



# VPM's R.Z. SHAH COLLEGE OF ARTS, SCIENCE & COMMERCE

Mithagar Road, Mulund (E) 400 081

## CERTIFICATE

This is to certify that **Gulshan Suryanarayan Chauhan** Roll No. 2153004 has completed his/her journal in the subject of Data Science under the program of B.Sc. (Computer Science) Semester-VI on behalf of University of Mumbai during the academic year 2021-2022.

He/She has completed the prescribed practical satisfactorily.

Examination Seat No.: \_\_\_\_\_

Date: \_\_\_\_\_

---

Subject In-charge

---

HOD/Coordinator

# INDEX

Sr. No	Title	Date
1	Practical of Data collection, Data curation and management for Unstructured data (NoSQL)	
2	Practical of Data collection, Data curation and management for Large-scale Data system (such as MongoDB)	
3	Practical of Principal Component Analysis	
4	Practical of Clustering	
5	Practical of Time-series forecasting	
6	Practical of Simple/Multiple Linear Regression	
7	Practical of Logistics Regression	
8	Practical of Hypothesis testing	
9	Practical of Analysis of Variance	
10	Practical of Decision Tree	

**Practical No: 1**

**Aim:** Practical of Data collection, Data curation and management for Unstructured data (NoSQL)

Couchdb

database----

rscript

Install couchdb

first

**Rscript code**

```
install.packages('sofa')
```

```
#devtools::install_gith
```

```
ub("ropensci/sofa")
```

```
library('sofa')
```

```
#creat
```

```
e
```

```
conne
```

```
ction
```

```
object
```

```
x<-
```

```
Cushi
```

```
on$ne
```

```
w()
```

```

#to check
whether
object
created
x$ping()

#create
database ty
db_create(
x,dbname
= 'ty')
db_list(x)

#create json doc
doc1<-'{"rollno":"01","name":"ABC","GRADE":"A"}'
doc_create(x,doc1,dbname
ame = "ty",docid =
"a_1") doc2<-
'{"rollno":"02","name"
:"PQR","GRADE":"A"
}'


doc3<-'{"rollno":"03","name":"xyz","GRADE":"B","REMARK":"PASS"}'
doc_create(x,doc3,dbname = "ty",docid = "a_3")

#CHANGES FEED
db_changes(x,"ty")

```

```

#search for id >
null so all docs
will display
db_query(x,dbname
me = "ty",
selector = list('_id'=list('$gt'=NULL)))$docs

#search for students with grade is A
db_query(x,dbname = "ty",selector = list(GRADE="A"))$docs

#search for students with remark =pass
db_query(x,dbname = "ty",selector = list(REMARK="PASS"))$docs

#return only certain fields where rollno>2
db_query(x,dbname = "ty",selector =
list(rollno=list('$gt'='02')),fields=c("name","GRADE"))$docs

#convert the result of a query
into a data frame using
jsonlite library("jsonlite")

res<-db_query(x,dbname = "ty",selector =
list('_id'=list('$gt'=NULL)),fields=c("name","rollno","GRADE","REMARK"),as="json"
")

```

```

#display

json doc

fromJSON(
res)$docs


#doc_delete(cush
ion,dbname,docid
)

doc_delete(x,dbn
ame = "ty",docid
= "a_2")

doc_get(x,dbnam
e = "ty",docid =
"a_2")

doc2<-'{ "name":"Sdrink","beer":"TEST","note":"yummy","note2":"yay"}'

doc_update(x,dbname = "ty",doc=doc2,docid="a_3",rev = "3-
b1fb56db955b142c6efd3b3c52fe9e1b")



doc3<-
'{"rollno":"
01",
"name":"R
UTU",
"GRADE":"A"}'

```

```
doc_update(x, dbname = "ty", doc=doc3, docid = "a_1", rev = "1-be7c98bddf8ea7c46f4f401ff387593d")
```

## Output:

```
R version 3.3.1 (2016-06-21) -- "Bug in Your Hair"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.
It is distributed under the terms of the GNU General Public License.
Type 'help()' for further information and 'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos; 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quite R.

[workspace loaded from ~/rdata]

> install.packages(sofa)
Error: package 'sofa' not found
> install.packages("sofa")
also installing the dependencies 'tribeard', 'uritools', 'httpcode', 'curl', 'jsonlite', 'uritools'

There are binary versions available but the source versions are later:
  binary source needs_compilation
uritools      0.5.2       0.7.0      FALSE
curl          0.5.2       0.6       TRUE
jsonlite      0.5.0       0.6       TRUE
  binaries will be installed
  trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.3/tribeard_0.3.0.zip'
  Content type 'application/zip' length 708397 bytes (689 KB)
downloaded 689 KB

  trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.3/uritools_3.7.0.zip'
  Content type 'application/zip' length 824800 bytes (805 KB)
downloaded 824800 bytes

  trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.3/httpcode_0.2.0.zip'
  Content type 'application/zip' length 26328 bytes (25 KB)
downloaded 25 KB

  trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.3/jsonlite_1.5.zip'
  Content type 'application/zip' length 1159497 bytes (1.1 MB)
```

```
> install.packages('curl')
-- package 'curl' successfully unpacked and MD5 sums checked
> install.packages('sofa')
-- package 'sofa' successfully unpacked and MD5 sums checked
> install.packages('tribeard')
-- package 'tribeard' successfully unpacked and MD5 sums checked
> install.packages('uritools')
-- package 'uritools' successfully unpacked and MD5 sums checked
> install.packages('httpcode')
-- package 'httpcode' successfully unpacked and MD5 sums checked
> install.packages('jsonlite')
-- package 'jsonlite' successfully unpacked and MD5 sums checked
> install.packages('uritools')
-- package 'uritools' successfully unpacked and MD5 sums checked
> install.packages('httpcode')
-- package 'httpcode' successfully unpacked and MD5 sums checked
> install.packages('curl')
-- package 'curl' successfully unpacked and MD5 sums checked
> devtools::install_github('ropensci/sofa')
Error: package 'sofa' not found
> library('sofa')
Warning message:
package 'sofa' was built under R version 3.3.3
> sofa
--> cushionnew()
> xc_cushionnew()
> xc_cushionnew()
> xc_piping()
> sofa
[1] "Welcome"
$version
[1] "2.3.0"
$gitsha
[1] "07e0c07"
$uid
[1] "a42adled9a458c27635222068f992a9f"
$features
$features[[1]]
[1] "pluggable-storage-engines"
$features[[2]]
[1] "scheduler"

$vendor
$vendor$name
```

```
Console / v2.0.0
> #doc_a_delete(x,dbname,docid)
> doc_a_delete(x,dbname = "ty", docid = "a_2")
[1] TRUE
> doc_a_create(x,dbname = "ty", docid = "a_2")
[1] "a_2"
> rev
[1] "2-82f1879cc7d3bef5574cc5cdf7c4094"
> doc_get(x,dbname = "ty", docid = "a_2")
Error: unexpected identifier
> doc2<-c("name","SdrTrnk","beer","TEST","note","yummy","note2","yay")
> doc_update(x,dbname = "ty", doc=doc2, docid="a_3", rev = "3-b1fb56db955b142c6efd3b3c52fe9e1b"
[1] TRUE
> doc_a_update(x,dbname = "ty", doc=doc3, docid = "a_1", rev = "1-be7c98bddf8ea7c46f4f401ff387593d")
[1] TRUE
> doc_a_create(x,dbname = "ty", docid = "a_1")
[1] "a_1"
> rev
[1] "2-8e881d6a3e0fbfd735da8ff70cff6cc"
```

```

Console <-
MySql <- dbConnect(MySQL(), user = "root", password = "root", host = "localhost", port = 3306)
# Characters $, %, +, ., and / are allowed. Must begin with a letter.
> db_create<-c(dbname = "ty")
> db_create
[1] TRUE
> db_list(x)
[1] "ty"
> #create json doc
> doc1<-("rollno":"01","name":"ABC","GRADE":"A")
> doc1<-c(doc1,dbname = "ty",docId = "a_1")
>Error: lexical error: invalid char in json text.
    at character position 12.
    (right here) ----^
> #create json doc
> doc2<-("rollno":"02","name":"XYZ","GRADE":"B")
> doc2<-c(doc2,dbname = "ty",docId = "a_2")
>Error: lexical error: invalid char in json text.
    at character position 12.
    (right here) ----^
> doc3<-("rollno":"03","name":"PQR","GRADE":"C")
> doc3<-c(doc3,dbname = "ty",docId = "a_3")
>Error: lexical error: invalid char in json text.
    at character position 12.
    (right here) ----^
[1] TRUE
> doc1
[1] "a_1"
> rev
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"
> doc2
[1] "2-g1AAAATHe2zLywb94MhgTmEQTM4VTC5ISXLIyU90ZMnILy7JAuoxJTIkyf____z8rkqGPo1QF1j1kd1Kwzzim"
> doc3
[1] "3-g1AAAATHe2zLywb94MhgTmEQTM4VTC5ISXLIyU90ZMnILy7JAuoxJTIkyf____z8rkqGPo1QF1j1kd1Kwzzim"
AvksselGccnp6c104ppjaeq5f0ebuwaqasnc6PBugyNaAponL5xkhdfG7nx1byBq7x0j9gFELc19wQDAVnnit"
[1] TRUE
> doc1
[1] "a_2"
> rev
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"
> doc2
[1] "2-g1AAAATHe2zLywb94MhgTmEQTM4VTC5ISXLIyU90ZMnILy7JAuoxJTIkyf____z8rkqGPo1QF1j1kd1Kwzzim"
> doc3
[1] "3-g1AAAATHe2zLywb94MhgTmEQTM4VTC5ISXLIyU90ZMnILy7JAuoxJTIkyf____z8rkqGPo1QF1j1kd1Kwzzim"
AvksselGccnp6c104ppjaeq5f0ebuwaqasnc6PBugyNaAponL5xkhdfG7nx1byBq7x0j9gFELc19wQDAVnnit"
[1] TRUE
> doc1
[1] "a_3"
> rev
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"

```

```

Console <-
> #CHANGES FEED
> ob_changes(x,"ty")
$results
$results[[1]]$seq
[1] "1-g1AAAATHe2zLywb94MhgTmEQTM4VTC5ISXLIyU90ZMnILy7JAuoxJTIkyf____z8rkqGPo1QF1j1kd1Kwzzim"
AvksselGccnp6c104ppjaeq5f0ebuwaqasnc6PBugyNaAponL5xkhdfG7nx1byBq7x0j9gFELc19wQDAVnnit"
$results[[1]]$id
[1] "a_1"
$results[[1]]$changes
$results[[1]]$changes[[1]]
$rev
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"

$results[[2]]$seq
$results[[2]]$id
[1] "a_2"
$results[[2]]$changes
$results[[2]]$changes[[1]]
$rev
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"

$results[[3]]$seq
$results[[3]]$id
[1] "a_3"
$results[[3]]$changes
$rev
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"

```

RStudio Environment

```

Console -/ 
[1] 0
> #search for id > null so all docs will display
> db_query(x,dbname = "ty",selector = list('_id'>list('$gt'=NULL)))$docs
[[1]]$_id
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"
[[1]]$_rev
[1] "1-1ddcb45704c37893389b050ddbd440a"
[[1]]$rollno
[1] "01"
[[1]]$name
[1] "ABC"
[[1]]$GRADE
[1] "A"

[[2]]
[[2]]$_id
[1] "a_2"
[[2]]$_rev
[1] "1-1ddcb45704c37893389b050ddbd440a"
[[2]]$rollno
[1] "02"
[[2]]$name
[1] "PQR"
[[2]]$GRADE
[1] "A"

[[3]]
[[3]]$_id
[1] "a_3"
[[3]]$_rev
[1] "3-b1fb56db955b142c6efd3b3c52fe9e1b"
[[3]]$rollno
[1] "03"

```

RStudio Environment

```

Console -/ 
[1] "PASS"

> #search for students with grade is A
> db_query(x,dbname = "ty",selector = list(GRADE="A"))$docs
[[1]]
[[1]]$_id
[1] "a_1"

[[1]]$_rev
[1] "1-be7c98bddf8ea7c46f4f401ff387593d"

[[1]]$rollno
[1] "01"

[[1]]$name
[1] "ABC"

[[1]]$GRADE
[1] "A"

[[2]]
[[2]]$_id
[1] "a_2"
[[2]]$_rev
[1] "1-1ddcb45704c37893389b050ddbd440a"
[[2]]$rollno
[1] "02"
[[2]]$name
[1] "PQR"
[[2]]$GRADE
[1] "A"

> #search for students with remark =pass
> db_query(x,dbname = "ty",selector = list(REMARK="PASS"))$docs
[[1]]
[[1]]$_id
[1] "a_3"

[[1]]$_rev
[1] "3-b1fb56db955b142c6efd3b3c52fe9e1b"

