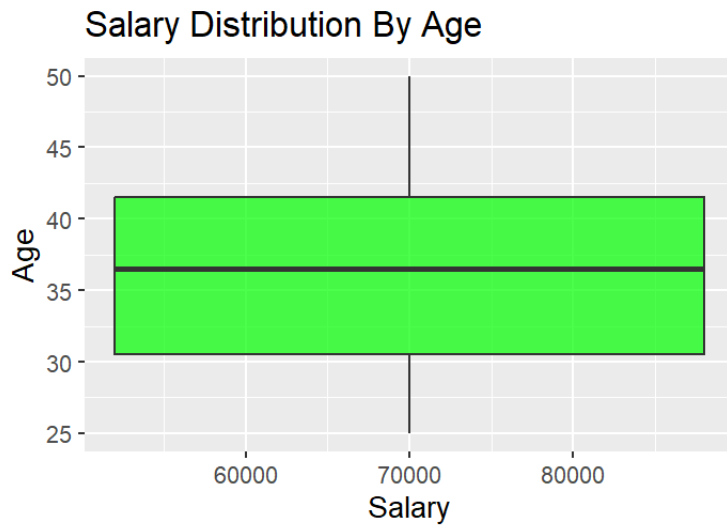
Describe Method From Describe of psych> descr_stats <- describe(data[,
ge", "Salary"))
> print("Detailed Descriptive Statistics:")
[1] "Detailed Descriptive Statistics:"
> print(descr_stats)
      vars  n   mean      sd median trimmed   mad   min   max
Age       1 10   36.5    7.95   36.5   36.25    8.9   25   50
Salary    2 10 72000.0 13613.72 76500.0 72500.00 14826.0 50000 90000
      range skew kurtosis      se
Age       25  0.16   -1.39    2.51
Salary 40000 -0.31   -1.57  4305.04

> cat("\nDescribe Method From Descr of SummaryTools")

Describe Method From Descr of SummaryTools> print(descr(data))
Descriptive Statistics
data
N: 10

-----
      Age      Salary
-----
Mean      36.50    72000.00
Std.Dev    7.95    13613.72
Min        25.00    50000.00
Q1         30.00    60000.00
Median     36.50    76500.00
Q3         42.00    82000.00
Max        50.00    90000.00
MAD        8.90    14826.00
IQR        11.00    20250.00
CV         0.22      0.19
Skewness   0.16     -0.31
SE.Skewness 0.69      0.69
Kurtosis  -1.39     -1.57
N.Valid    10.00    10.00
N          10.00    10.00
Pct.Valid  100.00   100.00

```



**Result:**

Thus, Statistical Analysis for a Given Dataset using is Analysed and Scaled.



**Aim:**

Implement a Decision Tree Classification on the Given Dataset.

**Procedure:****1. Load Required Libraries**

- Load the necessary libraries:
  - rpart for building decision tree models.
  - rpart.plot for visualizing decision trees.
  - caret for data splitting and model evaluation.

**Code:**

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

**2. Load the Dataset**

- Load the Iris dataset (built-in in R).
- Display the first few rows to understand the data structure.

**Code:**

```
data("iris")
print("First Few Rows of Dataset")
head(iris)
```

**3. Split the Data into Training and Testing Sets**

- Set a seed for reproducibility.
- Use createDataPartition to split the data into:
  - 80% training set
  - 20% testing set

**Code:**

```
set.seed(123)
train_index <- createDataPartition(iris$Species, p = 0.8, list = FALSE)
train_data <- iris[train_index, ]
test_data <- iris[-train_index, ]
```

**4. Train a Decision Tree Model**

- Build a decision tree classifier using rpart, predicting Species based on the features.

**Code:**

```
tree_model <- rpart(Species ~ ., data = train_data, method = "class")
print(tree_model)
```

## 5. Visualize the Decision Tree

- Plot the trained decision tree using `rpart.plot` with enhanced formatting.

**Code:**

```
rpart.plot(tree_model,
           main = "Decision Tree for Iris Dataset",
           type = 3,
           extra = 101,
           under = TRUE,
           tweak = 1.2,
           box.palette = "RdBu")
```

## 6. Make Predictions on Test Data

- Use the trained model to predict the species on the test dataset.

**Code:**

```
pred <- predict(tree_model, test_data, type = "class")
```

## 7. Evaluate Model Performance

- Create a confusion matrix to compare predicted vs actual labels.
- Print evaluation metrics like accuracy, sensitivity, specificity, etc.

**Code:**

```
conf_mat <- confusionMatrix(pred, test_data$Species)
print(conf_mat)
```

**Output:**

