Exp-1

Downloading and installing Hadoop on Ubuntu, Understanding different Hadoop modes, Startup scripts, Configuration files

Aim:

To successfully install, configure, and run Hadoop on a local system using a single-node setup.

Procedure:

1. **Install Java and SSH:**
   - Update your package lists and install OpenJDK 8 and SSH.

     sudo apt update

     sudo apt install openjdk-8-jdk

     java -version # Verify Java installation

     sudo apt install ssh
2. **Create Hadoop User:**
   - Add a dedicated user for Hadoop and generate SSH keys for passwordless SSH.

     sudo adduser hadoop

     su - hadoop # Switch to Hadoop user

     ssh-keygen -t rsa

     cat ~/.ssh/id_rsa.pub >> ~/.ssh/authorized_keys

     chmod 640 ~/.ssh/authorized_keys

     ssh localhost # Test SSH connection to localhost
3. **Download and Install Hadoop:**
   - Download the latest Hadoop version (3.3.6), extract the tarball, and move it to the desired location.

     wget https://downloads.apache.org/hadoop/common/hadoop-3.3.6/hadoop-3.3.6.tar.gz

     tar -xvzf hadoop-3.3.6.tar.gz

     mv hadoop-3.3.6 hadoop
4. **Configure Environment Variables:**
   - **Update. bashrc to include Hadoop and Java paths.**

     nano ~/.bashrc

     # Add the following lines at the end

     export JAVA_HOME=/usr/lib/jvm/java-8-openjdk-amd64

```
export HADOOP_HOME=$HOME/hadoop
export PATH=$PATH:$HADOOP_HOME/bin:$HADOOP_HOME/sbin
source ~/.bashrc  # Apply changes
```

5. **Edit Hadoop Configuration Files:**
   - Modify configuration files to set up the necessary Hadoop directories and services.
   - **core-site.xml:**

```
nano $HADOOP_HOME/etc/hadoop/core-site.xml
# Add between <configuration></configuration>:
<property>
  <name>fs.defaultFS</name>
  <value>hdfs://localhost:9000</value>
</property>
```

   - **hdfs-site.xml:**

```
nano $HADOOP_HOME/etc/hadoop/hdfs-site.xml
```

Add:

```
<property>
  <name>dfs.replication</name>
  <value>1</value>
</property>
<property>
  <name>dfs.namenode.name.dir</name>
  <value>file:///home/hadoop/hadoopdata/hdfs/namenode</value>
</property>
<property>
  <name>dfs.datanode.data.dir</name>
  <value>file:///home/hadoop/hadoopdata/hdfs/datanode</value>
</property>
```

   - **mapred-site.xml:**

```
cp $HADOOP_HOME/etc/hadoop/mapred-site.xml.template $HADOOP_HOME/etc/hadoop/mapred-site.xml
nano $HADOOP_HOME/etc/hadoop/mapred-site.xml
```

Add:

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

- **yarn-site.xml:**

```
nano $HADOOP_HOME/etc/hadoop/yarn-site.xml
```

Add:

```
<property>
   <name>yarn.nodemanager.aux-services</name>
   <value>mapreduce_shuffle</value>
</property>
```

6. **Format the NameNode:**
   - Format the HDFS NameNode.

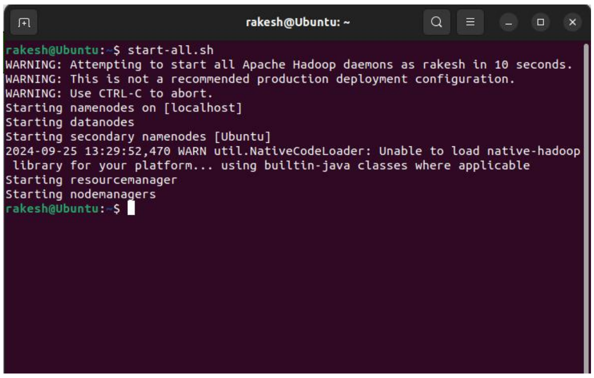
```
hdfs namenode -format
```

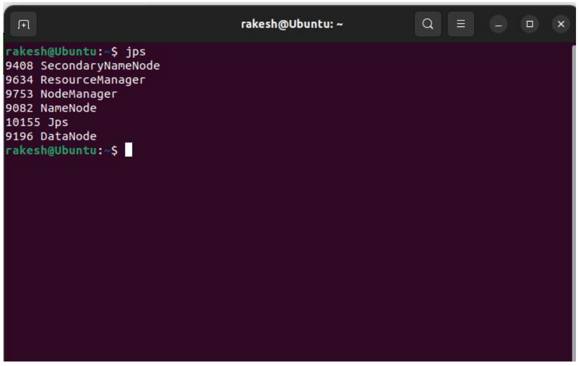
7. **Start Hadoop:**
   - Start Hadoop services (NameNode, DataNode, ResourceManager, and NodeManager).

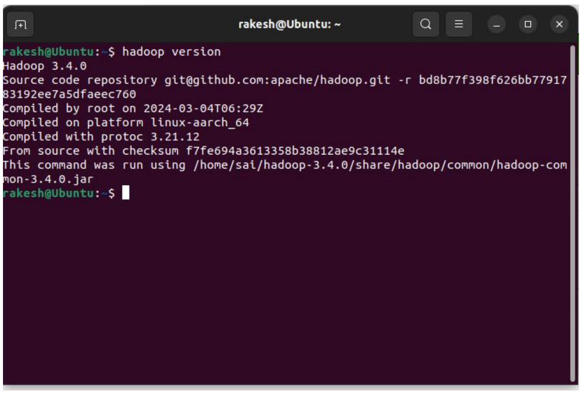
```
start-all.sh
jps  # Verify running services
```

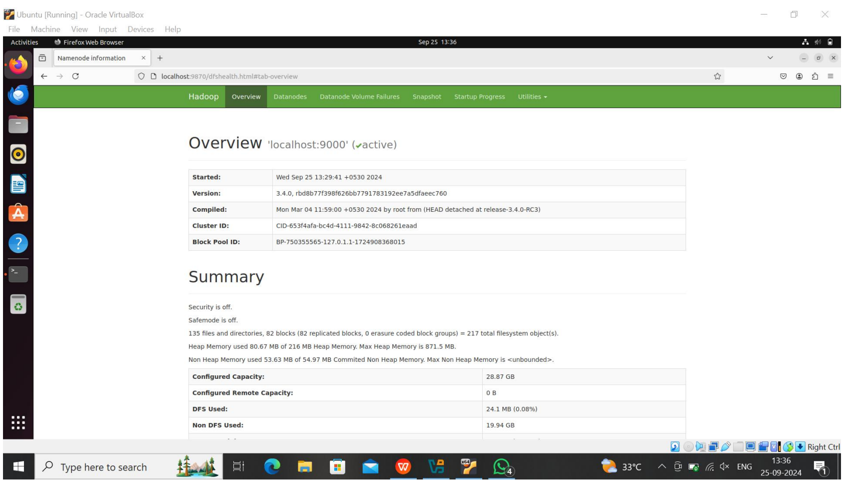
8. **Access Web Interfaces:**
   - Verify that Hadoop is running by accessing the following URLs:
     - **NameNode:** http://localhost:9870
     - **Resource Manager:** http://localhost:8088
9. **Stop Hadoop Cluster:**
   - Stop all Hadoop services.

```
stop-all.sh
```


rakesh@Ubuntu: ~
rakesh@Ubuntu:~$ start-all.sh
WARNING: Attempting to start all Apache Hadoop daemons as rakesh in 10 seconds.
WARNING: This is not a recommended production deployment configuration.
WARNING: Use CTRL-C to abort.
Starting namenodes on [localhost]
Starting datanodes
Starting secondary namenodes [Ubuntu]
2024-09-25 13:29:52,470 WARN util.NativeCodeLoader: Unable to load native-hadoop library for your platform... using builtin-java classes where applicable
Starting resourcemanager
Starting nodemanagers
rakesh@Ubuntu:~$


rakesh@Ubuntu: ~
rakesh@Ubuntu:~$ jps
9408 SecondaryNameNode
9634 ResourceManager
9753 NodeManager
9082 NameNode
10155 Jps
9196 DataNode
rakesh@Ubuntu:~$


rakesh@Ubuntu: ~
rakesh@Ubuntu:~$ hadoop version
Hadoop 3.4.0
Source code repository git@github.com:apache/hadoop.git -r bd8b77f398f626bb7791783192ee7a5dfaeec760
Compiled by root on 2024-03-04T06:29Z
Compiled on platform linux-aarch_64
Compiled with protoc 3.21.12
From source with checksum f7fe694a3613358b38812ae9c31114e
This command was run using /home/sai/hadoop-3.4.0/share/hadoop/common/hadoop-common-3.4.0.jar
rakesh@Ubuntu:~$


