Exp.No: 1

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

AIM:

To Download and install Hadoop, Understanding different Hadoop modes, Startup scripts, Configuration files.

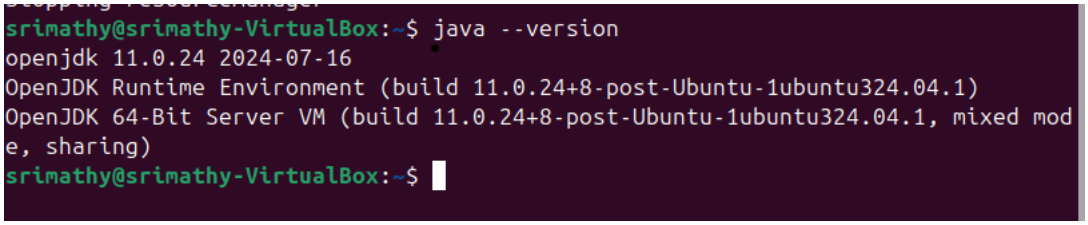
Procedure:

Step 1 : Install Java Development Kit
The default Ubuntu repositories contain Java 8 and Java 11 both. But, Install Java 8 because hive only works on this version. Use the following command to install it.

$sudo apt update&&sudo apt install openjdk-8-jdk

Step 2 : Verify the Java version
Once installed, verify the installed version of Java with the following command: **$**

java -version Output:



Step 3: Install SSH

SSH (Secure Shell) installation is vital for Hadoop as it enables secure communication between nodes in the Hadoop cluster. This ensures data integrity, confidentiality, and allows for efficient distributed processing of data across the cluster. **$sudo apt install ssh**

Step 4 : Create the hadoop user :
All the Hadoop components will run as the user that you create for Apache Hadoop, and the user will also be used for logging in to Hadoop's web interface. Run the command to create user and set password:

$ sudo adduser hadoop

Step 5 : Switch user
Switch to the newly created hadoop user:
$ su - hadoop

Step 6 : Configure SSH
Now configure password-less SSH access for the newly created hadoop user, so didn't enter the key to save file and passphrase. Generate an SSH keypair (generate Public and Private Key Pairs)first

$ ssh-keygen -t rsa

Step 7 : Set permissions :

Next, append the generated public keys from id_rsa.pub to authorized_keys and set proper permission:

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

$ chmod 640 ~/.ssh/authorized_keys

Step 8 : SSH to the localhost
Next, verify the password less SSH authentication with the following command:

$ ssh localhost

You will be asked to authenticate hosts by adding RSA keys to known hosts. Type yes and hit Enter to authenticate the localhost:

Step 9 : Switch user

Again switch to hadoop. So, First, change the user to hadoop with the following command: **$ su–hadoop**

Step 10 : Install hadoop
Next, download the latest version of Hadoop using the wget command:

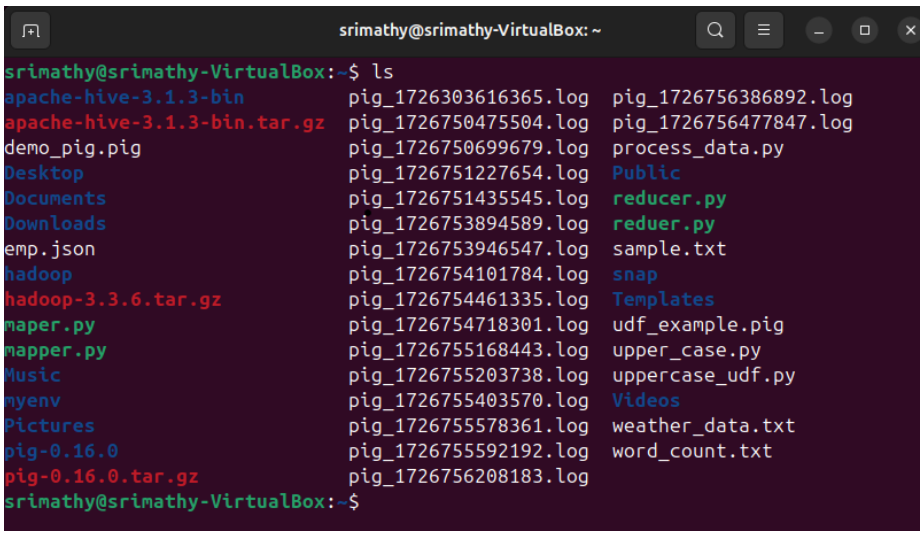
$ wgethttps://downloads.apache.org/hadoop/common/hadoop-3.3.6/hadoop-3.3.6.tar.gz Once

downloaded, extract the downloaded file:

$ tar -xvzf hadoop-3.3.6.tar.gz

Next, rename the extracted directory to hadoop:

$ mv hadoop-3.3.6 hadoop



Next, you will need to configure Hadoop and Java Environment Variables on your system. Open the ~/.bashrc file in your favorite text editor. Use nano editior , to pasting the code we use ctrl+shift+v for saving the file ctrl+x and ctrl+y ,then hit enter:

Next, you will need to configure Hadoop and Java Environment Variables on your system.

Open the ~/.bashrc file in your favorite text editor:

$ nano ~/.bashrc

Append the below lines to file.

```
export JAVA_HOME=/usr/lib/jvm/java-8-openjdk-amd64
export HADOOP_HOME=/home/hadoop/hadoop
export HADOOP_INSTALL=$HADOOP_HOME
export HADOOP_MAPRED_HOME=$HADOOP_HOME
export HADOOP_COMMON_HOME=$HADOOP_HOME
export HADOOP_HDFS_HOME=$HADOOP_HOME
export HADOOP_YARN_HOME=$HADOOP_HOME
export HADOOP_COMMON_LIB_NATIVE_DIR=$HADOOP_HOME/lib/native
export PATH=$PATH:$HADOOP_HOME/sbin:$HADOOP_HOME/bin
export HADOOP_OPTS="-Djava.library.path=$HADOOP_HOME/lib/native"
```

Save and close the file. Then, activate the environment variables with the following command:

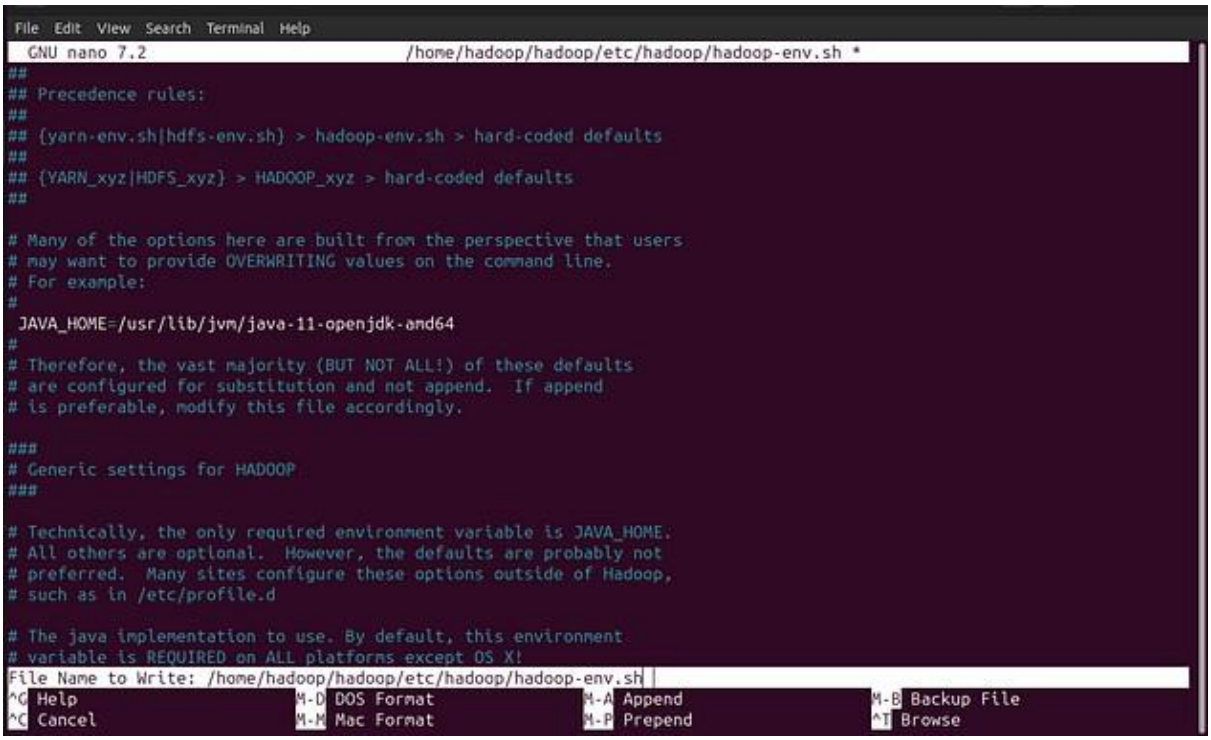
s$ source ~/.bashrc

Next, open the Hadoop environment variable file: **$ nano**

$HADOOP_HOME/etc/hadoop/hadoop-env.sh

Search for the “export JAVA_HOME” and configure it.

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



Save and close the file when you are finished.

Step 11 : Configuring Hadoop :
First, you will need to create the namenode and datanode directories inside the Hadoop user home directory. Run the following command to create both directories:
$ cd hadoop/
$mkdir -p ~/hadoopdata/hdfs/{namenode,datanode}

- Next, edit the core-site.xml file and update with your system hostname:

$nano $HADOOP_HOME/etc/hadoop/core-site.xml

Change the following name as per your system hostname:

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

Save and close the file.

Then, edit the hdfs-site.xml file:
$nano $HADOOP_HOME/etc/hadoop/hdfs-site.xml

- Change the NameNode and DataNode directory paths as shown below:

```
<configuration>
    <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>
</configuration>
```

- Then, edit the mapred-site.xml file:
  $nano $HADOOP_HOME/etc/hadoop/mapred-site.xml

- Make the following changes:

```
<configuration>
   <property>
      <name>yarn.app.mapreduce.am.env</name>
      <value>HADOOP_MAPRED_HOME=$HADOOP_HOME/home/hadoop/hadoop/bin/hadoop</value>
   </property>
   <property>
      <name>mapreduce.map.env</name>
      <value>HADOOP_MAPRED_HOME=$HADOOP_HOME/home/hadoop/hadoop/bin/hadoop</value>
   </property>
   <property>
      <name>mapreduce.reduce.env</name>
      <value>HADOOP_MAPRED_HOME=$HADOOP_HOME/home/hadoop/hadoop/bin/hadoop</value>
   </property>
</configuration>
```

- Then, edit the yarn-site.xml file:
  $nano $HADOOP_HOME/etc/hadoop/yarn-site.xml
- Make the following changes:

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

Save the file and close it.

Step 12 – Start Hadoop Cluster

Before starting the Hadoop cluster. You will need to format the Namenode as a hadoop user.

Run the following command to format the Hadoop Namenode:

$hdfs namenode –format

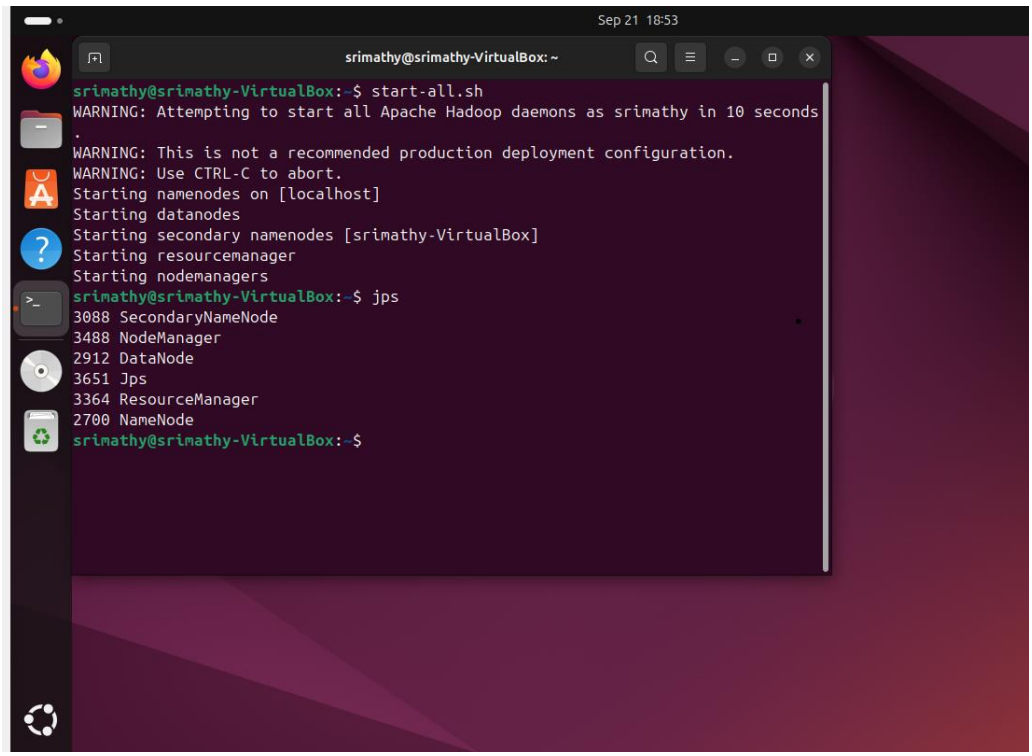
Once the namenode directory is successfully formatted with hdfs file system, you will see the message "Storage directory /home/hadoop/hadoopdata/hdfs/namenode has been successfully formatted "

Then start the Hadoop cluster with the following command.

$ start-all.sh

You can now check the status of all Hadoop services using the jps command:

$ jps

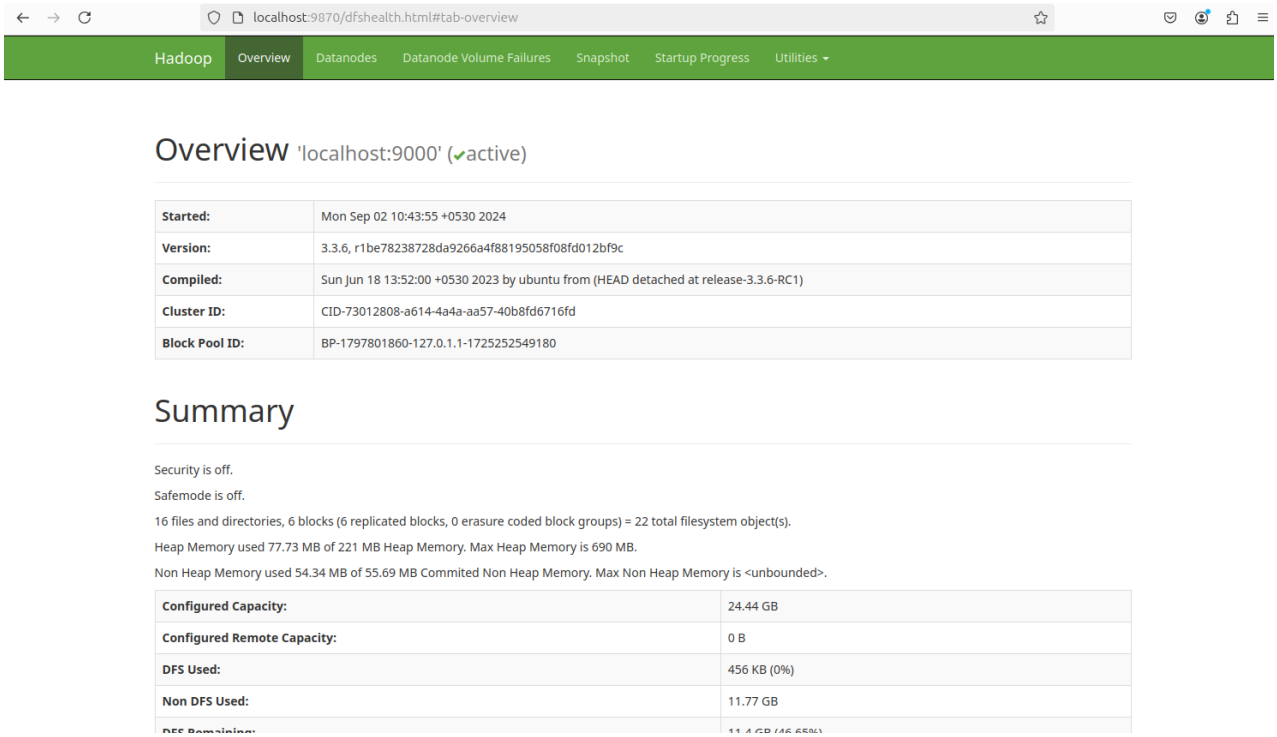


Step 13 – Access Hadoop Namenode and Resource Manager

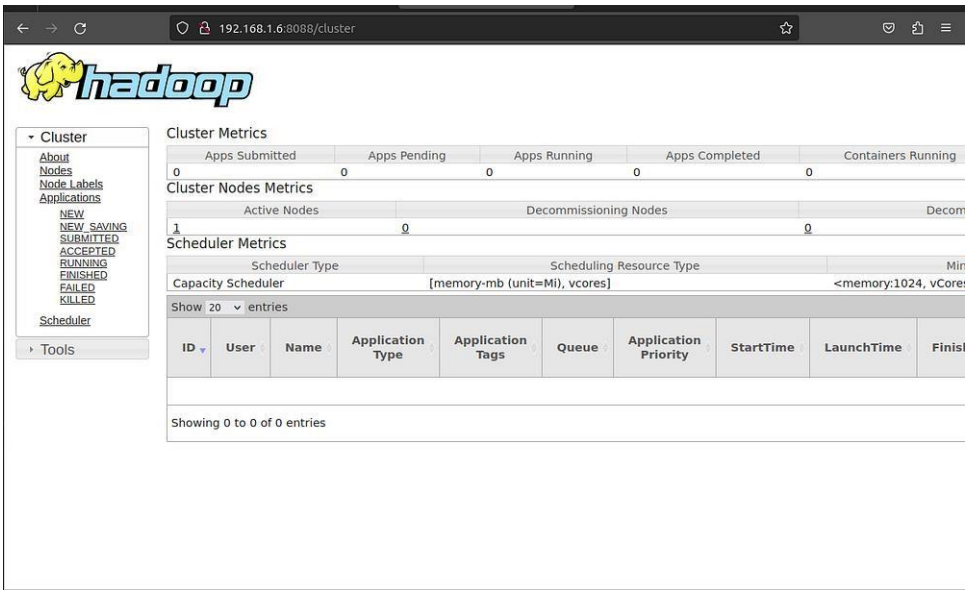
- First we need to know our ipaddress, In Ubuntu we need to install net-tools to run ipconfig command,
  If you installing net-tools for the first time switch to default user:
  $sudo apt install net-tools
- Then run ifconfig command to know our ip address: **ifconfig**

Here my ip address is 192.168.1.6.