```
> print("First Few Row of Dataset")
[1] "First Few Row of Dataset"
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1           5.1          3.5          1.4          0.2  setosa
2           4.9          3.0          1.4          0.2  setosa
3           4.7          3.2          1.3          0.2  setosa
4           4.6          3.1          1.5          0.2  setosa
5           5.0          3.6          1.4          0.2  setosa
6           5.4          3.9          1.7          0.4  setosa

> print(tree_model)
n= 120

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

1) root 120 80 setosa (0.33333333 0.33333333 0.33333333)
2) Petal.Length< 2.45 40 0 setosa (1.00000000 0.00000000 0.00000000) *
3) Petal.Length>=2.45 80 40 versicolor (0.00000000 0.50000000 0.50000000)
   6) Petal.Width< 1.75 42 3 versicolor (0.00000000 0.92857143 0.07142857) *
   7) Petal.Width>=1.75 38 1 virginica (0.00000000 0.02631579 0.97368421) *
```

```
> print(conf_mat)
```

Confusion Matrix and Statistics

Prediction	Reference		
	setosa	versicolor	virginica
setosa	10	0	0
versicolor	0	10	2
virginica	0	0	8

Overall Statistics

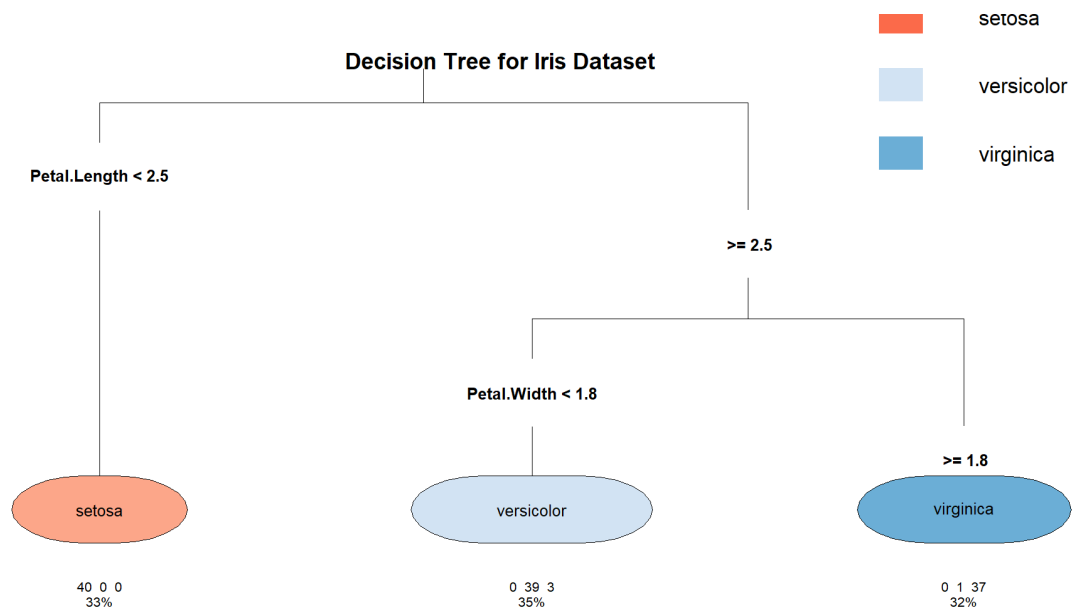
Accuracy : 0.9333  
95% CI : (0.7793, 0.9918)  
No Information Rate : 0.3333  
P-Value [Acc > NIR] : 8.747e-12

Kappa : 0.9

McNemar's Test P-Value : NA

Statistics by Class:

	Class: setosa	Class: versicolor	Class: virginica
Sensitivity	1.0000	1.0000	0.8000
Specificity	1.0000	0.9000	1.0000
Pos Pred Value	1.0000	0.8333	1.0000
Neg Pred Value	1.0000	1.0000	0.9091
Prevalence	0.3333	0.3333	0.3333
Detection Rate	0.3333	0.3333	0.2667
Detection Prevalence	0.3333	0.4000	0.2667
Balanced Accuracy	1.0000	0.9500	0.9000



**Result:**

The Decision Tree is Implemented Successfully.

**EXP NO: 5**

## **IMPLEMENT K-NEAREST NEIGHBOR ALGORITHM IN R**

**Aim:**

Implement a KNN Classification on the Given Dataset.

**Procedure:**

**1. Load Required Libraries**

- Load the necessary libraries:
  - class for KNN model.
  - ggplot2 for plotting.
  - GGally for advanced plots (pairwise plots).
  - caret for data partitioning and evaluation.

**Code:**