Ubuntu [Running] - Oracle VirtualBox
Sep 25 13:36
Namenode information
localhost:9870/dfshealth.html#tab-overview
Hadoop
Overview
Datanodes
Datanode Volume Failures
Snapshot
Startup Progress
Utilities
Overview 'localhost:9000' (active)
Started: Wed Sep 25 13:29:41 +0530 2024
Version: 3.4.0, rbd8b77f398f626bb7791783192ee7a5dfaeec760
Compiled: Mon Mar 04 11:59:00 +0530 2024 by root from (HEAD detached at release-3.4.0-RC3)
Cluster ID: CID-653f4afa-bc4d-4111-9842-8c068261eaad
Block Pool ID: BP-750355565-127.0.1.1-1724908368015
Summary
Security is off.
Safemode is off.
135 files and directories, 82 blocks (82 replicated blocks, 0 erasure coded block groups) = 217 total filesystem object(s).
Heap Memory used 80.67 MB of 216 MB Heap Memory. Max Heap Memory is 871.5 MB.
Non Heap Memory used 53.63 MB of 54.97 MB Commited Non Heap Memory. Max Non Heap Memory is <unbounded>.
Configured Capacity: 28.87 GB
Configured Remote Capacity: 0 B
DFS Used: 24.1 MB (0.08%)
Non DFS Used: 19.94 GB
Type here to search
33°C
ENG
13:36
25-09-2024

RESULT:

The step-by-step installation and configuration of Hadoop on Ubuntu system have been successfully completed.

Expt-2

Run a basic Word Count Map Reduce program to understand Map Reduce Paradigm.

AIM:

To run a basic Word Count MapReduce program using Hadoop.

PROCEDURE:

1. **Create Data File**:

   ```
   nano word_count_data.txt
   ```

   Example content for word_count_data.txt:

   Hadoop is a framework that allows for distributed processing of large data sets.

2. **Mapper Program (mapper.py)**:

   ```
   import sys
   for line in sys.stdin:
       line = line.strip()
       words = line.split()
       for word in words:
           print(f'{word}\t1')
   ```

3. **Reducer Program (reducer.py)**:

   ```
   import sys
   current_word = None
   current_count = 0
   word = None

   for line in sys.stdin:
       line = line.strip()
       word, count = line.split('\t', 1)

       try:
           count = int(count)
       except ValueError:
           continue
   ```

```
    if current_word == word:
        current_count += count
    else:
        if current_word:
            print(f'{current_word}\t{current_count}')
        current_count = count
        current_word = word

if current_word == word:
    print(f'{current_word}\t{current_count}')
```

4. **Set Hadoop Environment**:

```
hdfs dfs -mkdir /word_count_input
hdfs dfs -copyFromLocal word_count_data.txt /word_count_input
```

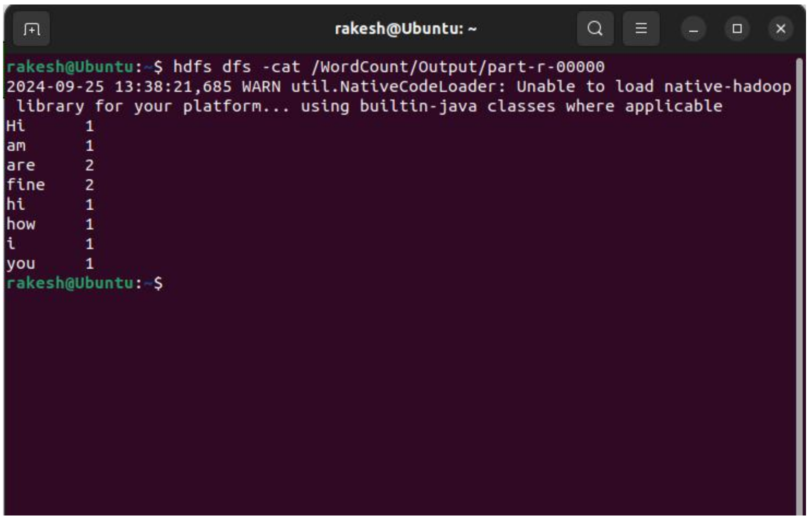
5. **Run Word Count Program**:

```
hadoop jar $HADOOP_HOME/share/hadoop/tools/lib/hadoop-streaming-*.jar \
-input /word_count_input/word_count_data.txt \
-output /word_count_output \
-mapper mapper.py \
-reducer reducer.py
```

6. **Check Output**:

```
hdfs dfs -cat /word_count_output/part-00000
```

OUTPUT:



RESULT:

Thus, the program for basic Word Count Map Reduce has been executed successfully.

Expt-3

Map Reduce program to process a weather dataset.

AIM:

To implement MapReduce program to process a weather dataset.

PROCEDURE:

1. **Create Weather Dataset**:

    ```
    nano weather_data.txt
    ```

    Example content:

    20220101 30.5

    20220102 29.8

2. **Mapper Program (mapper.py)**:

    ```
    #!/usr/bin/env python3
    import sys
    for line in sys.stdin:
        line = line.strip()
        month = line[4:6]  # Extracting month
        temp = line[7:11]  # Extracting temperature
        print(f'{month}\t{temp}')
    ```

3. **Reducer Program (reducer.py)**:

    ```
    #!/usr/bin/env python3
    import sys

    current_month = None
    current_max_temp = -float('inf')

    for line in sys.stdin:
        line = line.strip()
        month, temp = line.split('\t')

        try:
    ```

```
        temp = float(temp)
    except ValueError:
        continue

    if current_month == month:
        current_max_temp = max(current_max_temp, temp)
    else:
        if current_month:
            print(f'{current_month}\t{current_max_temp}')
        current_month = month
        current_max_temp = temp

if current_month == month:
    print(f'{current_month}\t{current_max_temp}')
```

4. **Run the Program**:

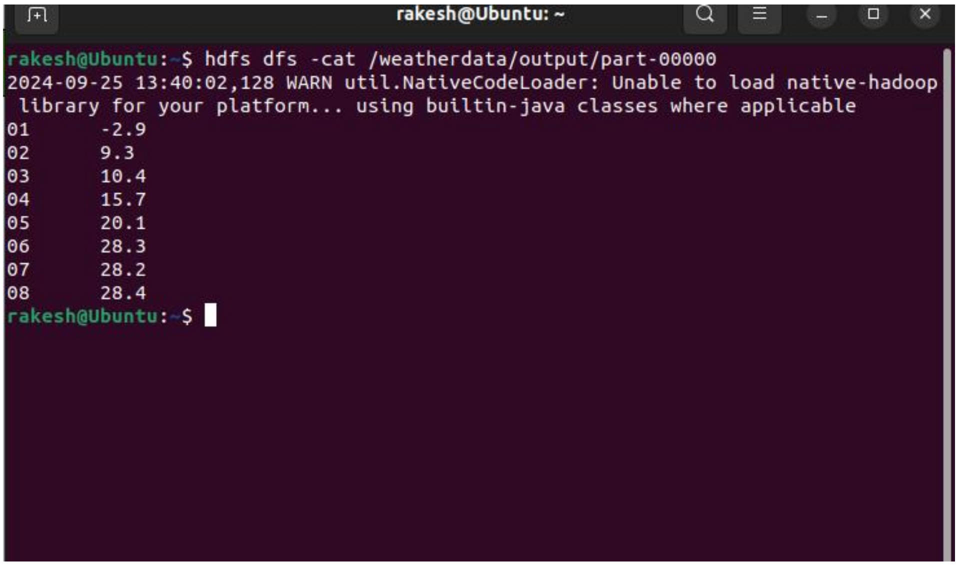
```
hdfs dfs -mkdir /weatherdata
hdfs dfs -copyFromLocal weather_data.txt /weatherdata

hadoop jar $HADOOP_HOME/share/hadoop/tools/lib/hadoop-streaming-*.jar \
-input /weatherdata/weather_data.txt \
-output /weatherdata/output \
-mapper mapper.py \
-reducer reducer.py
```

5. **Check Output**:

```
hdfs dfs -cat /weatherdata/output/part-00000
```

OUTPUT:



RESULT:

Thus, the program for weather dataset using Map Reduce has been executed successfully.

Expt-4

Create UDF (User Defined Functions) in Apache Pig and execute it in MapReduce / HDFS mode

AIM:

To create UDF in Apache Pig and execute it in MapReduce/HDFS mode.