- To access the Namenode, open your web browser and visit the URL http://your-serverip:9870.
- You should see the following screen:
  http://192.168.1.6:9870



To access Resource Manage, open your web browser and visit the URL http://your-serverip:8088. You should see the following screen: http://192.168.16:8088



Step 14 – Verify the Hadoop Cluster

At this point, the Hadoop cluster is installed and configured. Next, we will create some directories in the HDFS filesystem to test the Hadoop.

Let's create some directories in the HDFS filesystem using the following command:

```
$ hdfsdfs -mkdir /test1
$ hdfsdfs -mkdir /logs
```

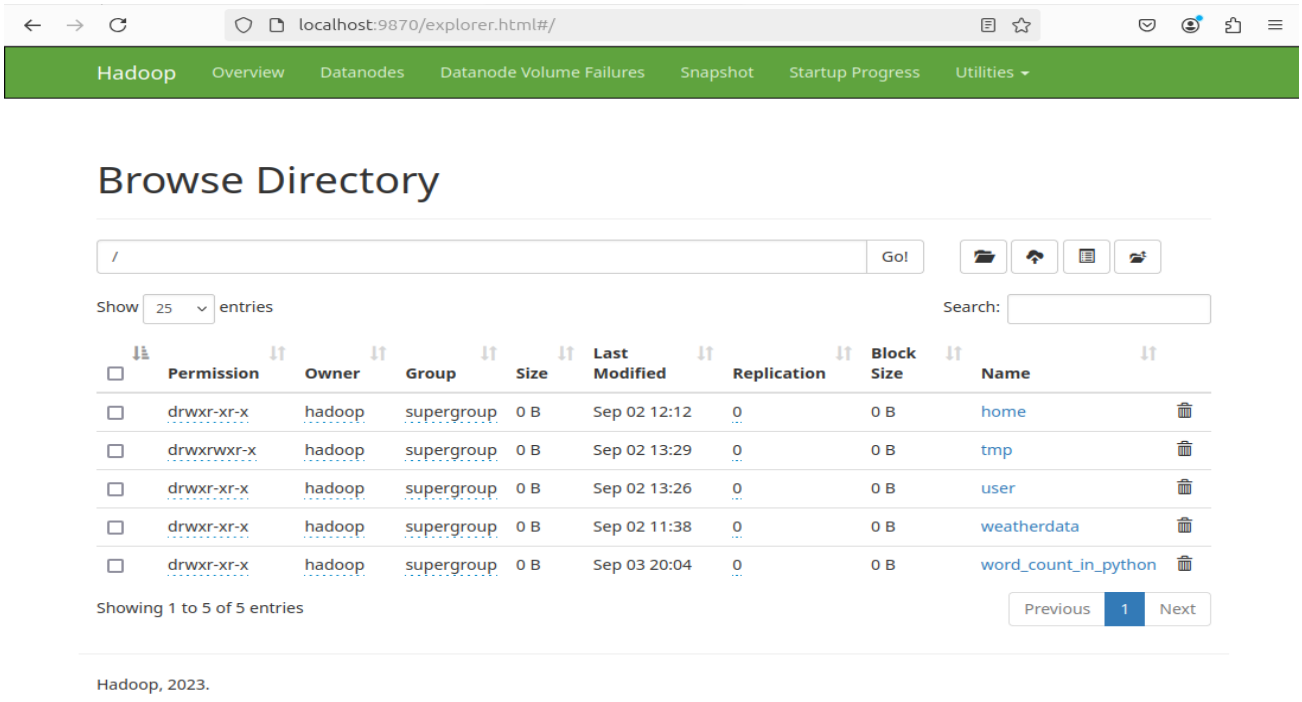
Next, run the following command to list the above directory:

Also, put some files to hadoop file system. For the example, putting log files from host machine to hadoop file system.

```
$ hdfs dfs -put /var/log/* /logs/
```

You can also verify the above files and directory in the Hadoop Namenode web interface.

Go to the web interface, click on the Utilities => Browse the file system. You should see your directories which you have created earlier in the following screen:



Step 15 – Stop Hadoop Cluster

To stop the Hadoop all services, run the following command:

```
$ stop-all.sh
```

```
srimathy@srimathy-VirtualBox:~$ jps
3088 SecondaryNameNode
3488 NodeManager
2912 DataNode
3651 Jps
3364 ResourceManager
2700 NameNode
srimathy@srimathy-VirtualBox:~$ stop-all.sh
WARNING: Stopping all Apache Hadoop daemons as srimathy in 10 seconds.
WARNING: Use CTRL-C to abort.
Stopping namenodes on [localhost]
Stopping datanodes
Stopping secondary namenodes [srimathy-VirtualBox]
Stopping nodemanagers
Stopping resourcemanager
srimathy@srimathy-VirtualBox:~$
```

Result:

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

Exp.No: 2

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

AIM:

To run a basic Word Count MapReduce program.

Procedure:

Step 1: Create Data File:

Create a file named "word_count_data.txt" and populate it with text data that you wish to analyse. Login with your hadoop user.

```
nano word_count.txt
```

Output: Type the below content in word_count.txt

Step 2: Mapper Logic - mapper.py:

Create a file named "mapper.py" to implement the logic for the mapper. The mapper will read input data from STDIN, split lines into words, and output each word with its count.

```
nano mapper.py
# Copy and paste the mapper.py code
```

```
#!/usr/bin/env python3
# import sys because we need to read and write data to STDIN and STDOUT
#!/usr/bin/python3
import sys
for line in sys.stdin:
    line = line.strip()    # remove leading and trailing whitespace
    words = line.split()   # split the line into words
    for word in words:
        print( '%s\t%s' % (word, 1))
```

.

Step 3: Reducer Logic - reducer.py:

Create a file named "reducer.py" to implement the logic for the reducer. The reducer will aggregate the occurrences of each word and generate the final output.

```
nano reducer.py
# Copy and paste the reducer.py code
```

reducer.py

```
#!/usr/bin/python3 from operator
import itemgetter 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( '%s\t%s' % (current_word, current_count))
current_count = count        current_word = word if
current_word == word:        print( '%s\t%s' %
(current_word, current_count))
```

Step 4: Prepare Hadoop Environment:

Start the Hadoop daemons and create a directory in HDFS to store your data.

```
start-all.sh hdfsdfs -mkdir /word_count_in_python hdfsdfs -copyFromLocal
/path/to/word_count.txt/word_count_in_python
```

Step 6: Make Python Files Executable:

Give executable permissions to your mapper.py and reducer.py files.

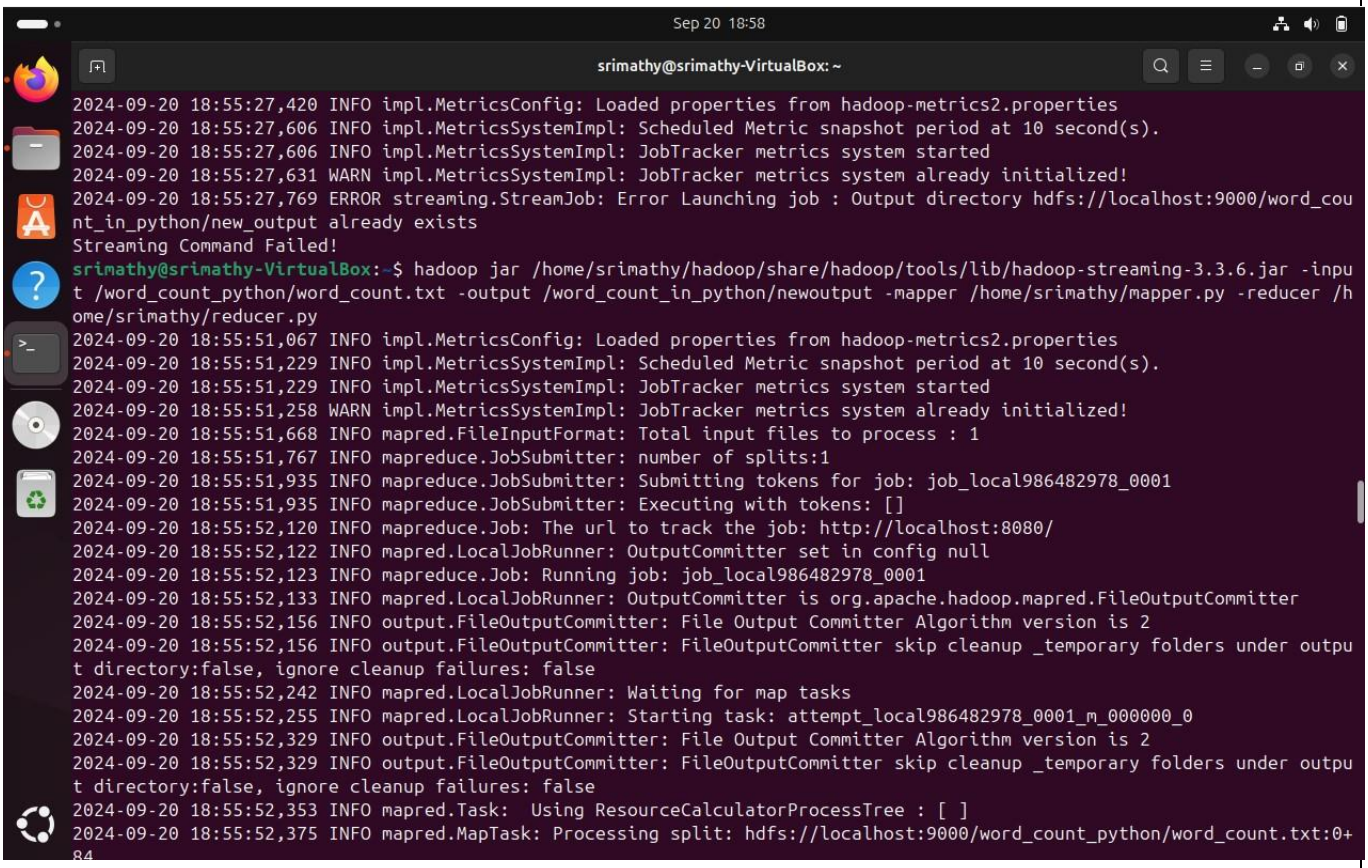
```
chmod 777 mapper.py reducer.py
```

Step 7: Run Word Count using Hadoop Streaming:

Download the latest hadoop-streaming jar file and place it in a location you can easily access.

Then run the Word Count program using Hadoop Streaming.

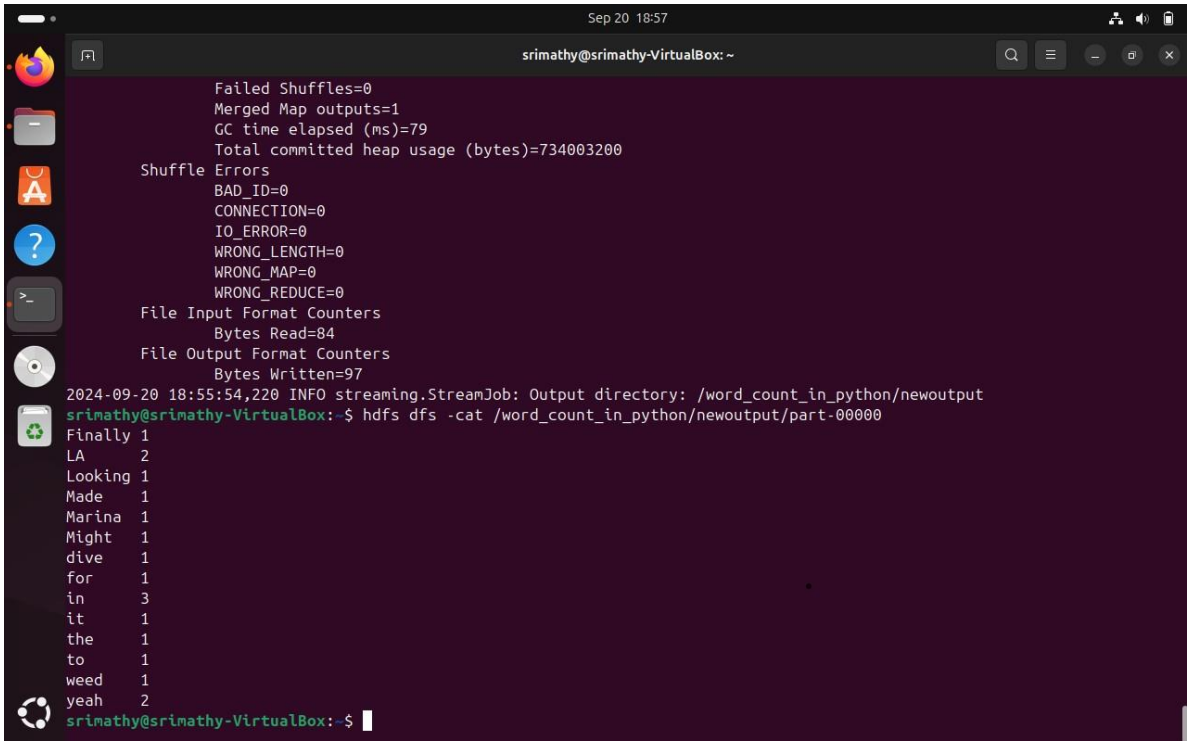
```
hadoop jar /path/to/hadoop-streaming-3.3.6.jar \     -input
/word_count_in_python/word_count_data.txt \
    -output /word_count_in_python/new_output \
    -mapper /path/to/mapper.py \
    -reducer /path/to/reducer.py
```



Step 8: Check Output:

Check the output of the Word Count program in the specified HDFS output directory.

hdfs dfs -cat /word_count_in_python/new_output/part-00000



Result:

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

Reg.No.: 210701260

Exp.No.: 3 Map Reduce program to process a weather dataset

AIM:

To implement MapReduce program to process a weather dataset.

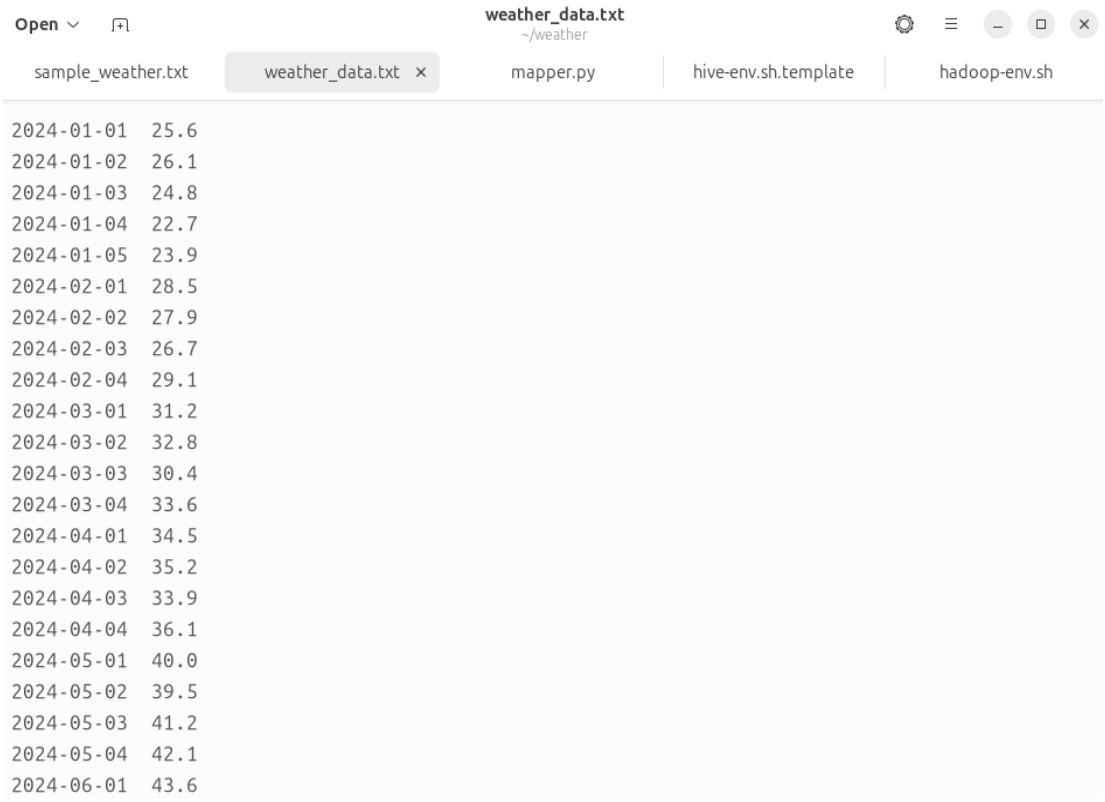
Procedure:

Step 1: Create Data File:

Create a file named "word_count_data.txt" and populate it with text data that you wish to analyse. Login with your hadoop user.

Download the dataset (weather data)

Output:



Step 2: Mapper Logic - mapper.py:

Create a file named "mapper.py" to implement the logic for the mapper. The mapper will read input data from STDIN, split lines into words, and output each word with its count.

```
nano mapper.py
# Copy and paste the mapper.py code
```

```
#!/usr/bin/env python

import sys

# input comes from STDIN (standard input)
# the mapper will get daily max temperature and group it by month. so output will be
(month,dailymax_temperature)
```

```
for line in sys.stdin:
   # remove leading and trailing whitespace
   line = line.strip()    # split
the line into words    words =
line.split()
   #See the README hosted on the weather website  which help us understand how each
position represents a column    month = line[10:12]    daily_max = line[38:45]    daily_max
= daily_max.strip()
   # increase counters    for
word in words:
      # write the results to STDOUT (standard output);
      # what we output here will be go through the shuffle proess and then
      # be the input for the Reduce step, i.e. the input for reducer.py
      #
      # tab-delimited; month and daily max temperature as output
print ('%s\t%s' % (month ,daily_max))
```

.