```
library(class)
library(ggplot2)
library(GGally)
library(caret)
```

**2. Load the Dataset**

- Load the Iris dataset.
- Display the first few rows to understand the structure.

**Code:**

```
data("iris")
print("First Few Rows of Dataset")
head(iris)
```

**3. Define a Normalize Function**

- Create a custom function to normalize (scale between 0 and 1) the numerical feature columns.

**Code:**

```
normalize <- function(x) {
  return((x - min(x)) / (max(x) - min(x)))
}
```

**4. Normalize the Feature Columns**

- Apply the normalization function to the first four feature columns.
- Add back the Species column separately.

**Code:**

```
iris_norm <- as.data.frame(lapply(iris[1:4], normalize))
iris_norm$Species <- iris$Species
```

**5. Split the Data into Training and Testing Sets**

- Set a random seed for reproducibility.
- Use createDataPartition to split:
  - 80% for training
  - 20% for testing

**Code:**

```
set.seed(123)
train_index <- createDataPartition(iris$Species, p = 0.8, list = FALSE)
train_data <- iris_norm[train_index, ]
test_data <- iris_norm[-train_index, ]
```

**6. Extract Training and Test Labels**

- Separate the labels (Species) from the feature data for both train and test sets.

**Code:**

```
train_labels <- train_data$Species
test_labels <- test_data$Species
```

**7. Train the KNN Model**

- Train the K-Nearest Neighbors model using:
  - Normalized feature columns
  - k = 5 neighbors.

**Code:**

```
knn_model <- knn(train = train_data[, 1:4], test = test_data[, 1:4], cl = train_labels, k = 5)
print(knn_model)
```

**8. Visualize the Data**

- Create visualizations to understand feature distributions:
  - Scatter plot of Sepal Length vs Sepal Width.
  - Pairwise plots (all feature combinations).

**Code:**

```
ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width, color = Species)) +
  geom_point() +
  labs(title = "Scatter Plot of Sepal Dimensions", x = "Sepal Length", y = "Sepal Width") +
  theme_minimal()
ggpairs(iris, aes(color = Species)) +
  theme_minimal()
```

## 9. Evaluate Model Performance

- Generate a confusion matrix comparing predictions and true labels.
- Print classification results including accuracy, sensitivity, and specificity.

### Code:

```
conf_mat <- confusionMatrix(knn_model, test_labels)
print(conf_mat)
```

### Output:

```
> print("First Few Row of Dataset")
[1] "First Few Row of Dataset"
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4          0.2  setosa
2          4.9         3.0          1.4          0.2  setosa
3          4.7         3.2          1.3          0.2  setosa
4          4.6         3.1          1.5          0.2  setosa
5          5.0         3.6          1.4          0.2  setosa
6          5.4         3.9          1.7          0.4  setosa
>
> print(knn_model)
[1] setosa      setosa      setosa      setosa      setosa
[6] setosa      setosa      setosa      setosa      setosa
[11] versicolor versicolor versicolor versicolor versicolor
[16] versicolor versicolor versicolor versicolor versicolor
[21] virginica  virginica  virginica  virginica  virginica
[26] virginica  virginica  virginica  virginica  virginica
Levels: setosa versicolor virginica
> print(conf_mat)
Confusion Matrix and Statistics

          Reference
Prediction setosa versicolor virginica
setosa      10           0           0
versicolor   0          10           0
virginica    0           0          10