```

```

Source
Console ~ / ~

> #search for students with remark -pass
> db_query(x,dbname = "ty",selector = list(REMARK=="PASS"))$docs
[[1]]
[[1]]$._id
[1] "a_3"

[[1]]$._rev
[1] "3-b1fb56db955b142c6efd3b3c52fe9e1b"

[[1]]$rollno
[1] "03"

[[1]]$name
[1] "xyz"

[[1]]$GRADE
[1] "B"

[[1]]$REMARK
[1] "PASS"

> #return only certain fields where rollno>2
> db_query(x,dbname = "ty",selector = list(rollno=list("Sgt"~'02')),fields=c("name","GRADE"))
$docs
[[1]]
[[1]]$name
[1] "xyz"

[[1]]$GRADE
[1] "B"

> #convert the result of a query into a data frame using jsonlite
> library("jsonlite")
Warning message:
package 'jsonlite' was built under R version 3.3.3
> res<-db_query(x,dbname = "ty",selector = list(_id=list("Sgt"=NULL)),fields=c("name","rol
lno","GRADE","REMARK"),as="json")
> #display json doc
> fromJSON(res)$docs
  name rollno GRADE REMARK
1 ABC      01     A <NA>
2 PQR      02     A <NA>
3 XYZ      03     B PASS
> #doc_delete(cushion,dbname = "ty",docid = "a_3")

```

```

File Edit Code View Plots Session Build Debug Profile Tools Help
D ~ Go To File Function Addins ~

Source
Console ~ / ~

> xyz
[1] "xyz"
> #doc_delete(cushion,dbname,docid)
> doc_delete(x,dbname = "ty",docid = "a_2")
$ok
[1] TRUE

$id
[1] "a_2"

$rev
[1] "2-82f1879cc7d73bef5574cc5cdf7c4094"

> doc_get(x,dbname = "ty",docid = "a_2")
Error: (404) - deleted
> doc2<- '{"name":"Shrink","beer":"TEST","note":"yummy","note2":"yay"}'
> doc_update(x,dbname = "ty",doc=doc2,docid="a_3",rev = "3-b1fb56db955b142c6efd3b3c52fe9e1b")
$ok
[1] TRUE

$id
[1] "a_3"

$rev
[1] "4-ee42fic3bfc1fd646764c4d94333c038"

> doc3<- {"rollno": "01", "name": "UZMA", "GRADE": "A"}
Error: unexpected ',' in "doc3<- {"rollno": "01", "
> doc3<- {"rollno": "01", "name": "UZMA", "GRADE": "A"} "
Error: unexpected ',' in "doc3<- {"rollno": "01", "
> doc3<- {"rollno": "01", "name": "UZMA", "GRADE": "A"} "
Error: unexpected ',' in "doc3<- {"rollno": "01", "
> doc3<- {"rollno": "01", "name": "UZMA", "GRADE": "A"} "
Error: unexpected ',' in "doc3<- {"rollno": "01", "
> doc3<- {"rollno": "01", "name": "UZMA", "GRADE": "A"} "
Error: unexpected ',' in "doc3<- {"rollno": "01", "
+ "name": "UZMA",
+ "GRADE": "A"
> doc_update(x,dbname = "ty",doc=doc3,docid = "a_1",rev = "1-be7c98bddf8ea7c46f4f401ff387593
d")
$ok
[1] TRUE

$id
[1] "a_1"

$rev
[1] "2-8e881d6a3e0fbdf735da8ff70cff6cc"

```

## **Practical No. 2**

**Aim:** Practical of Data collection, Data curation and management for Large-scale Data system (such as MongoDB)

- MongoDB Create database
- MongoDB Drop Database
- MongoDB Create collection
- MongoDB Drop collection
- MongoDB Insert Document
- MongoDB Query Document
- MongoDB Update Document
- Delete document in MongoDB
- MongoDB Projection
- limit() and skip() method in MongoDB
- Sorting of Documents in MongoDB
- MongoDB Indexing

Starting server with mongo or mongodb

C:\>**mongo**

>db

Test

- Create Database in MongoDB

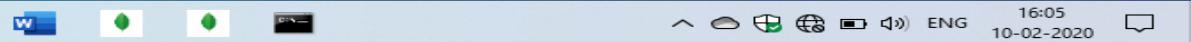
Once you are in the MongoDB shell, create the database in MongoDB by typing this command:

**use database\_name**

For example: create a database “tycs”:

```
> use tycs  
switched to db tycs
```

```
MongoDB Enterprise > use tycs
switched to db tycs
MongoDB Enterprise > show dbs
admin    0.000GB
config   0.000GB
local    0.000GB
tycs     0.000GB
MongoDB Enterprise >
```



create a collection **user** and insert a document in it.

```
> db.user.insert({name: "Asif", age: 20})
```

**O/P:** WriteResult({ "nInserted" : 1 })

**>show dbs**

```
admin 0.000GB
```

```
config 0.000GB
```

```
local 0.000GB
```

```
tycs 0.000GB
```

- MongoDB Drop Database

The syntax to drop a Database is:

```
>db.dropDatabase()
```

**O/P:**

```
{ "dropped" : "Testdb", "ok" : 1 }
```

```
MongoDB Enterprise > show dbs
```

```
admin 0.000GB
```

```
config 0.000GB
```

```
local 0.000GB
```

```
tycs 0.000GB
```

**O/P:**

```
MongoDB Enterprise > db.dropDatabase()
{ "dropped" : "tycs", "ok" : 1 }
MongoDB Enterprise > show dbs
admin      0.000GB
config     0.000GB
local      0.000GB
MongoDB Enterprise >
```

- Create Collection in MongoDB

Method 1: Creating the Collection in MongoDB on the fly

```
MongoDB Enterprise > use tycs
```

```
switched to db tycs
```

```
MongoDB Enterprise > db.tycs.insert({name:"Asif
khan",age:21,website:"www.google.com"})
```

**O/P:**

```
WriteResult({ "nInserted" : 1 })
```

Syntax: **db.collection\_name.find()**

```
MongoDB Enterprise > db.tycs.find()
```

**o/p:**

```
{ "_id" : ObjectId("5e410808e3755b1e06a63d1d"), "name" : "Asif khan", "age" : 21,
"website" : "www.google.com" }
```

```
show collections
```

```
MongoDB Enterprise > show collections
```

**O/P:**

```
tycs
```

```
user
```

- Drop collection in MongoDB

**SYNTAX:**

```
db.collection_name.drop()
```

MongoDB Enterprise > use students  
switched to db students

MongoDB Enterprise >**show collections**  
students  
teachers  
tycs  
user

MongoDB Enterprise >**db.user.drop()**  
true  
MongoDB Enterprise >**show collections**  
students  
teacher  
tycs

MongoDB Insert Document

**Syntax to insert a document into the collection:**

```
db.collection_name.insert()
```

```
>db.tycs.insert(  
... {  
...   name: "ASIF",  
...   age: 20,  
...   email: "asif@gmail.com",  
...   course: [ { name: "MongoDB", duration: 7 }, { name: "Java", duration: 30 } ]  
... }  
...)  
O/P:  
WriteResult({ "nInserted" : 1 })
```

**Verification:**

Syntax:

```
db.collection_name.find()
```

```
>db.tycs.find()
```

```
{ "_id" : ObjectId("5c2d37734fa204bd77e7fc1c"), "name" : "ASIF", "age" : 20, "email" : "asif@gmail.com", "course" : [ { "name" : "MongoDB", "duration" : 7 }, { "name" : "Java", "duration" : 30 } ] }
```

MongoDB Example: Insert Multiple Documents in collection

MongoDB Enterprise > **var beginners=**

```
... [
... "studentID":1001,
... "studentName":"Asif",
... "age":20
... ],
... ]
```

- MongoDB Query Document using find() method

Querying all the documents in JSON format

MongoDB Enterprise > db.students.find().pretty()

```
{
    "_id" : ObjectId("5e410f3fe3755b1e06a63d1e"),
    "studentID" : 1001,
    "studentName" : "Asif",
    "age" : 20
}
```

- **Query Document based on the criteria**

```
> db.students.find({StudentName : "Asif"}).pretty()
{
    "_id" : ObjectId("5c281c90c23e08d1515fd9cc"),
    "StudentId" : 1001,
    "StudentName" : "Asif",
    "age" : 20
}
```

- **Updating Document using update() method**

#### Syntax:

```
db.collection_name.update(criteria, update_data)
```

```
>use tycs
switched to db tycs
>show collections
```

```

beginnersbook
students
tycs
>db.createCollection("got")
{ "ok" : 1 }
> var abc = [
... {
...   "_id" : ObjectId("59bd2e73ce524b733f14dd65"),
...   "name" : "Asif",
...   "age" : 20
... },
... ];
> db.got.find().pretty()
{
  "_id" : ObjectId("59bd2e73ce524b733f14dd65"),
  "name" : "steve",
  "age" : 20
}

```

### To update multiple documents with the update() method:

```
db.got.update({ "name":"Jon Snow" },
{$set:{ "name":"Kit Harington" }},{multi:true})
```

Updating Document using save() method

#### Syntax:

```
db.collection_name.save( {_id:ObjectId(), new_document} )
```

To get the \_id of a document, you can either type this command:

```
db.got.find().pretty()
```

```

> db.got.find({ "name": "Asif" }).pretty()
{
  "_id" : ObjectId("59bd2e73ce524b733f14dd65"),
  "name" : "Asif",
  "age" : 20
}
> db.got.find().pretty()
{
  "_id" : ObjectId("59bd2e73ce524b733f14dd65"),
  "name" : "Steve",
  "age" : 20
}
```

- MongoDB Delete Document from a Collection

#### Syntax of remove() method:

```
db.collection_name.remove(delete_criteria)
```

#### Delete Document using remove() method

```
> db.students.find().pretty()
{
  "_id" : ObjectId("59bcecc7668dcce02aaa6fed"),
  "StudentId" : 1001,
  "StudentName" : "Steve",
  "age" : 30
}
```

```
db.students.remove({ "StudentId": 3333 })
```

#### Output:

```
WriteResult({ "nRemoved" : 1 })
```

To verify whether the document is actually deleted. Type the following command:

```
db.students.find().pretty()
```

It will list all the documents of students collection.

```
> use tycs
switched to db_tycs
> db.students.find().pretty()
{
  "_id" : ObjectId("5c281c90c23e08d1515fd9cc"),
  "StudentId" : 1001,
  "StudentName" : "Asif",
  "age" : 20
}
{
  "_id" : ObjectId("5c2d38934fa204bd77e7fc1d"),
  "StudentId" : 1001,
  "StudentName" : "Steve",
  "age" : 30
}
```

#### Remove all Documents

```
db.collection_name.remove({ })
```

- MongoDB Projection

**Syntax:**

```
db.collection_name.find({},{field_key:1 or 0})
```

```
> db.students.find().pretty()
{
    "_id" : ObjectId("5c281c90c23e08d1515fd9cc"),
    "StudentId" : 1001,
    "StudentName" : "Steve",
    "age" : 20
}
> db.students.find({},{"_id": 0, "StudentId" : 1})
{ "StudentId" : 1001 }
{ "StudentId" : 1002 }
```

```
> db.students.find({},{"_id": 0, "StudentName" : 0, "age" : 0})
{ "StudentId" : 1001 }
{ "StudentId" : 1002 }
• MongoDB – limit() and skip() method
```

**The limit() method in MongoDB****Syntax:**

```
db.collection_name.find().limit(number_of_documents)
db.studentdata.find({student_id : {$gt:2002} }).pretty()
db.studentdata.find({student_id : {$gt:2002} }).limit(1).pretty()
```

**MongoDB Skip() Method**

```
db.studentdata.find({student_id : {$gt:2002} }).limit(1).skip(1).pretty()
```

- MongoDB sort() method

**Sorting Documents using sort() method****Syntax of sort() method:**

```
db.collecttion_name.find().sort({field_key:1 or -1})
```

1 is for ascending order and -1 is for descending order. The default value is 1.