Step 3: Reducer Logic - reducer.py:

Create a file named "reducer.py" to implement the logic for the reducer. The reducer will aggregate the occurrences of each word and generate the final output.

```
nano reducer.py
# Copy and paste the reducer.py code
```

reducer.py

```
#!/usr/bin/env python

from operator import itemgetter import sys
#reducer will get the input from stdid which will be a collection of key, value(Key=month , value=
daily max temperature)
#reducer logic: will get all the daily max temperature for a month and find max temperature for the
month
#shuffle will ensure that key are sorted(month)
current_month = None
current_max = 0 month =
None

# input comes from STDIN for
line in sys.stdin:
   # remove leading and trailing whitespace    line
= line.strip()
   # parse the input we got from mapper.py    month,
daily_max = line.split('\t', 1)

   # convert daily_max (currently a string) to float    try:
```

```
        daily_max = float(daily_max)      except
ValueError:
        # daily_max was not a number, so silently
        # ignore/discard this line
continue

    # this IF-switch only works because Hadoop shuffle process sorts map output
    # by key (here: month) before it is passed to the reducer
if current_month == month:          if daily_max > current_max:
current_max = daily_max      else:          if current_month:
            # write result to STDOUT
            print ('%s\t%s' % (current_month, current_max))
current_max = daily_max
        current_month = month

# output of the last month if current_month == month:
print ('%s\t%s' % (current_month, current_max))
```

Step 4: Prepare Hadoop Environment:

Start the Hadoop daemons and create a directory in HDFS to store your data.

```
start-all.sh
```

Step 6: Make Python Files Executable:

Give executable permissions to your mapper.py and reducer.py files.

```
chmod 777 mapper.py reducer.py
```

Step 7: Run the program using Hadoop Streaming:

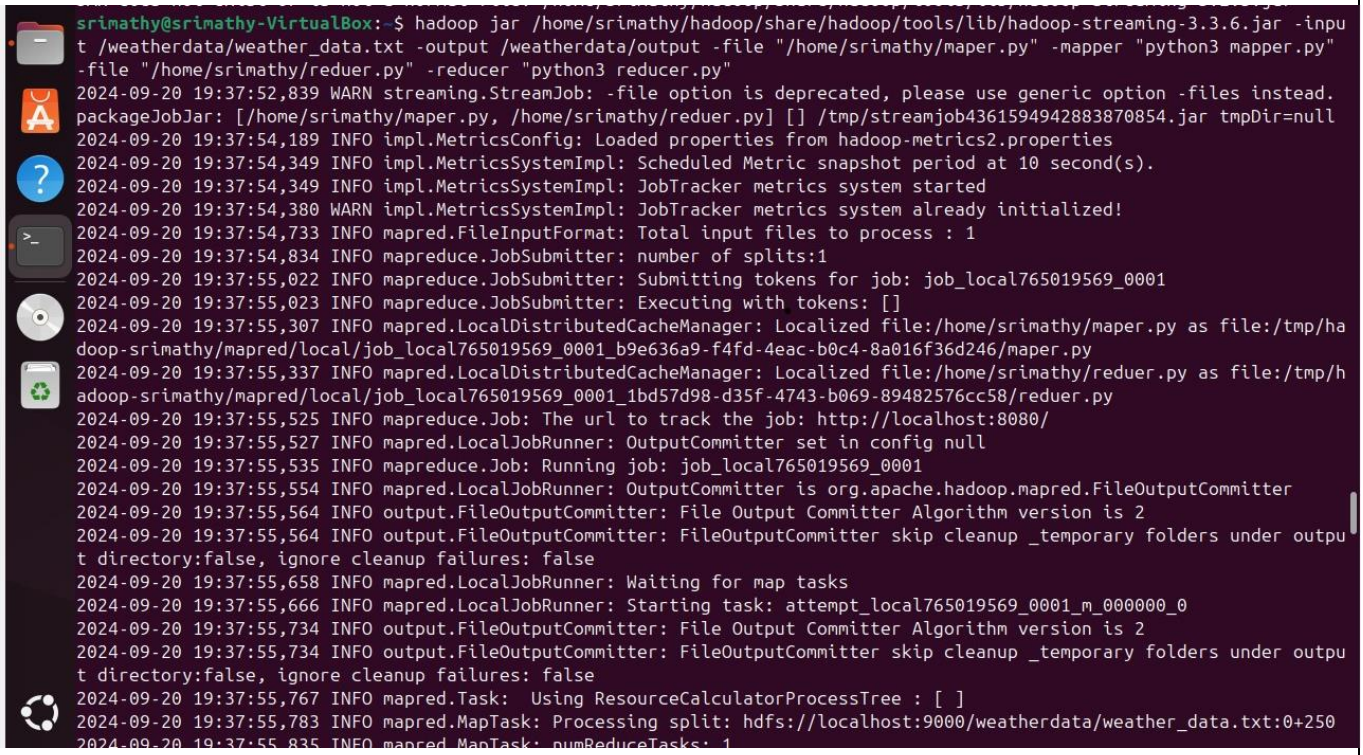
Download the latest hadoop-streaming jar file and place it in a location you can easily access.

Then run the program using Hadoop Streaming.

```
hadoop fs -mkdir -p /weatherdata

hadoop fs -copyFromLocal /home/sx/Downloads/dataset.txt /weatherdata

hdfs dfs -ls /weatherdata

hadoop jar /home/sx/hadoop-3.2.3/share/hadoop/tools/lib/hadoop-streaming-3.2.3.jar \
  -input /weatherdata/dataset.txt \
  -output /weatherdata/output \
```

```
-file "/home/sx/Downloads/mapper.py" \
-mapper "python3 mapper.py" \
-file "/home/sx/Downloads/reducer.py" \
-reducer "python3 reducer.py"
```

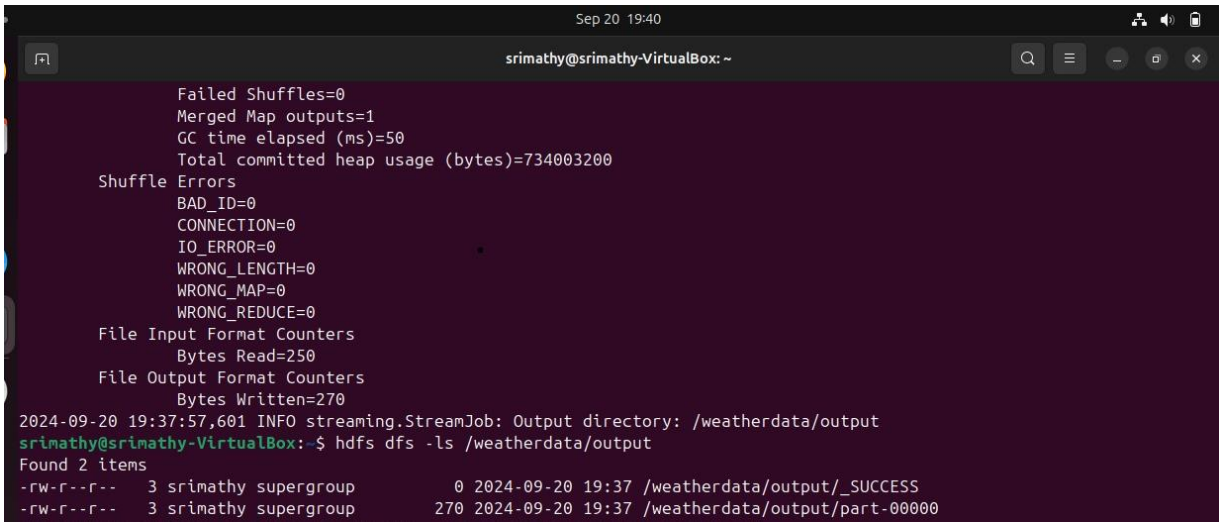
hdfs dfs -text /weatherdata/output/* > /home/sx/Downloads/outputfile.txt



Step 8: Check Output:

Check the output of the program in the specified HDFS output directory.

hdfs dfs -text /weatherdata/output/* > /home/sx/Downloads/output/ /part-00000



After copy and paste the above output in your local file give the below command to remove the directory from hdfs : hadoop fs -rm -r /weatherdata/output

Result:

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

Exp.No.: 4 **Create UDF in PIG**

Step-by-step installation of Apache Pig on Hadoop cluster on Ubuntu Pre-requisite:

· Ubuntu 16.04 or higher version running (I have installed Ubuntu on Oracle VM (Virtual Machine) VirtualBox),

· Run Hadoop on ubuntu (I have installed Hadoop 3.2.1 on Ubuntu 16.04). You may refer to my blog "How to install Hadoop installation" click here for Hadoop installation).

Pig installation steps

Step 1: Login into Ubuntu

Step 2: Go to https://pig.apache.org/releases.html and copy the path of the latest version of pig that you want to install. Run the following comment to download Apache Pig in Ubuntu:

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

Step 3: To untar pig-0.16.0.tar.gz file run the following command:

$ tar xvzf pig-0.16.0.tar.gz

Step 4: To create a pig folder and move pig-0.16.0 to the pig folder, execute the following command:

$ sudo mv /home/hadoop/pig-0.16.0 /home/hadoop/pig

Step 5: Now open the .bashrc file to edit the path and variables/settings for pig. Run the following command:

$ sudo nano .bashrc

Add the below given to .bashrc file at the end and save the file.

#PIG settingsexport PIG_HOME=/home/hdoop/pigexport
PATH=$PATH:$PIG_HOME/binexport

PIG_CLASSPATH=$PIG_HOME/conf:$HADOOP_INSTALL/etc/hadoop/export PIG_CONF_DIR=$PIG_HOME/confexport JAVA_HOME=/usr/lib/jvm/java-8-openjdkamd64export PIG_CLASSPATH=$PIG_CONF_DIR:$PATH#PIG setting ends

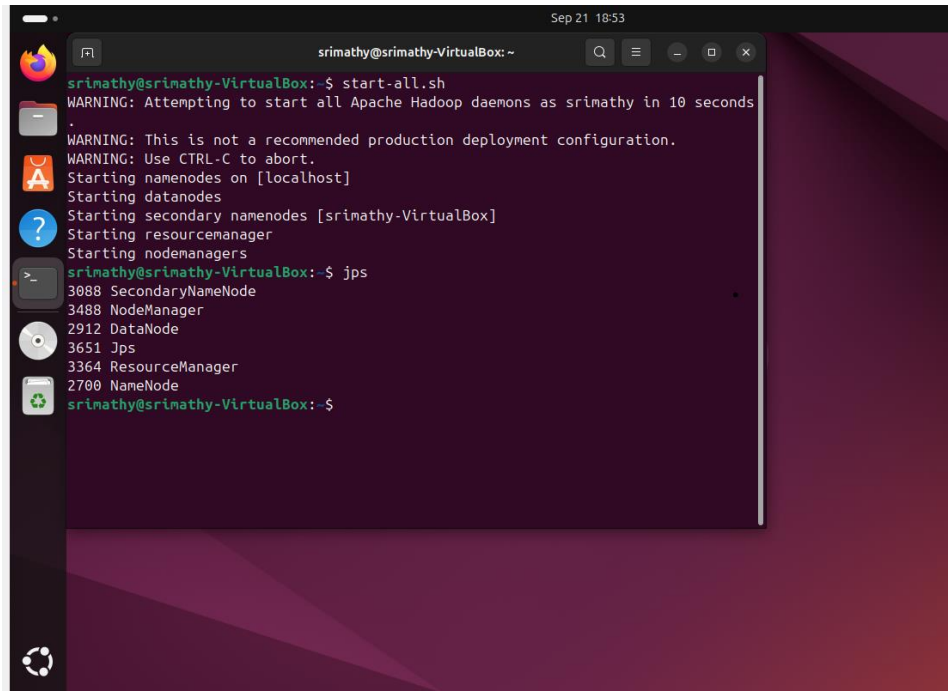
```
 GNU nano 7.2                          .bashrc

export JAVA_HOME=/usr/lib/jvm/java-11-openjdk-amd64
export HADOOP_HOME=/home/hadoop/hadoop
export HADOOP_INSTALL=$HADOOP_HOME
export HADOOP_MAPRED_HOME=$HADOOP_HOME
export HADOOP_COMMON_HOME=$HADOOP_HOME
export HADOOP_HDFS_HOME=$HADOOP_HOME
export HADOOP_YARN_HOME=$HADOOP_HOME
export HADOOP_COMMON_LIB_NATIVE=$HADOOP_HOME/lib/native
export PATH=$PATH:$HADOOP_HOME/bin:$HADOOP_HOME/sbin
export HADOOP_OPTS="-Djava.library.path=$HADOOP_HOME/lib/native"


# PIG settings
export PIG_HOME=/home/hadoop/pig
export PATH=$PATH:$PIG_HOME/bin
export PIG_CLASSPATH=$PIG_HOME/conf:$HADOOP_INSTALL/etc/hadoop
export PIG_CONF_DIR=$PIG_HOME/conf
export JAVA_HOME=/usr/lib/jvm/java-11-openjdk-amd64
export PIG_CLASSPATH=$PIG_CONF_DIR:$PIG_CLASSPATH
# PIG settings end
```

Step 6: Run the following command to make the changes effective in the .bashrc file:

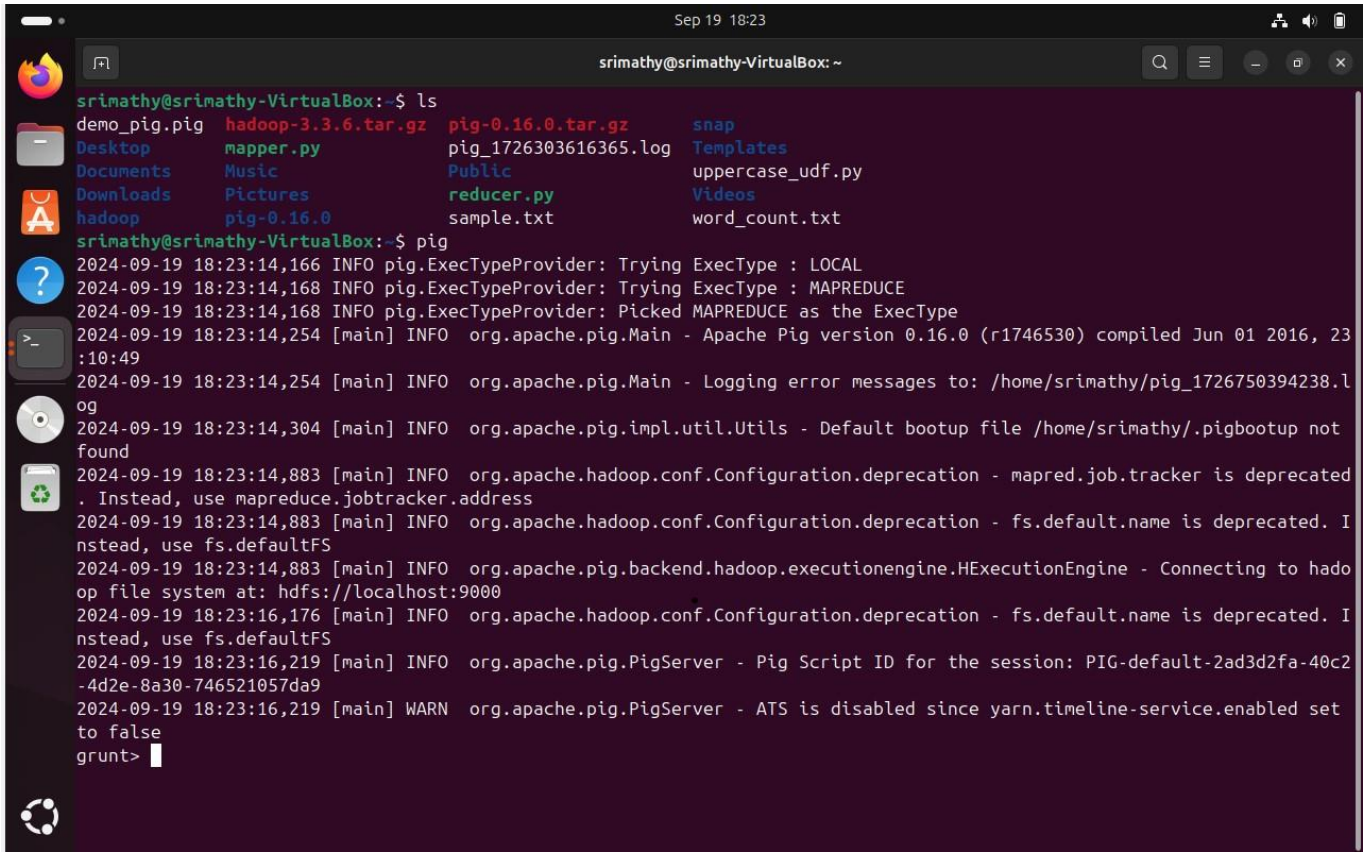
$ source .bashrc

Step 7: To start all Hadoop daemons, navigate to the hadoop-3.2.1/sbin folder and run the following commands:

$ ./start-dfs.sh$ ./start-yarn$ jps



Step 8: Now you can launch pig by executing the following command: $ pig



Step 9: Now you are in pig and can perform your desired tasks on pig. You can come out of the pig by the quit command:

> quit;

Reg.No.: 210701260

CREATE USER DEFINED FUNCTION(UDF)

Aim :

To create User Define Function in Apache Pig and execute it on map reduce.

