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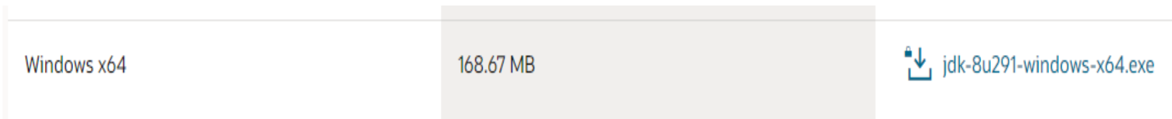
PRACTICAL NO : 1

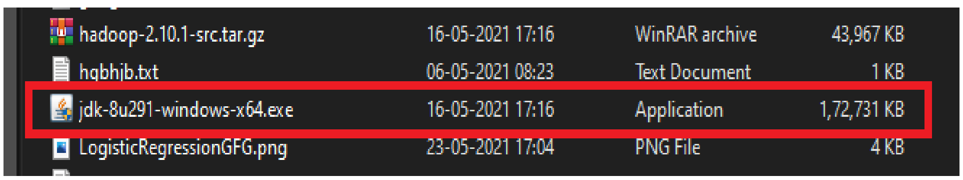
Aim: Install, configure and run Hadoop and HDFS

Description:

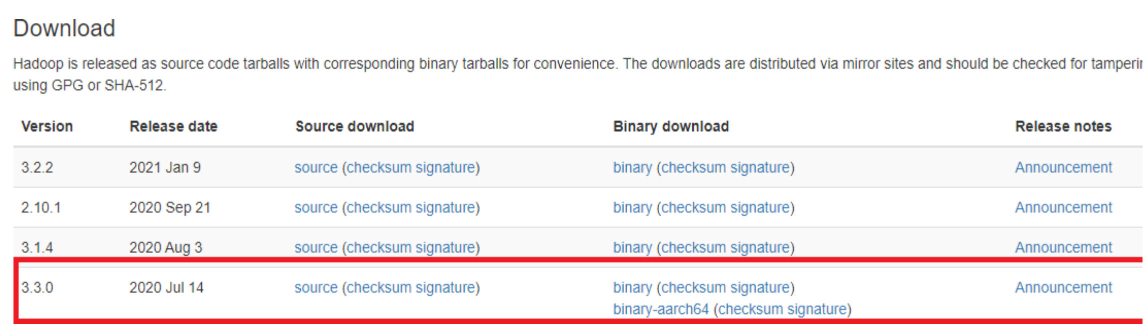
Hadoop Installation.

Step 1: downlaod java jdk first .the package size 168.67MB





Step 2: download Hadoop binaries from the official website. The binary package size is about 342 MB.

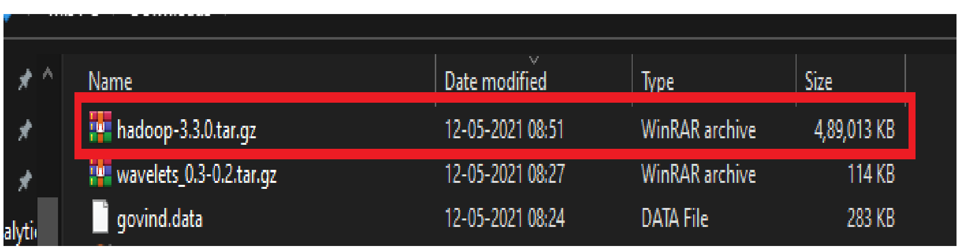


Download

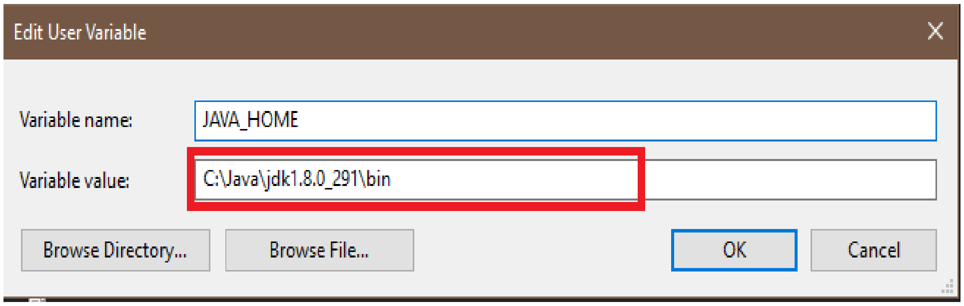
Hadoop is released as source code tarballs with corresponding binary tarballs for convenience. The downloads are distributed via mirror sites and should be checked for tamperi using GPG or SHA-512.

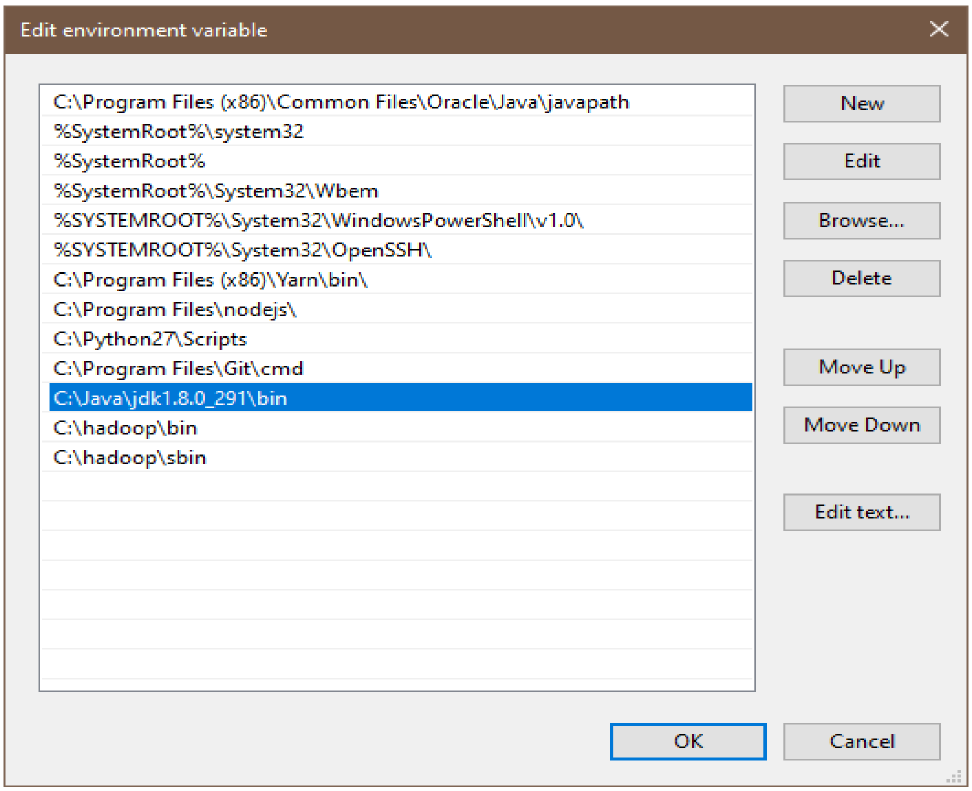
Version	Release date	Source download	Binary download	Release notes
3.2.2	2021 Jan 9	source (checksum signature)	binary (checksum signature)	Announcement
2.10.1	2020 Sep 21	source (checksum signature)	binary (checksum signature)	Announcement
3.1.4	2020 Aug 3	source (checksum signature)	binary (checksum signature)	Announcement
3.3.0	2020 Jul 14	source (checksum signature)	binary (checksum signature) binary-aarch64 (checksum signature)	Announcement

Step 3: After finishing the file download, we should unpack the package using 7zip int two steps. First, we should extract the hadoop-3.2.1.tar.gz library, and then, we should unpack the extracted tar file:



Step 4: When the “Advanced system settings” dialog appears, go to the “Advanced” tab and click on the “Environment variables” button located on the bottom of the dialog.





Step 5: Check the version of java

```
C:\Windows\system32\cmd.exe
Microsoft Windows [Version 10.0.19041.928]
(c) Microsoft Corporation. All rights reserved.

C:\Users\hp>javac
Usage: javac <options> <source files>
where possible options include:
  -g                         Generate all debugging info
  -g:none                    Generate no debugging info
  -g:{lines,vars,source}     Generate only some debugging info
  -nowarn                    Generate no warnings
  -verbose                   Output messages about what the compiler is doing
  -deprecation               Output source locations where deprecated APIs are used
  -classpath <path>          Specify where to find user class files and annotation process
  -cp <path>                 Specify where to find user class files and annotation process
  -sourcepath <path>         Specify where to find input source files
  -bootclasspath <path>      Override location of bootstrap class files
  -extdirs <dirs>            Override location of installed extensions
  -endorseddirs <dirs>       Override location of endorsed standards path
  -proc:{none,only}          Control whether annotation processing and/or compilation is d
  -processor <class1>[,<class2>,<class3>...] Names of the annotation processors to run; by
```

```
C:\Users\hp>java -version
java version "1.8.0_291"
Java(TM) SE Runtime Environment (build 1.8.0_291-b10)
Java HotSpot(TM) 64-Bit Server VM (build 25.291-b10, mixed mode)
```