Procedure:

Step 1: Install and Configure Apache Pig

1. **Download Apache Pig**:

   Download the latest version of Pig from the official website:

   wget https://dlcdn.apache.org/pig/pig-0.16.0/pig-0.16.0.tar.gz

2. **Extract Pig**:

   tar xvzf pig-0.16.0.tar.gz

3. **Move Pig Directory**:

   Move the extracted Pig files to a dedicated folder:

   sudo mv pig-0.16.0 /usr/local/pig

4. **Set Environment Variables**:

   Edit the .bashrc file to set up Pig environment variables:

   nano ~/.bashrc

   Append the following lines:

   export PIG_HOME=/usr/local/pig

   export PATH=$PATH:$PIG_HOME/bin

   export PIG_CLASSPATH=$HADOOP_HOME/conf

   Apply the changes:

   source ~/.bashrc

5. **Verify Pig Installation**:

   Run the following command to verify if Pig has been installed correctly:

   pig -version

Step 2: Create Sample Data for the Pig Job

1. **Create a Sample Data File**: Create a sample text file (sample.txt) with some dummy data:

   nano sample.txt

   Add the following content:

   1,John

   2,Jane

   3,Joe

   4,Emma

2. **Upload the Data File to HDFS**: Upload the sample file to Hadoop's distributed file system (HDFS):

   hdfs dfs -mkdir /piginput

   hdfs dfs -put sample.txt /piginput

Step 3: Write Pig Script for the UDF

1. **Create the Pig Script**:

   Create a new Pig script (demo_pig.pig):

   nano demo_pig.pig

   Write the following code in the script to load and display the data:

   pig

   -- Load data from HDFS

   data = LOAD '/piginput/sample.txt' USING PigStorage(',') AS (id:int, name:chararray);

   -- Display the loaded data

   DUMP data;

Step 4: Write the UDF in Python

1. **Create the Python UDF**:

   Create a Python file (uppercase_udf.py) to convert text to uppercase:

   nano uppercase_udf.py

   def uppercase(text):

```
    return text.upper()

if __name__ == "__main__":
    import sys
    for line in sys.stdin:
        line = line.strip()
        print(uppercase(line))
```

2. **Upload the Python UDF to HDFS**:

   Upload the UDF to HDFS:

   ```
   hdfs dfs -mkdir /udfs
   hdfs dfs -put uppercase_udf.py /udfs
   ```

Step 5: Update Pig Script to Use UDF

1. **Modify the Pig Script to Include UDF**:

   Edit the demo_pig.pig script to register the UDF and process the data:

   ```
   nano demo_pig.pig
   ```

   Modify the script as follows:

   pig

   -- Register the Python UDF script

   ```
   REGISTER '/udfs/uppercase_udf.py' USING jython AS myudf;
   ```

   -- Load data from HDFS

   ```
   data = LOAD '/piginput/sample.txt' USING PigStorage(',') AS (id:int, name:chararray)
   ```

   -- Apply UDF to convert names to uppercase

   ```
   uppercased_data = FOREACH data GENERATE myudf.uppercase(name);
   ```

   -- Display the transformed data

   ```
   DUMP uppercased_data;
   ```

Step 6: Run the Pig Script

1. **Run the Pig Script**:

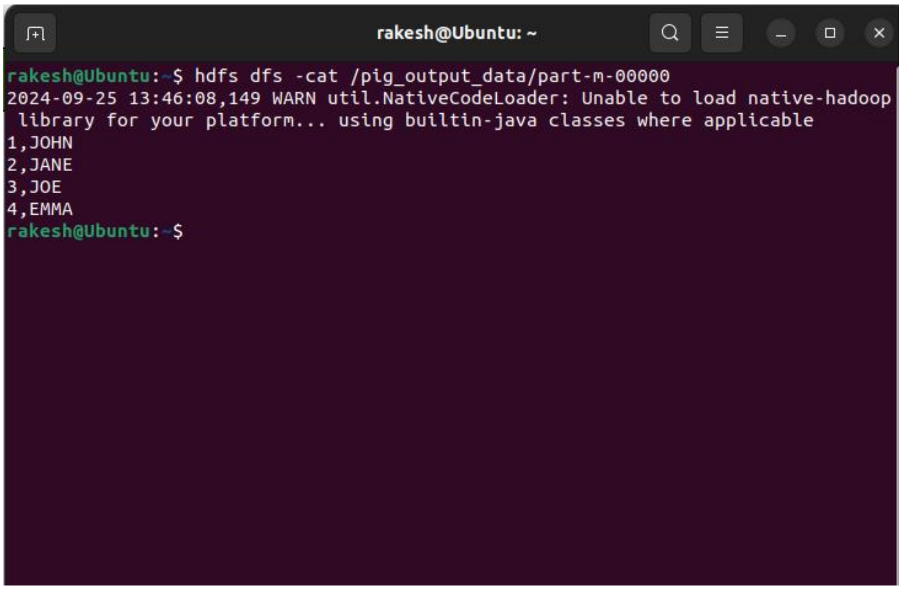
   Run the Pig script using the following command:

   pig -x mapreduce demo_pig.pig

2. **View Output**

   hdfs dfs -cat /pigoutput/part-m-00000

OUTPUT:



RESULT:

Thus, UDF in Apache Pig has been created and executed in MapReduce/HDFS mode successfully.

Ex No 5

Create tables in Hive and write queries to access the data in the table

AIM:

To create tables in Hive and write queries to access the data in the table.

PROCEDURE:

Step 1: Download and Install Hive

1. **Download Hive**:

   Download Hive from the official website:

   wget https://downloads.apache.org/hive/hive-3.1.2/apache-hive-3.1.2-bin.tar.gz

2. **Extract Hive**:

   tar -xvf apache-hive-3.1.2-bin.tar.gz

3. **Move Hive Directory**:

   sudo mv apache-hive-3.1.2-bin /usr/local/hive

4. **Set Hive Environment Variables**:

   Edit .bashrc to configure Hive:

   nano ~/.bashrc

   Add the following lines:

   export HIVE_HOME=/usr/local/hive

   export PATH=$PATH:$HIVE_HOME/bin

   Apply the changes:

   source ~/.bashrc

5. **Configure Hive**:

Configure Hive to use MySQL as its metastore by editing the Hive configuration file (hive-site.xml):

nano $HIVE_HOME/conf/hive-site.xml

Add the following configuration for MySQL connection:

```
<property>
   <name>javax.jdo.option.ConnectionURL</name>
   <value>jdbc:mysql://localhost/metastore</value>
</property>
<property>
   <name>javax.jdo.option.ConnectionDriverName</name>
   <value>com.mysql.jdbc.Driver</value>
</property>
<property>
   <name>javax.jdo.option.ConnectionUserName</name>
   <value>root</value>
</property>
<property>
   <name>javax.jdo.option.ConnectionPassword</name>
   <value>password</value>
</property>
```

6. **Start Hive**:

   Once everything is configured, start Hive by simply typing:

   ```
   hive
   ```

Step 2: Create a Database and Table in Hive

1. **Create a Database**:

In the Hive terminal, create a new database:

```
CREATE DATABASE financials;
```

2. **Use the Database**:

```
USE financials;
```

3. **Create a Table**:

Create a table to store financial data:

```
CREATE TABLE finance_table (
   id INT,
   name STRING
)
```

4. **Insert Data into the Table**:

Insert sample data into the finance_table:

```
INSERT INTO TABLE finance_table VALUES (1, 'Alice'), (2, 'Bob'), (3, 'Charlie');
```

Step 3: Store the Output in HDFS

1. **Create a Partitioned Table**:

   For optimized storage, create a partitioned table by year:

```
CREATE TABLE partitioned_finance_table (
   id INT,
   name STRING
)
PARTITIONED BY (year INT)
```

2. **Insert Data into the Partitioned Table**:

```
INSERT INTO partitioned_finance_table PARTITION (year=2023) VALUES (1, 'Alice'), (2, 'Bob');
```

```
INSERT INTO partitioned_finance_table PARTITION (year=2024) VALUES (3, 'Charlie');
```

3. **Create a Bucketed Table**:

Create a bucketed table to improve query performance:

```
CREATE TABLE bucketed_finance_table (
  id INT,
  name STRING
)
CLUSTERED BY (id) INTO 4 BUCKETS
```

4. **Insert Data into the Bucketed Table**:

```
INSERT INTO TABLE bucketed_finance_table VALUES (1, 'Alice'), (2, 'Bob'), (3, 'Charlie');
```

Step 4: View the Output in HDFS

1. **Create an ORC Table**:

Use ORC (Optimized Row Columnar) format for efficient storage:

```
CREATE TABLE orc_finance_table (
  id INT,
  name STRING
)
```

2. **Insert Data into the ORC Table**:

```
INSERT INTO TABLE orc_finance_table SELECT * FROM finance_table;
```

3. **View the Output in HDFS**:

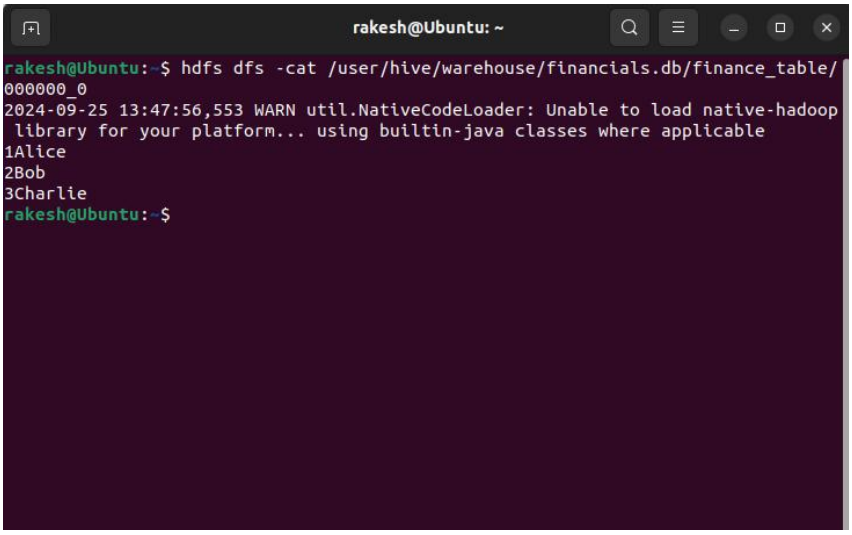
You can view the output by navigating to the HDFS directory where Hive stores the data. Use the following command to view the stored data:

```
hdfs dfs -ls /user/hive/warehouse/financials.db/finance_table
```

To view the contents of the ORC table:

```
hdfs dfs -cat /user/hive/warehouse/financials.db/orc_finance_table/000000_0
```

OUTPUT:



RESULT:

Thus, to create tables in Hive and write queries to access the data in the table was completed successfully.

Ex No 6

Import a JSON file from the command line. Apply the following actions with the data present in the JSON file where, projection, aggregation, remove, count, limit, skip and sort

AIM:

To import a JSON file from the command line and apply the following actions with the data present in the JSON file where, projection, aggregation, remove, count, limit, skip and sort using jq tool.

PROCEDURE:

- Create a json file 'employees.json' and provide data in it.
- Open the command prompt.
- Navigate to the folder where employees.json is stored.
- Load and view the JSON data with jq.
- Use the jq commands for projection, aggregation, removal, counting, limiting, and sorting operations.

employees.json:

```
[
  {
    "id": 1,
    "name": "Alice Johnson",
    "department": "Engineering",
    "age": 29,
    "salary": 70000
  },
  {
    "id": 2,
    "name": "Bob Smith",
    "department": "Marketing",
    "age": 35,
```

"salary": 55000
},
{
"id": 3,
"name": "Charlie Davis",
"department": "Engineering",
"age": 25,
"salary": 60000
},
{
"id": 4,
"name": "Dana Lee",
"department": "Human Resources",
"age": 40,
"salary": 65000
},
{
"id": 5,
"name": "Eve Martinez",
"department": "Finance",
"age": 45,
"salary": 75000
}
]

OUTPUT:

Running jq queries:

I. Projection:

```
rakesh@Ubuntu: ~
rakesh@Ubuntu:~$ python3  process_data.py
Raw JSON Data: [
{"name": "John Doe", "age": 30, "department": "HR", "salary": 50000},
{"name": "Jane Smith", "age": 25, "department": "IT", "salary": 60000},
{"name": "Alice Johnson", "age": 35, "department": "Finance", "salary": 70000},
{"name": "Bob Brown", "age": 28, "department": "Marketing", "salary": 55000},
{"name": "Charlie Black", "age": 45, "department": "IT", "salary": 80000}
]
```

II. Aggregation:

```
Aggregation: Calculate total salary
Total Salary: 315000
```

III. Count:

```
Count: Number of employees earning more than 50000
Number of High Earners (>50000): 4
```

IV. Remove:

```
Filtered DataFrame (IT department removed):
            name  age department  salary
0       John Doe   30         HR   50000
2  Alice Johnson   35    Finance   70000
3      Bob Brown   28  Marketing   55000
```

V. Limit:

```
Limit: Top 5 highest salary
            name  age department  salary
4  Charlie Black   45         IT   80000
2  Alice Johnson   35    Finance   70000
1     Jane Smith   25         IT   60000
3      Bob Brown   28  Marketing   55000
0       John Doe   30         HR   50000
```

VI. Skip:

```
Skipped DataFrame (First 2 rows skipped):
            name  age department  salary
2  Alice Johnson   35    Finance   70000
3      Bob Brown   28  Marketing   55000
4  Charlie Black   45         IT   80000
```

VII. Sort:

```
Sorted DataFrame by Name:
            name  age department  salary
2  Alice Johnson   35    Finance   70000
3      Bob Brown   28  Marketing   55000
4  Charlie Black   45         IT   80000
1     Jane Smith   25         IT   60000
0       John Doe   30         HR   50000
```

RESULT:

Thus to import a JSON file from the command line and apply the following actions with the data present in the JSON file where, projection, aggregation, remove, count, limit, skip and sort using jq tool is completed successfully.

Ex No 7

Implement Linear and Logistic Regression in R

AIM:

To Implement Linear and Logistic Regression using R

PROCEDURE:

- Collect and load the dataset from sources like CSV files or databases.
- Clean and preprocess the data, including handling missing values and encoding categorical variables.
- Split the dataset into training and testing sets to evaluate model performance.
- Normalize or standardize the features to ensure consistent scaling. 5.Choose the appropriate model: Linear Regression for continuous outcomes.
- Train the model on the training data using the `fit` method.
- Make predictions on the testing data using the `predict` method.
- Evaluate the model using metrics like Mean Squared Error (MSE) for Linear Regression or accuracy and confusion matrix for Logistic Regression.
- Visualize the results with plots, such as scatter plots for Linear Regression or decision boundaries for Logistic Regression.
- Fine-tune the model by adjusting hyperparameters or applying regularization Techniques.

CODE:

LinearRegression.R:

```
# Sample data

heights <- c(150, 160, 165, 170, 175, 180, 185)

weights <- c(55, 60, 62, 68, 70, 75, 80)

# Create a data frame

data <- data.frame(heights, weights)

# Fit a linear regression model

linear_model <- lm(weights ~ heights, data = data)

# Print the summary of the model
```

```
print(summary(linear_model))
# Plotting the data and regression line
plot(data$heights, data$weights,
    main = "Linear Regression: Weight vs. Height",
    xlab = "Height (cm)",
    ylab = "Weight (kg)",
    pch = 19, col = "blue")
# Add regression line
abline(linear_model, col = "red", lwd = 2)
```

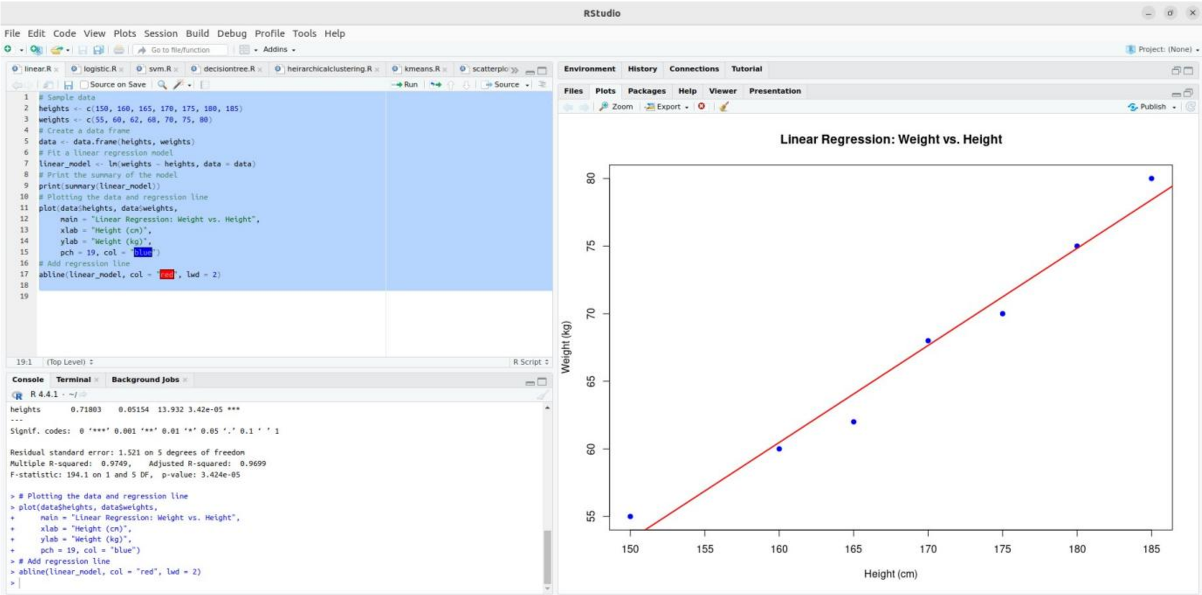
LogisticRegression.R:

```
# Load the dataset
data(mtcars)
# Convert 'am' to a factor (categorical variable)
mtcars$am <- factor(mtcars$am, levels = c(0, 1), labels = c("Automatic", "Manual"))
# Fit a logistic regression model
logistic_model <- glm(am ~ mpg, data = mtcars, family = binomial)
# Print the summary of the model
print(summary(logistic_model))
# Predict probabilities for the logistic model
predicted_probs <- predict(logistic_model, type = "response")
# Display the predicted probabilities
print(predicted_probs)
# Plotting the data and logistic regression curve
plot(mtcars$mpg, as.numeric(mtcars$am) - 1,
    main = "Logistic Regression: Transmission vs. MPG",
    xlab = "Miles Per Gallon (mpg)",
    ylab = "Probability of Manual Transmission",
```