PROCEDURE:

Create a sample text file

hadoop@Ubuntu:~/Documents$ nano sample.txt

Paste the below content to sample.txt

1,John

2,Joe

3,Emma

4,Peter

hadoop@Ubuntu:~/Documents$ hadoop fs -put sample.txt /home/hadoop/piginput/

Create PIG File

hadoop@Ubuntu:~/Documents$ nano demo_pig.pig

paste the below the content to demo_pig.pig

-- Load the data from HDFS

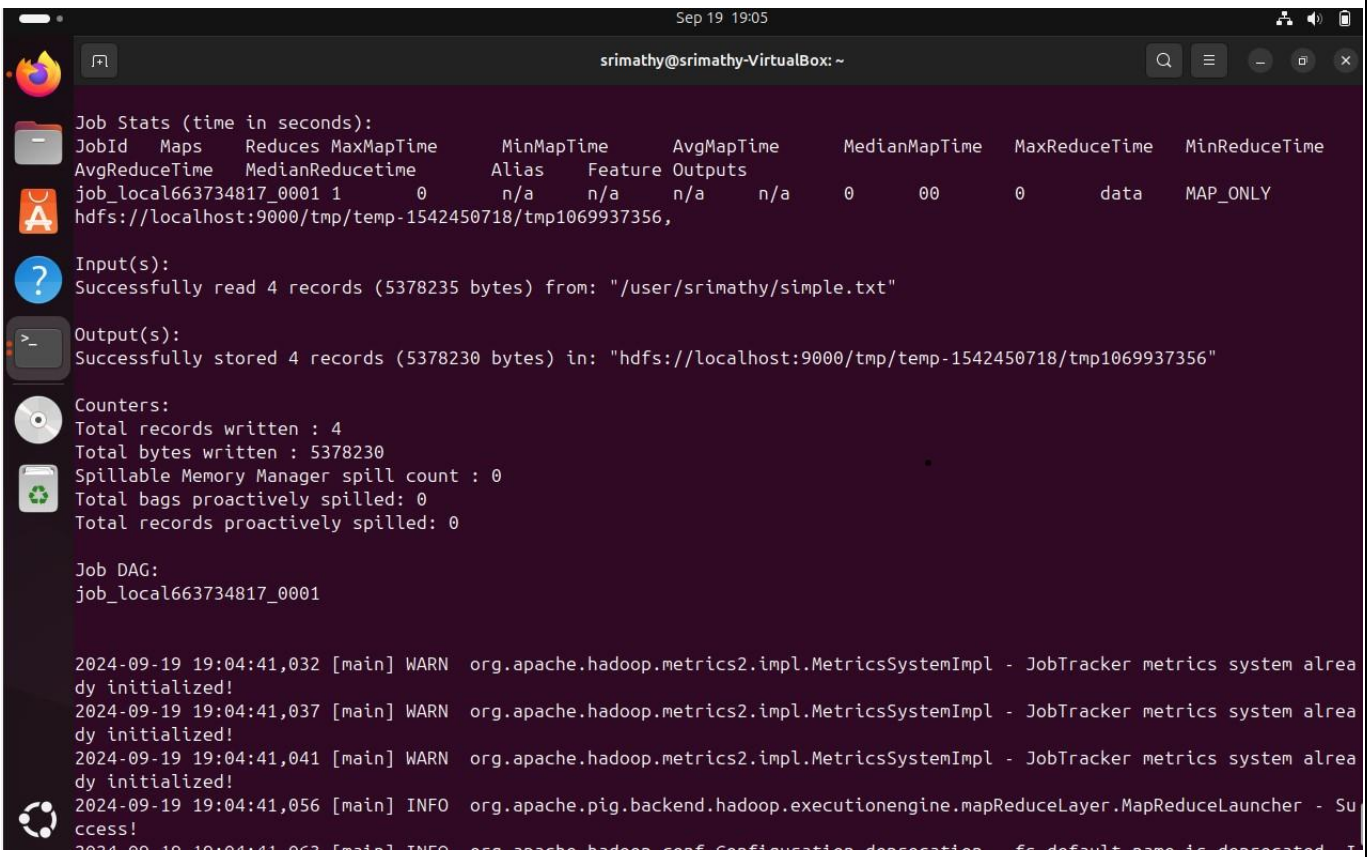
data = LOAD '/home/hadoop/piginput/sample.txt' USING PigStorage(',') AS (id:int>

-- Dump the data to check if it was loaded correctly

DUMP data;

---------- **Run the above file**

hadoop@Ubuntu:~/Documents$ pig demo_pig.pig



Create udf file an save as uppercase_udf.py

uppercase_udf.py

```
def uppercase(text): return text.upper()


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

Create the udfs folder on hadoop

hadoop@Ubuntu:~/Documents$ hadoop fs -mkdir /home/hadoop/udfs

put the upppercase_udf.py in to the abv folder

hadoop@Ubuntu:~/Documents$ hdfs dfs -put uppercase_udf.py /home/hadoop/udfs/

hadoop@Ubuntu:~/Documents$ nano udf_example.pig copy and paste the below content on udf_example.pig

-- Register the Python UDF script

```
REGISTER 'hdfs:///home/hadoop/udfs/uppercase_udf.py' USING jython AS udf;

-- Load some data
data = LOAD 'hdfs:///home/hadoop/sample.txt' AS (text:chararray);

-- Use the Python UDF
uppercased_data = FOREACH data GENERATE udf.uppercase(text) AS uppercase_text;

-- Store the result
STORE uppercased_data INTO 'hdfs:///home/hadoop/pig_output_data';
```

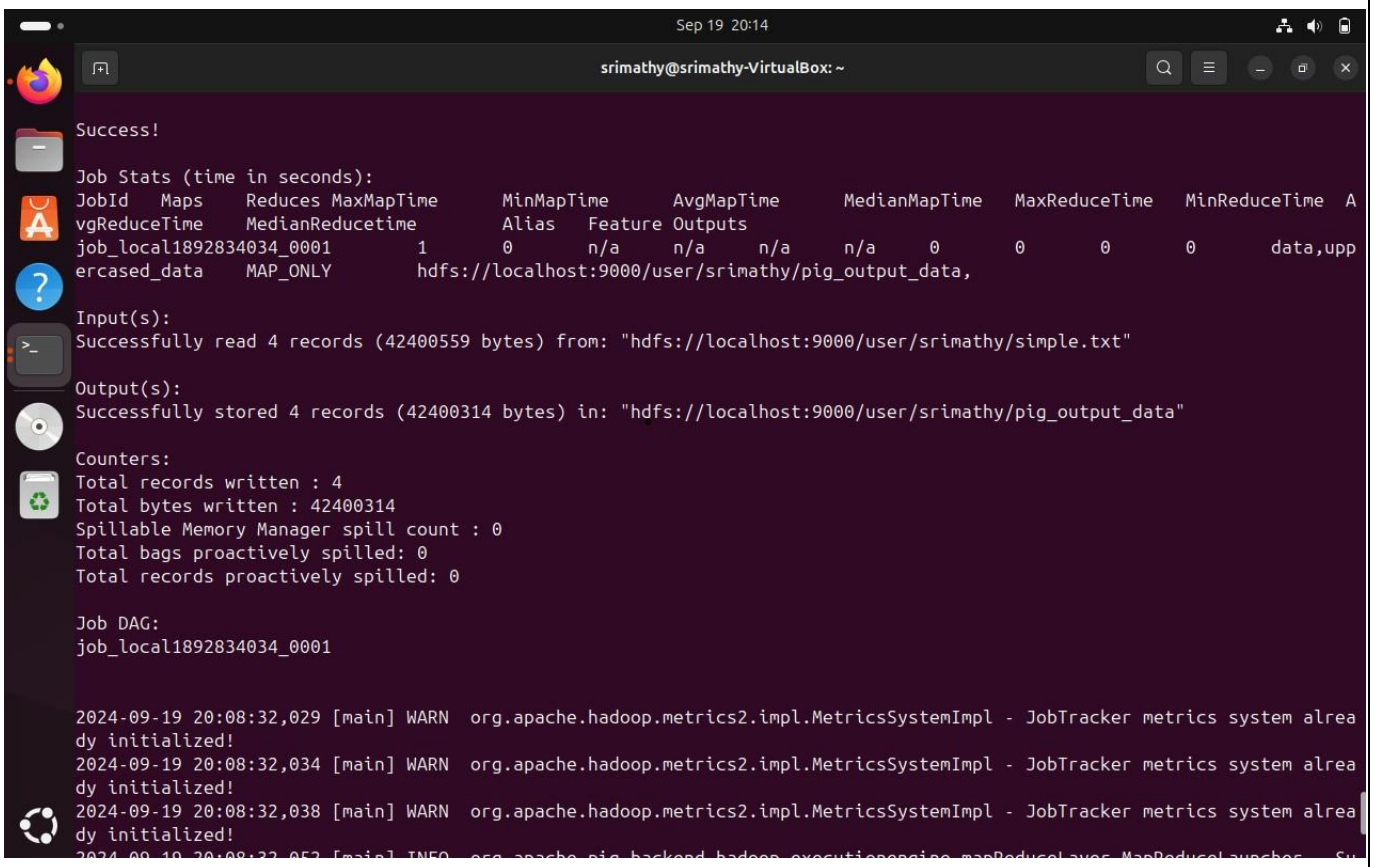
---

place sample.txt file on hadoop

hadoop@Ubuntu:~/Documents$ hadoop fs -put sample.txt /home/hadoop/

To Run the pig file

hadoop@Ubuntu:~/Documents$ pig -f udf_example.pig



To check the output file is created

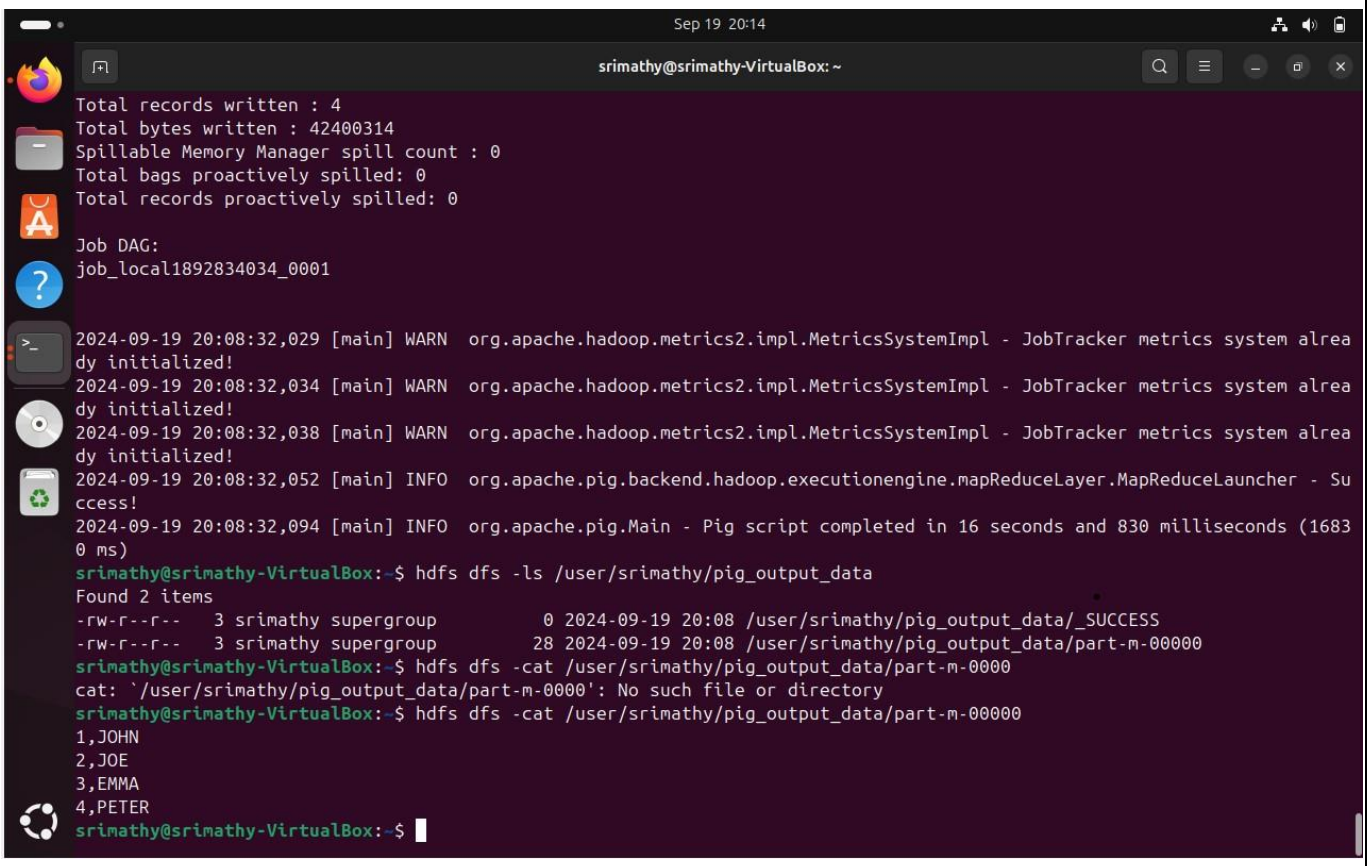
hadoop@Ubuntu:~/Documents$ hdfs dfs -ls /home/hadoop/pig_output_data

Found 2 items

If you need to examine the files in the output folder, use:

To view the output

hadoop@Ubuntu:~/Documents$ hdfs dfs -cat /home/hadoop/pig_output_data/part-m00000



Result:

Thus the program to create User Define Function in Apache Pig and execute it on map reduce has been done successfully.

Exp.No.:5 **Installation of Hive on Ubuntu**

Aim:

To Download and install Hive, Understanding Startup scripts, Configuration files.

Procedure:

Step 1: Download and extract it

Download the Apache hive and extract it use tar, the commands given below:

$wgethttps://downloads.apache.org/hive/hive-3.1.2/apache-hive-3.1.2-bin.tar.gz

```
/apache-hive-3.1.2-bin.tar.gz
--2024-09-02 12:26:15--  https://archive.apache.org/dist/hive/hive-3.1.2/apache-
hive-3.1.2-bin.tar.gz
Resolving archive.apache.org (archive.apache.org)... 65.108.204.189, 2a01:4f9:1a
:a084::2
Connecting to archive.apache.org (archive.apache.org)|65.108.204.189|:443... con
nected.
HTTP request sent, awaiting response... 200 OK
Length: 278813748 (266M) [application/x-gzip]
Saving to: ‘apache-hive-3.1.2-bin.tar.gz’

apache-hive-3.1.2-b 100%[===================>] 265.90M  1.20MB/s    in 2m 57s

2024-09-02 12:29:13 (1.50 MB/s) - ‘apache-hive-3.1.2-bin.tar.gz’ saved [27881374
8/278813748]
```

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

```
apache-hive-3.1.2-bin/LICENSE
apache-hive-3.1.2-bin/NOTICE
apache-hive-3.1.2-bin/RELEASE_NOTES.txt
apache-hive-3.1.2-bin/binary-package-licenses/asm-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/com.google.protobuf-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/com.ibm.icu.icu4j-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/com.sun.jersey-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/com.thoughtworks.paranamer-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/javax.transaction.transaction-api-
LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/javolution-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/jline-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/NOTICE
apache-hive-3.1.2-bin/binary-package-licenses/org.abego.treelayout.core-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/org.antlr-LICENSE
apache-hive-3.1.2-bin/binary-package-licenses/org.antlr.antlr4-LICENSE
```

Step 2: Place different configuration properties in Apache Hive

In this step, we are going to do two things ○ Placing

Hive Home path in bashrc file

$*nano .bashrc*

And append the below lines in it

```
#HIVE settings
export HIVE_HOME=/home/hadoop/apache-hive-3.1.2
export PATH=$PATH:$HIVE_HOME/bin
#HIVE settings end
```

2. Exporting **Hadoop path in Hive-config.sh** (To communicate with the Hadoop eco system we are defining Hadoop Home path in hive config field) **Open the hiveconfig.sh as shown in below** *$cd apache-hive-3.1.2-bin/bin*
$cp hive-env.sh.template hive-env.sh
$nano hive-env.sh
Append the below commands on it export HADOOP_HOME=/home/Hadoop/Hadoop
export HIVE_CONF_DIR=/home/Hadoop/apache-hive-3.1.2/conf

```
# Set HADOOP_HOME to point to a specific hadoop install directory
# HADOOP_HOME=${bin}/../../hadoop
export HADOOP_HOME=/home/hadoop/hadoop


# Hive Configuration Directory can be controlled by:
# export HIVE_CONF_DIR=
export HIVE_CONF_DIR=/home/hadoop/apache-hive-3.1.2-bin/conf
# Folder containing extra libraries required for hive compilation/execution can be controlled by:
```

Step 3: Install mysql

1. Install mysql in Ubuntu by running this command:

$sudo apt update
$sudo apt install mysql-server

2. *Alter username and password for MySQLby running below commands:*
$sudomysql

Pops command line interface for MySQLand run the below SQL queries to change username and set password
mysql> SELECT user, host, plugin FROM mysql.user WHERE user = 'root';
mysql> ALTER USER 'root'@'localhost' IDENTIFIED WITH 'mysql_native_password' BY 'your_new_password';
mysql> FLUSH PRIVILEGES;

Step 4:Config hive-site.xml

Config the hive-site.xml by appending this xml code and change the username and password according to your MySQL.
$cd apache-hive-3.1.2-bin/bin
$cp hive-default.xml.template hive-site.xml
$nano hive-site.xml
Append these lines into it
Replace root as your username of MySQL
Replaceyour_new_password as with your password of MySQL
<configuration>
<property>
<name>javax.jdo.option.ConnectionURL</name>
<value>jdbc:mysql://localhost/metastore?createDatabaseIfNotExist=true</value>
</property>

```
<property>
<name>javax.jdo.option.ConnectionDriverName</name>
<value>com.mysql.cj.jdbc.Driver</value>
</property>

<property>
<name>javax.jdo.option.ConnectionUserName</name>
<value>root</value>
</property>

<property>
<name>javax.jdo.option.ConnectionPassword</name>
<value>your_new_password</value>
</property>

<property>
<name>datanucleus.autoCreateSchema</name>
<value>true</value>
</property>

<property>
<name>datanucleus.fixedDatastore</name>
<value>true</value>
</property>

<property>
<name>datanucleus.autoCreateTables</name>
<value>True</value>
</property>