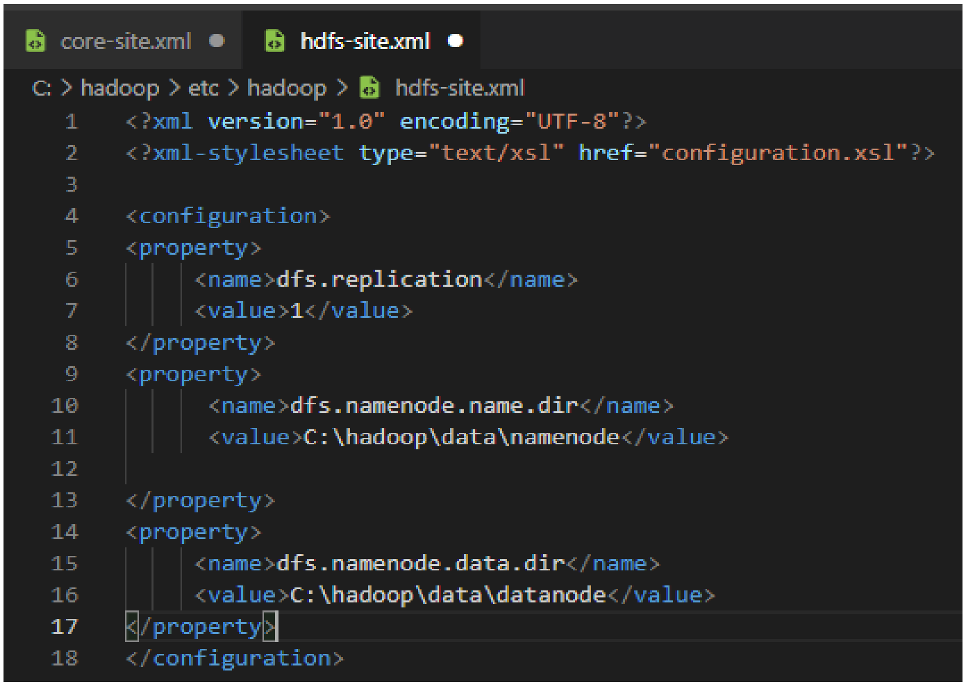
Step 6: Configuration core-site.xml

```
container-executor.cfg     07-07-2020 01:03     CFG File
core-site.xml              19-05-2021 17:57     XML File
hadoop-env.cmd             19-05-2021 17:57     Windows Comma...
```

```
core-site.xml
C: > hadoop > etc > hadoop > core-site.xml
<?xml version="1.0" encoding="UTF-8"?>
<?xml-stylesheet type="text/xsl" href="configuration.xsl"?>

<configuration>

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

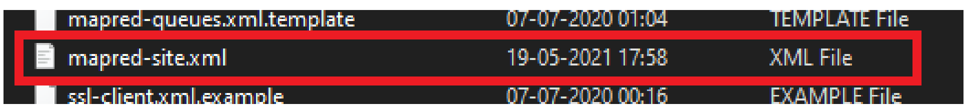
Step 7: Configuration core-site.xml

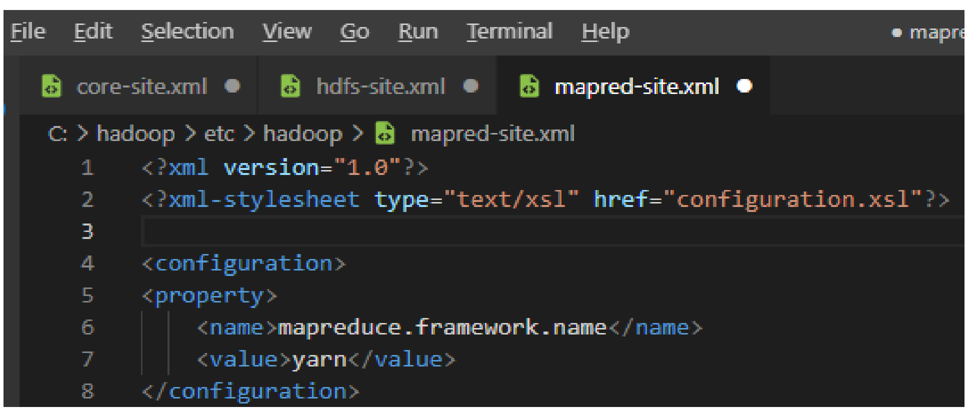
```
hdfs-rbf-site.xml     07-07-2020 00:26     XML File
hdfs-site.xml         19-05-2021 17:58     XML File
httpfs-env.sh         07-07-2020 00:25     Shell Script
```




```xml
<?xml version="1.0" encoding="UTF-8"?>
<?xml-stylesheet type="text/xsl" href="configuration.xsl"?>

<configuration>
<property>
    <name>dfs.replication</name>
    <value>1</value>
</property>
<property>
     <name>dfs.namenode.name.dir</name>
     <value>C:\hadoop\data\namenode</value>

</property>
<property>
    <name>dfs.namenode.data.dir</name>
    <value>C:\hadoop\data\datanode</value>
</property>
</configuration>
```

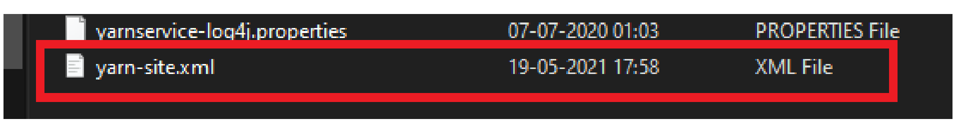
Step 8: Configuration core-site.xml

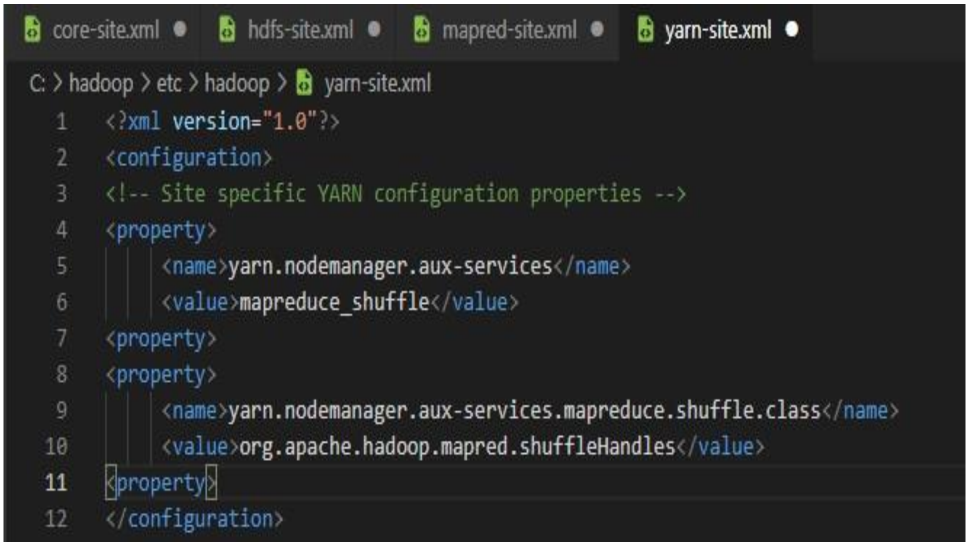




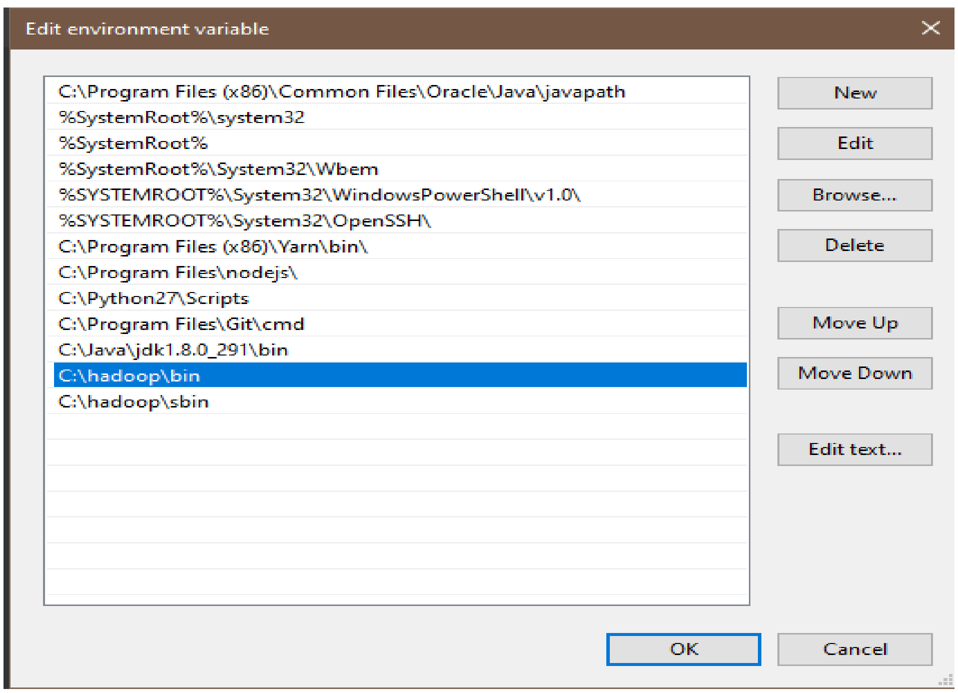

```xml
<?xml version="1.0"?>
<?xml-stylesheet type="text/xsl" href="configuration.xsl"?>