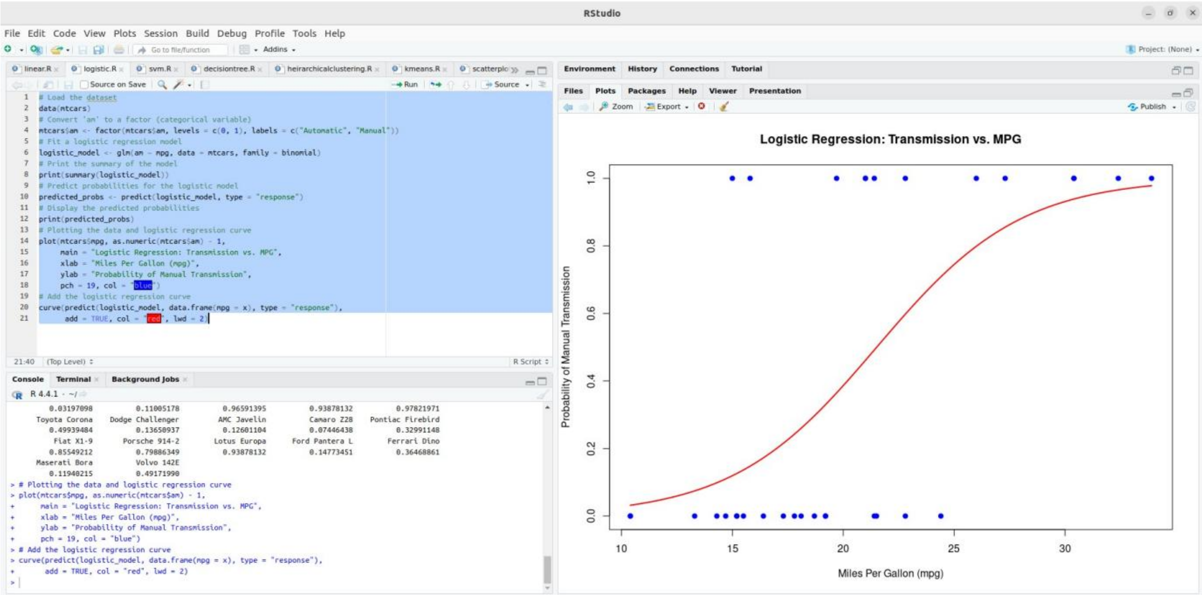
```
      pch = 19, col = "blue")
# Add the logistic regression curve
curve(predict(logistic_model, data.frame(mpg = x), type = "response"),
      add = TRUE, col = "red", lwd = 2)
```

OUTPUT:

Linear Regression:



Logistic Regression:



RESULT:

Thus to Implement Linear and Logistic Regression using R has been successfully executed.

Ex No 8

Implement SVM/Decision tree classification techniques

AIM:

To Implement SVM/Decision tree classification techniques using R.

PROCEDURE:

- Collect and load the dataset from sources like CSV files or databases.
- Clean and preprocess the data, including handling missing values and encoding categorical variables.
- Split the dataset into training and testing sets to evaluate model performance.
- Normalize or standardize the features, especially for SVM, to ensure consistent scaling.
- Choose the appropriate model: SVM for margin-based classification, Decision Tree for rule-based classification.
- Train the model on the training data using the ‘fit’ method.
- Make predictions on the testing data using the ’predict’ method.
- Evaluate the model using metrics like accuracy, confusion matrix, precision, and recall.
- Visualize the results with plots, such as decision boundaries for SVM or tree structures for Decision Trees.
- Fine-tune the model by adjusting hyperparameters like `C` for SVM or

`max_depth` for Decision Trees.

CODE:

SVM.R:

```
# Install and load the e1071 package (if not already installed)

install.packages("e1071")

library(e1071)

# Load the iris dataset
```

```
data(iris)
# Inspect the first few rows of the dataset
head(iris)
# Split the data into training (70%) and testing (30%) sets
set.seed(123) # For reproducibility
sample_indices <- sample(1:nrow(iris), 0.7 * nrow(iris))
train_data <- iris[sample_indices, ]
test_data <- iris[-sample_indices, ]
# Fit the SVM model
svm_model <- svm(Species ~ ., data = train_data, kernel = "radial")
# Print the summary of the model
summary(svm_model)
# Predict the test set
predictions <- predict(svm_model, newdata = test_data)
# Evaluate the model's performance
confusion_matrix <- table(Predicted = predictions, Actual = test_data$Species)
print(confusion_matrix)
# Calculate accuracy
accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix)
cat("Accuracy:", accuracy * 100, "%\n")
```

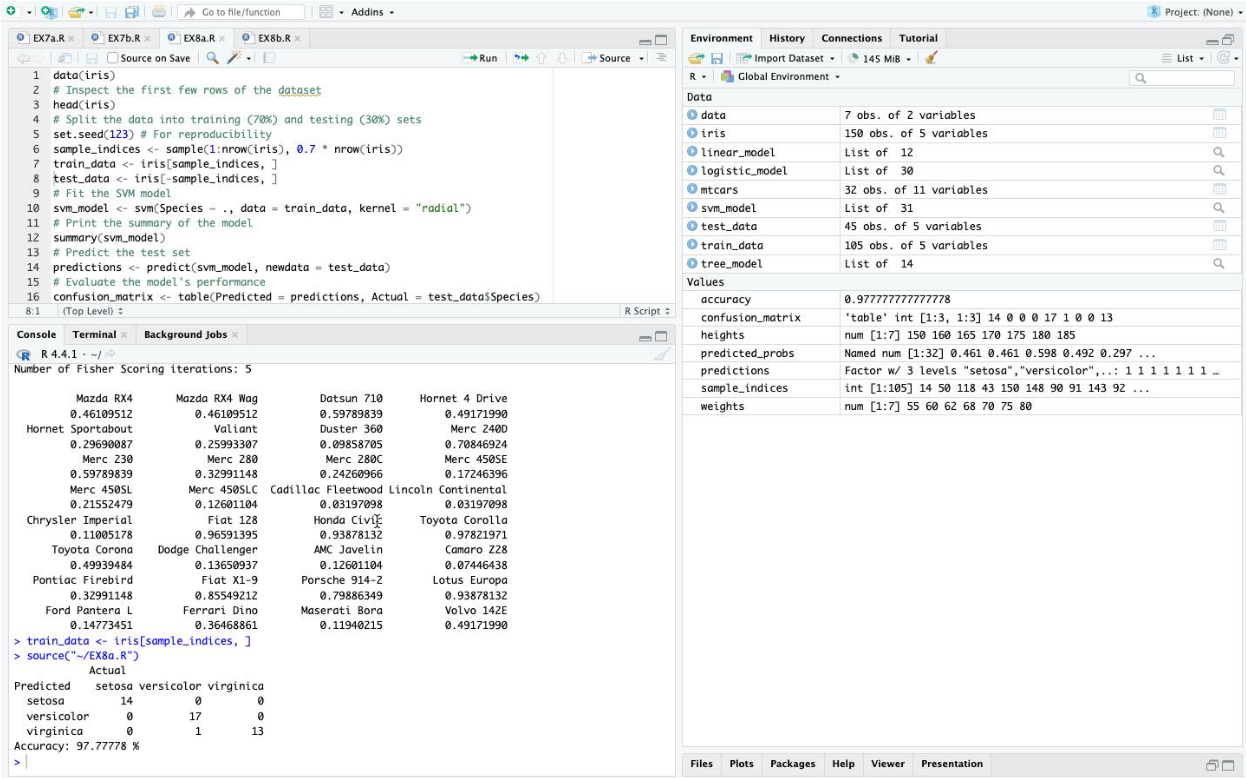
Decision Tree.R:

```
# Install and load the rpart package (if not already installed)
install.packages("rpart")
library(rpart)
# Load the iris dataset
data(iris)
# Split the data into training (70%) and testing (30%) sets
```