Overall Statistics

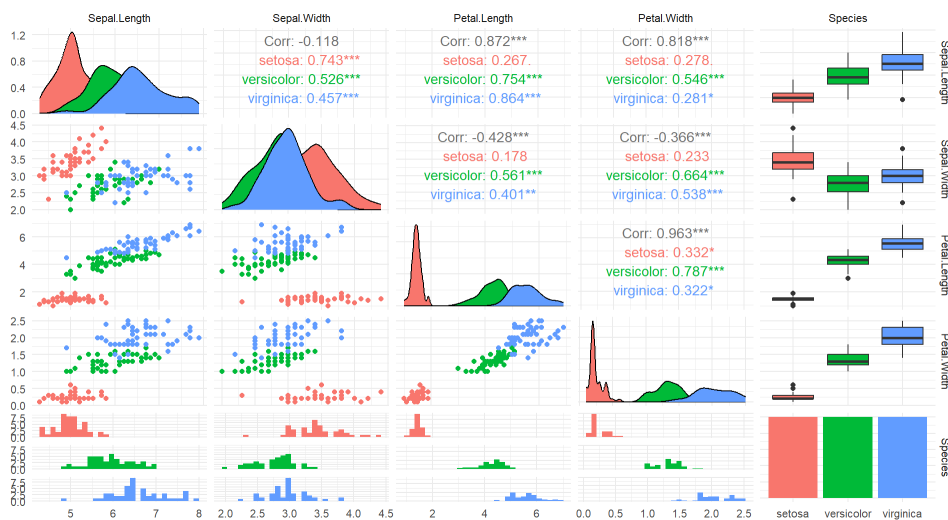
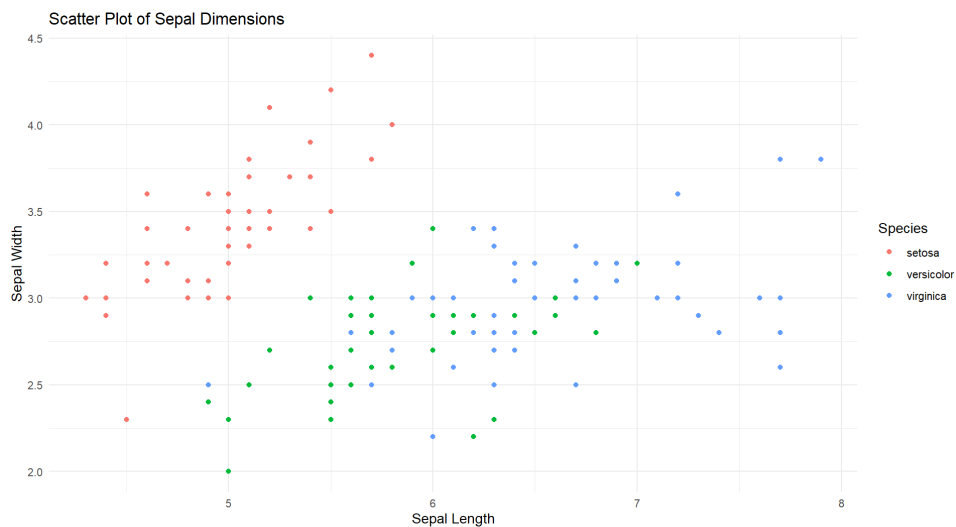
               Accuracy : 1
               95% CI : (0.8843, 1)
    No Information Rate : 0.3333
    P-Value [Acc > NIR] : 4.857e-15

               Kappa : 1

McNemar's Test P-Value : NA
```

## Statistics by Class:

	Class: setosa	Class: versicolor
Sensitivity	1.0000	1.0000
Specificity	1.0000	1.0000
Pos Pred Value	1.0000	1.0000
Neg Pred Value	1.0000	1.0000
Prevalence	0.3333	0.3333
Detection Rate	0.3333	0.3333
Detection Prevalence	0.3333	0.3333
Balanced Accuracy	1.0000	1.0000
	Class: virginica	
Sensitivity	1.0000	
Specificity	1.0000	
Pos Pred Value	1.0000	
Neg Pred Value	1.0000	
Prevalence	0.3333	
Detection Rate	0.3333	
Detection Prevalence	0.3333	
Balanced Accuracy	1.0000	





**Result:**

The KNN Classification is Successfully Implemented.

**Aim:**

Implement a Naïve Bayes Classification on the Given Dataset.

**Procedure:****1. Load Required Libraries**

- Load the necessary libraries:
  - e1071 for the Naive Bayes model.
  - ggplot2 for visualization.
  - caret for data partitioning and evaluation.

**Code:**

```
library(e1071)
library(ggplot2)
library(caret)
```

**2. Load the Dataset**

- Load the Iris dataset.
- Display the first few rows for a quick overview.

**Code:**

```
data("iris")
print("First Few Rows of Dataset")
head(iris)
```

**3. Split the Data into Training and Testing Sets**

- Set a random seed to ensure reproducibility.
- Split the data into:
  - 80% for training
  - 20% for testing

**Code:**

```
set.seed(123)
train_index <- createDataPartition(iris$Species, p = 0.8, list = FALSE)
train_data <- iris[train_index, ]
test_data <- iris[-train_index, ]
```

**4. Extract Training and Test Labels**

- Assign the Species column as the labels for training and testing.

**Code:**

```
train_labels <- train_data$Species
test_labels <- test_data$Species
```

## 5. Train the Naive Bayes Model

- Train the Naive Bayes classifier using the training data.

**Code:**

```
nb_model <- naiveBayes(Species ~ ., data = train_data)
print(nb_model)
```

## 6. Visualize the Data

- Create a scatter plot of Sepal Length vs Sepal Width colored by species.

**Code:**