**For example:** collection studentdata contains following documents:

```
> db.studentdata.find().pretty()
```

```
{  
    "_id" : ObjectId("59bf63380be1d7770c3982af"),  
    "student_name" : "Steve",  
    "student_id" : 1001,  
    "student_age" :1002  
}
```

Let's display the student\_id of all the documents in **descending order**:

```
> db.studentdata.find({}, {"student_id": 1, _id:0}).sort({"student_id": -1})  
{ "student_id" : 1001 }  
{ "student_id" : 1002 }
```

To display the student\_id field of all the students in **ascending order**:

```
> db.studentdata.find({}, {"student_id": 1, _id:0}).sort({"student_id": 1})  
{ "student_id" : 1001 }  
{ "student_id" : 1002 }
```

```
Administrator: Command Prompt - mongo Beginnersbook.com □ X  
> db.studentdata.find({}, {"student_id": 0, _id:0}).sort({"student_id": 1})  
{ "student_name" : "Steve", "student_age" : 22 }  
{ "student_name" : "Carol", "student_age" : 22 }  
{ "student_name" : "Tim", "student_age" : 23 }  
>
```

- **MongoDB Indexing with Example**

**How to create index in MongoDB**

```
db.collection_name.createIndex({field_name: 1 or -1})
```

The value 1 is for ascending order and -1 is for **descending order**.

Let's create the index on student\_name field in **ascending order**:

```
db.studentdata.createIndex({student_name: 1})
```

**Output:**

```
{  
    "createdCollectionAutomatically" : false,  
    "numIndexesBefore" : 1,  
    "numIndexesAfter" : 2,
```

```
        "ok" : 1
    }
```

- MongoDB – Finding the indexes in a collection

```
db.collection_name.getIndexes()
> db.studentdata.getIndexes()
[
  {
    "v" : 2,
    "key" : {
      "_id" : 1
    },
    "name" : "_id_",
    "ns" : "test.studentdata"
  },
]
```

- MongoDB –droping the indexes in a collection

```
> db.studentgrades.dropIndexes( )
{
  "nIndexesWas" : 1,
  "msg" : "non-_id indexes dropped for collection",
  "ok" : 1
}
> █
```

### **Practical No. 3**

**Aim:** Practical of Principal Component Analysis

1]

```
data_iris<-iris[1:4]  
Cov_data<-cov(data_iris)  
Eigen_data<-eigen(Cov_data)  
PCA_data<-princomp(data_iris,cor="False")  
Eigen_data$values
```

2]

```
PCA_data$sdev^2  
PCA_data$loadings[,1:4]  
Eigen_data$vectors  
summary(PCA_data)  
biplot(PCA_data)  
screeplot(PCA_data,type="lines")
```

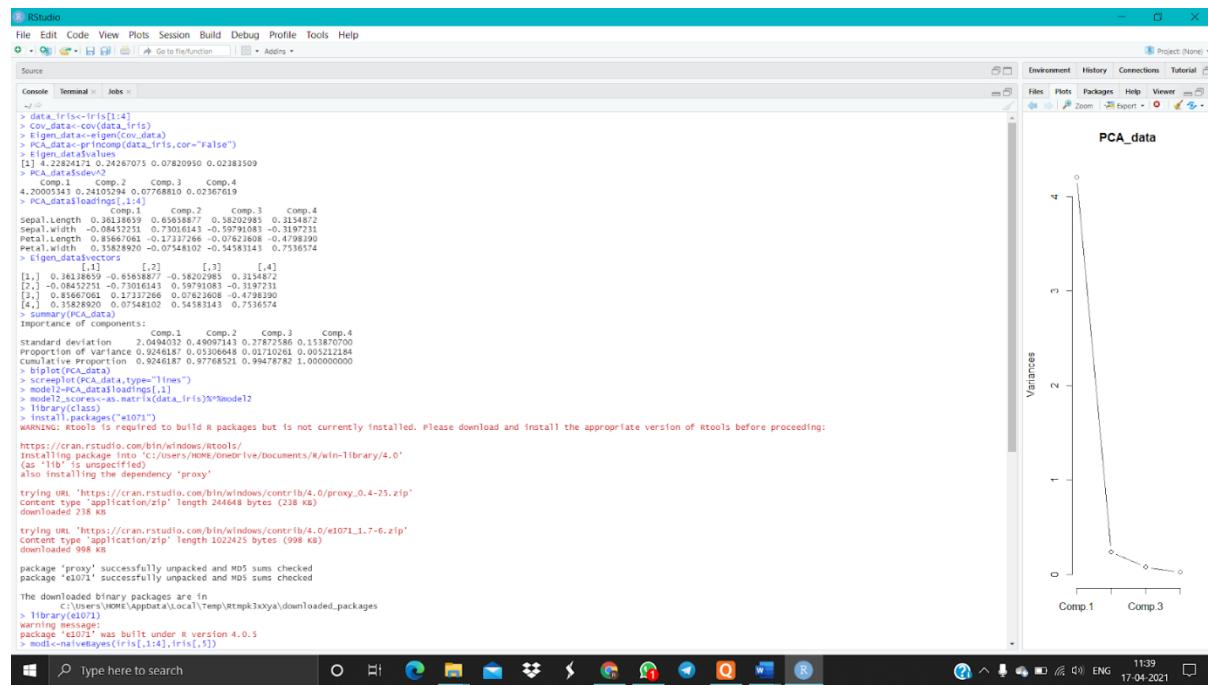
```

model2=PCA_data$loadings[,1]
model2_scores<-as.matrix(data_iris)%*%model2
library(class)
install.packages("e1071")
library(e1071)

mod1<-naiveBayes(iris[,1:4],iris[,5])
mod2<-naiveBayes(model2_scores,iris[,5])
table(predict(mod1,iris[,1:4]),iris[,5])
table(predict(mod2,model2_scores),iris[,5])

```

## Output:



RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Console Terminal Jobs

```
~/Documents/R/iris/iris.R
WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:
https://cran.rstudio.com/bin/windows/tools/
Installing package into 'C:/Users/HOME/OneDrive/Documents/R/win-library/4.0'
(as 'lib' is unspecified)
also installing the dependency 'proxy'

trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/proxy_0.4-25.zip'
Content type 'application/zip' length 244848 bytes (238 kB)
downloaded 238 kB

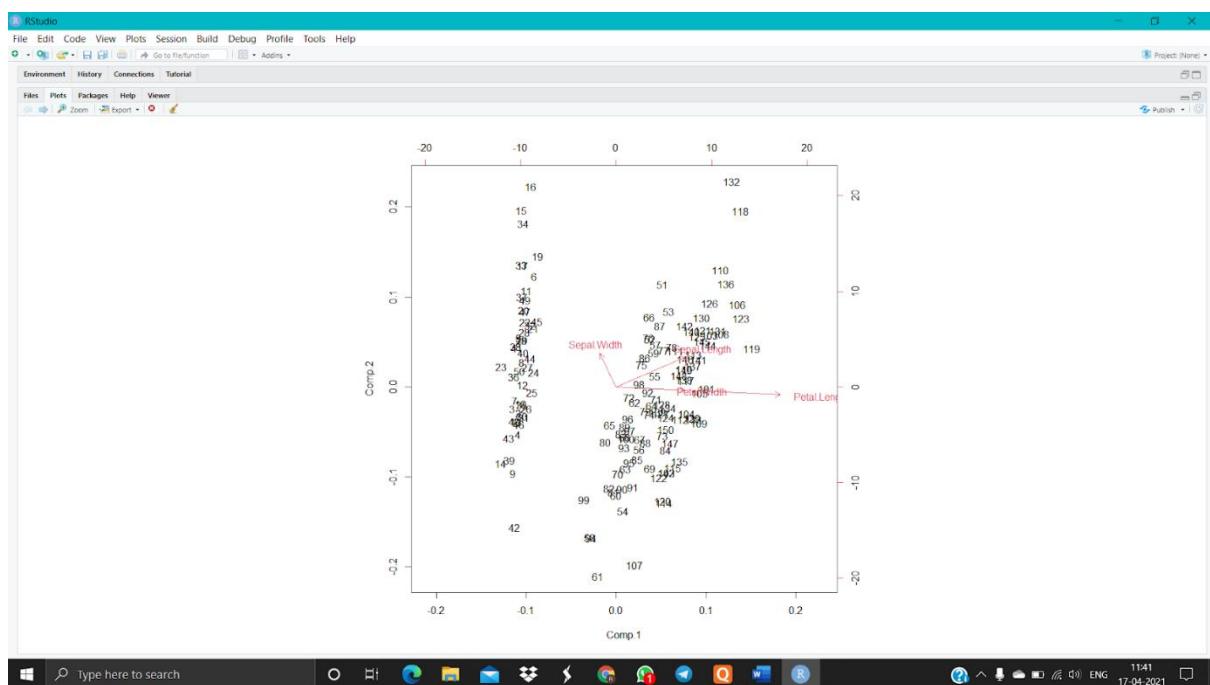
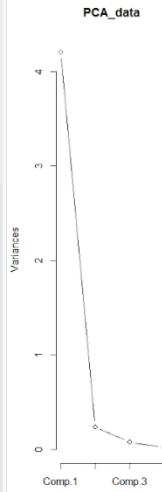
trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/e1071_1.7-6.zip'
Content type 'application/zip' length 1022425 bytes (998 kB)
downloaded 998 kB

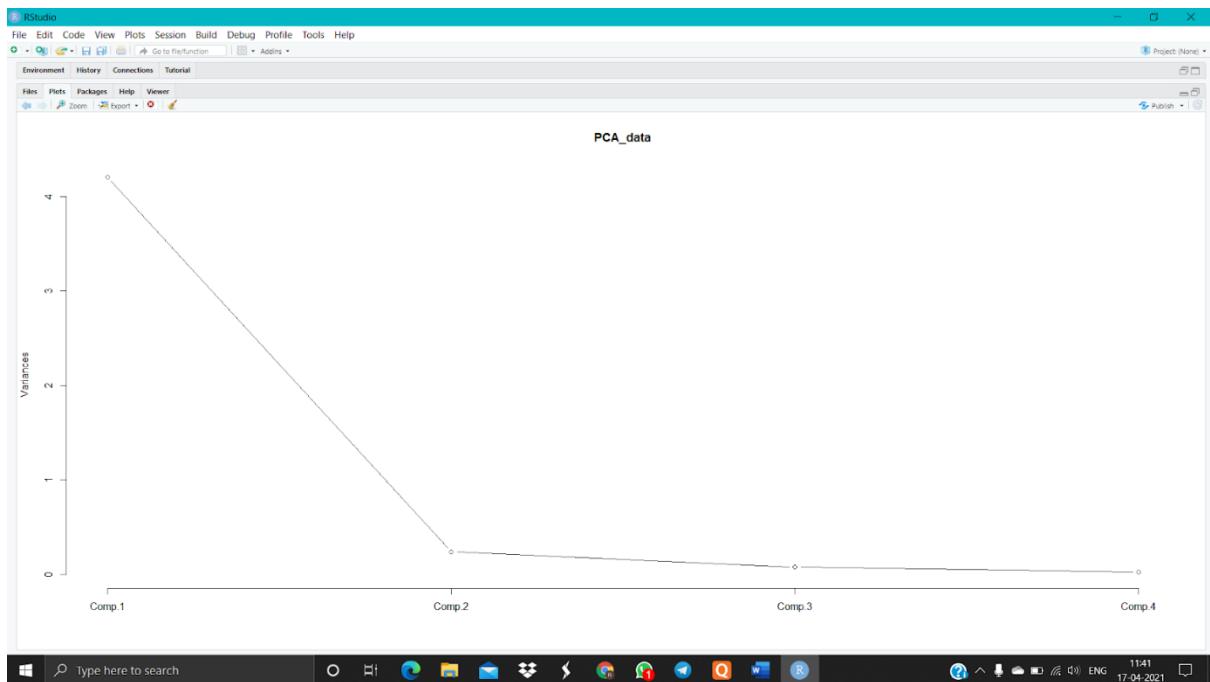
package 'proxy' successfully unpacked and MD5 sums checked
package 'e1071' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
  C:/Users/HOME/AppData/Local/Temp/RtmpJ3xyA/downloaded_packages
Warning message:
package 'e1071' was built under R version 4.0.5
> library(e1071)
> mod1<-naiveBayes(iris[,1:4],iris[,5])
> mod2<-naiveBayes(iris[,1:4],iris[,5])
> table(predict(mod1,iris[,1:4]),iris[,5])

  setosa versicolor virginica
setosa      50          0          0
versicolor    0         46          5
virginica     0          4        45
> table(predict(mod2,mod2_scores),iris[,5])

  setosa versicolor virginica
setosa      50          0          0
versicolor    0         46          5
virginica     0          4        45
> table(predict(mod1,iris[,1:4]),iris[,5])
```