</configuration>
```

Step 5: Setup MySQL java connector:

First, you'll need to download the MySQL Connector/J, which is the JDBC driver for MySQL. You can download it from the below link

https://drive.google.com/file/d/1QFhB7Kvcat7a4LzDRe6GcmZva1yAxKz/view?usp=drive_link

Copy the downloaded MySQL Connector/J JAR file to the Hive library directory. By default, the Hive library directory is usually located at*/path/to/apache-hive-3.1.2/lib/*on Ubuntu. Use the following command to copy the JAR file:

$sudo cp /path/to/mysql-connector-java-8.0.15.jar /path/to/apache-hive-3.1.2/lib/ Replace /path/to/ with the actual path to the JAR file.

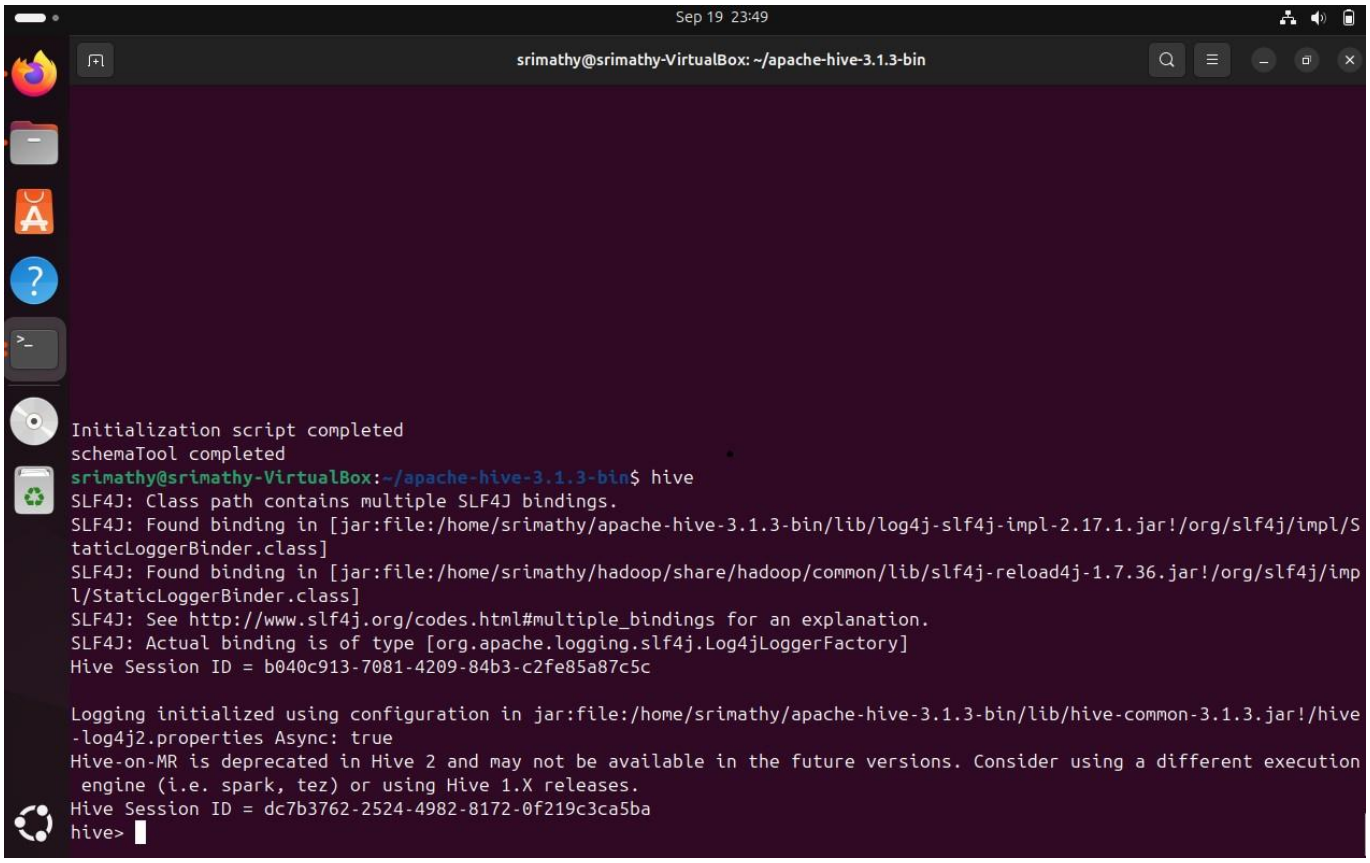
Step 6:Initialize the Hive Metastore Schema:

Run the following command to initialize the Hive metastore schema:

$$HIVE_HOME/bin/schematool -initSchema -dbTypemysql

Step 7: Start hive:

You can test Hive by running the Hive shell: Copy code hive You should be able to run Hive queries, and metadata will be stored in your MySQL database. *$hive*



Result:

Thus, the Apache Hive installation is completed successfully on Ubuntu.

Exp.No.: 5a

Design and test various schema models to optimize data storage and retrieval Using Hive

Aim:

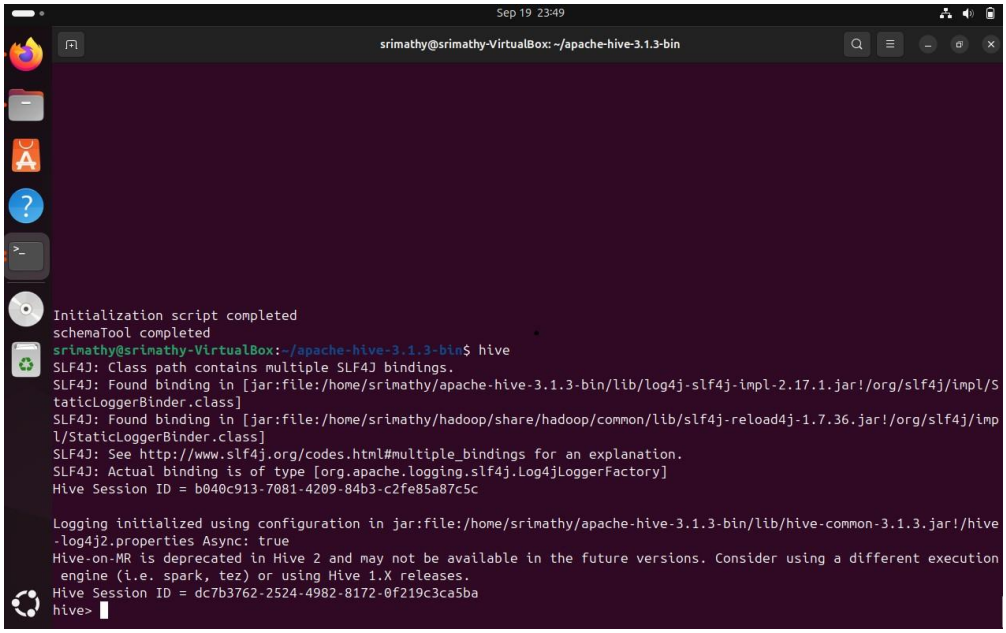
To Design and test various schema models to optimize data storage and retrieval Using Hbase.

Procedure:

Step 1: Start Hive

Open a terminal and start Hive by running:

$hive



Step 2: Create a Database

Create a new database in Hive: hive>CREATE DATABASE financials;

```
hive> CREATE DATABASE financials;
OK
Time taken: 0.063 seconds
```

Step 3: Use the Database*:*

Switch to the newly created database: hive>use financials;

Step 4: Create a Table:

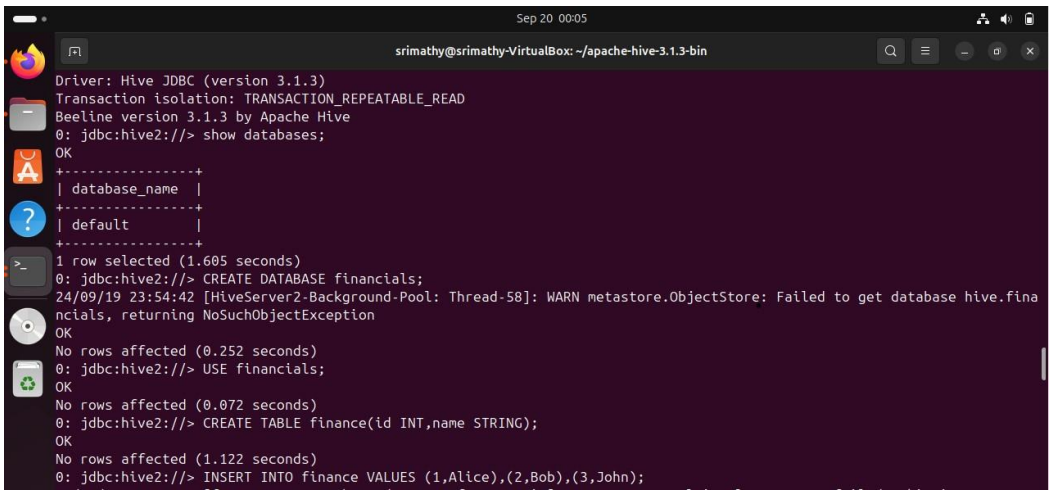
Create a simple table in your database:

hive>CREATE TABLE finance_table(id INT, name STRING);

Step 5: Load Sample Data:

You can insert sample data into the table:

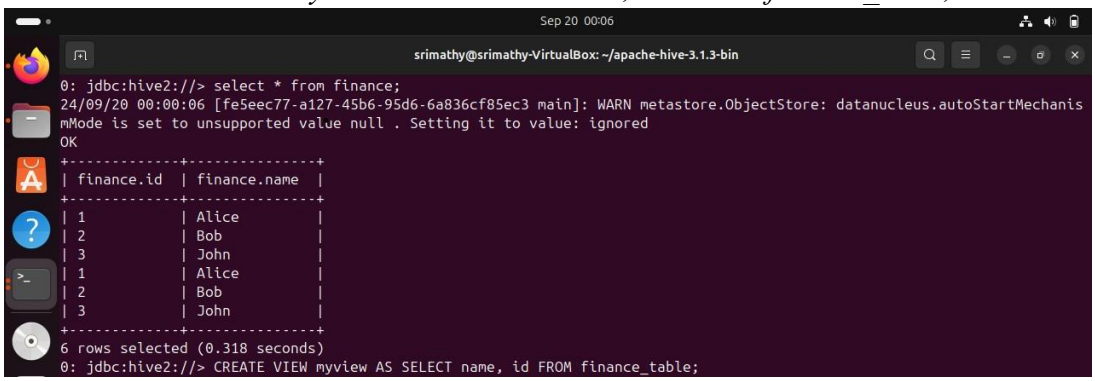
hive>INSERT INTO finance_tableVALUES (1, 'Alice'), (2, 'Bob'), (3, 'Charlie');



Step 6: Query Your Data

Use SQL-like queries to retrieve data from your table:

hive>CREATE VIEW myview AS SELECT name, id FROM finance_table;



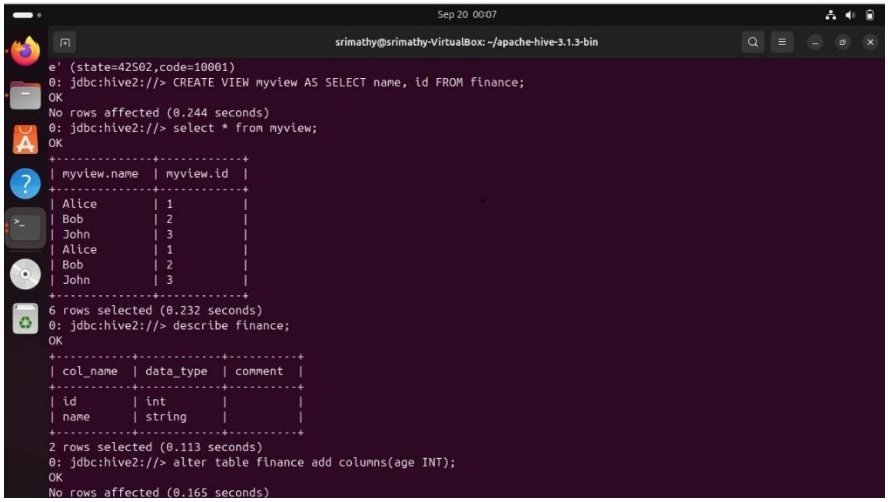
Step 7: View the data:

*To see the data in the view, you would need to query the view hive>SELECT*FROM myview;*

Step 8: Describe a Table:

You can describe the structure of a table using the DESCRIBE command:

hive>DESCRIBE finance_table;

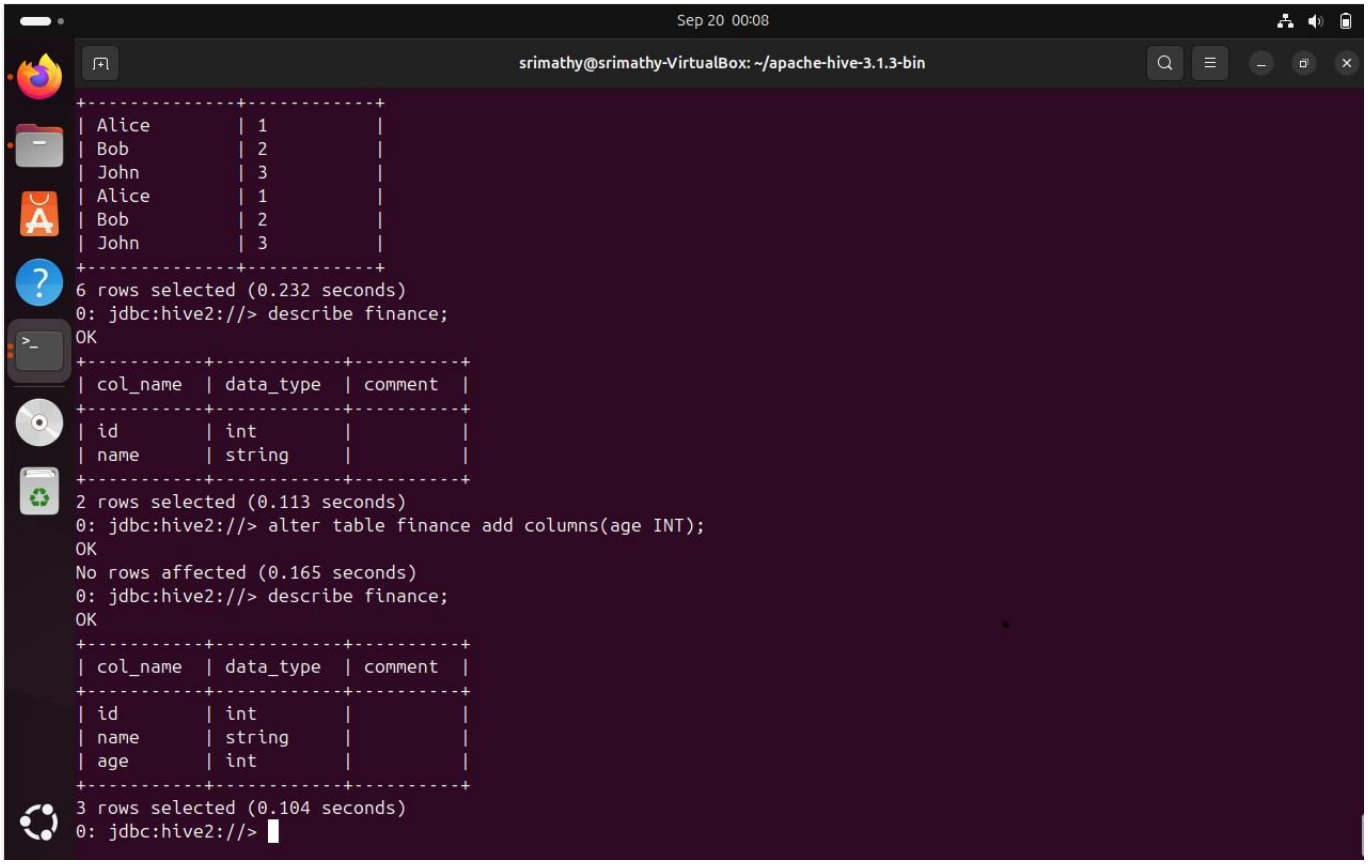


Step 9: Alter a Table:

You can alter the table structure by adding a new column: hive>ALTER TABLE finance_table ADD COLUMNS (age INT);

Step 10: Quit Hive:

To exit the Hive CLI, simply type: hive>quit;



Result:

Thus, the usage of various commands in Hive has been successfully completed.

Ex.No.: 6

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

AIM:
To import a JASON file from the command line and apply the following actions with the data present in the JASON file where, projection, aggregation, remove, count, limit, skip and sort.

PROCEDURE:
1. Required Packages Installation
• Install Pandas
Pandas is required for manipulating and analyzing data.
Installation:
▪ pip install pandas
• Install HDFS
HDFS provides a Python interface to interact with Hadoop Distributed File System (HDFS).
Installation:
▪ pip install hdfs
• Optional Packages
These packages may help when working with large datasets or different formats:
o PyArrow (for Apache Arrow support):
▪ pip install pyarrow
o HDFS3 (alternative to HDFS):
▪ pip install hdfs3

2. Create a json file (for example: emp.json) with the following content:

```
[
   {"name": "Alice", "salary": 60000, "department": "HR"},
   {"name": "Bob", "salary": 55000, "department": "Finance"},
   {"name": "Charlie", "salary": 70000, "department": "IT"},
   {"name": "David", "salary": 45000, "department": "Sales"},
   {"name": "Eve", "salary": 80000, "department": "IT"}
]
```

3. Copy the json file to the hdfs directory using the command:
$ hdfs dfs copyFromLocal /path/to/emp.json /home/hadoop
Also give the necessary permissions if not already given using the command:
$ hdfs dfs -chmod 777 /home/hadoop

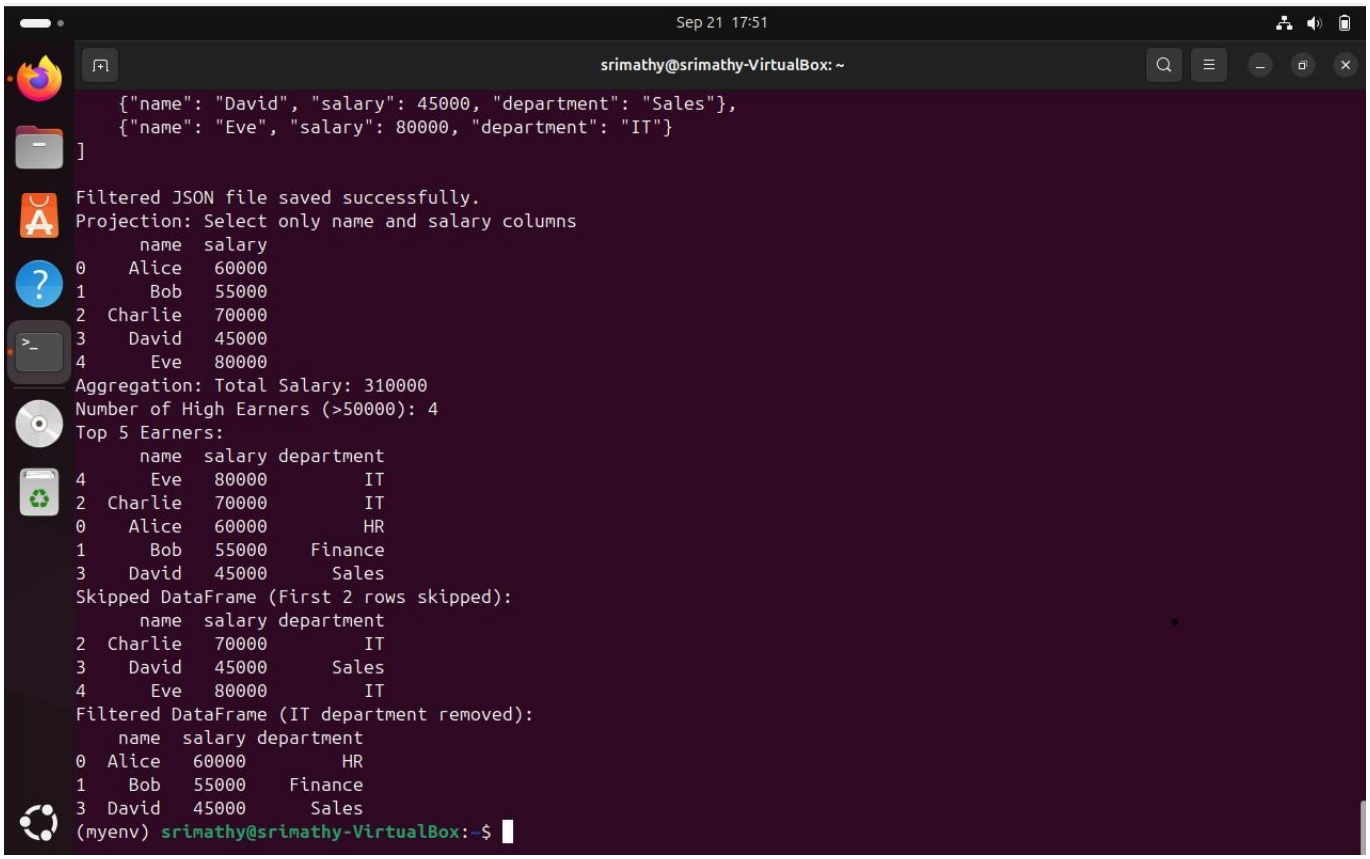
4. Python Script: process_data.py
The following script reads a JSON file from HDFS, processes it using Pandas, and performs several operations such as projection, aggregation, counting, limiting, skipping, and filtering.