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

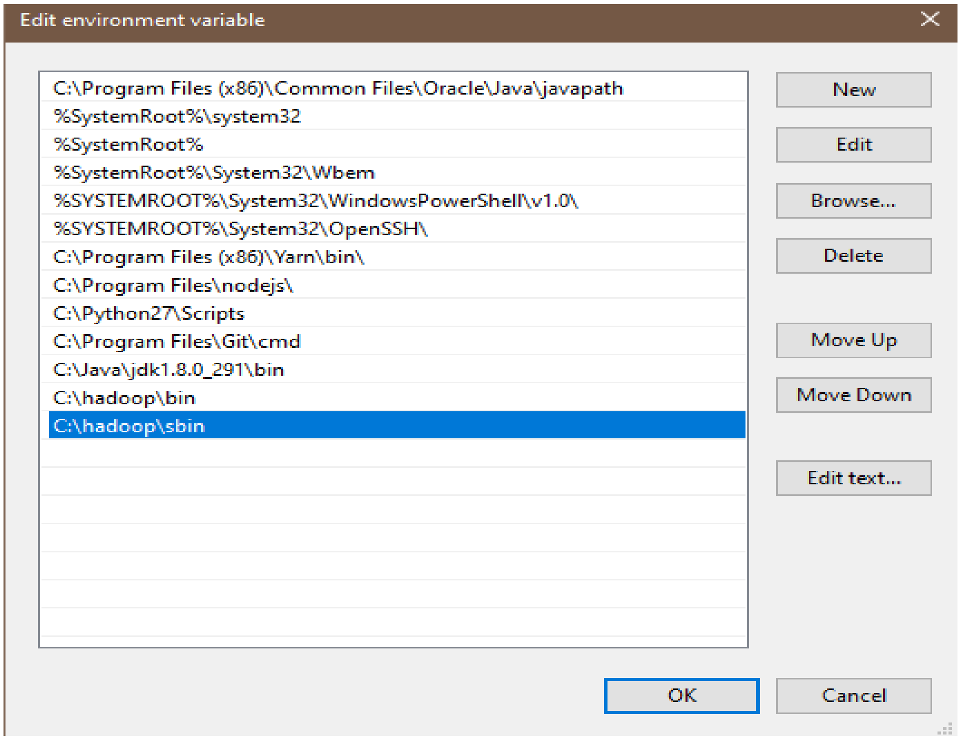
Step 9: Configuration core-site.xml



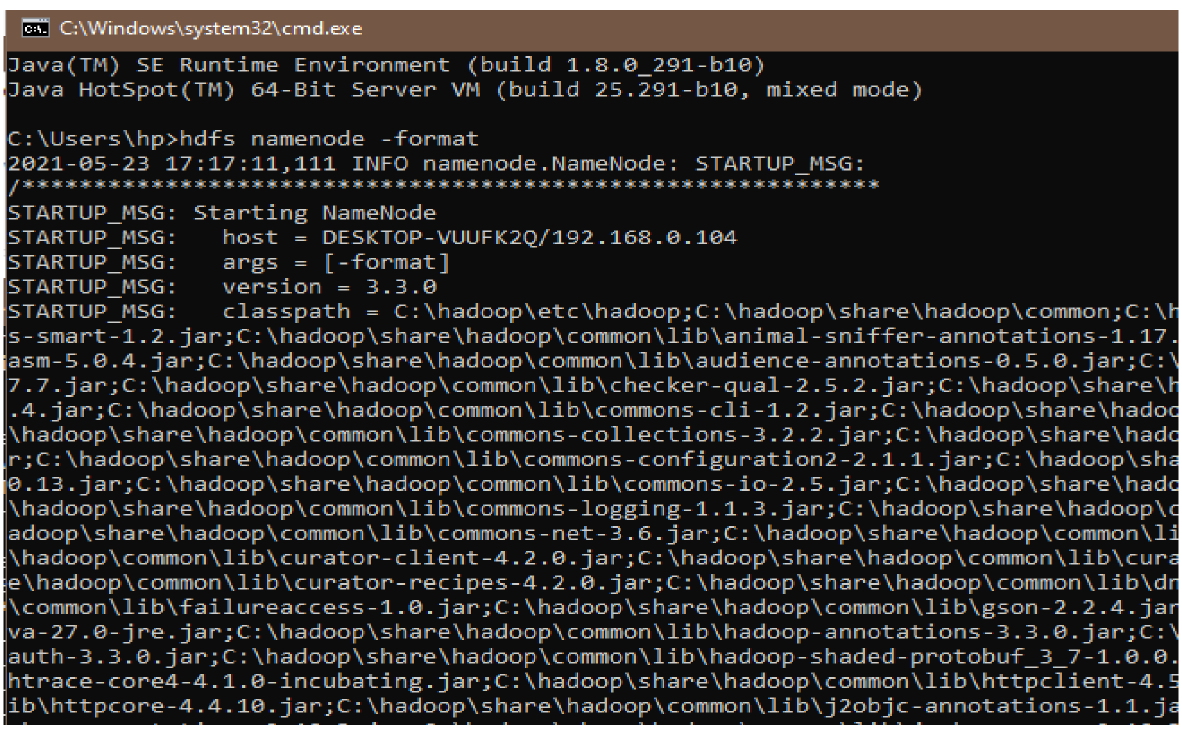


Step 10: When the “Advanced system settings” dialog appears, go to the “Advanced” tab and click on the “Environment variables” button located on the bottom of the dialog.





Step 11: let's check Hadoop install Successfully



```
Apache Hadoop Distribution
DEPRECATED: Use of this script to execute hdfs command is deprecated.
Instead use the hdfs command for it.
2021-05-23 17:19:33,116 INFO namenode.NameNode: STARTUP_MSG:
/************************************************************
STARTUP_MSG: Starting NameNode
STARTUP_MSG:   host = DESKTOP-VUUFK2Q/192.168.0.104
STARTUP_MSG:   args = []
STARTUP_MSG:   version = 3.3.0
STARTUP_MSG:   classpath = C:\hadoop\etc\hadoop;C:\hadoop\share\hadoop\common;C:\hadoop\share\hadoop\common\lib\accessor
s-smart-1.2.jar;C:\hadoop\share\hadoop\common\lib\animal-sniffer-annotations-1.17.jar;C:\hadoop\share\hadoop\common\lib\
asm-5.0.4.jar;C:\hadoop\share\hadoop\common\lib\audience-annotations-0.5.0.jar;C:\hadoop\share\hadoop\common\lib\avro-1.
7.7.jar;C:\hadoop\share\hadoop\common\lib\checker-qual-2.5.2.jar;C:\hadoop\share\hadoop\common\lib\commons-beanutils-1.9
.4.jar;C:\hadoop\share\hadoop\common\lib\commons-cli-1.2.jar;C:\hadoop\share\hadoop\common\lib\commons-codec-1.11.jar;C:
\hadoop\share\hadoop\common\lib\commons-collections-3.2.2.jar;C:\hadoop\share\hadoop\common\lib\commons-compress-1.19.ja
r;C:\hadoop\share\hadoop\common\lib\commons-configuration2-2.1.1.jar;C:\hadoop\share\hadoop\common\lib\commons-daemon-1.
0.13.jar;C:\hadoop\share\hadoop\common\lib\commons-io-2.5.jar;C:\hadoop\share\hadoop\common\lib\commons-lang3-3.7.jar;C:
\hadoop\share\hadoop\common\lib\commons-logging-1.1.3.jar;C:\hadoop\share\hadoop\common\lib\commons-math3-3.1.1.jar;C:\h
adoop\share\hadoop\common\lib\commons-net-3.6.jar;C:\hadoop\share\hadoop\common\lib\commons-text-1.4.jar;C:\hadoop\share
\hadoop\common\lib\curator-client-4.2.0.jar;C:\hadoop\share\hadoop\common\lib\curator-framework-4.2.0.jar;C:\hadoop\shar
e\hadoop\common\lib\curator-recipes-4.2.0.jar;C:\hadoop\share\hadoop\common\lib\dnsjava-2.1.7.jar;C:\hadoop\share\hadoop
```

```
Apache Hadoop Distribution
        at com.ctc.wstx.sr.StreamScanner.throwParseError(StreamScanner.java:491)
        at com.ctc.wstx.sr.StreamScanner.throwParseError(StreamScanner.java:475)
        at com.ctc.wstx.sr.BasicStreamReader.reportWrongEndElem(BasicStreamReader.java:3365)
        at com.ctc.wstx.sr.BasicStreamReader.readEndElem(BasicStreamReader.java:3292)
        at com.ctc.wstx.sr.BasicStreamReader.nextFromTree(BasicStreamReader.java:2911)
        at com.ctc.wstx.sr.BasicStreamReader.next(BasicStreamReader.java:1123)
        at org.apache.hadoop.conf.Configuration$Parser.parseNext(Configuration.java:3347)
        at org.apache.hadoop.conf.Configuration$Parser.parse(Configuration.java:3141)
        at org.apache.hadoop.conf.Configuration.loadResource(Configuration.java:3034)
        ... 9 more
```

Step 12: Let check bin

```
C:\Windows\system32\cmd.exe

C:\Users\hp>cd C:\hadoop\sbin

C:\hadoop\sbin>start-all.cmd
This script is Deprecated. Instead use start-dfs.cmd and start-yarn.cmd
starting yarn daemons

C:\hadoop\sbin>
```

PRACTICAL NO : 2

Aim: Implement Decision tree classification techniques

Description:

Decision tree builds classification or regression models in the form of a tree structure. It breaks down a dataset into smaller and smaller subsets while at the same time an associated decision tree is incrementally developed. The final result is a tree with **decision nodes** and **leaf nodes**

Step 1: The package "party" has the function ctree() which is used to create and analyze decison tree.

```
> install.packages("party")
```

Step 2: Load the party package. It will automatically load other# dependent packages Print some records from data set readingSkills.

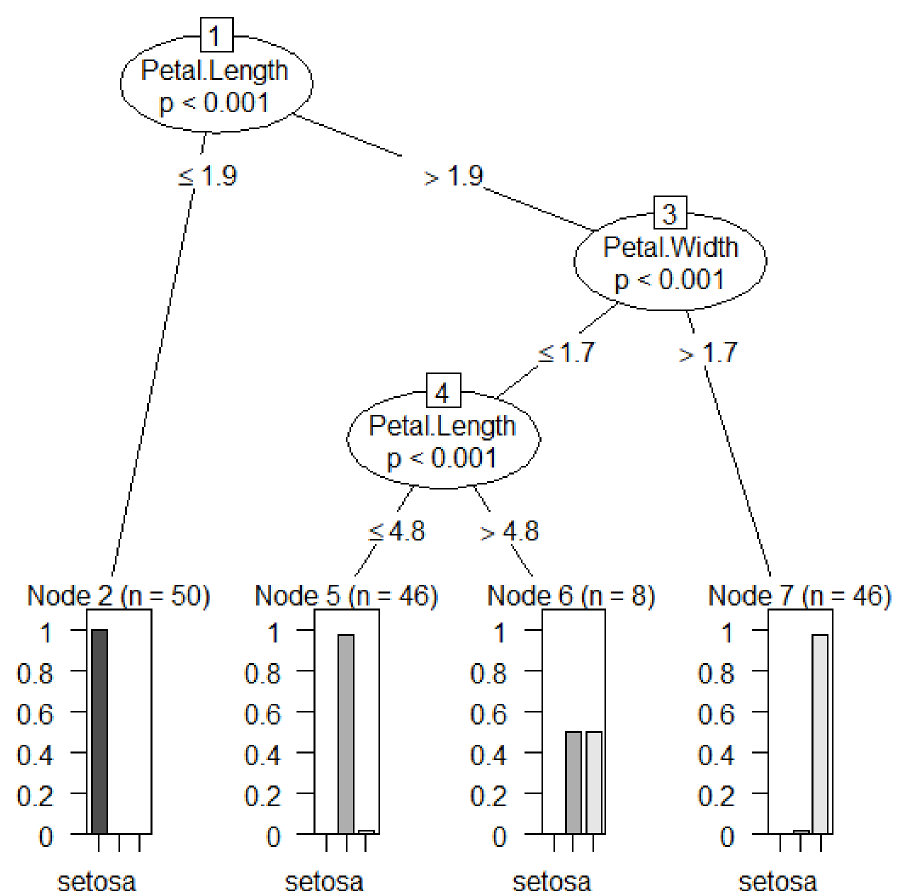
```
> library("party")
> print(head(readingSkills))
  nativeSpeaker age shoeSize    score
1           yes   5 24.83189 32.29385
2           yes   6 25.95238 36.63105
3            no  11 30.42170 49.60593
4           yes   7 28.66450 40.28456
5           yes  11 31.88207 55.46085
6           yes  10 30.07843 52.83124
>
```

Step 3 : Call function ctree to build a decision tree. The first parameter is a formula, which defines a target variable and a list of independent variables.