## Practical No. 4

Aim: Practical of Clustering

"K-means Clustering "

```

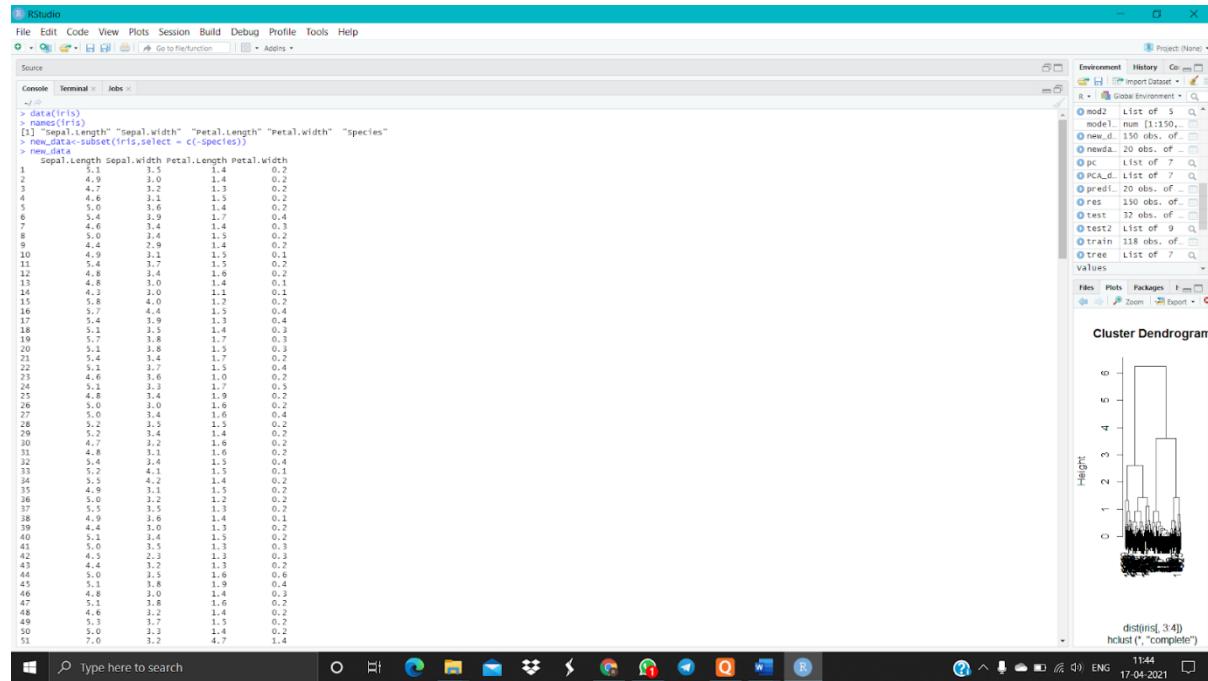
data(iris)
names(iris)
new_data<-subset(iris,select = c(-Species))
new_data
cl<-kmeans(new_data,3)
cl
data<-new_data
wss<-sapply(1:15,function(k){kmeans(data,k)$tot.withinss})

```

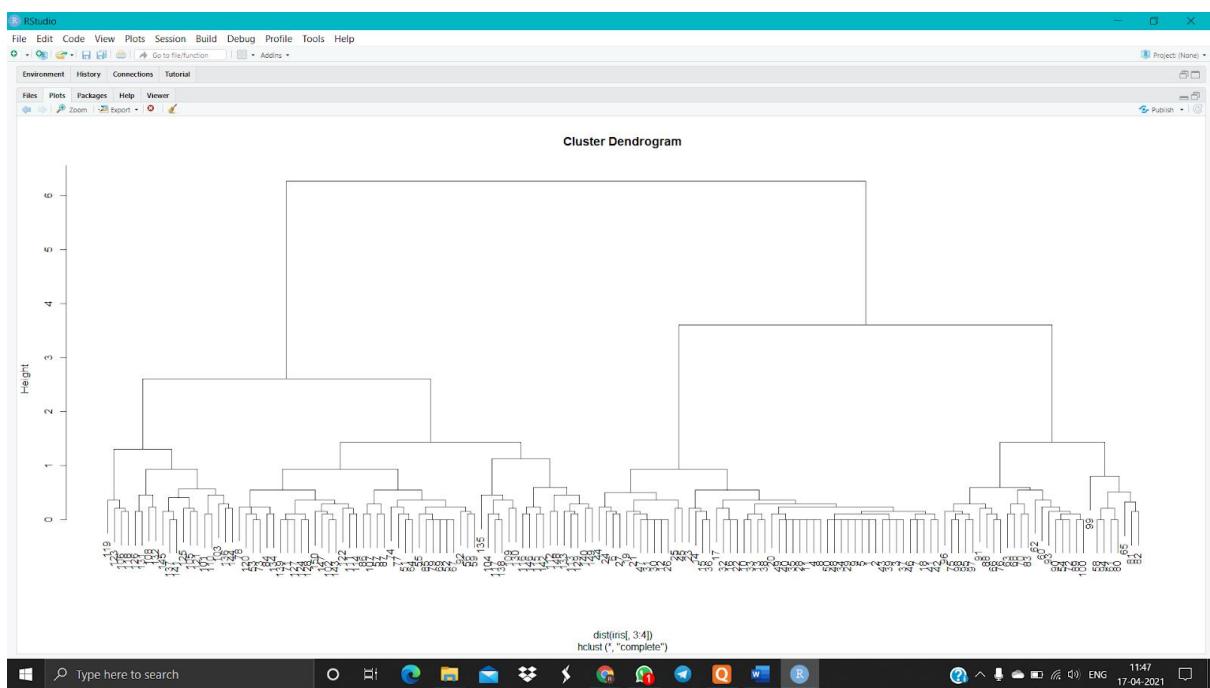
wss

```
plot(1:15,wss,type="b",pch=19,frame=FALSE,xlab = "Number of clusters K",ylab = "Total within-clusters sums of squares")  
  
library(cluster)  
  
clusplot(new_data,cl$cluster,color=TRUE,shade=TRUE,labels=2,lines=0)  
  
cl$cluster  
  
cl$centers  
  
"agglomerative clustering "  
  
clusters<-hclust(dist(iris[,3:4]))  
  
plot(clusters)  
  
clusterCut<-cutree(clusters,3)  
  
table(clusterCut,iris$Species)
```

## Output:







**Practical No:05**

**Aim:** Practical of Time-Series Forecasting

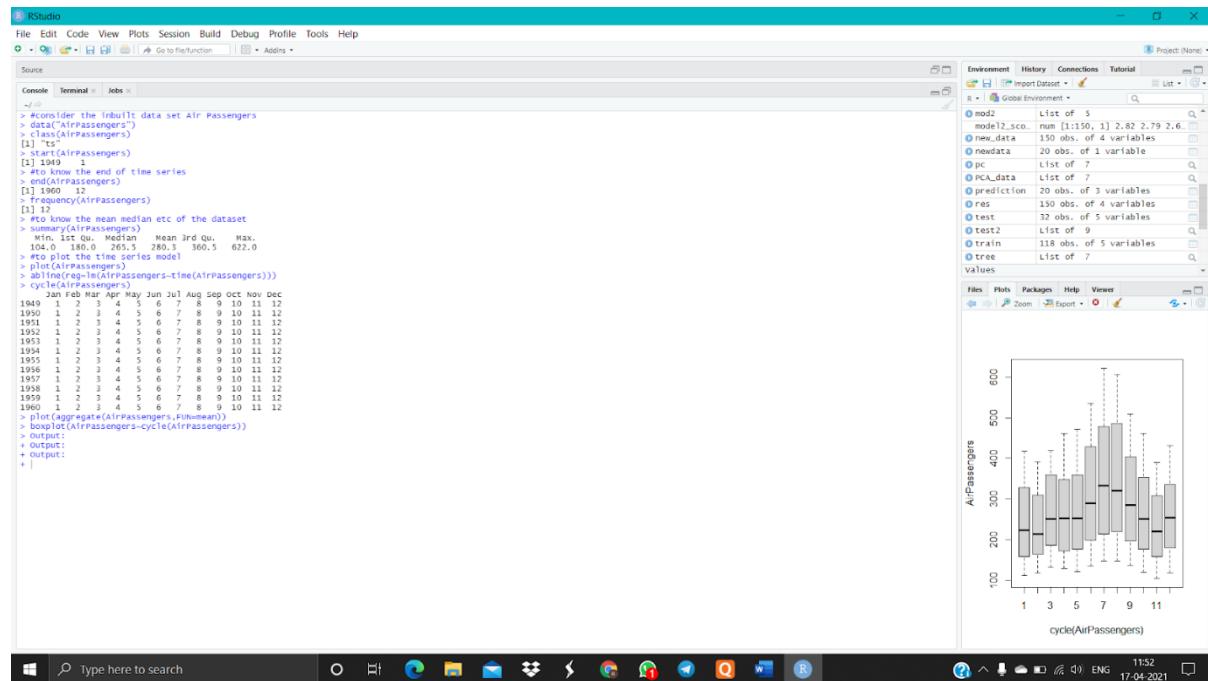
```
#consider the inbuilt data set Air Passengers  
data("AirPassengers")  
class(AirPassengers)  
start(AirPassengers)  
#to know the end of time series  
end(AirPassengers)  
frequency(AirPassengers)  
#to know the mean median etc of the dataset  
summary(AirPassengers)  
#to plot the time series model  
plot(AirPassengers)  
abline(reg=lm(AirPassengers~time(AirPassengers)))
```