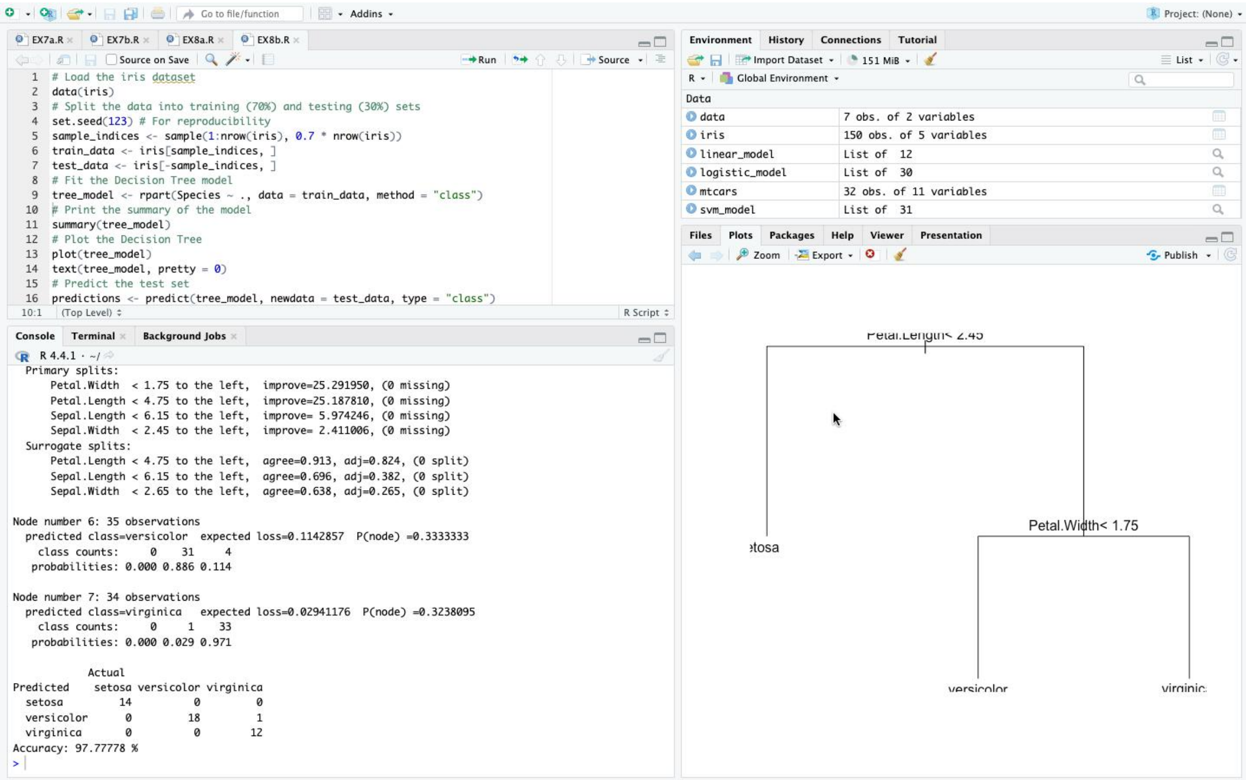
```
set.seed(123) # For reproducibility
sample_indices <- sample(1:nrow(iris), 0.7 * nrow(iris))
train_data <- iris[sample_indices, ]
test_data <- iris[-sample_indices, ]
# Fit the Decision Tree model
tree_model <- rpart(Species ~ ., data = train_data, method = "class")
# Print the summary of the model
summary(tree_model)
# Plot the Decision Tree
plot(tree_model)
text(tree_model, pretty = 0)
# Predict the test set
predictions <- predict(tree_model, newdata = test_data, type = "class")
# Evaluate the model's performance
confusion_matrix <- table(Predicted = predictions, Actual = test_data$Species)
print(confusion_matrix)
# Calculate accuracy
accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix)
cat("Accuracy:", accuracy * 100, "%\n")
```

OUTPUT:

SVM in R:



Decision tree:



RESULT:

Thus, Implement SVM and Decision tree classification techniques has been successfully executed.

Ex No 9

Implement clustering techniques – Hierarchical and K-Means

AIM:

To Implement clustering techniques – Hierarchical and K-Means using R.

PROCEDURE:

- Collect and load the dataset from sources like CSV files or databases.
- Clean and preprocess the data, including handling missing values and scaling features.
- Determine the number of clusters (K) for K-Means, or decide on the stopping criterion for Hierarchical Clustering.
- Choose the appropriate clustering algorithm: K-Means for partitioning, Hierarchical for nested clustering.
- Apply the K-Means algorithm using fit_predict to assign data points to clusters.
- Apply the Hierarchical Clustering algorithm using Agglomerative Clustering for hierarchical clusters.
- Visualize the clusters with scatter plots for K-Means, and dendrograms for Hierarchical Clustering.
- Evaluate clustering performance using metrics like silhouette score or inertia (for K-Means).
- Fine-tune the clustering by adjusting the number of clusters or linkage criteria.
- Interpret the results to understand the structure and relationships within the data.

CODE:

Hierarchical Clustering.R:

```
# Load the iris dataset
data(iris)
# Use only the numeric columns for clustering (exclude the Species column)
iris_data <- iris[, -5]
# Standardize the data
iris_scaled <- scale(iris_data)
```

```
# Compute the distance matrix
distance_matrix <- dist(iris_scaled, method = "euclidean")
# Perform hierarchical clustering using the "complete" linkage method
hc_complete <- hclust(distance_matrix, method = "complete")
# Plot the dendrogram
plot(hc_complete, main = "Hierarchical Clustering Dendrogram", xlab = "", sub = "", cex =
0.6)
# Cut the tree to form 3 clusters
clusters <- cutree(hc_complete, k = 3)
# Print the cluster memberships
print(clusters)
# Add the clusters to the original dataset
iris$Cluster <- as.factor(clusters)
# Display the first few rows of the updated dataset
head(iris)
```

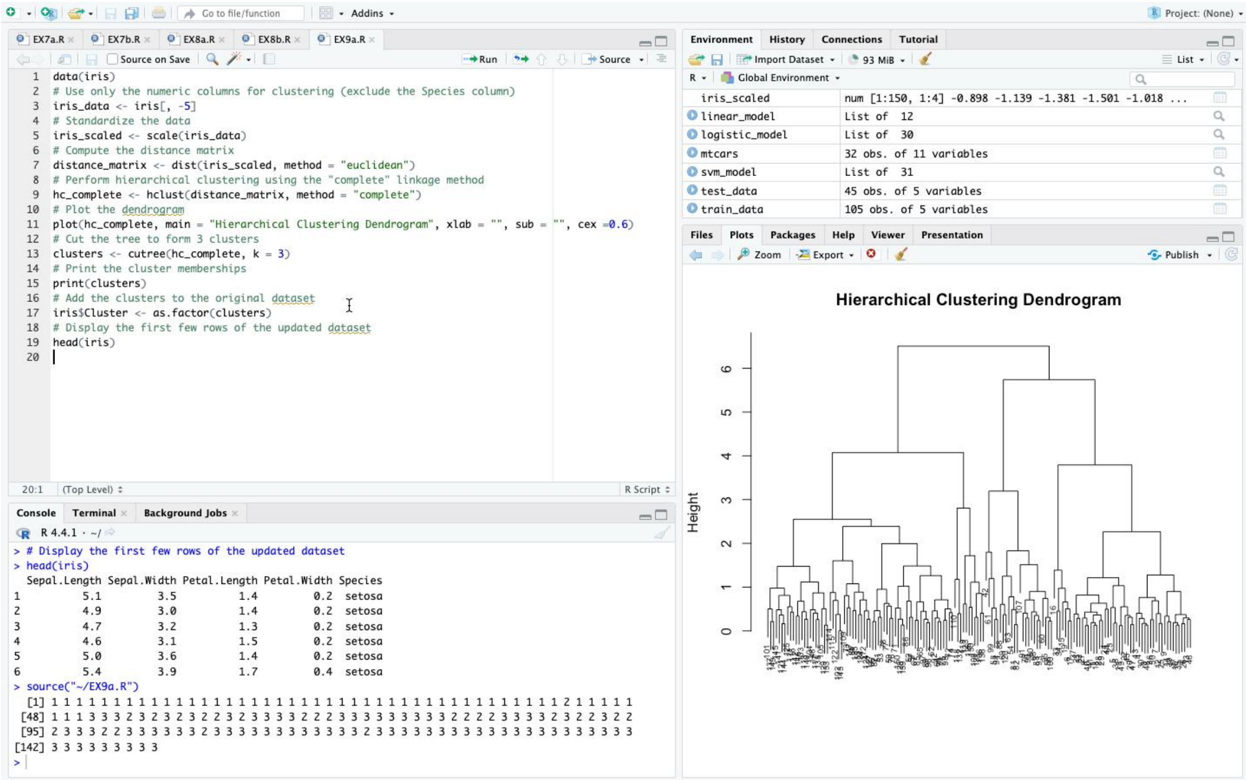
K-Means Clustering.R:

```
# Load the iris dataset
data(iris)
# Use only the numeric columns for clustering (exclude the Species column)
iris_data <- iris[, -5]
# Standardize the data
iris_scaled <- scale(iris_data)
# Set the number of clusters
set.seed(123) # For reproducibility
k <- 3 # Number of clusters
# Perform K-Means clustering
kmeans_result <- kmeans(iris_scaled, centers = k, nstart = 25)
```