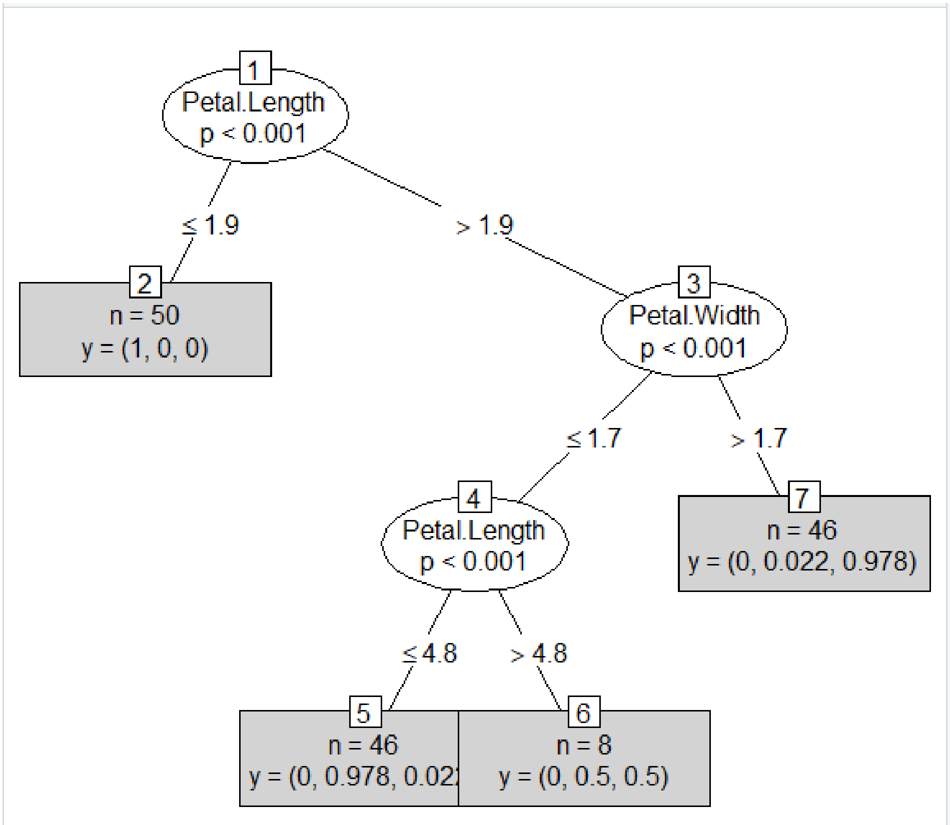
```
> library("party")
> str(iris)
'data.frame':   150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1
```

```
> iris_ctree <- ctree(Species ~ Sepal.Length + Sepal.Width + Petal.Length + Peta
l.Width, data=iris)
> print(iris_ctree)

         Conditional inference tree with 4 terminal nodes

Response:  Species
Inputs:  Sepal.Length, Sepal.Width, Petal.Length, Petal.Width
Number of observations:  150

1) Petal.Length <= 1.9; criterion = 1, statistic = 140.264
  2)*  weights = 50
1) Petal.Length > 1.9
  3) Petal.Width <= 1.7; criterion = 1, statistic = 67.894
    4) Petal.Length <= 4.8; criterion = 0.999, statistic = 13.865
      5)*  weights = 46
    4) Petal.Length > 4.8
      6)*  weights = 8
  3) Petal.Width > 1.7
    7)*  weights = 46
> plot(iris_ctree)
```

Output :




```
> plot(iris_ctree, type="simple")
```


1
Petal.Length
p < 0.001
≤ 1.9
> 1.9
2
n = 50
y = (1, 0, 0)
3
Petal.Width
p < 0.001
≤ 1.7
> 1.7
4
Petal.Length
p < 0.001
7
n = 46
y = (0, 0.022, 0.978)
≤ 4.8
> 4.8
5
n = 46
6
n = 8
y = (0, 0.5, 0.5)

PRACTICAL NO : 3

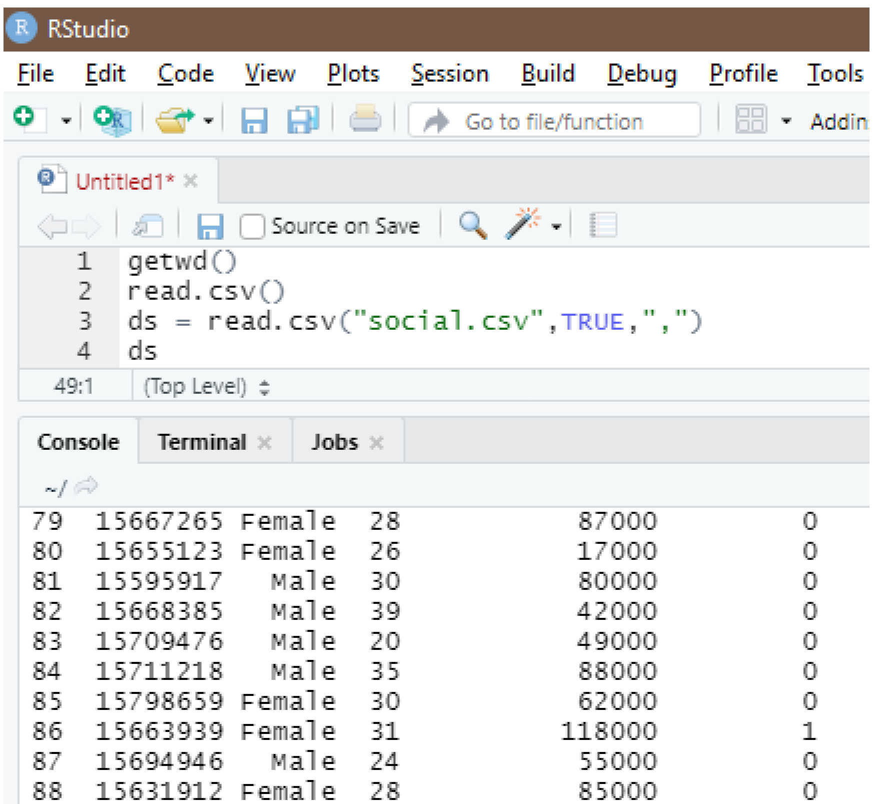
Aim: Classification using SVM

Description:

A support vector machine (SVM) is a supervised machine learning model that uses classification algorithms for two-group classification problems. After giving an SVM model sets of labeled training data for each category, they're able to categorize new text

The implementation is explained in the following steps:

Step 1: Importing the dataset



Step 2: Selecting columns 3-5

```
> ds = ds[3:5]
> ds[3:5]
Error in `[.data.frame`(ds, 3:5) : undefined
> ds
   Age EstimatedSalary Purchased
1   19           19000         0
2   35           20000         0
3   26           43000         0
4   27           57000         0
5   19           76000         0
6   27           58000         0
7   27           84000         0
8   32          150000         1
9   25           33000         0
10  35           65000         0
11  26           80000         0
12  26           52000         0
```

Step 3: install package

```
> install.packages("caTools")
```

Step 4: Splitting the dataset

```
> library(caTools)
> set.seed(123)
> split = sample.split(ds$Purchased, SplitRatio = 0.75)
> training_set = subset(ds, split == TRUE)
> test_set = subset(ds, split == FALSE)
> ds
   Age EstimatedSalary Purchased
1   19           19000         0
2   35           20000         0
3   26           43000         0
4   27           57000         0
5   19           76000         0
6   27           58000         0
7   27           84000         0
8   32          150000         1
9   25           33000         0
10  35           65000         0
```

Step 5: Feature Scaling

```
332  48          119000        1
333  42           65000        0
 [ reached 'max' / getOption("max.print") -- omitted 67 rows ]
> test_set[-3] = scale(test_set[-3])
> training_set[-3] = scale(training_set[-3])
> test_set[-3] = scale(test_set[-3])
> test_set[-3]
            Age EstimatedSalary
2   -0.30419063     -1.51354339
4   -1.05994374     -0.32456026
5   -1.81569686      0.28599864
9   -1.24888202     -1.09579256
12  -1.15441288     -0.48523366
18   0.64050076     -1.32073531
19   0.73496990     -1.25646596
20   0.92390818     -1.22433128
22   0.82943904     -0.58163769
29  -0.87100546     -0.77444577
32  -1.05994374      2.24621408
34  -0.96547460     -0.74231109
35  -1.05994374      0.73588415
38  -0.77653633     -0.58163769
45  -0.96547460      0.54307608
46  -1.43782030     -1.51354339
```

Step 6: Fitting SVM to the training set

```
> install.packages('e1071')
```

```
> library(e1071)
> classifier = svm(formula = Purchased ~ .,
+                  data = training_set,
+                  type = 'C-classification',
+                  kernel = 'linear')
> classifier

Call:
svm(formula = Purchased ~ ., data = training_set, type = "C-classification",
    kernel = "linear")


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

Number of Support Vectors:  116
```

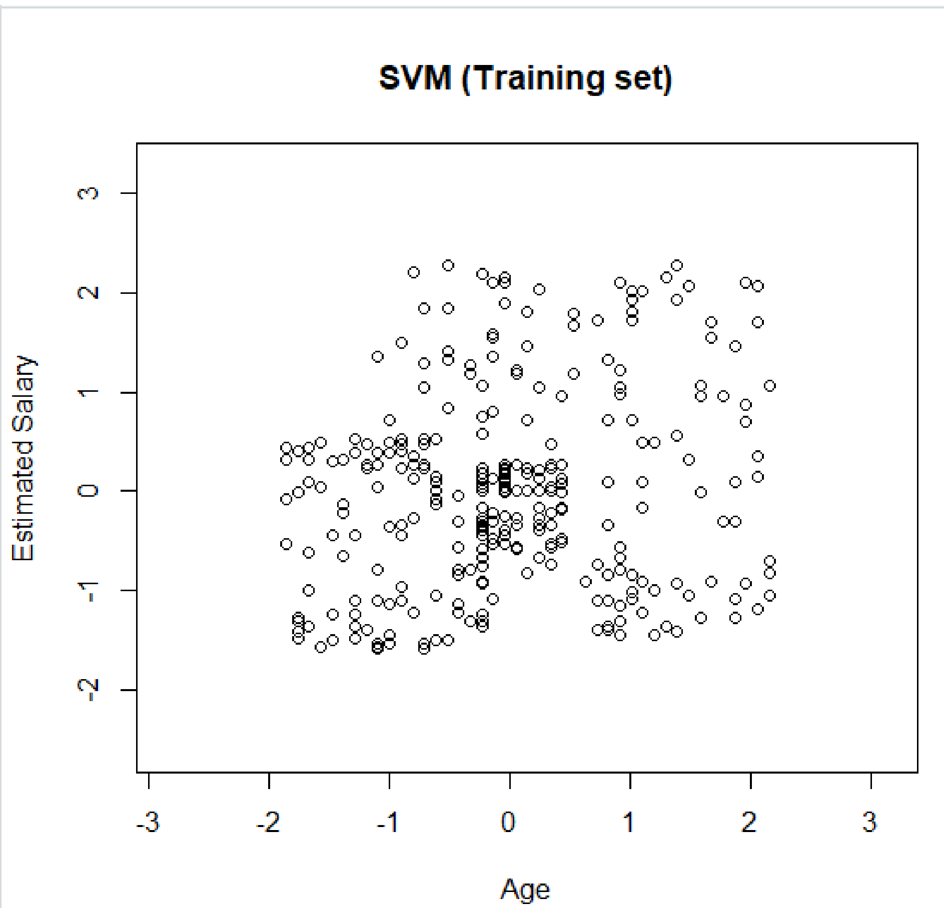
Step 7: Predicting the test set result

```
> y_pred = predict(classifier, newdata = test_set[-3])
> y_pred
  2   4   5   9  12  18  19  20  22  29  32  34  35  38  45  46  48  52  66 
  0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0 
 69  74  75  82  84  85  86  87  89 103 104 107 108 109 117 124 126 127 131 
  0   0   0   0   0   0   0   0   0   0   1   0   0   0   0   0   0   0   0 
134 139 148 154 156 159 162 163 170 175 176 193 199 200 208 213 224 226 228 
  0   0   0   0   0   0   0   0   0   0   0   0   0   0   1   1   1   0   1 
229 230 234 236 237 239 241 255 264 265 266 273 274 281 286 292 299 302 305 
  0   1   1   1   0   1   1   1   0   1   1   1   1   1   0   1   1   1   0 
307 310 316 324 326 332 339 341 343 347 353 363 364 367 368 369 372 373 380 
  1   0   0   0   0   1   0   1   0   1   1   0   1   1   1   0   1   0   1 
383 389 392 395 400 
  1   0   0   0   0 
Levels: 0 1
```