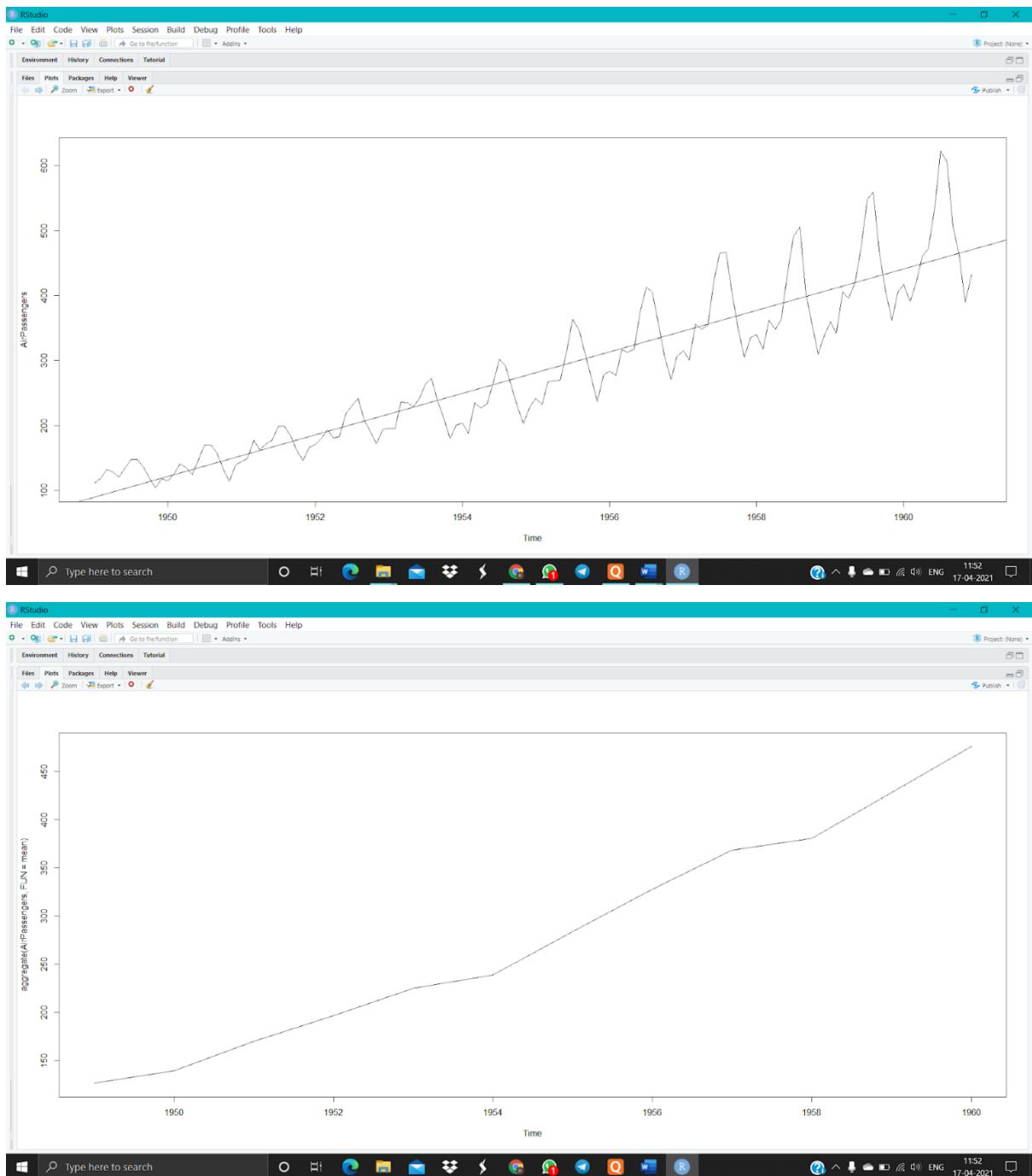
```

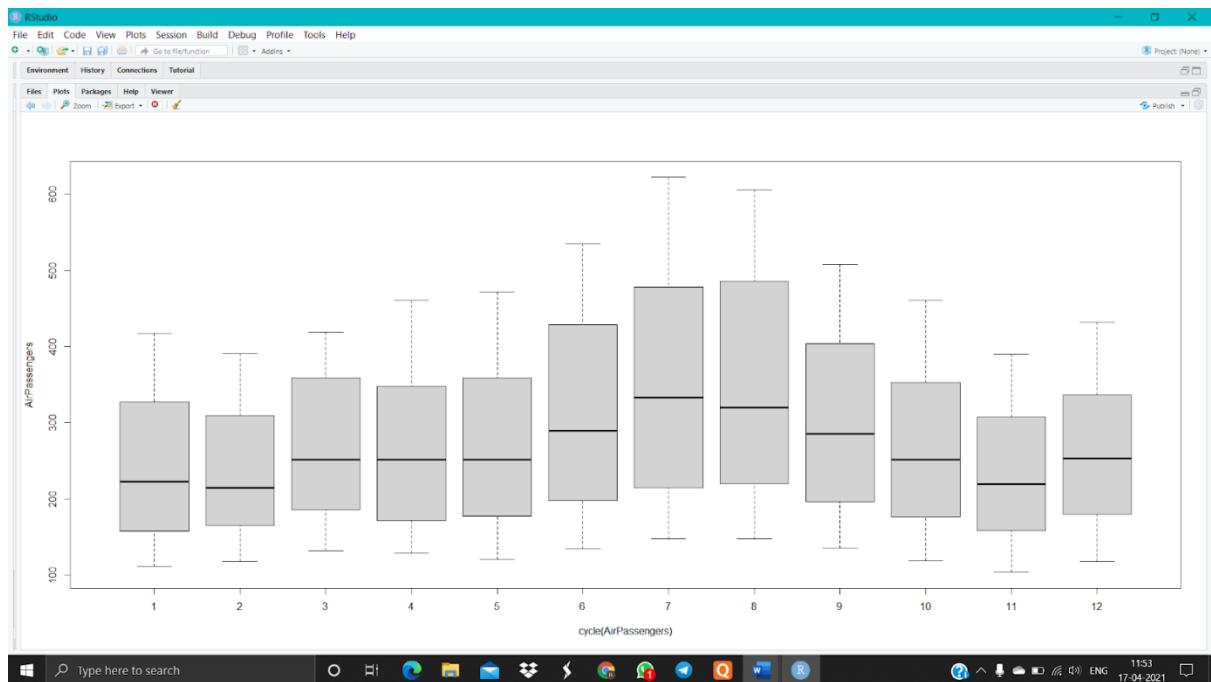
cycle(AirPassengers)
plot(aggregate(AirPassengers,FUN=mean))
boxplot(AirPassengers~cycle(AirPassengers))

```

## Output:







### Practical No:06

**Aim:** Practical Of Simple /Multiple Linear Regression

#consider some data set

```
height<-c(102,117,105,141,135,115,138,144,137,100,131,119,115,121,113)
```

```
weight<-c(61,46,62,54,60,69,51,50,46,64,48,56,64,48,59)
```

#lm is for Linear Regression

```
student<-lm(weight~height)
```

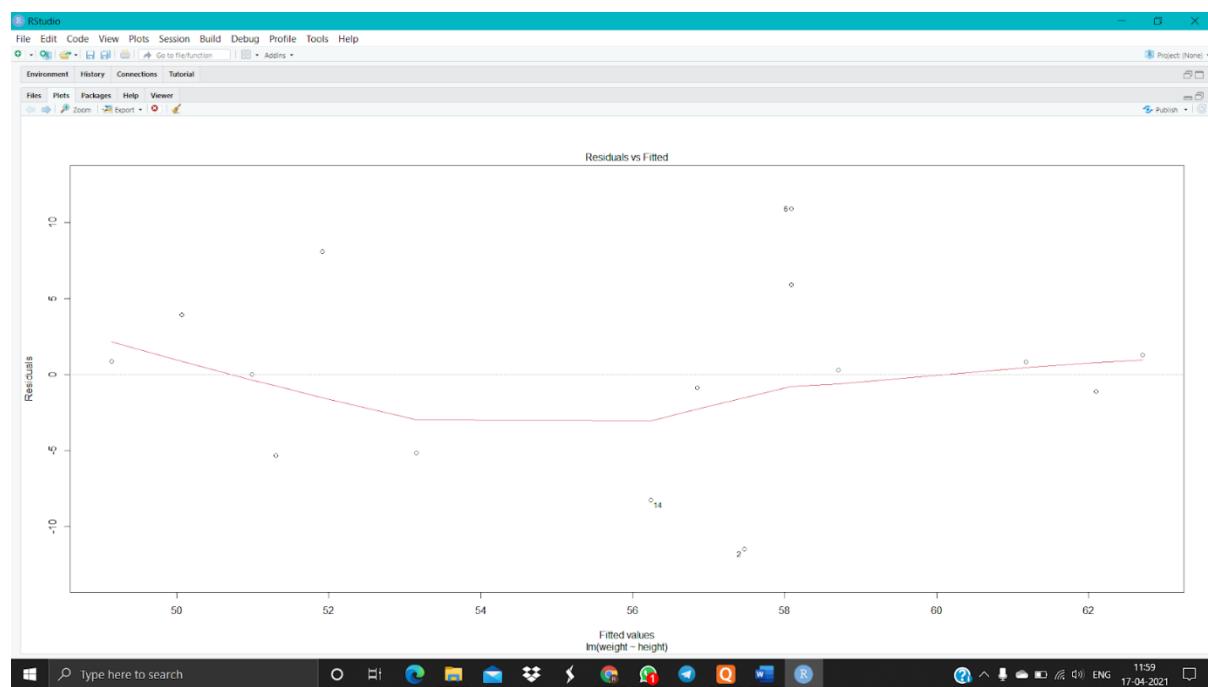
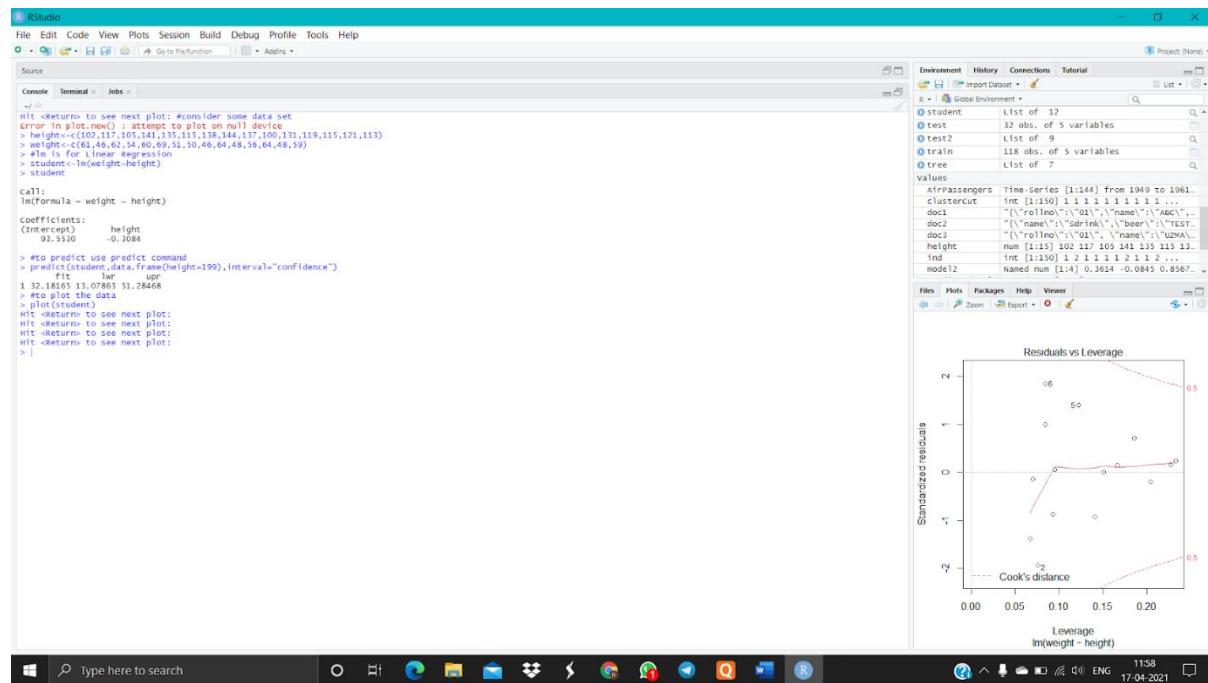
student

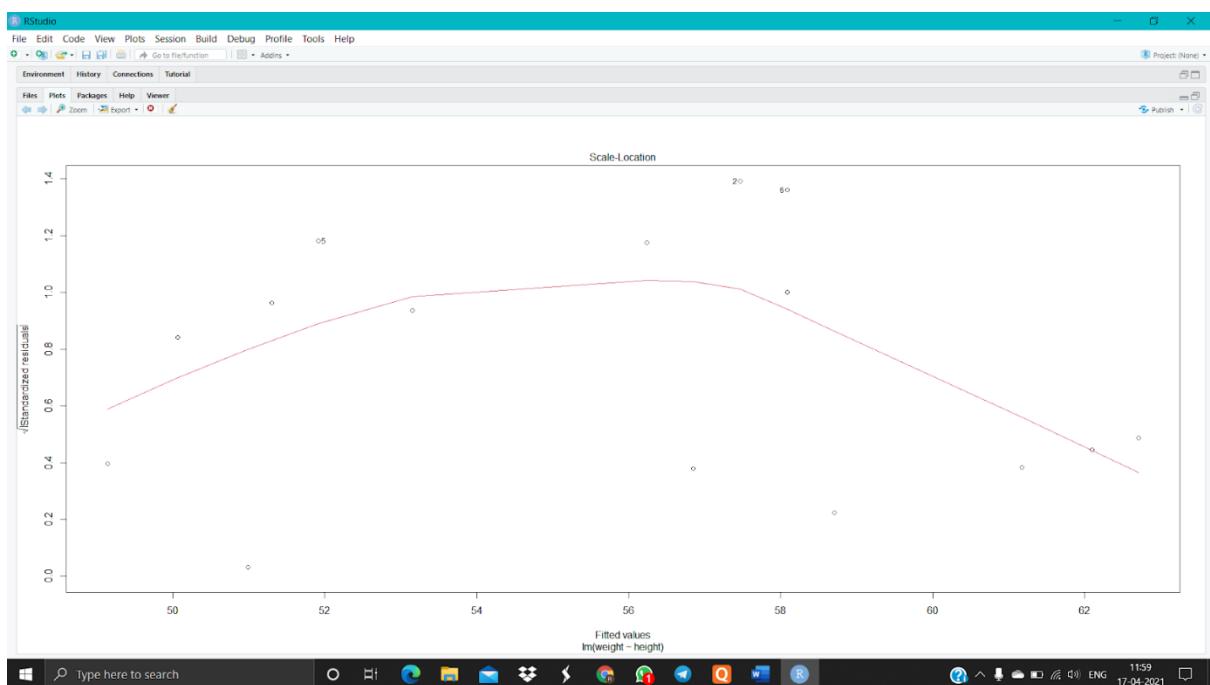
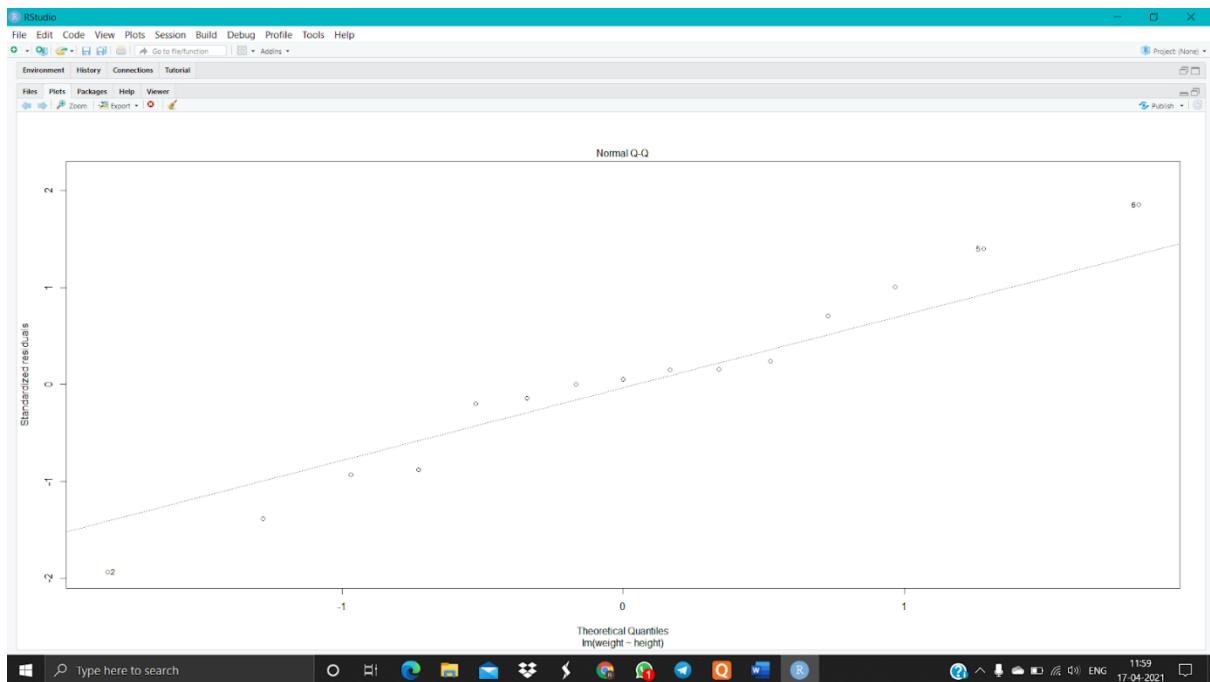
#to predict use predict command