```
#process_data.py
from hdfs import InsecureClient
import pandas as pd
import json
# Connect to HDFS
hdfs_client = InsecureClient('http://localhost:9870', user='hdfs')
# Read JSON data from HDFS
try:
with hdfs_client.read('/home/hadoop/emp.json', encoding='utf-8') as reader:
json_data = reader.read()  # Read the raw data as a string
if not json_data.strip():  # Check if data is empty
raise ValueError("The JSON file is empty.")
print(f"Raw JSON Data: {json_data[:1000]}")  # Print first 1000 characters for debugging
data = json.loads(json_data)  # Load the JSON data
except json.JSONDecodeError as e:
print(f"JSON Decode Error: {e}")
exit(1)
except Exception as e:
print(f"Error reading or parsing JSON data: {e}")
exit(1)
# Convert JSON data to DataFrame
try:
df = pd.DataFrame(data)
except ValueError as e:
print(f"Error converting JSON data to DataFrame: {e}")
exit(1)
# Projection: Select only 'name' and 'salary' columns
projected_df = df[['name', 'salary']]
# Aggregation: Calculate total salary
total_salary = df['salary'].sum()
# Count: Number of employees earning more than 50000
high_earners_count = df[df['salary'] > 50000].shape[0]
# Limit: Get the top 5 highest earners
top_5_earners = df.nlargest(5, 'salary')
# Skip: Skip the first 2 employees
skipped_df = df.iloc[2:]
# Remove: Remove employees from a specific department (e.g., 'Sales')
filtered_df = df[df['department'] != 'IT']
# Save the filtered result back to HDFS
filtered_json = filtered_df.to_json(orient='records')
try:
    with hdfs_client.write('/home/hadoop/filtered_employees.json', encoding='utf-8', overwrite=True) as
writer:
        writer.write(filtered_json)
    print("Filtered JSON file saved successfully.")
except Exception as e:
```

```
    print(f"Error saving filtered JSON data: {e}")
    exit(1)
# Print results
print(f"Projection: Select only name and salary columns\n{projected_df}")
print(f"Aggregation: Total Salary: {total_salary}")
print(f"Number of High Earners (>50000): {high_earners_count}")
print(f"Top 5 Earners: \n{top_5_earners}")
print(f"Skipped DataFrame (First 2 rows skipped): \n{skipped_df}")
print(f"Filtered DataFrame (IT department removed): \n{filtered_df}")
```

5. Run the Script

Execute the Python script by running the following command in your terminal:



RESULT:

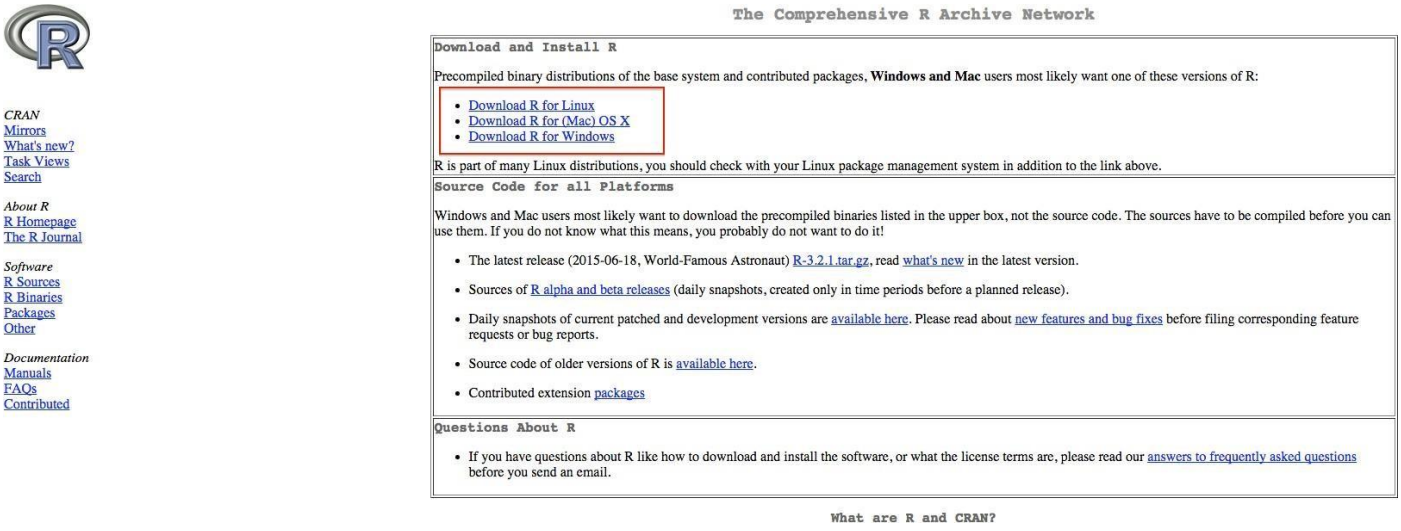
Thus to import a JASON file from the command line and apply the following actions with the data present in the JASON file where, projection, aggregation, remove, count, limit, skip and sort has been executed and verified successfully.

Reg.No: 210701260

Installation guide for R and RStudio

Step 1 – Install R

1. Download the R installer from https://cran.r---project.org/



The Comprehensive R Archive Network

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R Homepage
The R Journal

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R Sources
R Binaries
Packages
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Documentation
Manuals
FAQs
Contributed

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- Download R for Linux
- Download R for (Mac) OS X
- Download R for Windows

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2015-06-18, World-Famous Astronaut) R-3.2.1.tar.gz, read what's new in the latest version.
- Sources of R alpha and beta releases (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are available here. Please read about new features and bug fixes before filing corresponding feature requests or bug reports.
- Source code of older versions of R is available here.
- Contributed extension packages

Questions About R

- If you have questions about R like how to download and install the software, or what the license terms are, please read our answers to frequently asked questions before you send an email.

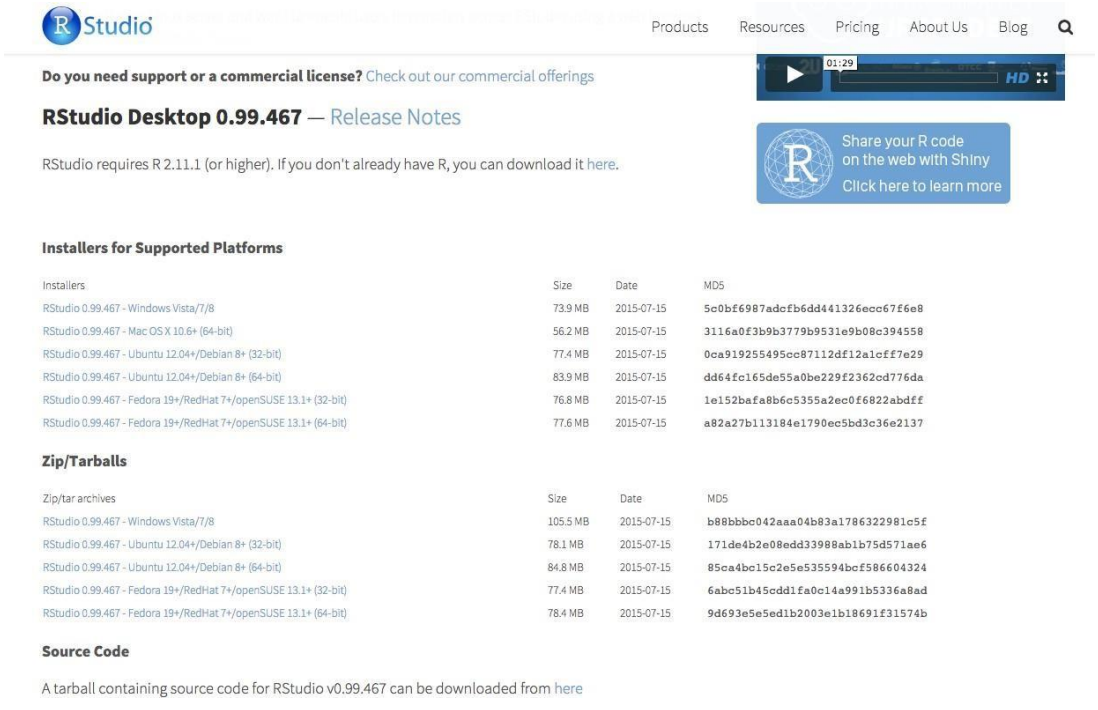
What are R and CRAN?

Figure 1. Screenshot of http://cran.csiro.au/

2. Run the installer. Default settings are fine. If you do not have admin rights on your laptop, then ask you local IT support. In that case, it is important that you also ask them to give you full permissions to the R directories. Without this, you will not be able to install additional packages later

Step 2 – Install RStudio

1. Download RStudio: https://www.rstudio.com/products/rstudio/download/



RStudio

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RStudio Desktop 0.99.467 — Release Notes

RStudio requires R 2.11.1 (or higher). If you don't already have R, you can download it here.

Share your R code on the web with Shiny
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Installers for Supported Platforms

Installers	Size	Date	MD5
RStudio 0.99.467 - Windows Vista/7/8	73.9 MB	2015-07-15	5c0bf6987adcfb6dd441326ecc67f6e8
RStudio 0.99.467 - Mac OS X 10.6+ (64-bit)	56.2 MB	2015-07-15	3116a0f3b9b3779b9531e9b08c394558
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (32-bit)	77.4 MB	2015-07-15	0ca919255495cc87112df12a1cff7e29
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (64-bit)	83.9 MB	2015-07-15	dd64fc165de55a0be229f2362cd776da
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	76.8 MB	2015-07-15	1e152bafa8b6c5355a2ec0f6822abdff
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	77.6 MB	2015-07-15	a82a27b113184e1790ec5bd3c36e2137

Zip/Tarballs

Zip/tar archives	Size	Date	MD5
RStudio 0.99.467 - Windows Vista/7/8	105.5 MB	2015-07-15	b88bbbc042aaa04b83a1786322981c5f
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (32-bit)	78.1 MB	2015-07-15	171de4b2e08edd33988ab1b75d571ae6
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (64-bit)	84.8 MB	2015-07-15	85ca4bc15c2e5e535594bcf586604324
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	77.4 MB	2015-07-15	6abc51b45cdd1fa0c14a991b5336a8ad
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	78.4 MB	2015-07-15	9d693e5e5ed1b2003e1b18691f31574b

Source Code

A tarball containing source code for RStudio v0.99.467 can be downloaded from here

Figure 2. Download RStudio on https://www.rstudio.com/products/rstudio/download/

2. Once the installation of R has completed successfully (and not before), run the RStudio installer.
3. If you do not have administrative rights on your laptop, step 2 may fail. Ask your IT Support or download a pre---built zip archive of RStudio which doesn't need installing. The link for this is towards the bottom of the download page, highlighted in Image 2.

    a. Download the appropriate archive for your system (Windows/Linux only – the Mac version can be installed into your personal "Applications" folder without admin rights).

    b. Double clicking on the zip archive should automatically unpack it on most Windows machines.

Step 3 – Check that R and RStudio are working

1. Open RStudio. It should open a window that looks similar to image 3 below.

2. In the left hand window, by the '>'sign, type '4+5'(without the quotes) and hit enter. An output line reading '[1] 9' should appear. This means that R and RStudio are working.

3. If this is not successful, contact us or your local IT support for further advice

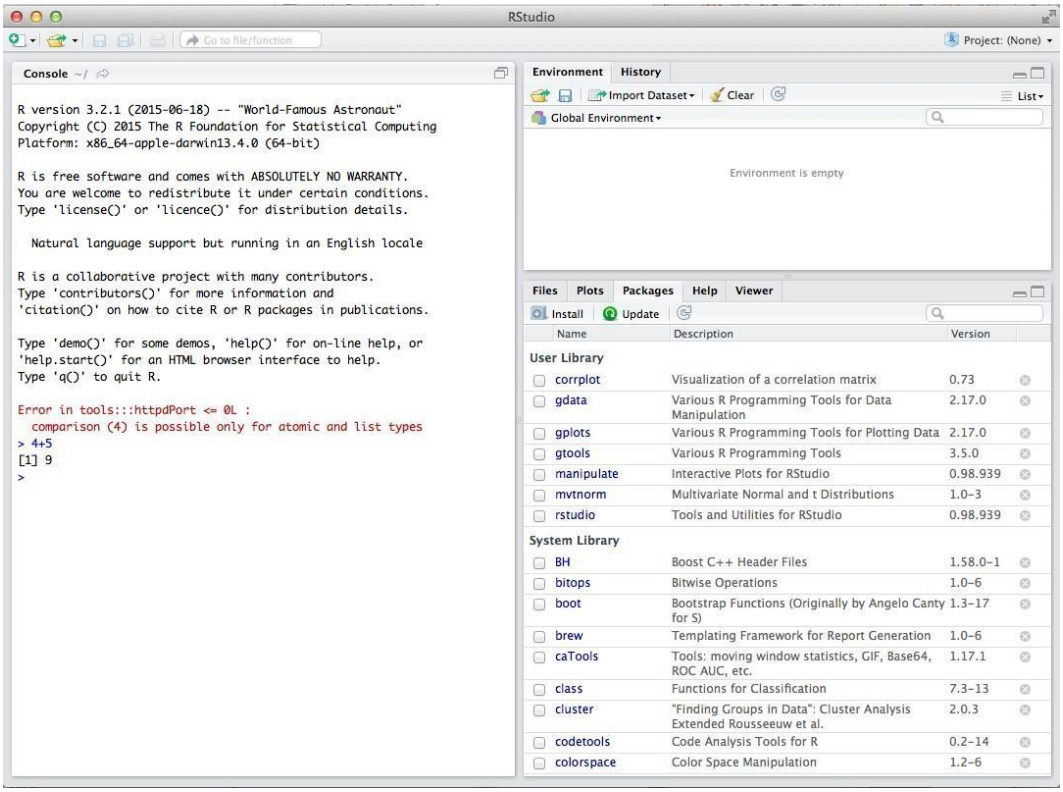


Figure 3. Running R with RStudio

Step 4 – Install R packages required for the workshop

1. Click on the tab ‘ Packages’ then ‘Install’ as shown in Image 4. Or Tools ---> Install packages.
2. Install the following packages: mixOmics version 6.1.0, mvtnorm, RColorBrewer, corrplot, igraph (see Image 4). For apple mac users, if you are unable to install the mixOmics imported library rgl, you will need to install the XQuartz software first https://www.xquartz.org/
3. Check that the packages are installed by typing ‘library(mixOmics)’ (without the quotes) in the prompt and press enter (see Image 5).
4. Then type ‘sessionInfo()’ and check that mixOmics version 6.1.0 has been installed (image 6).

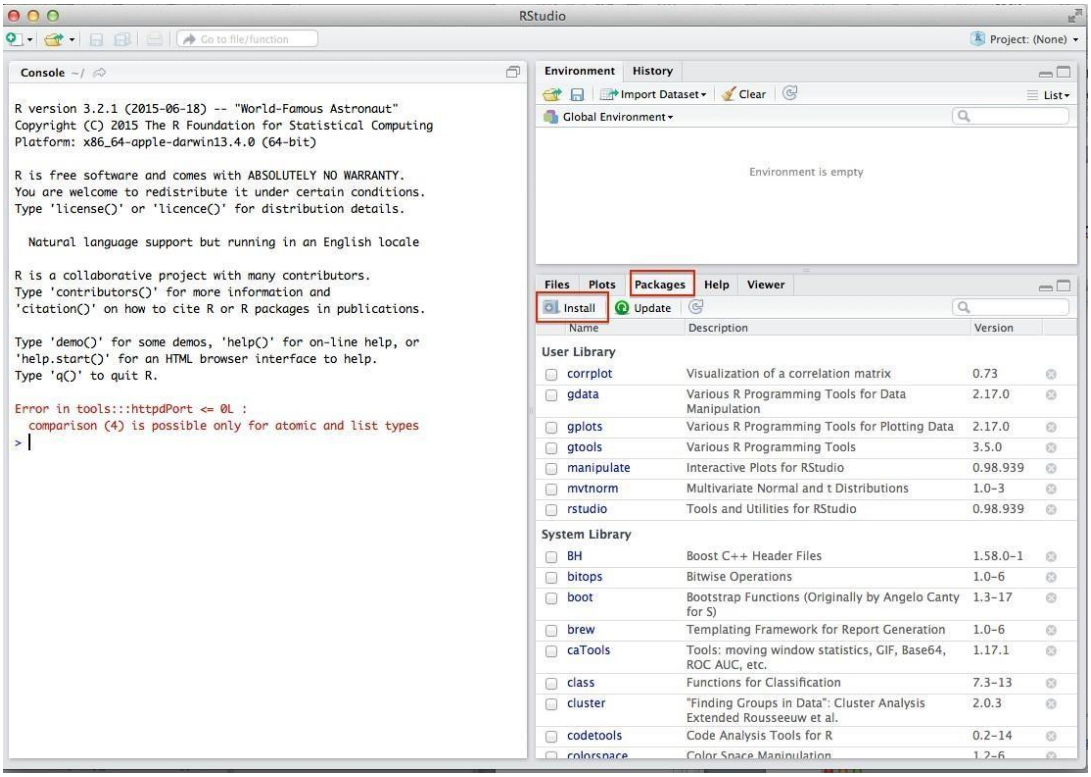


Figure 4. Click on Install to install R packages.

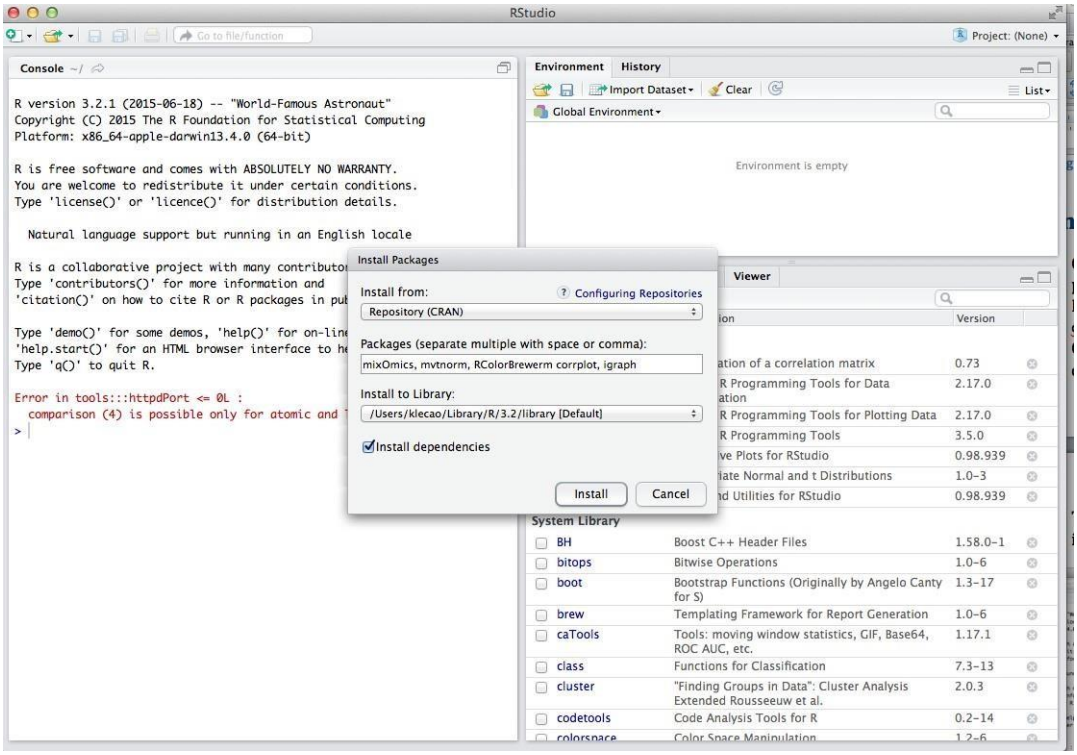


Figure 5. Specify the list of packages to be installed

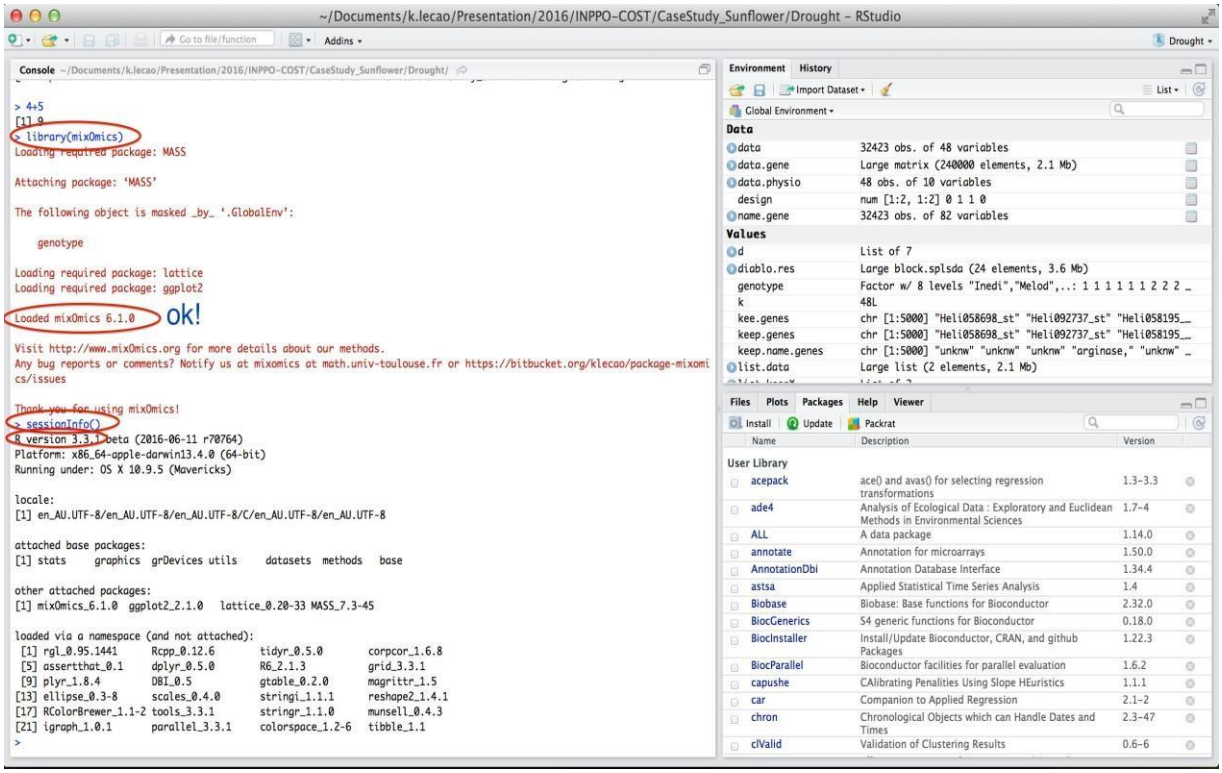


Figure 6. Check that the package mixOmics is installed and has the version 6.1.0.

Reg.No: 210701260

Exp.No: 7

IMPLEMENT LINEAR AND LOGISTIC REGRESSION

AIM:

To write an R code to implement linear and logistic regression.

PROCEDURE:

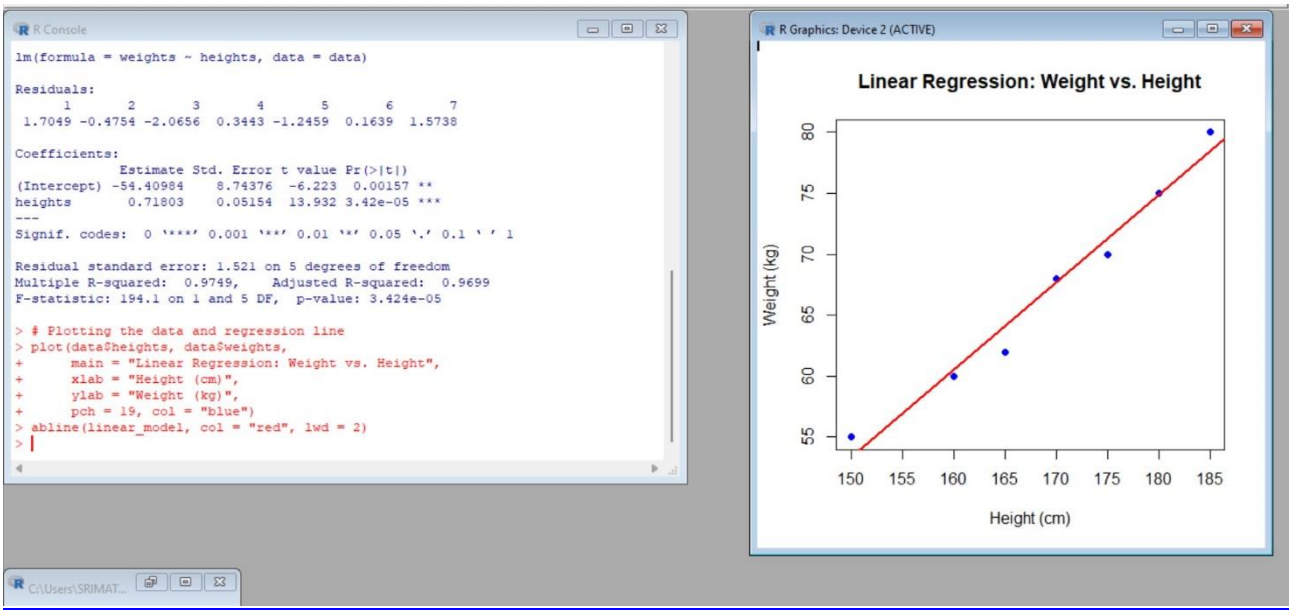
1. Create sample data for heights and weights, fit a linear regression model, and plot the data with the regression line.
2. Use the sample data to create a data frame for the regression model.
3. Fit the linear regression model using the `lm()` function and display the summary.
4. Plot the data points and add the regression line using the `plot()` and `abline()` functions.
5. Load the `mtcars` dataset, convert the 'am' variable to a factor, fit a logistic regression model using the `glm()` function, and plot the probabilities.

PROGRAM CODE:

a)Linear regression