```
ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width, color = Species)) +
  geom_point() +
  labs(title = "Scatter Plot of Sepal Dimensions", x = "Sepal Length", y = "Sepal
Width") +
  theme_minimal()
```

## 7. Make Predictions on the Test Data

- Predict the species for the test dataset using the trained model.

**Code:**

```
pred <- predict(nb_model, test_data)
```

## 8. Evaluate Model Performance

- Generate a confusion matrix to compare the predicted labels and true labels.
- Print evaluation metrics like accuracy, sensitivity, and specificity.

**Code:**

```
conf_mat <- confusionMatrix(pred, test_labels)
print(conf_mat)
```

**Output:**

```
> print("First Few Rows of Dataset")
[1] "First Few Rows of Dataset"
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1           5.1         3.5          1.4          0.2  setosa
2           4.9         3.0          1.4          0.2  setosa
3           4.7         3.2          1.3          0.2  setosa
4           4.6         3.1          1.5          0.2  setosa
5           5.0         3.6          1.4          0.2  setosa
6           5.4         3.9          1.7          0.4  setosa
```

```
> print(nb_model)
```

Naive Bayes Classifier for Discrete Predictors

Call:

```
naiveBayes.default(x = X, y = Y, laplace = laplace)
```

A-priori probabilities:

```
Y
  setosa versicolor virginica
0.3333333 0.3333333 0.3333333
```

Conditional probabilities:

```
      Sepal.Length
Y      [,1]      [,2]
setosa  4.9800 0.3567661
versicolor 5.9400 0.4903165
virginica 6.6375 0.6949221
```

```
      Sepal.Width
Y      [,1]      [,2]
setosa  3.3700 0.3450752
versicolor 2.7700 0.3267556
virginica 3.0125 0.3123012
```

```
      Petal.Length
Y      [,1]      [,2]
setosa  1.4650 0.1717930
versicolor 4.2325 0.4676112
virginica 5.6225 0.5775667
```

```
      Petal.Width
Y      [,1]      [,2]
setosa  0.2400 0.0928191
versicolor 1.3275 0.2087662
virginica 2.0700 0.2662176
```

```
> print(cont_mat)
```

Confusion Matrix and Statistics

```
      Reference
Prediction  setosa versicolor virginica
setosa      10         0         0
versicolor   0        10         2
virginica    0         0         8
```

Overall Statistics

```
Accuracy : 0.9333
95% CI : (0.7793, 0.9918)
No Information Rate : 0.3333
P-Value [Acc > NIR] : 8.747e-12
```

```
Kappa : 0.9
```

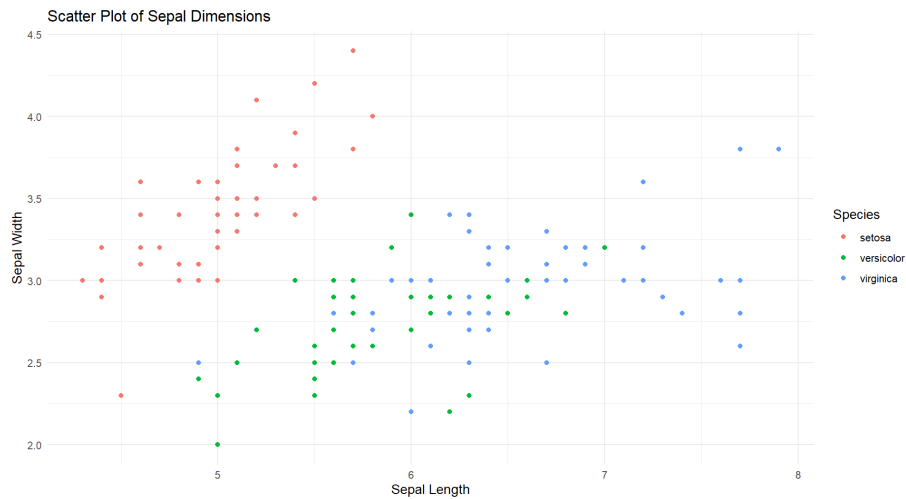
```
Mcnemar's Test P-Value : NA
```

### Statistics by Class:

	Class: setosa	Class: versicolor
Sensitivity	1.0000	1.0000
Specificity	1.0000	0.9000
Pos Pred Value	1.0000	0.8333
Neg Pred Value	1.0000	1.0000
Prevalence	0.3333	0.3333
Detection Rate	0.3333	0.3333
Detection Prevalence	0.3333	0.4000
Balanced Accuracy	1.0000	0.9500

	Class: virginica
Sensitivity	0.8000
Specificity	1.0000
Pos Pred Value	1.0000
Neg Pred Value	0.9091
Prevalence	0.3333
Detection Rate	0.2667
Detection Prevalence	0.2667
Balanced Accuracy	0.9000



### Result:

The Naïve Bayes Classification is Successfully Implemented.

**Aim:**

Implement a Linear Regression on the Given Dataset.

**Procedure:****1. Load Required Libraries**

- Load the necessary libraries:
  - ggplot2 for visualization.
  - caret for splitting the data and evaluating the model.

**Code:**