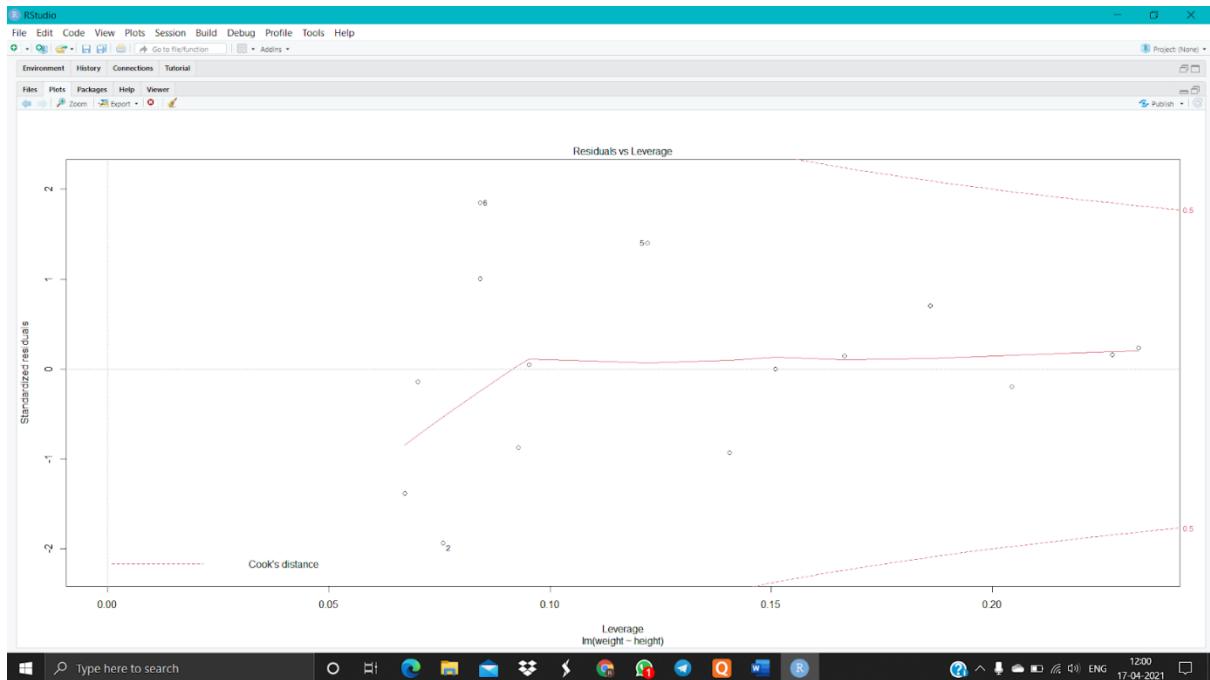
```
predict(student,data.frame(height=199),interval="confidence")
```

```
#to plot the data
plot(student)
```

## Output:







## Practical No: 07

**Aim:** Practical of Logistic Regression

```
library(datasets)
ir_data<-iris
head(ir_data)
str(ir_data)
levels(ir_data$Species)
sum(is.na(ir_data))
```

```

ir_data<-ir_data[1:100,]
set.seed(100)
samp<-sample(1:100,80)
ir_test<-ir_data[samp,]
ir_ctrl<-ir_data[-samp,]
install.packages("ggplot2")
library(ggplot2)
library(ggplot2)
install.packages("GGally")
ggpairs(ir_test)
y<-ir_test$Species;
x<-ir_test$Sepal.Length
glfit<-glm(y~x,family='binomial')
summary(glfit)
newdata<-data.frame(x=ir_ctrl$Sepal.Length)
predicted_val<-predict(glfit,newdata,type="response")
prediction<-data.frame(ir_ctrl$Sepal.Length,ir_ctrl$Species,predicted_val)
prediction

qplot(prediction[,1],round(prediction[,3]),col=prediction[,2],xlab='sepal.Length',ylab='prediction using logistic Reg')

```

### **Output:**

**RStudio**

File Edit Code View Plots Session Build Debug Profile Tools Help

Source

```

Console Terminal Jobs ×
~/d
> library(datasets)
> ir控件
> head(ir_data)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1       5.1       3.5        1.4       0.2    setosa
2       4.9       3.0        1.4       0.2    setosa
3       4.7       3.2        1.3       0.2    setosa
4       4.6       3.1        1.5       0.2    setosa
5       5.0       3.6        1.4       0.4    setosa
6       5.4       3.9        1.7       0.4    setosa
> str(ir_data)
'data.frame': 150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 1 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3.0 3.2 3.1 3.6 3.9 3.4 4.5 4.5 4.5 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa", "versicolor", "virginica"
   [1] "setosa"      "versicolor"   "virginica"
   ...$mcn$mcn$mcn$mcn
[1] 0
> ir_data=ir_data[1:100,]
> set.seed(100)
> sample=sample[1:1:100,80]
> ir_test=ir_data[samp,]
> ir_train=ir_data[-samp,]
> ir_all=pack.ir(ir_all3)
WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:
https://cran.rstudio.com/bin/windows/Rtools/
Installing package into 'C:/users/onebive/onedrive/documents/R/win-library/4.0'
(as you are a member of the 'root' group).
also installing the dependencies: 'gridspace', 'c11n', 'crayon', 'utf8', 'farver', 'labeling', 'lifecycle', 'munsell', 'RColorBrewer', 'viridisLite', 'ellipsis', 'fansi', 'magrittr', 'pillar', 'pkgconfig', 'vctrs', 'digest', 'glue', 'gttable', 'gridbase', 'gridExtra', 'tidyverse', 'tibble', 'wtre'
trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/colorspace_2.0-0.zip'
Content type 'application/zip' length 2647275 bytes (2.5 MB)
downloaded 2.5 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/ci_2.4.0.zip'
Content type 'application/zip' length 50429 bytes (49 kB)
downloaded 50429 bytes

trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/crayon_1.4.1.zip'
Content type 'application/zip' length 141732 bytes (138 kB)
downloaded 138 kB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/utf8_1.2.1.zip'
Content type 'application/zip' length 209830 bytes (204 kB)
downloaded 209 kB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/farver_2.1.0.zip'
Content type 'application/zip' length 1751664 bytes (1.7 MB)
downloaded 1.7 kB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/labeling_0.4.2.zip'
Content type 'application/zip' length 62727 bytes (61 kB)

```

12:09 17-04-2021

**RStudio**

File Edit Code View Plots Session Build Debug Profile Tools Help

Source

```

Console Terminal Jobs ×
~/d
package 'reshape' successfully unpacked and NAMESPACE sums checked
package 'tidyverse' successfully unpacked and NAMESPACE sums checked
package 'Ggally' successfully unpacked and NAMESPACE sums checked
The downloaded binary packages are in
C:/Users/ONEAppdata/Local/Temp/rtmpk3xyxa/downloaded_packages
> ggpairs()
Error in ggpairs(fit_test) : could not find function "ggpairs"
> yc<-ir_test$Species;
> xc<-ir_test$Sepal.Length
> gl<-iris$Species,family='binomial')
> summary(glfit)

call:
glm(formula = y ~ x, family = "binomial")

Deviance Residuals:
Min      1Q      Median      3Q      Max 
-1.96338 -0.50121  0.04079  0.45923  2.76238 

Coefficients:
Estimate Std. Error z value Pr(>z)
(Intercept) -25.386 5.517 -4.601 4.20e-06 ***
x             4.675 1.017 4.596 4.31e-06 ***
...
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

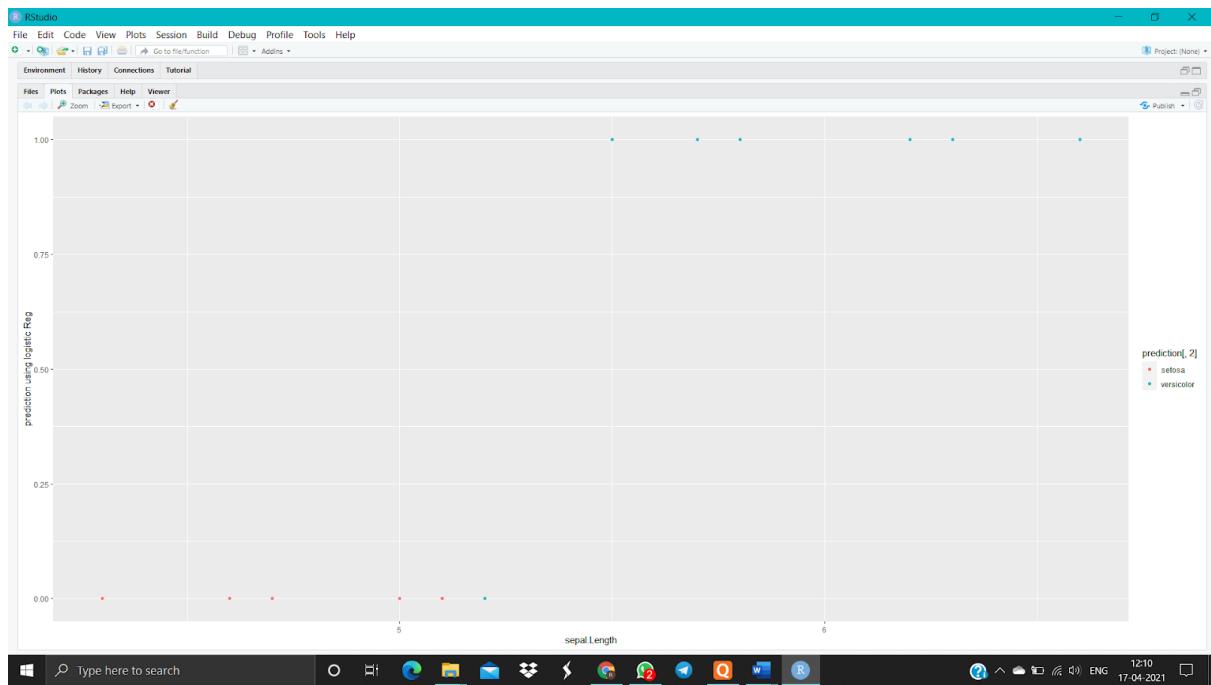
(Dispersion parameter for binomial family taken to be 1)

null deviance: 110.854 on 79 degrees of freedom
residual deviance: 56.716 on 78 degrees of freedom
AIC: 60.716

Number of Fisher Scoring Iterations: 6
> newdata<-data.frame(x=ir_ctrl$Sepal.Length)
> predicted_val<-predict(glfit,newdata,type="response")
> predicted_val<-data.frame(ir_ctrl$Sepal.Length,ir_ctrl$Species,predicted_val)
> prediction
  ir_ctrl.Sepal.Length ir_ctrl.Species predicted_val
1                     5.0      setosa       0.17602704
2                     4.7      setosa       0.031871367
3                     4.6      setosa       0.020210042
4                     5.0      setosa       0.020210042
5                     4.6      setosa       0.020210042
6                     4.3      setosa       0.0050468194
7                     4.6      setosa       0.020210042
8                     5.2      setosa       0.254235573
9                     5.2      setosa       0.254235573
10                    5.0      setosa       0.17602704
11                    5.0      setosa       0.114037011
12                    6.6      versicolor   0.995801728
13                    5.2      versicolor   0.692779173
14                    5.8      versicolor   0.849266736
15                    6.2      versicolor   0.973736995
16                    6.0      versicolor   0.993803728
17                    5.5      versicolor   0.384877616