```
# Linear Regression
heights <- c(150, 160, 165, 170, 175, 180, 185)
weights <- c(55, 60, 62, 68, 70, 75, 80)
data <- data.frame(heights, weights)
linear_model <- lm(weights ~ heights, data = data)
print(summary(linear_model))


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

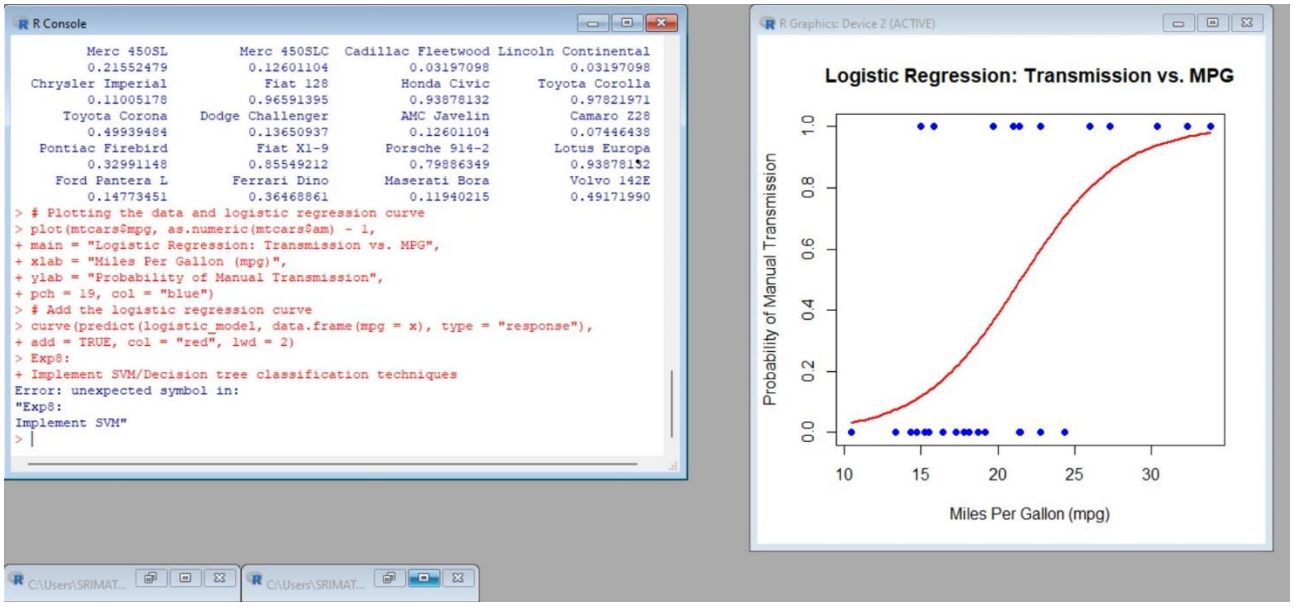
OUTPUT:



b) Logistic regression

```
# Logistic Regression
data(mtcars)
mtcars$am <- factor(mtcars$am, levels = c(0, 1), labels = c("Automatic", "Manual"))
logistic_model <- glm(am ~ mpg, data = mtcars, family = binomial)
print(summary(logistic_model))

# Plotting Logistic Regression
predicted_probs <- predict(logistic_model, type = "response")
print(predicted_probs)
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")
curve(predict(logistic_model, data.frame(mpg = x), type = "response"),
                                                    add = TRUE, col = "red", lwd = 2)
```

OUTPUT:



RESULT:

Thus the R program to implement Linear and Logistic Regression has been executed and verified successfully.

Reg.No: 210701260

Exp.No: 8

IMPLEMENT SVM/DECISION TREE CLASSIFICATION TECHNIQUES

AIM:

To write an R code to implement SVM/decision tree classification techniques.

PROCEDURE:

1. Install and load the required packages (e1071 for SVM and rpart for Decision Tree) and load the iris dataset.
2. Split the dataset into training (70%) and testing (30%) sets using a reproducible random sampling method.
3. Fit the SVM model with a radial kernel using the training data, print the model summary, and evaluate its performance using a confusion matrix and accuracy calculation.
4. Fit the Decision Tree model using the rpart function with the training data, print the model summary, visualize the tree, and evaluate its performance using a confusion matrix and accuracy calculation.
5. Predict the test set results for both SVM and Decision Tree models and assess their accuracy.

PROGRAM CODE:

a) SVM IN 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")
```

OUTPUT:

```
> # 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")
Error in svm(Species ~ ., data = train_data, kernel = "radial") :
  could not find function "svm"
> library(e1071)
>
> library(e1071)
>
> # Fit the SVM model
> svm_model <- svm(Species ~ ., data = train_data, kernel = "radial")
> # Print the summary of the model
> summary(svm_model)

Call:
svm(formula = Species ~ ., data = train_data, kernel = "radial")


Parameters:
   SVM-Type:  C-classification
 SVM-Kernel:  radial
       cost:  1

Number of Support Vectors:  45

 ( 7 18 20 )


Number of Classes:  3

Levels:
 setosa versicolor virginica


> # 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)
            Actual
Predicted    setosa versicolor virginica
  setosa         14          0         0
  versicolor      0         17         0
  virginica       0          1        13
> # Calculate accuracy
> accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix)
> cat("Accuracy:", accuracy * 100, "%\n")
Accuracy: 97.77778 %
```

b) Decision tree in 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:

```
package 'rpart' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
        C:\Users\SRIMATHY.R\AppData\Local\Temp\RtmpGsl1Wc\downloaded_packages
> 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)
Call:
rpart(formula = Species ~ ., data = train_data, method = "class")
  n= 105
```

```
         CP nsplit  rel error    xerror       xstd
1 0.5294118      0 1.00000000 1.2058824 0.06232572
2 0.3970588      1 0.47058824 0.5441176 0.07198662
3 0.0100000      2 0.07352941 0.1176471 0.03997857

Variable importance
 Petal.Width Petal.Length Sepal.Length  Sepal.Width
          34           32           21           13

Node number 1: 105 observations,    complexity param=0.5294118
  predicted class=virginica   expected loss=0.647619  P(node) =1
    class counts:    36    32    37
   probabilities: 0.343 0.305 0.352
  left son=2 (36 obs) right son=3 (69 obs)
  Primary splits:
      Petal.Length < 2.45 to the left,  improve=35.54783, (0 missing)
      Petal.Width  < 0.8  to the left,  improve=35.54783, (0 missing)
      Sepal.Length < 5.45 to the left,  improve=24.79179, (0 missing)
      Sepal.Width  < 3.25 to the right, improve=12.34670, (0 missing)
  Surrogate splits:
      Petal.Width  < 0.8  to the left,  agree=1.000, adj=1.000, (0 split)
      Sepal.Length < 5.45 to the left,  agree=0.924, adj=0.778, (0 split)
      Sepal.Width  < 3.25 to the right, agree=0.819, adj=0.472, (0 split)

Node number 2: 36 observations
  predicted class=setosa      expected loss=0  P(node) =0.3428571
    class counts:    36     0     0
   probabilities: 1.000 0.000 0.000

Node number 3: 69 observations,    complexity param=0.3970588
  predicted class=virginica   expected loss=0.4637681  P(node) =0.6571429
```

```
  Surrogate splits:
      Petal.Length < 4.75 to the left,  agree=0.913, adj=0.824, (0 split)
      Sepal.Length < 6.15 to the left,  agree=0.696, adj=0.382, (0 split)
      Sepal.Width  < 2.65 to the left,  agree=0.638, adj=0.265, (0 split)

Node number 6: 35 observations
  predicted class=versicolor  expected loss=0.1142857  P(node) =0.3333333
    class counts:     0    31     4
   probabilities: 0.000 0.886 0.114

Node number 7: 34 observations
  predicted class=virginica   expected loss=0.02941176  P(node) =0.3238095
    class counts:     0     1    33
   probabilities: 0.000 0.029 0.971