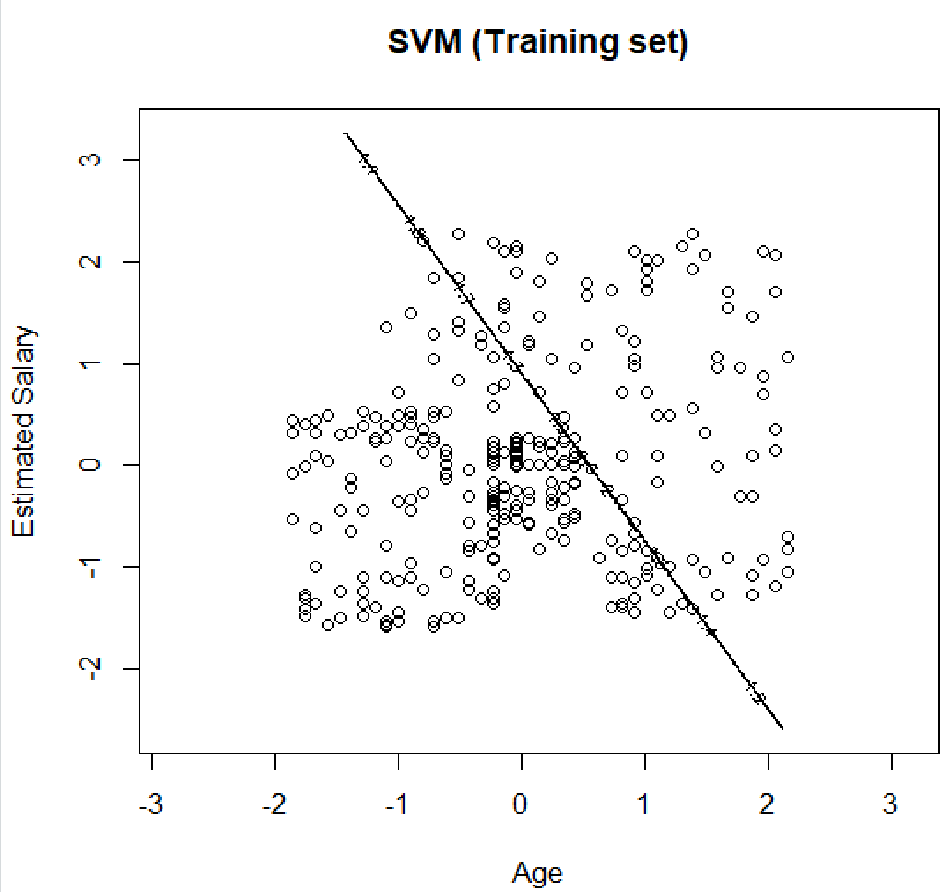
```
> cm = table(test_set[, 3], y_pred)
> cm
   y_pred
     0  1
  0 57  7
  1 13 23
```

Step 8: Visualizing the Training set results

```
> set = training_set
> X1 = seq(min(set[, 1]) - 1, max(set[, 1]) + 1, by = 0.01)
> X2 = seq(min(set[, 2]) - 1, max(set[, 2]) + 1, by = 0.01)
```

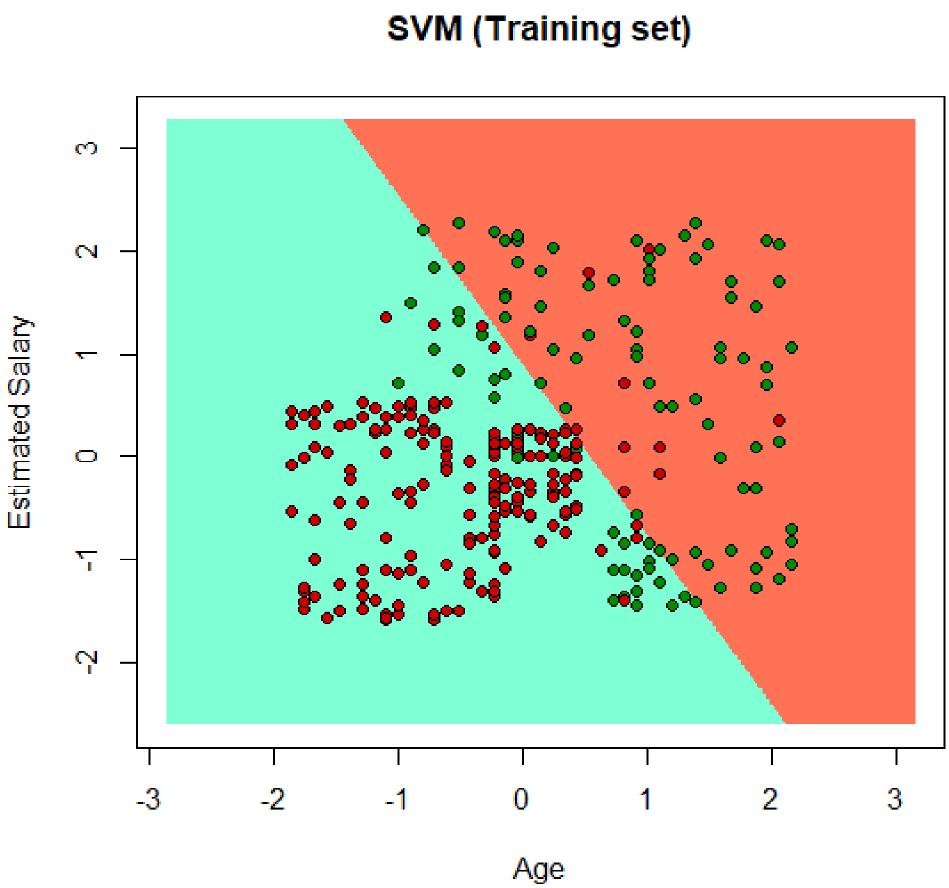


```
> grid_set = expand.grid(X1, X2)
> colnames(grid_set) = c('Age', 'EstimatedSalary')
> y_grid = predict(classifier, newdata = grid_set)
> plot(set[, -3],
+      main = 'SVM (Training set)',
+      xlab = 'Age', ylab = 'Estimated Salary',
+      xlim = range(X1), ylim = range(X2))
```




```
> contour(X1, X2, matrix(as.numeric(y_grid), length(X1), length(X2)), add = TRUE)
> points(grid_set, pch = '.', col = ifelse(y_grid == 1, 'coral1', 'aquamarine'))
> points(set, pch = 21, bg = ifelse(set[, 3] == 1, 'green4', 'red3'))
```

Output:

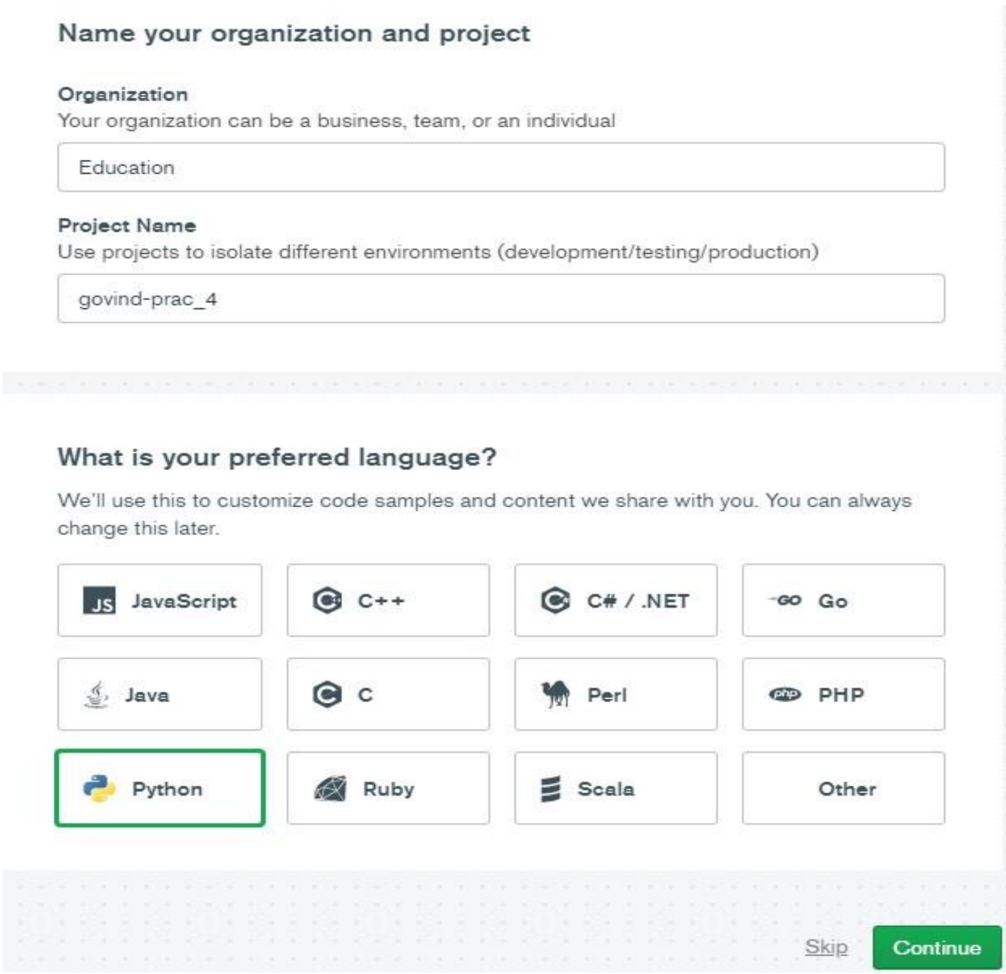

SVM (Training set)
Estimated Salary
Age
-3
-2
-1
0
1
2
3

PRACTICAL NO : 4

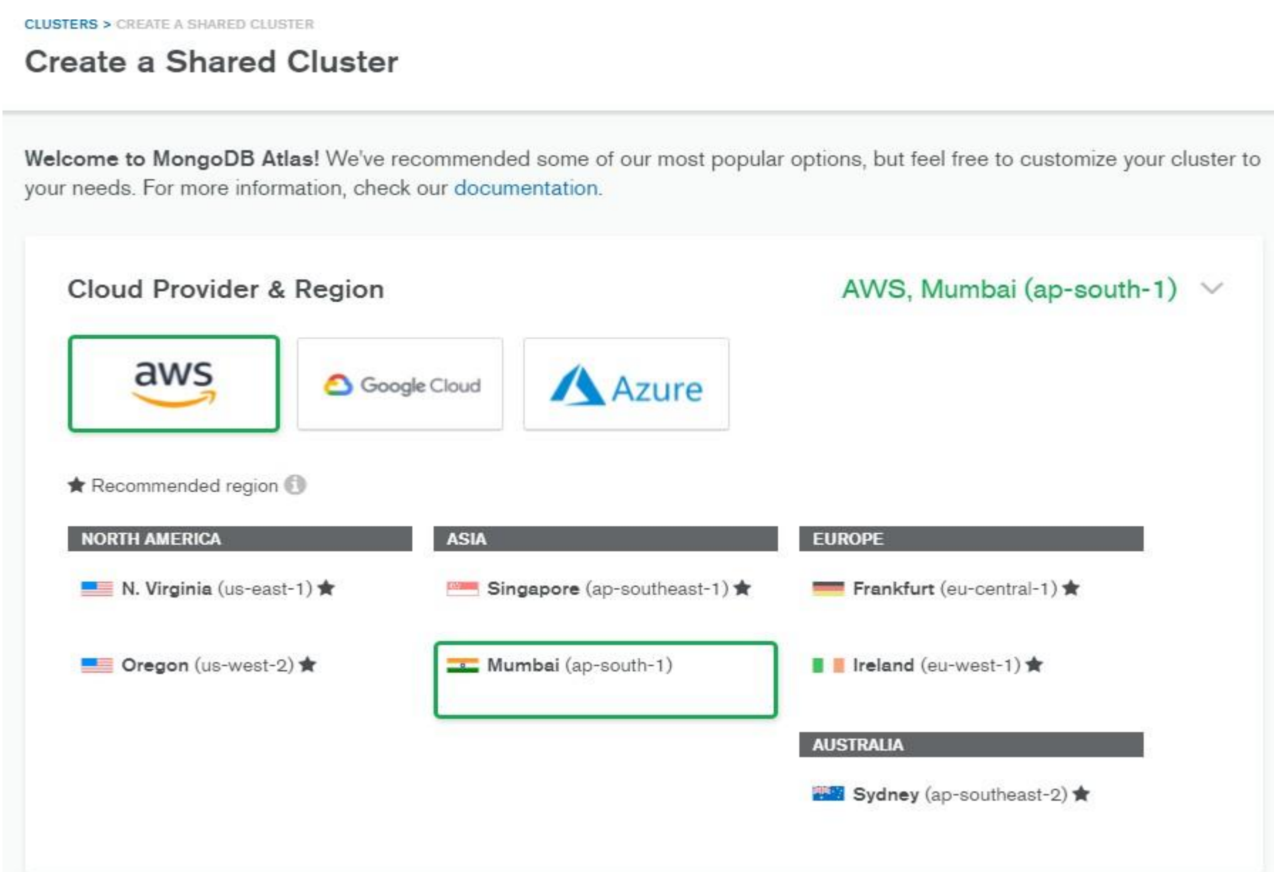
Aim: Implement an application that stores big data in Hbase / MongoDB and manipulate it using R / Python

Description:

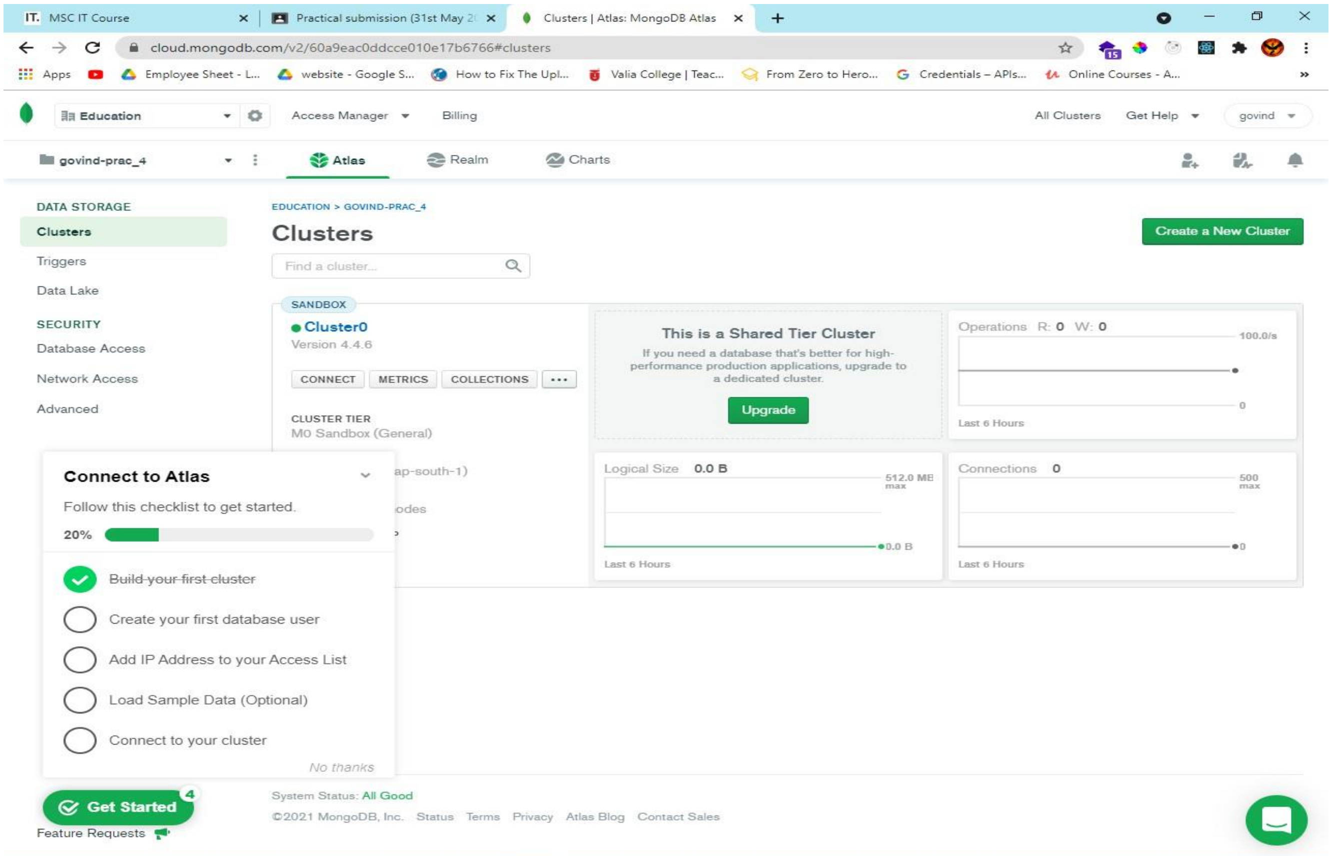
MongoDB is a source-available cross-platform document-oriented database program. Classified as a NoSQL database program, MongoDB uses JSON-like documents with optional schemas. MongoDB is developed by MongoDB Inc. and licensed under the Server Side Public License



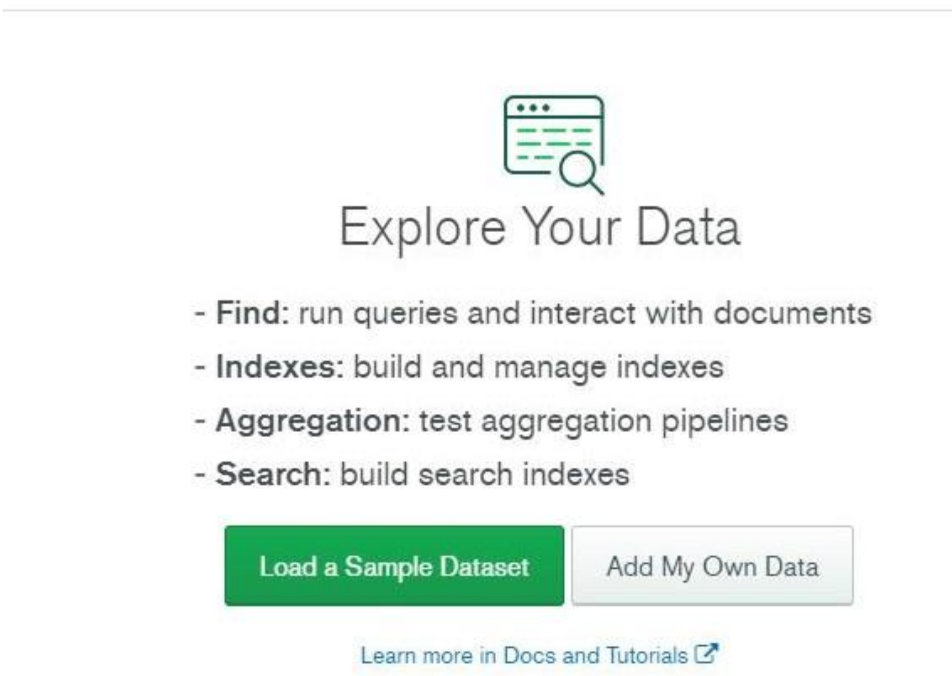
Step 1 : Sign up and create a cluster.



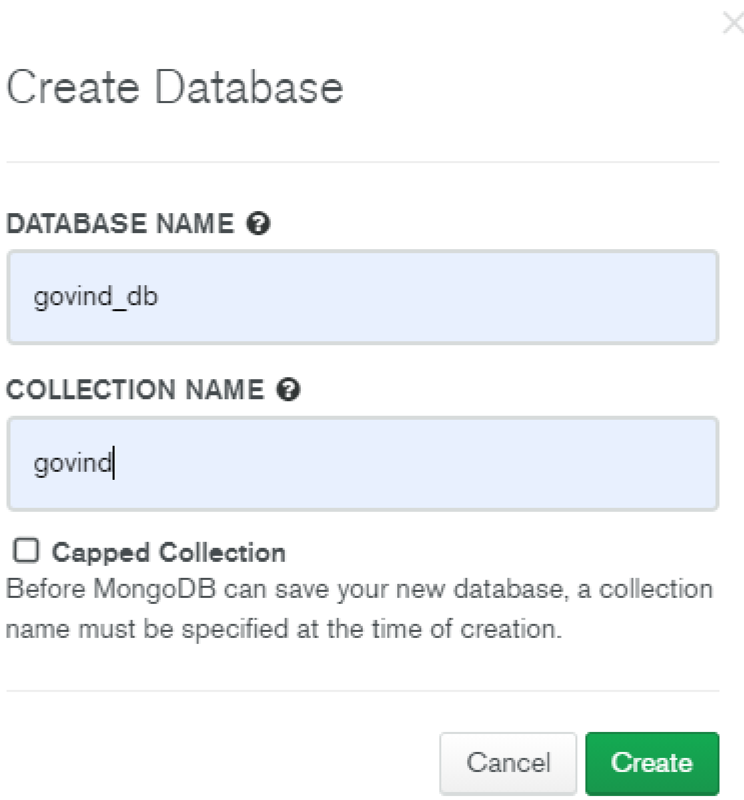
This is the home page of mongoDB Atlas.