```
library(ggplot2)
library(caret)
```

**2. Load the Dataset**

- Load the Headbrain dataset from a CSV file.
- Display the first few rows to inspect the data.

**Code:**

```
df <- read.csv("C:/Users/karthick.S/OneDrive/Documents/231801079-4/SAC/headbrain.csv")
print("First Few Rows of Dataset")
head(df)
```

**3. Split the Data into Training and Testing Sets**

- Set a random seed for reproducibility.
- Split the data into:
  - 70% for training
  - 30% for testing

**Code:**

```
set.seed(123)
index <- createDataPartition(df$Brain.Weight.grams., p = 0.7, list = FALSE)
train <- df[index, ]
test <- df[-index, ]
```

**4. Train the Linear Regression Model**

- Train a linear regression model to predict Brain.Weight.grams. based on Head.Size.cm.3..

**Code:**

```
print("Linear Regression Model")
model <- lm(Brain.Weight.grams. ~ Head.Size.cm.3., data = train)
print(model)
```

## 5. Make Predictions on the Test Data

- Use the trained model to predict brain weight values for the test dataset.

**Code:**

```
pred <- predict(model, newdata = test)
```

## 6. Evaluate Model Performance

- Use postResample to calculate evaluation metrics:
  - RMSE (Root Mean Squared Error)
  - R-squared (Coefficient of Determination)
  - MAE (Mean Absolute Error)

**Code:**

```
evaluation <- postResample(pred, test$Brain.Weight.grams.)  
cat("RMSE:", evaluation["RMSE"], "\n")  
cat("R-squared:", evaluation["Rsquared"], "\n")  
cat("MAE:", evaluation["MAE"], "\n")
```

## 7. Visualize the Data

- Plot the scatter points of the original data.
- Overlay the regression line based on the model's predictions.

**Code:**

```
x_vals <- seq(min(df$Head.Size.cm.3.) - 100, max(df$Head.Size.cm.3.) + 100,  
length.out = 1000)  
pred_line <- data.frame(Head.Size.cm.3. = x_vals)  
pred_line$Brain.Weight.grams. <- predict(model, newdata = pred_line)  
  
plot(df$Head.Size.cm.3., df$Brain.Weight.grams.,  
col = "green", pch = 19,  
xlab = "Head Size (cm³)",  
ylab = "Brain Weight (grams)",  
main = "Head Size vs Brain Weight with Regression Line")  
  
lines(pred_line$Head.Size.cm.3., pred_line$Brain.Weight.grams., col = "red", lwd =  
2)
```

**Output:**

```
> print("First Few Rows of Dataset")  
[1] "First Few Rows of Dataset"  
> head(df)  
  Gender Age.Range Head.Size.cm.3. Brain.Weight.grams.  
1      1         1         4512         1530  
2      1         1         3738         1297  
3      1         1         4261         1335  
4      1         1         3777         1282  
5      1         1         4177         1590  
6      1         1         3585         1300
```

```
> print("Linear Regression Model")
[1] "Linear Regression Model"
> model <- lm(Brain.Weight.grams. ~ Head.Size.cm.3., data = train)
> print(model)
```

Call:

```
lm(formula = Brain.Weight.grams. ~ Head.Size.cm.3., data = train)
```

Coefficients:

(Intercept)	Head.Size.cm.3.
329.6963	0.2635