> # 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)
            Actual
Predicted    setosa versicolor virginica
  setosa         14          0         0
  versicolor      0         18         1
  virginica       0          0        12
> # Calculate accuracy
> accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix)
> cat("Accuracy:", accuracy * 100, "%\n")
Accuracy: 97.77778 %
```

RESULT:

Thus the R program to implement SVM/decision tree classification techniques has been executed and verified successfully.

Reg.No: 210701260

Exp.No: 9

IMPLEMENT CLUSTERING TECHNIQUES – HIERARCHICAL AND KMEANS

AIM:

To write an R code to implement hierarchical and k-means clustering techniques.

PROCEDURE:

1. Load the iris dataset and use only the numeric columns for clustering by excluding the Species column.
2. Standardize the data to ensure all variables have equal weight in the clustering process.
3. Compute the distance matrix using the Euclidean method and perform hierarchical clustering using the "complete" linkage method, plot the dendrogram, and cut the tree to form 3 clusters.
4. Perform K-means clustering by setting the number of clusters, run the clustering algorithm, and add cluster assignments to the original dataset.
5. Display the first few rows of the updated dataset and plot the clusters using ggplot2 for visualization.

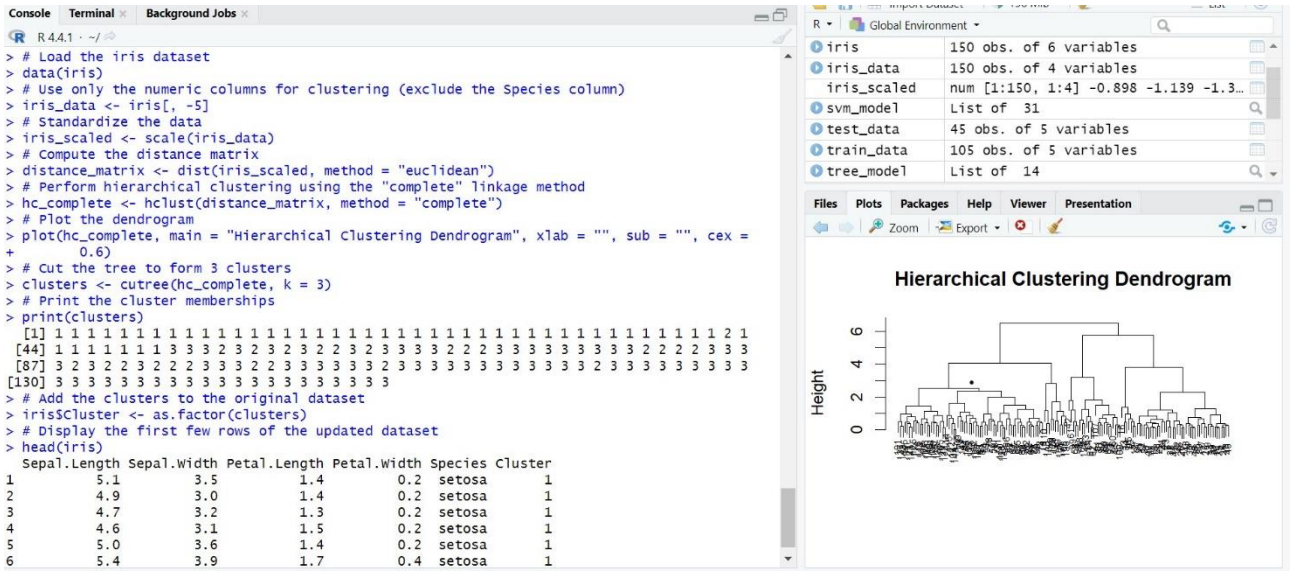
PROGRAM CODE:

a) HIERARCHIAL CLUSTERING

```
# 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)
```

OUTPUT:



```
> # 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)
  [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 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1
 [44] 1 1 1 1 1 1 1 3 3 3 2 3 2 3 2 3 2 2 3 2 2 3 2 3 3 3 3 3 3 3 3 3 2 2 2 2 3 3 3
 [87] 3 2 3 2 2 3 3 2 2 2 3 3 3 2 2 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3
[130] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
> # Add the clusters to the original dataset
> iris$Cluster <- as.factor(clusters)
> # Display the first few rows of the updated dataset
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species Cluster
1          5.1         3.5          1.4         0.2  setosa       1
2          4.9         3.0          1.4         0.2  setosa       1
3          4.7         3.2          1.3         0.2  setosa       1
4          4.6         3.1          1.5         0.2  setosa       1
5          5.0         3.6          1.4         0.2  setosa       1
6          5.4         3.9          1.7         0.4  setosa       1
```

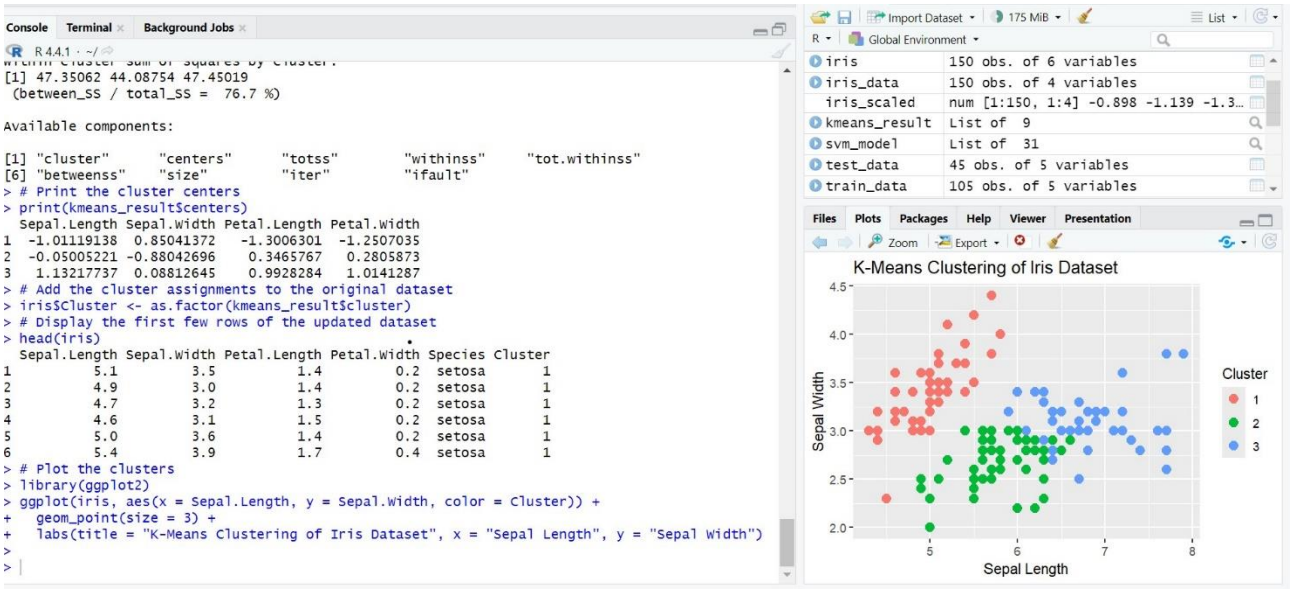
iris	150 obs. of 6 variables
iris_data	150 obs. of 4 variables
iris_scaled	num [1:150, 1:4] -0.898 -1.139 -1.3…
svm_model	List of 31
test_data	45 obs. of 5 variables
train_data	105 obs. of 5 variables
tree_model	List of 14

b) K-MEANS CLUSTERING

```
# 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:



RESULT:

Thus the R program to implement hierarchical and k-means clustering techniques has been executed and verified successfully.

Reg.No: 210701260

Exp.No:10

VISUALIZE DATA USING ANY PLOTTING FRAMEWORK

AIM:

To write an R code to visualize data using plotting framework such as scatter plot, bar char, histogram and box plot.

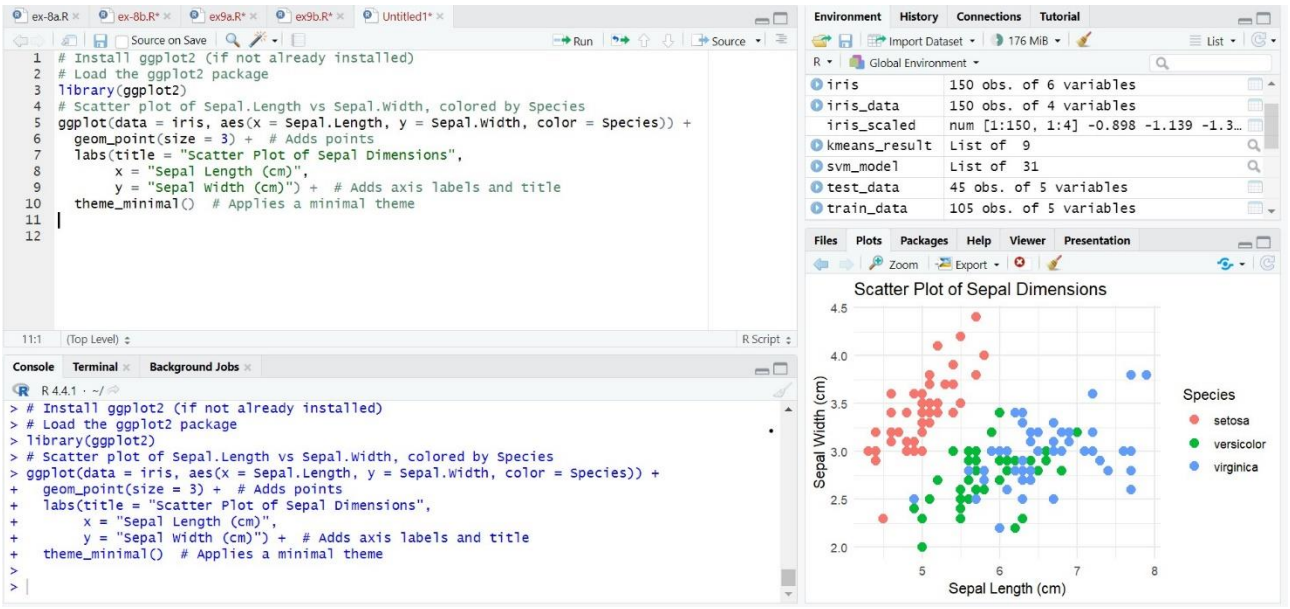
PROCEDURE:

1. Install and Load ggplot2: Ensure the ggplot2 package is installed and loaded to use its plotting functions.
2. Scatter Plot: Create a scatter plot of Sepal Length vs. Sepal Width, colored by Species, to visualize the relationship between these two variables across different species in the iris dataset.
3. Bar Chart: Generate a bar chart to show the count of different Species in the iris dataset, using bars filled with a specified color to represent the counts.
4. Histogram: Create a histogram of Sepal Length to visualize the frequency distribution of this variable within the dataset, specifying the bin width and colors for the histogram bars.
5. Box Plot: Plot a box plot of Sepal Length for each Species to compare the distribution and central tendency of Sepal Length across the different species in the dataset.

1) SCATTER PLOT

```
# 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
```

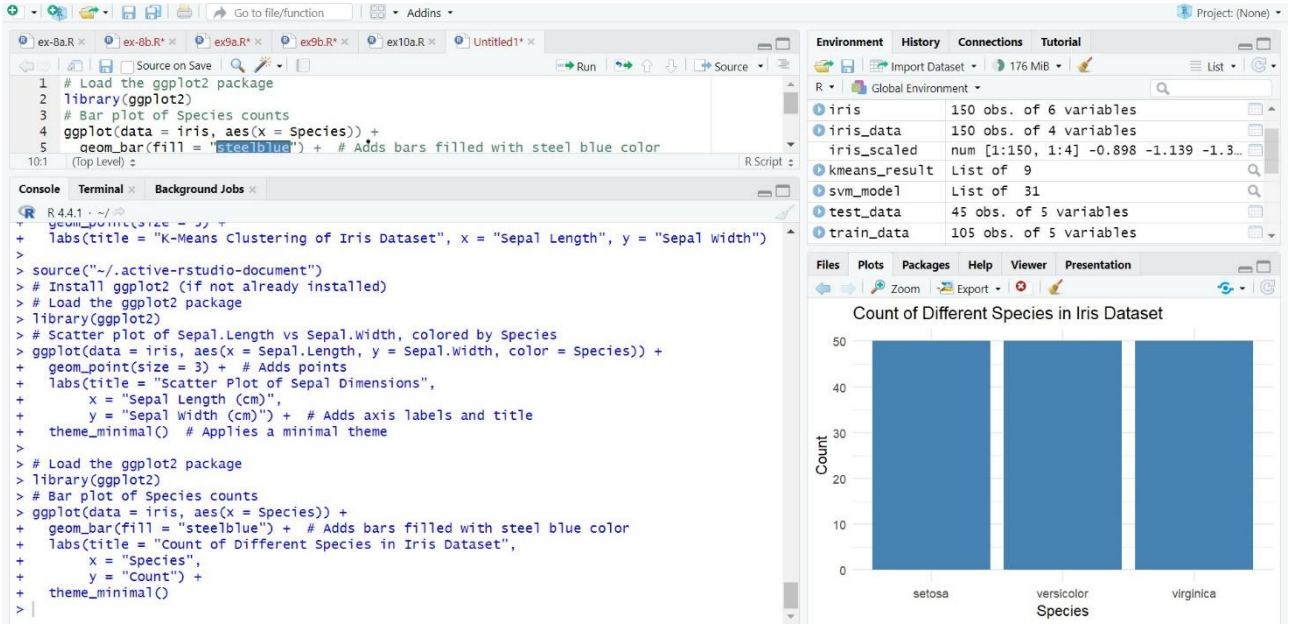
OUTPUT:



2) BAR CHART

```
# 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()
```

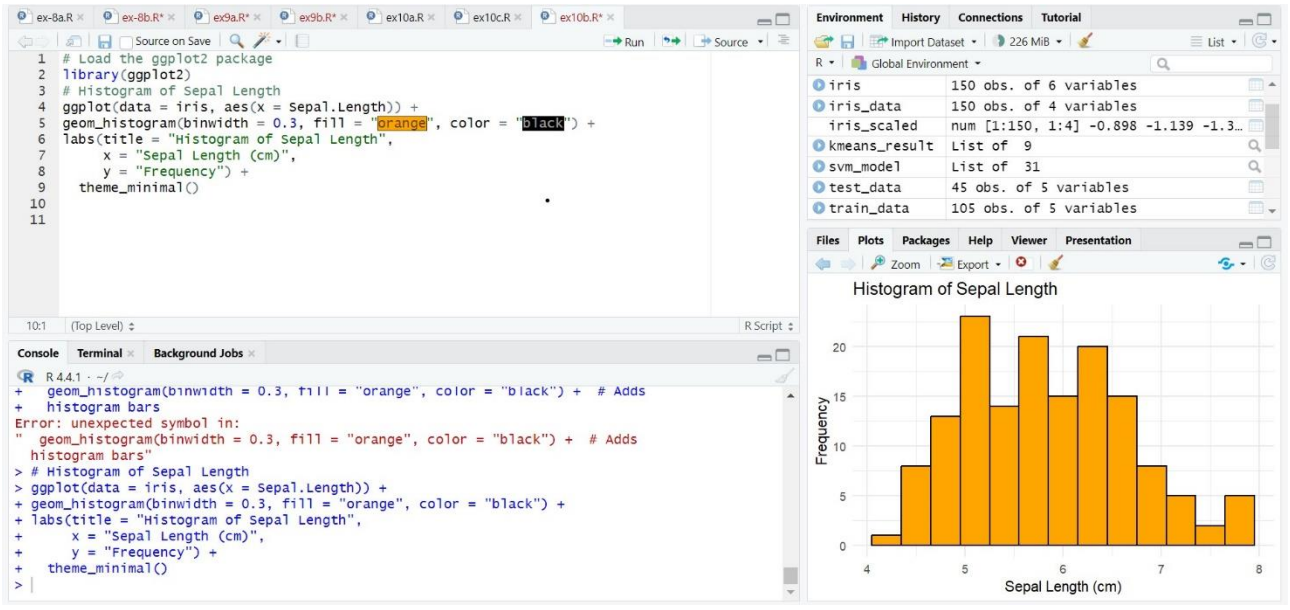
OUTPUT:



3) HISTOGRAM

```
# 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()
```

OUTPUT:

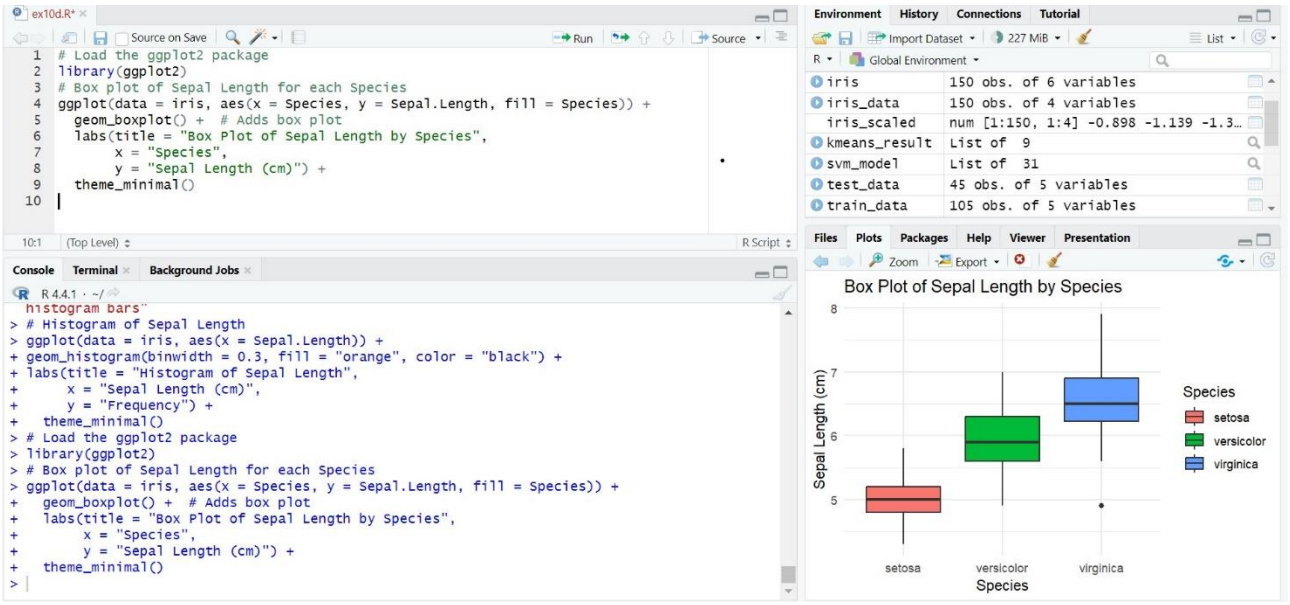


4)BOX PLOT

```
 # 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:



RESULT:

Thus the R program to visualize data using plotting framework such as scatter plot, bar char, histogram and box plot has been executed and verified successfully.