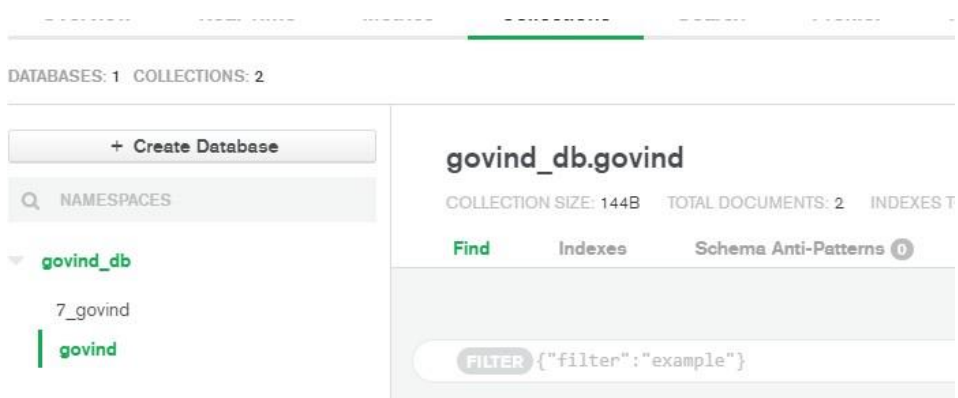
Step 2 : Click on collections to create and view existing databases.



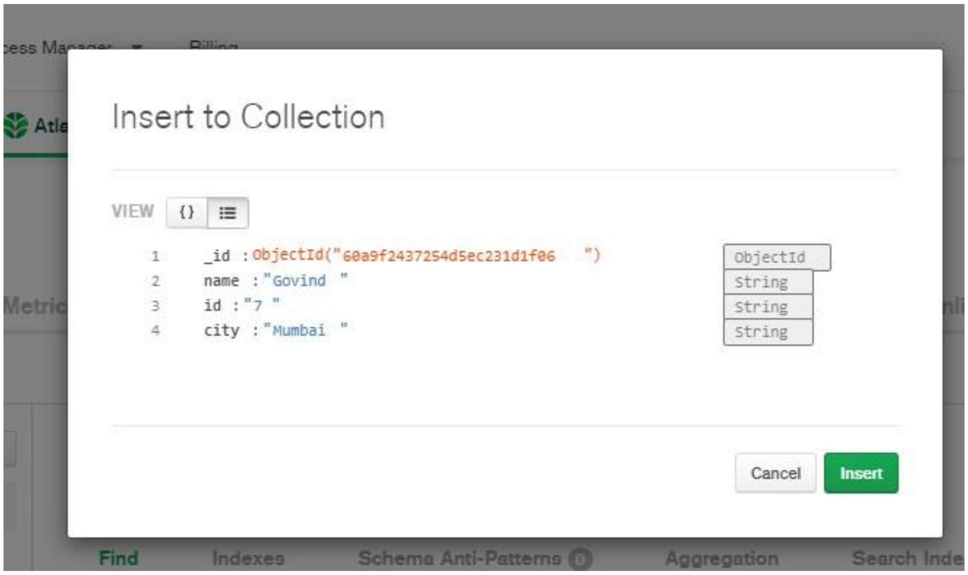
Step 3 : Click on 'Add My Own Data' to create a database.



Step 4 : Click on insert document to add records.



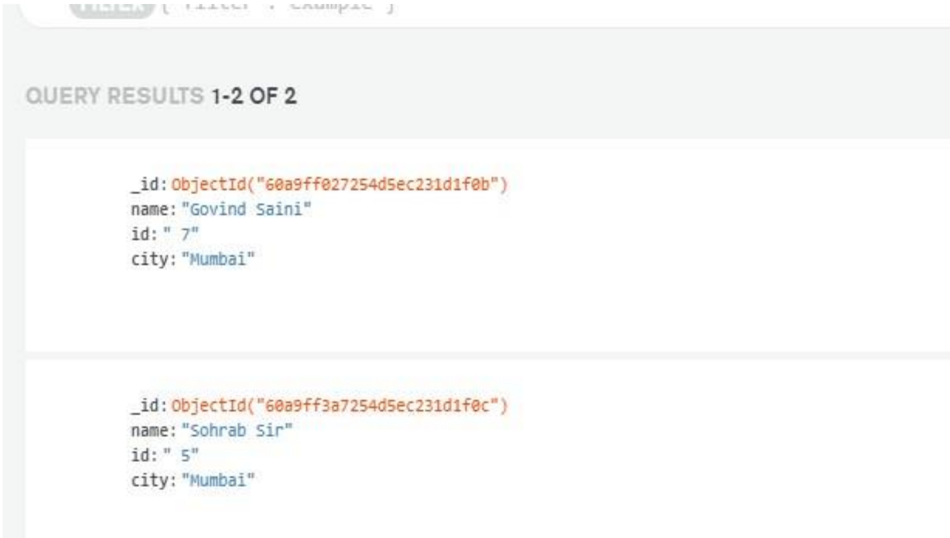
Since MongoDB is a No-SQL database, so you can add 'n' number of columns for any row/record.



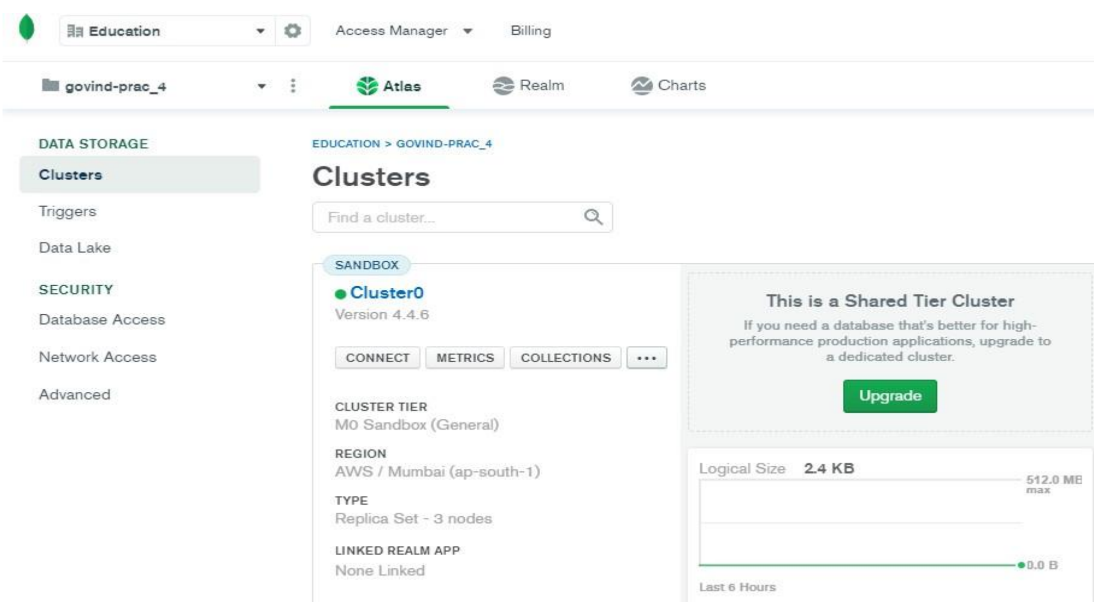
Perform updating data

Performing deleting data

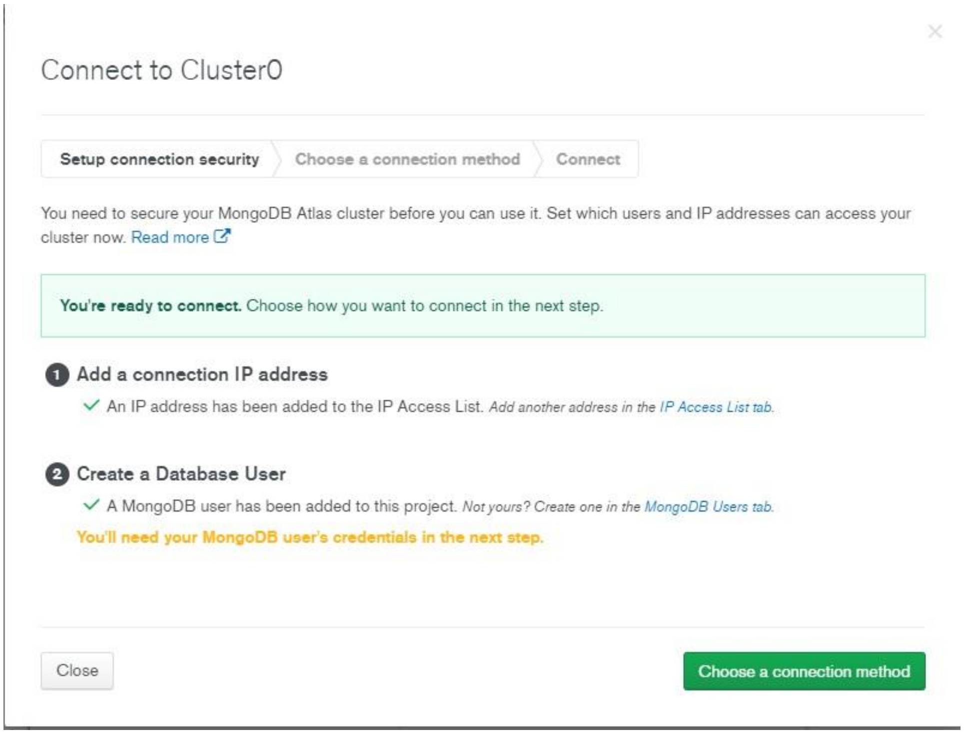
Performing Insert data



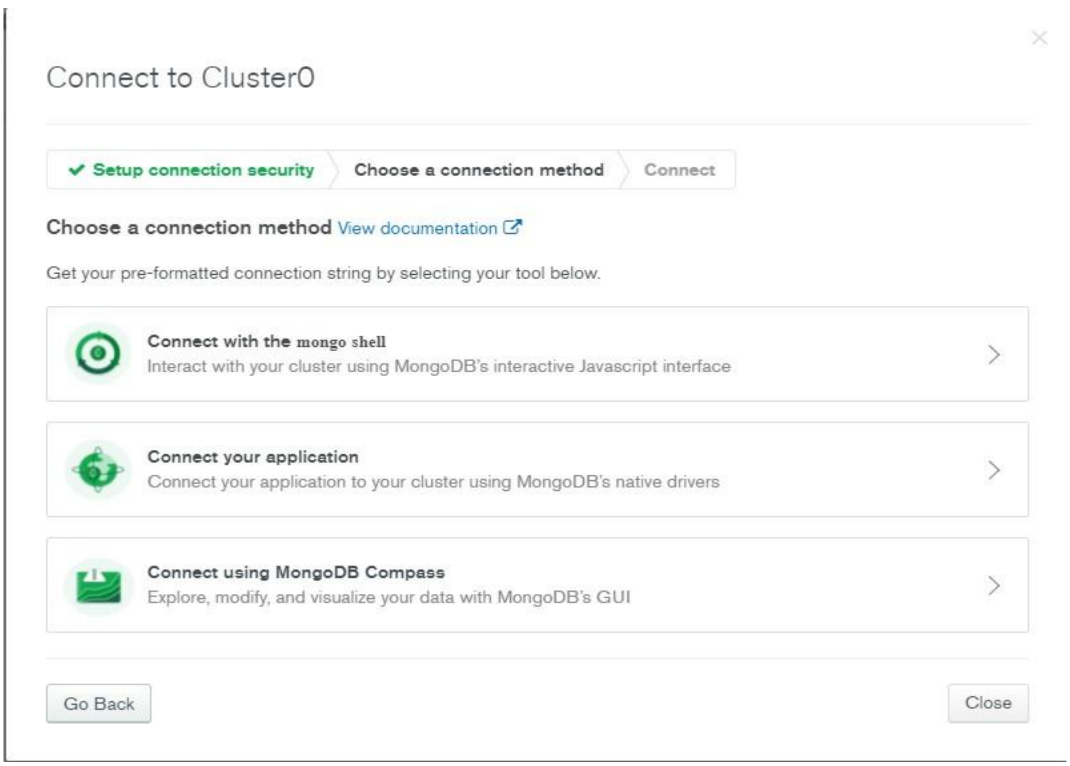
Step 5 : To start with the connection click on Overview, and then click on Connect.