```

12:10 17-04-2021



## **Practical No:08**

**Aim:** Practical of Hypothesis testing

#Entering the data

```
>x=c(6.2,6.6,7.1,7.4,7.6,7.9,8,8.3,8.4,8.5,8.6,8.8,8.8,9.1,9.2,9.4,9.7,9.9,10.2,10.4,10.8,11.3,11.9)
```

#one-sample Hypothesis test

```
>t.test(x-9,alternative = "two.sided",conf.level = 0.95)
```

#Two-sample hypothesis test

```
>x=c(481,421,421,422,425,427,431,434,437,439,446,447,448,454,463,465)
```

```
>y=c(429,430,430,431,36,437,440,441,445,446,447)
```

```
>test2<-t.test(x,y,alternative = "two.sided",mu=0,var.equal = F,conf.level = 0.95)
```

```
>test2
```

**Output:**

```

RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Source Terminal Jobs
~/d/ > #entering the data
> x<-c(2.5,6.7,1.7,4.7,6.7,9.8,8.3,8.4,8.5,8.6,8.8,8.9,1.9,2.9,4.9,7.9,9.10,2.10,4.10,8.11,3.11,9)
> #one sample hypothesis test
> t.test(x,alternative = "two.sided",conf.level = 0.95)
One Sample t-test

data: x
t = -0.41475, df = 22, p-value = 0.6823
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
-0.765569 0.3043829
sample estimates:
mean of x
mean of y
-0.180087

Two Sample t-test

data: x and y
t = 1.0939, df = 10, p-value = 0.2998
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-1.533866 4.623710
sample estimates:
mean of x mean of y
441.3125 401.0909
> test2

```

welch Two Sample t-test

```

data: x and y
t = 1.0939, df = 10, p-value = 0.2998
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-1.533866 4.623710
sample estimates:
mean of x mean of y
441.3125 401.0909
> 
```

## Practical No:09

**Aim:** Practical Of Analysis Of Variance

```

ftest<-read.csv(file.choose(),sep=",",header = T)

var.test(ftest$time_g1,ftest$time_g2,alternative = "two.sided")

//one way anova

names(data1)

summary(data1)

head(data1)

anv<-aov(formula=satindex~dept,data=data1)

summary(anv)

//two way anova

```

```

data2<-read.csv(file.choose(),sep=",",header=T)
names(data2)
summary(data2)
head(data2)
anv1<-aov(formula = satindex~dept+exp+dept*exp,data=data2)
summary(anv1)

```

### **Output:**

```

Console Terminal × Jobs ×
> ftest<-read.csv(file.choose(),sep=",",header = T)
> var.test(ftest$time_g1,ftest$time_g2,alternative = "two.sided")
    F test to compare two variances

data:  ftest$time_g1 and ftest$time_g2
F = 1.459, num df = 13, denom df = 13, p-value = 0.5053
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.4683787 4.5448881
sample estimates:
ratio of variances
1.459016

> ftest
   time_g1 time_g2
1       85     83
2       95     85
3      105     96
4       85     94
5       90    102
6       97    100
7      104     94
8       95     95
9       88     88
10      90     92
11      94     95
12      95     94
13      86     95
14      92     90
>

```

```

> data1<-read.csv(file.choose(),sep=",",header=T)
> names(data1)
[1] "satindex" "dept"
> summary(data1)
   satindex           dept
  Min. :51.00    CS      :13
  1st Qu.:59.00  FINANCE :12
  Median :66.00  MARKETING:12
  Mean   :65.59
  3rd Qu.:71.00
  Max.   :77.00
> head(data1)
  satindex dept
1       75 FINANCE
2       56 FINANCE
3       72 FINANCE
4       59 FINANCE
5       62 FINANCE
6       66 FINANCE
> anv<-aov(formula=satindex~dept,data=data1)
> summary(anv)
             Df Sum Sq Mean Sq F value Pr(>F)
dept          2  220.1  110.03  2.308  0.115
Residuals    34 1620.9   47.67
> |

```

---

```

> data2<-read.csv(file.choose(),sep=",",header=T)
> names(data2)
[1] "satindex" "dept"      "exp"
> summary(data2)
   satindex           dept      exp
  Min. :51.00    CS      :12    gt5:18
  1st Qu.:59.00  FINANCE :12    lt5:18
  Median :66.00  MARKETING:12
  Mean   :65.31
  3rd Qu.:71.00
  Max.   :77.00
> head(data2)
  satindex dept exp
1       75 FINANCE lt5
2       56 FINANCE lt5
3       72 FINANCE lt5
4       59 FINANCE lt5
5       62 FINANCE lt5
6       66 FINANCE lt5
> anv1<-aov(formula = satindex~dept+exp+dept*exp,data=data2)
> summary(anv1)
             Df Sum Sq Mean Sq F value Pr(>F)
dept          2  164.2  82.11  1.679  0.204
exp           1    78.0   78.03  1.595  0.216
dept:exp      2   20.2   10.11  0.207  0.814
Residuals    30 1467.2   48.91
> |

```

## **Practical No: 10**

**Aim:** Practical of Decision Tree

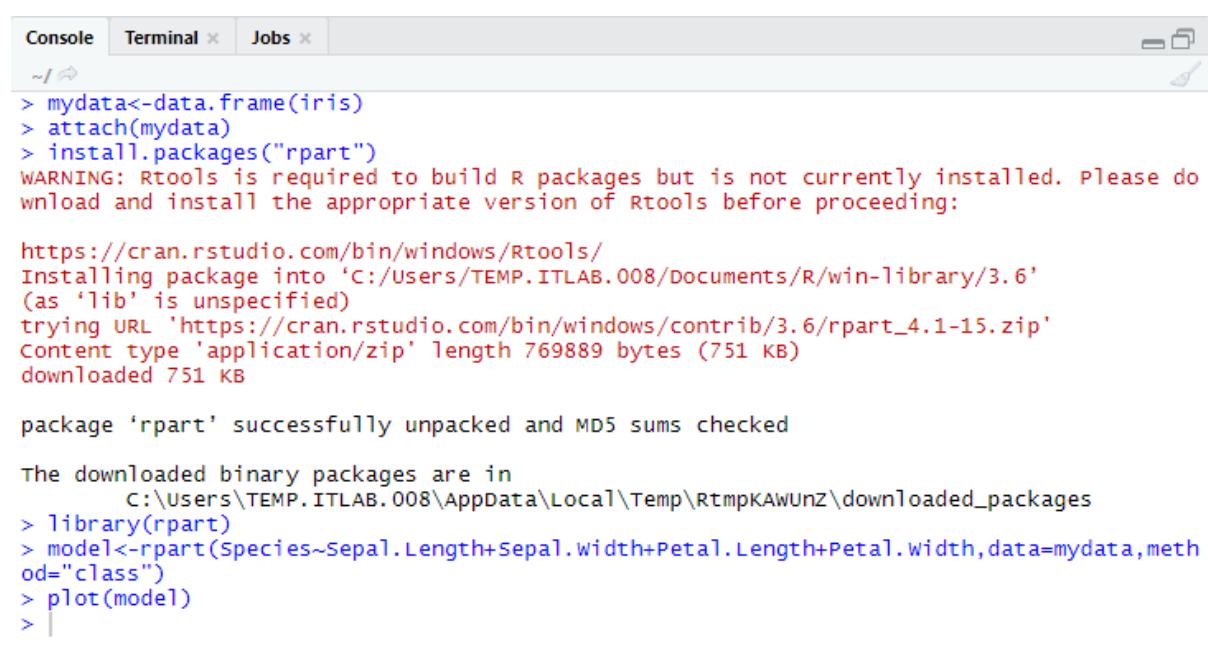
```
mydata<-data.frame(iris)
attach(mydata)
install.packages("rpart")
library(rpart)
model<-
rpart(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=my
data,method="class")
plot(model)
text(model,use.n=TRUE,all=TRUE,cex=0.8)
install.packages("tree")
library(tree)
model1<-
tree(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=myd
ata,method="class",split="gini")
plot(model1)
```

```

text(model,all=TRUE,cex=0.6)
install.packages("party")
library(party)
model2<-
ctree(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=my
data)
plot(model2)
library(tree)
mydata<-data.frame(iris)
attach(mydata)
model<-
tree(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=myd
ata,method="class",control=tree.control(nobs=150,mincut=10))
plot(model1)
text(model,all=TRUE,cex=0.6)
predict(model,iris)
model2<-
ctree(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=my
data,controls=ctree_control(maxdepth=2))
plot(model2)

```

## **Output:**



The screenshot shows the RStudio interface with the 'Console' tab selected. The console window displays the following R session:

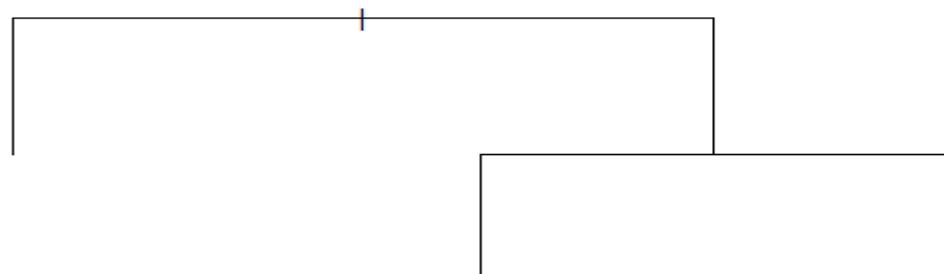
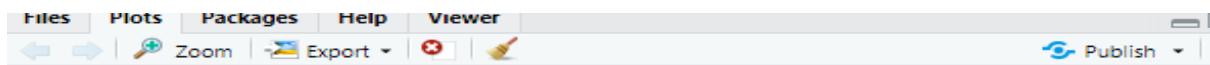
```

Console Terminal × Jobs ×
~/
> mydata<-data.frame(iris)
> attach(mydata)
> install.packages("rpart")
WARNING: Rtools is required to build R packages but is not currently installed. Please do
wnload and install the appropriate version of Rtools before proceeding:
https://cran.rstudio.com/bin/windows/Rtools/
Installing package into 'C:/Users/TEMP.ITLAB.008/Documents/R/win-library/3.6'
(as 'lib' is unspecified)
trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/rpart_4.1-15.zip'
Content type 'application/zip' length 769889 bytes (751 KB)
downloaded 751 KB

package 'rpart' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
  C:\Users\TEMP.ITLAB.008\AppData\Local\Temp\RtmpKAWUnZ\downloaded_packages
> library(rpart)
> model<-rpart(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata,meth
od="class")
> plot(model)
>

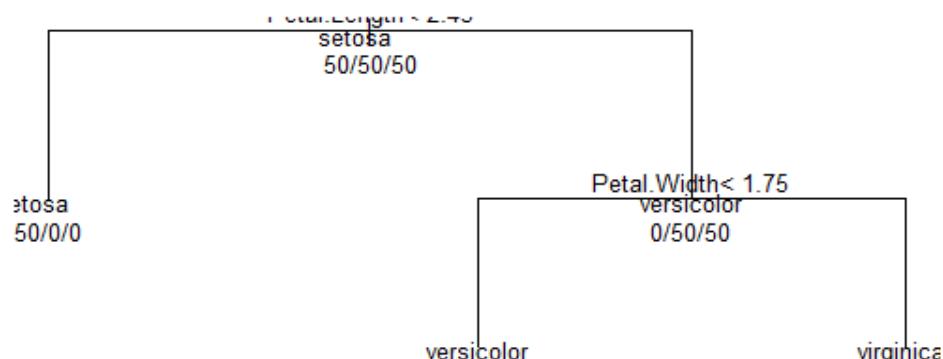
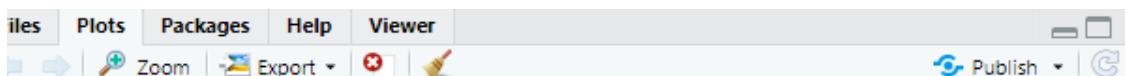
```



```
> text(model,use.n=TRUE,all=TRUE,cex=0.8)
> install.packages("tree")
WARNING: Rtools is required to build R packages but is not currently installed. Please
download and install the appropriate version of Rtools before proceeding:
https://cran.rstudio.com/bin/windows/Rtools/
Installing package into 'C:/Users/TEMP.ITLAB.008/Documents/R/win-library/3.6'
(as 'lib' is unspecified)
trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/tree_1.0-40.zip'
Content type 'application/zip' length 179039 bytes (174 KB)
downloaded 174 KB

package 'tree' successfully unpacked and MD5 sums checked

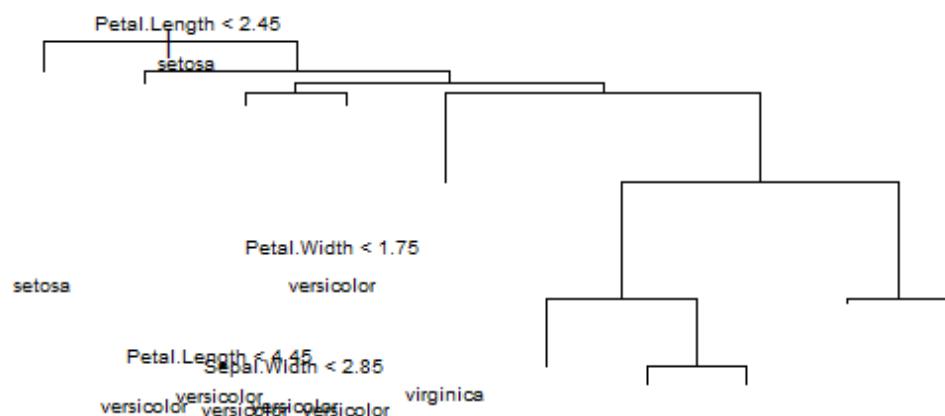
The downloaded binary packages are in
      C:\Users\TEMP.ITLAB.008\AppData\Local\Temp\RtmpKAWUnz\downloaded_packages
> library(tree)
> model1<-tree(species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata,me
thod="class",split="gini")
> |
```

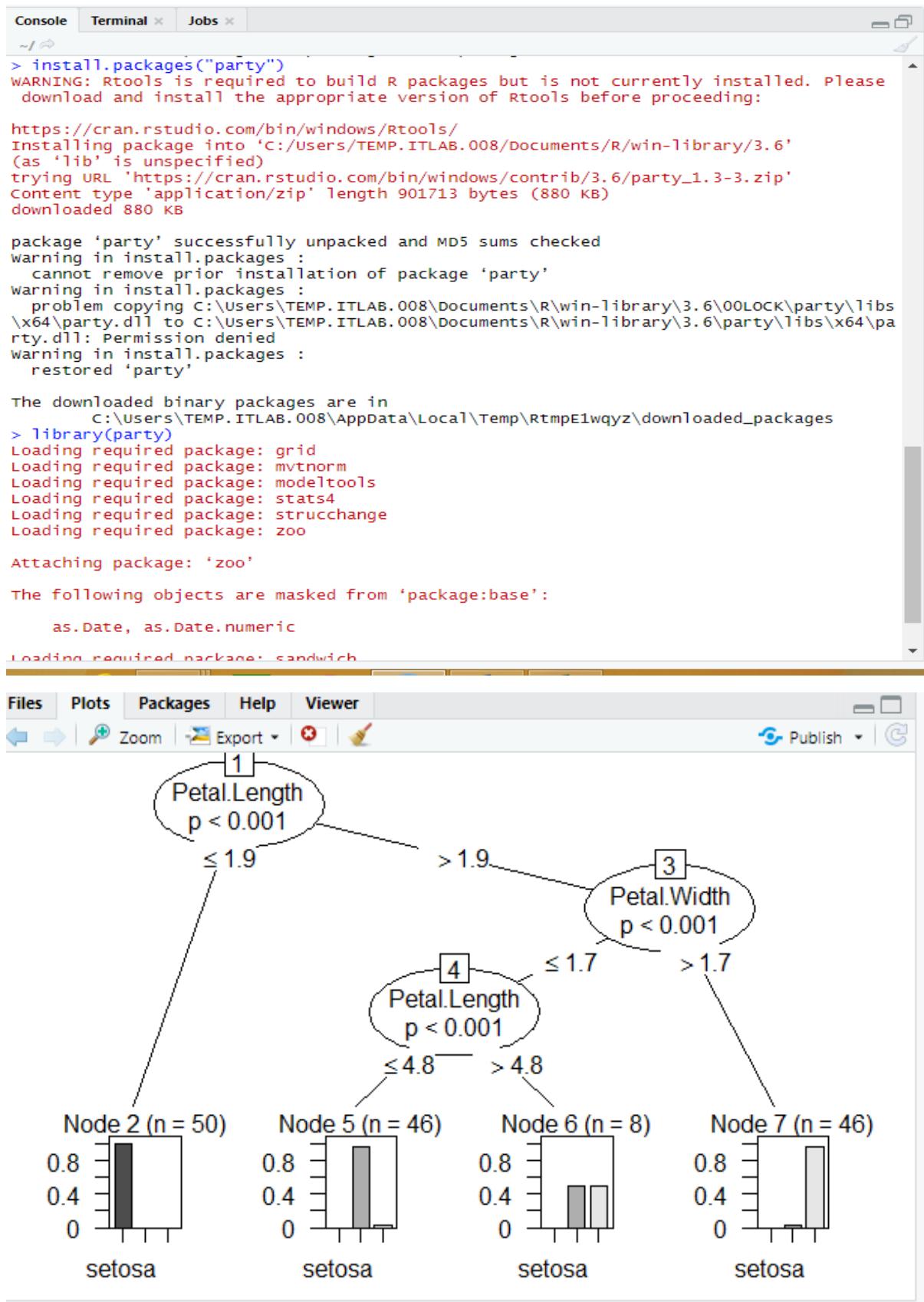


```

> model<-tree(species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata,method="class",control=tree.control(nobs=150,mincut=10))
> plot(model1)
> model<-tree(species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata,method="class",control=tree.control(nobs=150,mincut=10))
> model1<-tree(species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata,method="class",split="gini")
> plot(model1)
> text(model1,all=TRUE,cex=0.6)
>

```

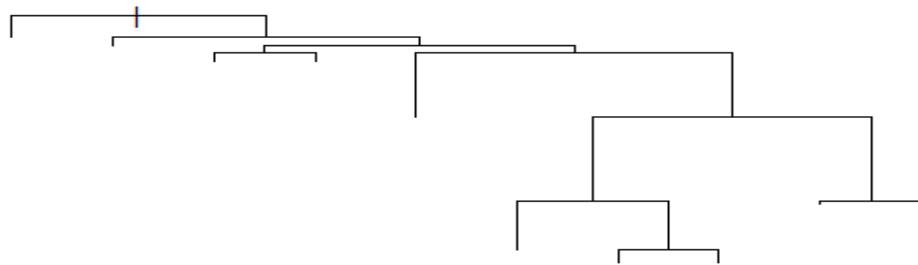




```

> model2<-ctree(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata)
> plot(model2)
> library(tree)
> mydata<-data.frame(iris)
> attach(mydata)
> model<-tree(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata,method="class",control=tree.control(nobs=150,mincut=10))
> plot(model1)
>

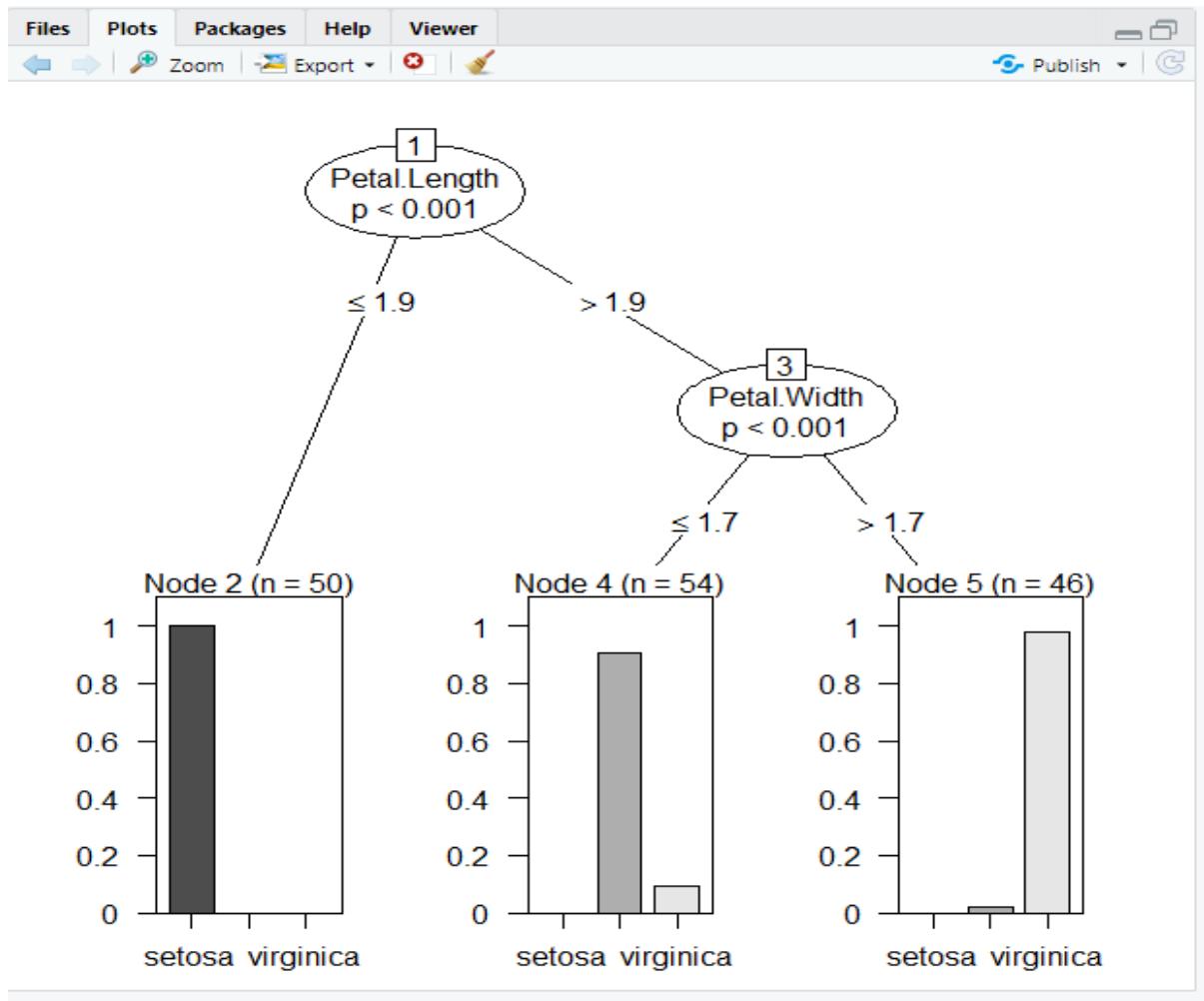
```



```

> model2<-ctree(Species~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=mydata,control=ctree_control(maxdepth=2))
> text(model,all=TRUE,cex=0.6)
> predict(model,iris)
  setosa versicolor virginica
1      1 0.00000000 0.00000000
2      1 0.00000000 0.00000000
3      1 0.00000000 0.00000000
4      1 0.00000000 0.00000000
5      1 0.00000000 0.00000000
6      1 0.00000000 0.00000000
7      1 0.00000000 0.00000000
8      1 0.00000000 0.00000000
9      1 0.00000000 0.00000000
10     1 0.00000000 0.00000000
11     1 0.00000000 0.00000000
..    .. .. .. ..

```



Class: TYCS

Name: Gulshan Suryanarayan Chauhan

No.: 2153004