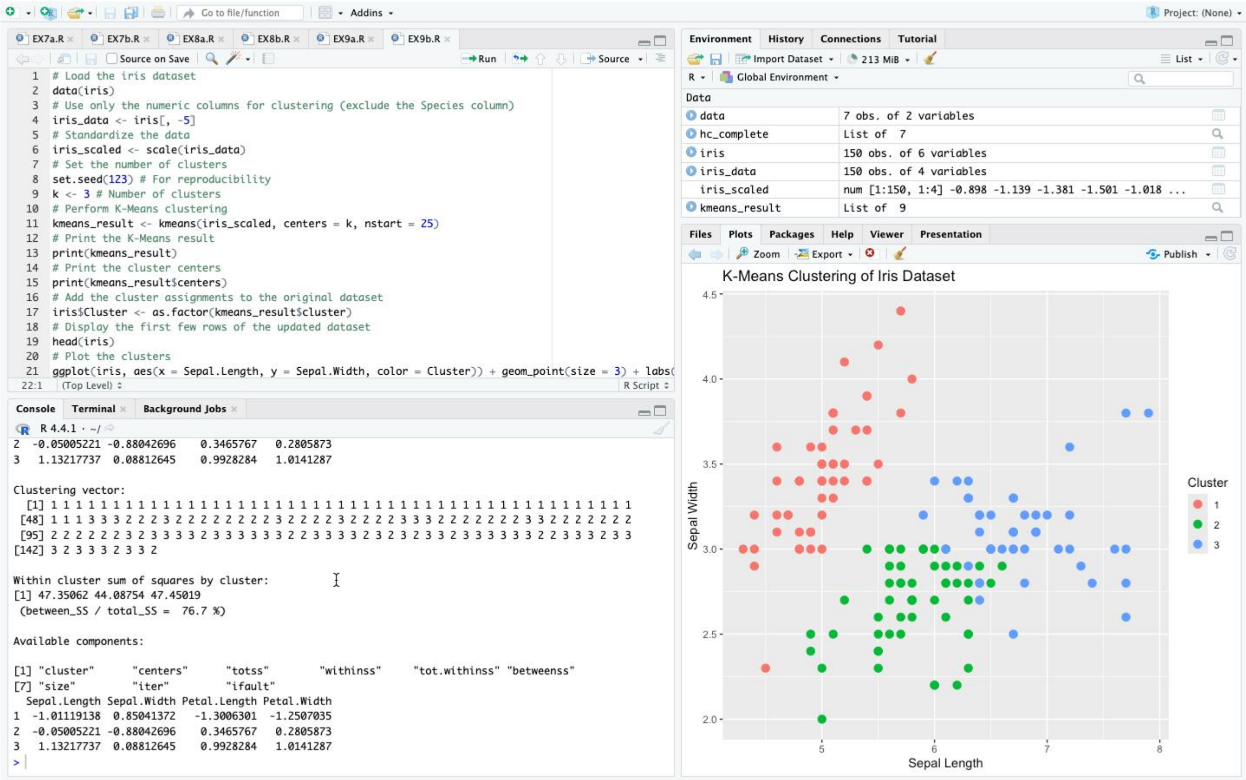
```
# Print the K-Means result
print(kmeans_result)
# Print the cluster centers
print(kmeans_result$centers)
# Add the cluster assignments to the original dataset
iris$Cluster <- as.factor(kmeans_result$cluster)
# Display the first few rows of the updated dataset
head(iris)
# Plot the clusters
library(ggplot2)
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Cluster)) +
  geom_point(size = 3) +
  labs(title = "K-Means Clustering of Iris Dataset", x = "Sepal Length", y = "Sepal Width")
```

OUTPUT:

Hierarchical Clustering:



K-Means Clustering:



RESULT:

Thus, to implement clustering techniques – Hierarchical and K-Means using R has been successfully executed.

Ex No 10

Visualize Data using Any plotting Framework

AIM:

To Visualize Data using Any plotting Frame work using R programming.

PROCEDURE:

- Install Plotly using pip install plotly if it’s not already installed.
- Import the necessary libraries: import plotly.express as px and import pandas as pd.
- Load your dataset into a DataFrame using pd.read_csv() or other data loading methods.
- Explore the dataset to understand its structure, variables, and potential visualizations.
- Choose the appropriate Plotly function (e.g., px.scatter, px.bar,px.line) based on the type of data and the desired plot.
- Define the x and y axes by specifying the columns from the DataFrame.
- Customize the plot by adding titles, labels, color coding, and other plot-specific attributes.
- Add interactive elements like hover data, tooltips, or facet plots for deeper insights.
- Render the plot using fig.show() to display it in a web browser or inline in a notebook.
- Save the plot to an HTML file or as a static image using fig.write_html() or fig.write_image().

CODE:

Scatter Plot.R:

```
# Install ggplot2 (if not already installed)

install.packages("ggplot2")

# Load the ggplot2 package

library(ggplot2)

# Scatter plot of Sepal.Length vs Sepal.Width, colored by Species

ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width, color = Species)) +
```

```
  geom_point(size = 3) + # Adds points
  labs(title = "Scatter Plot of Sepal Dimensions",
       x = "Sepal Length (cm)",
       y = "Sepal Width (cm)") + # Adds axis labels and title
  theme_minimal() # Applies a minimal theme
```

Bar Chart.R:

```
# Install ggplot2 (if not already installed)
install.packages("ggplot2")
# Load the ggplot2 package
library(ggplot2)
# Bar plot of Species counts
ggplot(data = iris, aes(x = Species)) +
  geom_bar(fill = "steelblue") + # Adds bars filled with steel blue color
  labs(title = "Count of Different Species in Iris Dataset",
       x = "Species",
       y = "Count") +
  theme_minimal()
```

Histogram.R:

```
# Install ggplot2 (if not already installed)
install.packages("ggplot2")
# Load the ggplot2 package
library(ggplot2)
# Histogram of Sepal Length
ggplot(data = iris, aes(x = Sepal.Length)) +
```

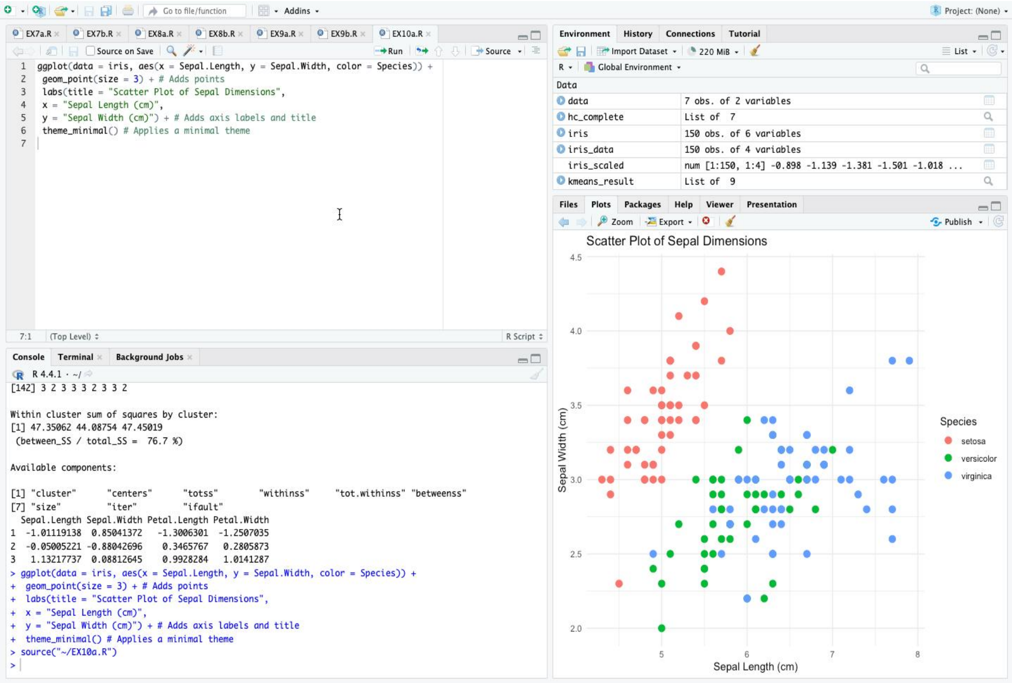
```
  geom_histogram(binwidth = 0.3, fill = "orange", color = "black") + # Adds histogram bars
  labs(title = "Histogram of Sepal Length",
       x = "Sepal Length (cm)",
       y = "Frequency") +
  theme_minimal()
```

Box Plot.R:

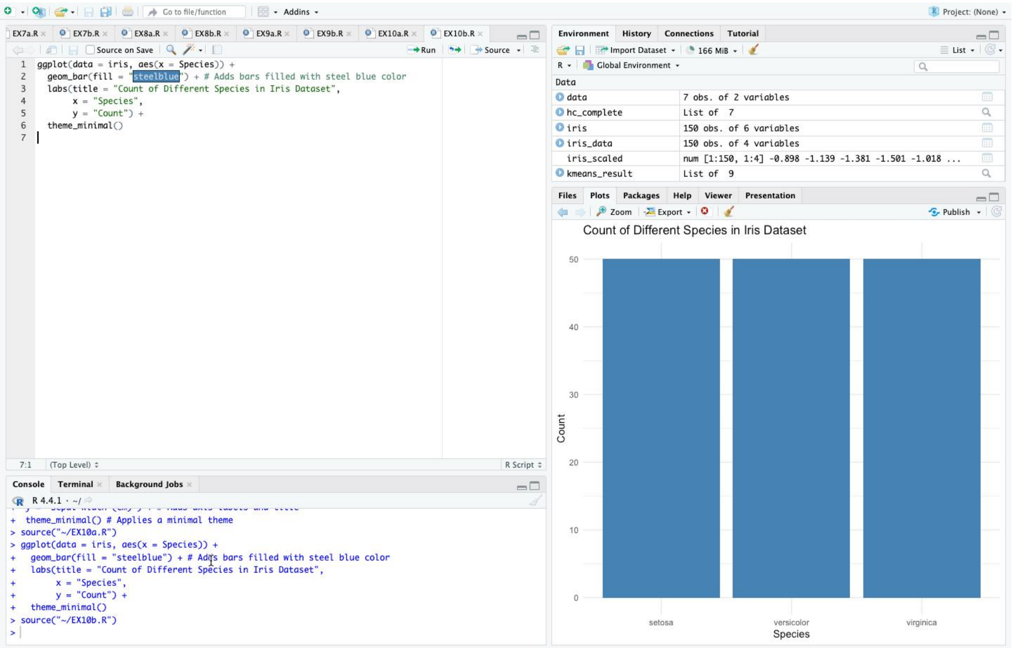
```
# Install ggplot2 (if not already installed)
install.packages("ggplot2")
library(ggplot2)
# Box plot of Sepal Length for each Species
ggplot(data = iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() + # Adds box plot
  labs(title = "Box Plot of Sepal Length by Species",
       x = "Species",
       y = "Sepal Length (cm)") +
  theme_minimal()
```

OUTPUT:

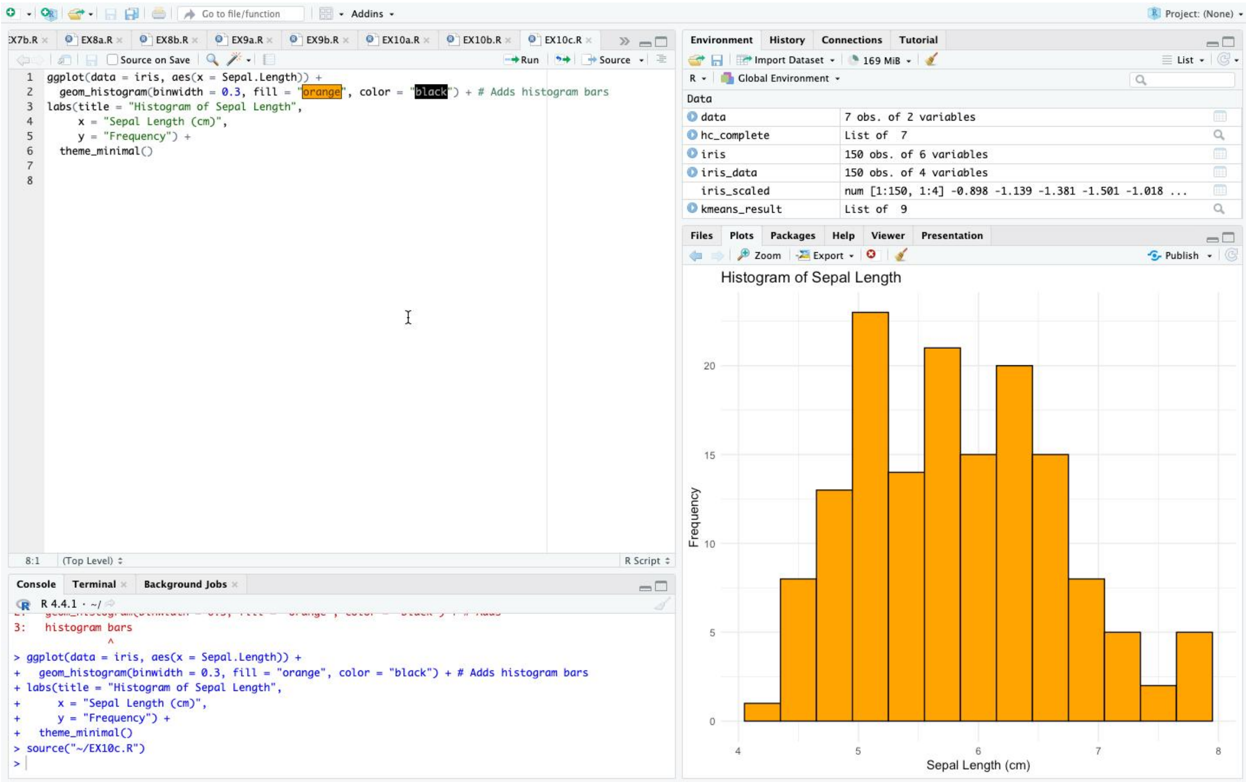
Scatter Plot:



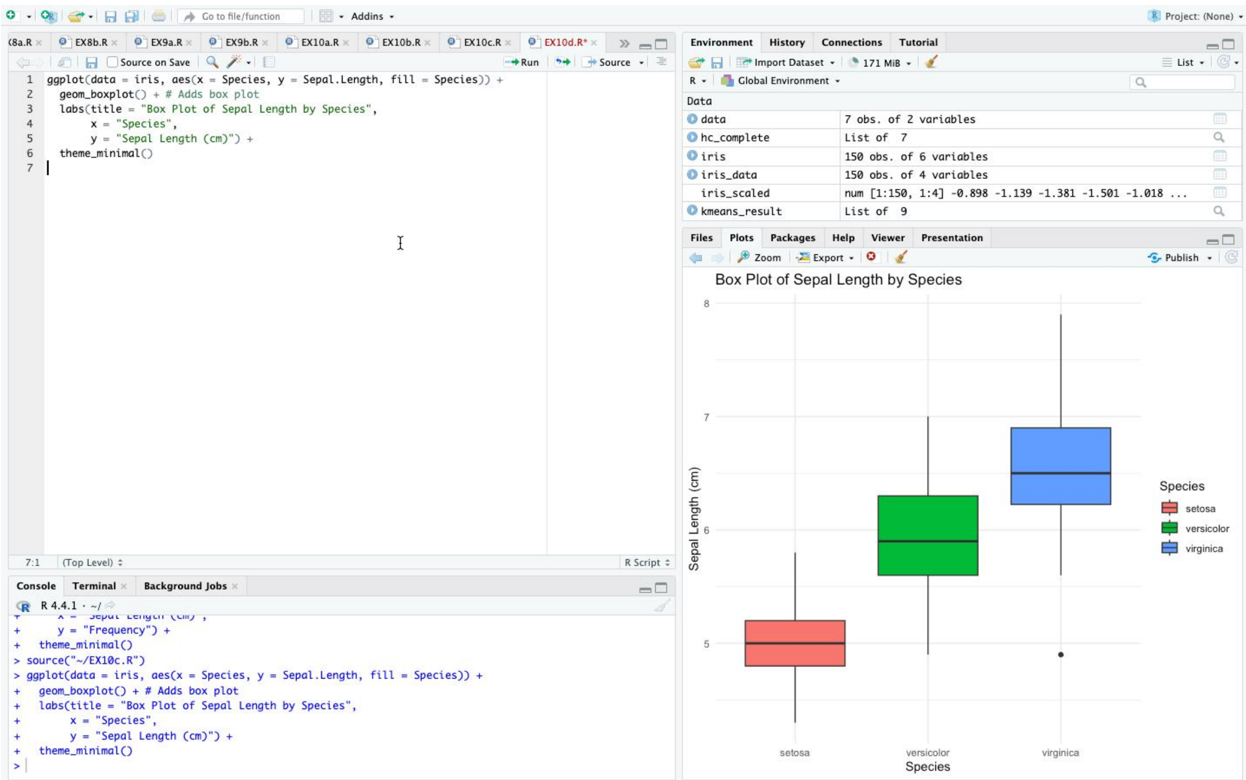
Bar Chart:



Histogram:



Box Plot:



RESULT:

Thus, Visualizing Data using any plotting framework using R programming has been successfully executed.