```
> cat("RMSE:", evaluation["RMSE"], "\n")
```

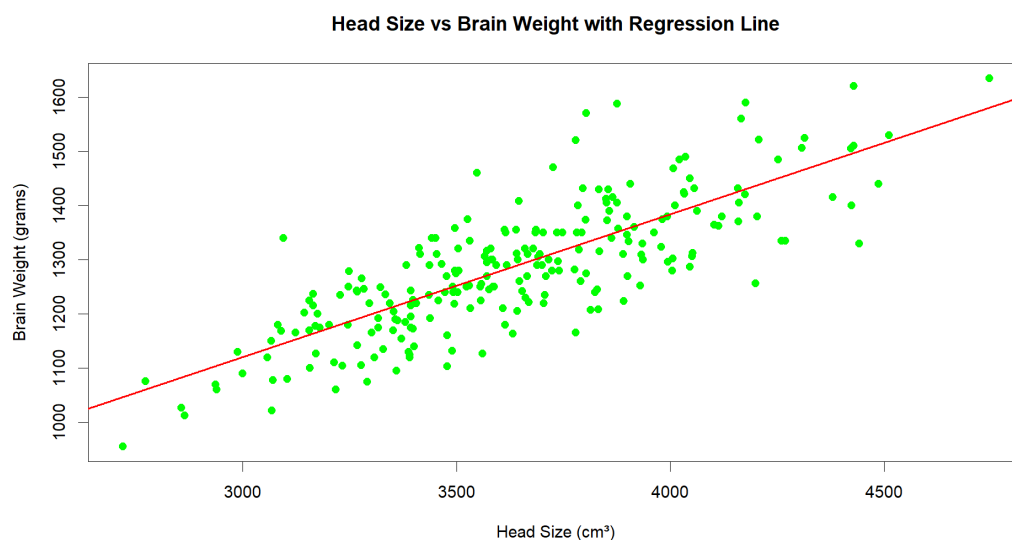
RMSE: 75.80924

```
> cat("R-squared:", evaluation["Rsquared"], "\n")
```

R-squared: 0.5921795

```
> cat("MAE:", evaluation["MAE"], "\n")
```

MAE: 59.80292



### Result:

The Linear Regression is Successfully Implemented.



**EXP NO: 8**

## **IMPLEMENT K-MEANS CLUSTERING ALGORITHM IN R**

**Aim:**

Implement a Kmeans Clustering on the Given Dataset.

**Procedure:**

**Procedure for Performing and Evaluating K-means Clustering in R**

**1. Load Required Libraries**

- Load the necessary libraries:
  - ggplot2 for plotting.
  - cluster for silhouette analysis.
  - factoextra for easy visualization of clustering.

**Code:**

```
library(ggplot2)
library(cluster)
library(factoextra)
```

**2. Load the Dataset**

- Load the Iris dataset.
- Remove the Species column to focus only on the numeric features for clustering.

**Code:**

```
data(iris)
iris_data <- iris[, -5]
head(iris_data)
```

**3. Determine the Optimal Number of Clusters Using Elbow Method**

- Use the Within-Cluster Sum of Squares (WSS) method to decide how many clusters are appropriate.

**Code:**

```
fviz_nbclust(iris_data, kmeans, method = "wss") +
  ggtitle("Elbow Method for Optimal K")
```

**4. Apply K-means Clustering with 3 Clusters**

- Set a random seed for reproducibility.
- Apply K-means clustering specifying 3 clusters (since Iris has 3 species).

**Code:**

```
set.seed(123)
kmeans_model <- kmeans(iris_data, centers = 3, nstart = 25)
```

**5. Print Cluster Centers and Cluster Assignments**

- View the center points of the clusters and how the data points were assigned.

**Code:**

```
print(kmeans_model$centers)
print(kmeans_model$cluster)
```

## 6. Visualize the Clusters

- Visualize the clustering result using a scatter plot with convex hulls around clusters.

**Code:**

```
fviz_cluster(kmeans_model, data = iris_data, geom = "point", ellipse.type =
"convex") +
  ggtitle("K-means Clustering on Iris Dataset")
```

## 7. Evaluate the Clustering (Silhouette Analysis)

- Perform silhouette analysis to assess the quality of the clustering.

**Code:**

```
silhouette_score <- silhouette(kmeans_model$cluster, dist(iris_data))
fviz_silhouette(silhouette_score)
```

**Output:**

```
> head(iris_data)
```

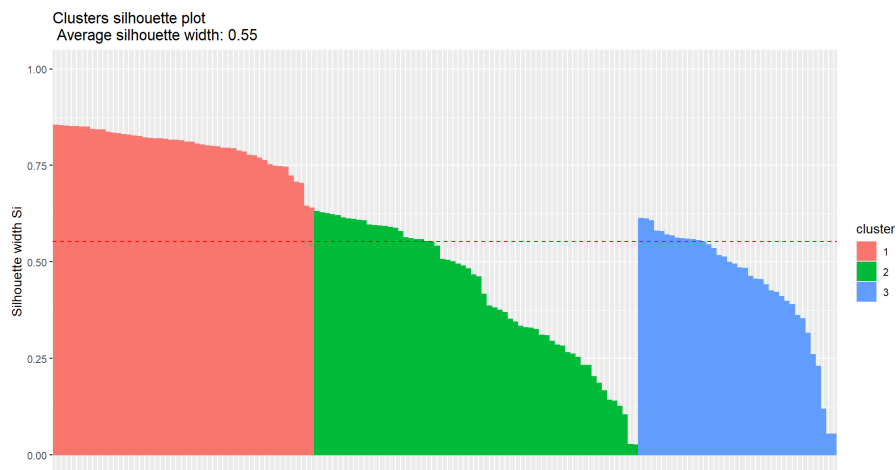
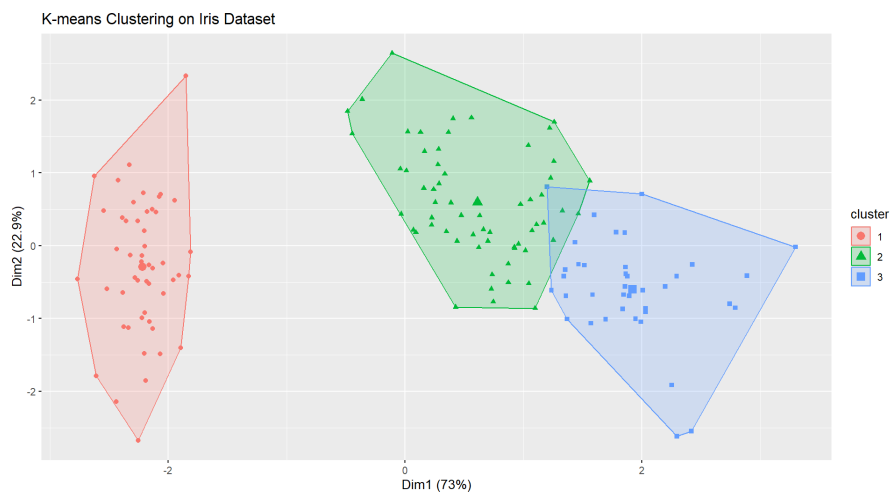
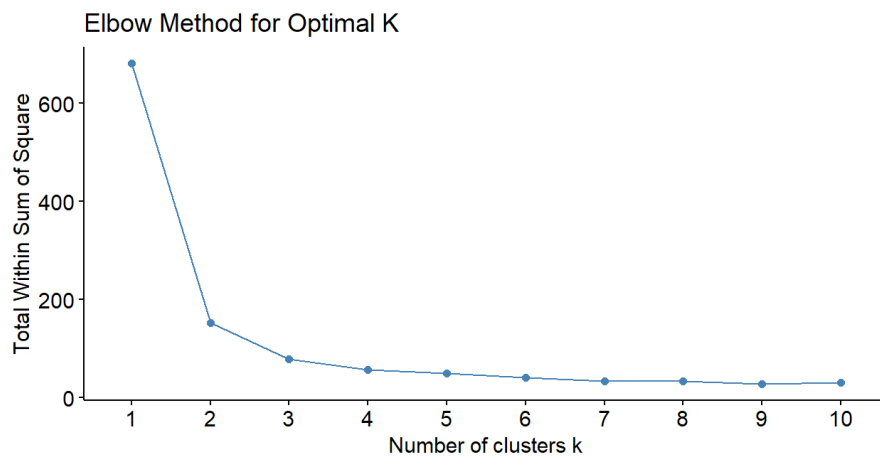
	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	5.1	3.5	1.4	0.2
2	4.9	3.0	1.4	0.2
3	4.7	3.2	1.3	0.2
4	4.6	3.1	1.5	0.2
5	5.0	3.6	1.4	0.2
6	5.4	3.9	1.7	0.4

```
> print(kmeans_model$centers)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	5.006000	3.428000	1.462000	0.246000
2	5.901613	2.748387	4.393548	1.433871
3	6.850000	3.073684	5.742105	2.071053

```
> print(kmeans_model$cluster)
[1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[31] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 3 2 2 2 2 2 2 2
[61] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 2 2 2 2 2 2 2 2 2 2 2
[91] 2 2 2 2 2 2 2 2 2 2 3 2 3 3 3 3 2 3 3 3 3 3 3 2 2 3 3 3 2
[121] 3 2 3 2 3 3 2 2 3 3 3 3 3 2 3 3 3 3 2 3 3 3 2 3 3 3 2
```

```
> fviz_silhouette(silhouette_score)
  cluster size ave.sil.width
1         1   50         0.80
2         2   62         0.42
3         3   38         0.45
```



## Result:

The Kmeans is Successfully Implemented.