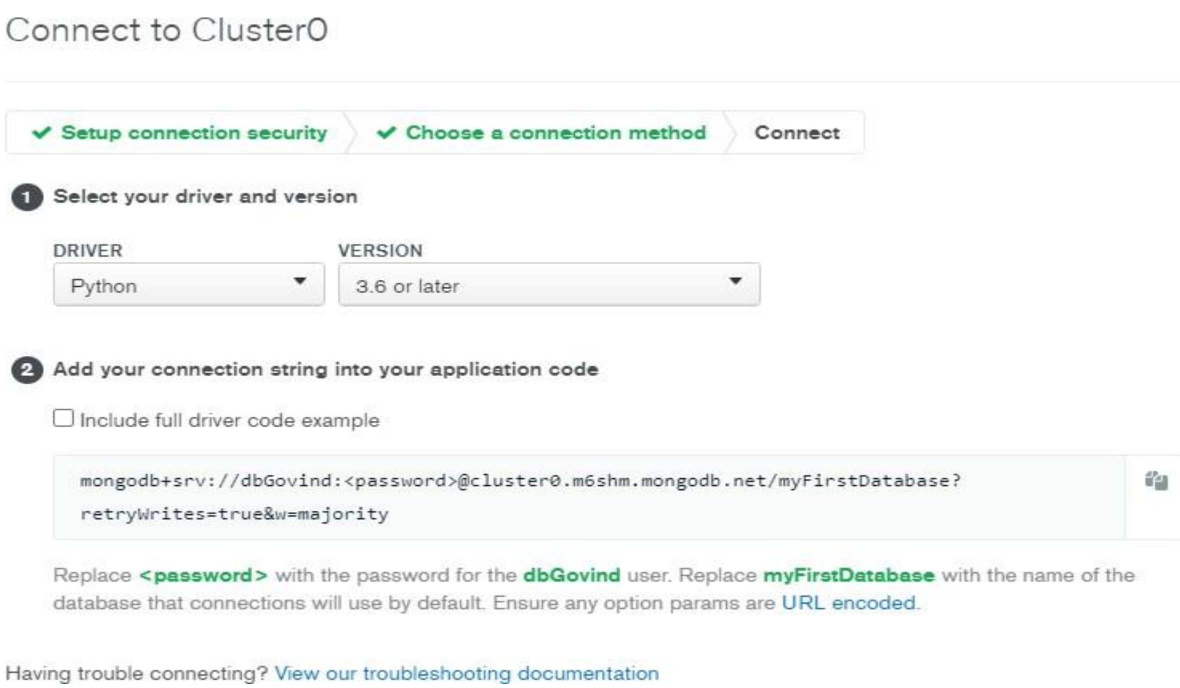
Step 6 : Select on add your current IP and create a MongoDB user.



Step 7 : Click on 'Connect your application'.



Step 8 : Select the driver as 'Python' and version as '3.6 or later'. (Select the version as 3.6 or later only if your Python's version is 3.6 or later.)



Step 9 : Write the code given below in a Python file.

```
prac4.py - C:/Python27/prac4.py (2.7.17)
File Edit Format Run Options Window Help

import pymongo
from pymongo import MongoClient
client = pymongo.MongoClient("mongodb+srv://dbGovind:GmongoDB123@c
db = client.get_database('govind_db')
records = db.govind
db = client.test
print(records.count_documents({}))
print(list(records.find()))
```

Output :

```
======================== RESTART: C:/Python27/prac.py ========================
2[{"_id":{"$oid":"60a9ff027254d5ec231d1f0b"},"name":"Govind Saini","id":" 7","city"
:"Mumbai"}{"_id":{"$oid":"60a9ff3a7254d5ec231d1f0c"},"name":"Sohrab Sir","id":" 5",
"city":"Mumbai"}]
>>> 
```

PRACTICAL NO : 5

Aim: write program in R of Naive baye's theorem

Description:

Naive Bayes is a Supervised Non-linear classification algorithm in R Programming. Naive Bayes classifiers are a family of simple probabilistic classifiers based on applying Baye's theorem with strong(Naive) independence assumptions between the features or variables

 # Loading data

```
> data(iris)
> str(iris)
'data.frame':   150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ 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 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1
```

 # Installing Packages

```
> install.packages("e1071")

> install.packages("caTools")

> install.packages("caret")
```

 # Loading package

```
> library(e1071)
> library(caTools)
> library(caret)
Loading required package: lattice
Loading required package: ggplot2
```

 # Splitting data into train and test data

```
> split <- sample.split(iris, SplitRatio = 0.7)
> train_cl <- subset(iris, split == "TRUE")
> test_cl <- subset(iris, split == "FALSE")
>
> train_scale <- scale(train_cl[, 1:4])
> test_scale <- scale(test_cl[, 1:4])
>
> set.seed(120)  # Setting Seed
> classifier_cl <- naiveBayes(Species ~ ., data = train_cl)
> classifier_cl

Naive Bayes Classifier for Discrete Predictors

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

A-priori probabilities:
Y
    setosa versicolor  virginica
 0.3333333  0.3333333  0.3333333

Conditional probabilities:
            Sepal.Length
Y                [,1]      [,2]
  setosa     5.046667 0.3848272
  versicolor 5.963333 0.5268536
  virginica  6.553333 0.6693967

            Sepal.Width
Y                [,1]      [,2]
  setosa     3.413333 0.4256705
  versicolor 2.823333 0.3470897
  virginica  2.956667 0.3136914

            Petal.Length
Y                [,1]      [,2]
  setosa     1.466667 0.1561019
  versicolor 4.320000 0.4759020
  virginica  5.496667 0.5738457

            Petal.Width
Y                 [,1]      [,2]
  setosa     0.2766667 0.1135124
  versicolor 1.3533333 0.1960530
  virginica  2.0433333 0.2568823
```

Predicting on test data'

```
> y_pred <- predict(classifier_cl, newdata = test_cl)
> cm <- table(test_cl$Species, y_pred)
> cm
            y_pred
             setosa versicolor virginica
  setosa         20          0         0
  versicolor      0         19         1
  virginica       0          2        18
>
```

Model Evauation

```
> confusionMatrix(cm)
Confusion Matrix and Statistics

            y_pred
             setosa versicolor virginica
  setosa         20          0         0
  versicolor      0         19         1
  virginica       0          2        18

Overall Statistics

               Accuracy : 0.95
                 95% CI : (0.8608, 0.9896)
    No Information Rate : 0.35
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.925

 Mcnemar's Test P-Value : NA

Statistics by Class:

                     Class: setosa Class: versicolor Class: virginica
Sensitivity                 1.0000            0.9048           0.9474
Specificity                 1.0000            0.9744           0.9512
Pos Pred Value              1.0000            0.9500           0.9000
Neg Pred Value              1.0000            0.9500           0.9750
Prevalence                  0.3333            0.3500           0.3167
Detection Rate              0.3333            0.3167           0.3000
Detection Prevalence        0.3333            0.3333           0.3333
Balanced Accuracy           1.0000            0.9396           0.9493
```

PRACTICAL NO : 6

Aim: Write a Program showing implementation of Regression model.

Description:

Regression is a method to mathematically formulate relationship between variables that in due course can be used to estimate, interpolate and extrapolate. Suppose we want to estimate the weight of individuals, which is influenced by height, diet, workout, etc. Here, *Weight* is the **predicted** variable

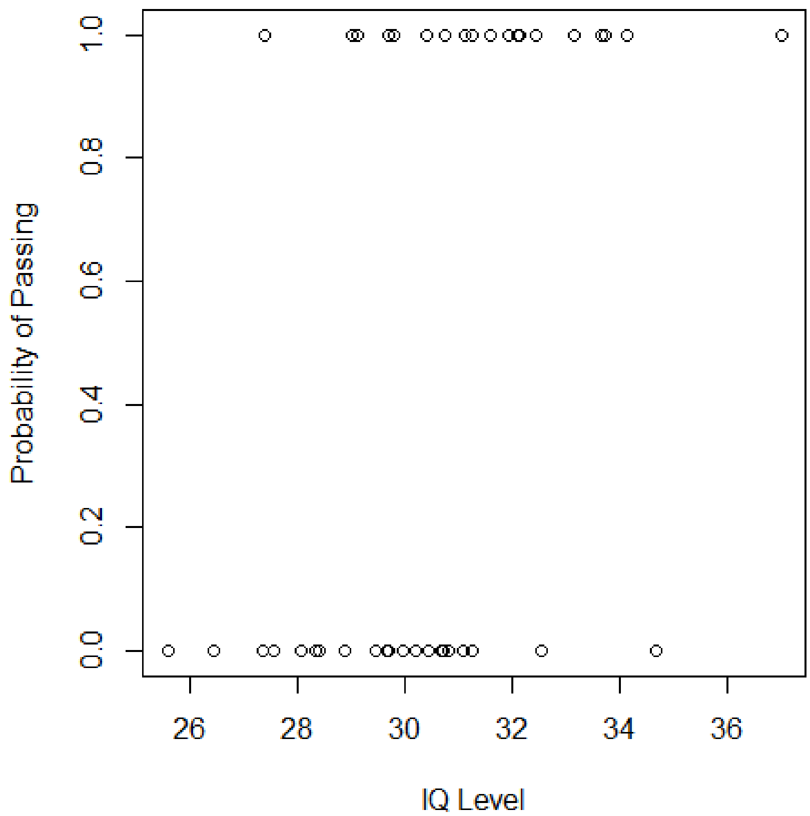
Lets implementation of Regression Model some Example:

```
> IQ <- rnorm(40, 30, 2)

> IQ <- sort(IQ)

> result <- c(0, 0, 0, 1, 0, 0, 0, 0, 0, 1,
+ 1, 0, 0, 0, 1, 1, 0, 0, 1, 0,
+ 0, 0, 1, 0, 0, 1, 1, 0, 1, 1,
+ 1, 1, 1, 0, 1, 1, 1, 1, 0, 1)
```

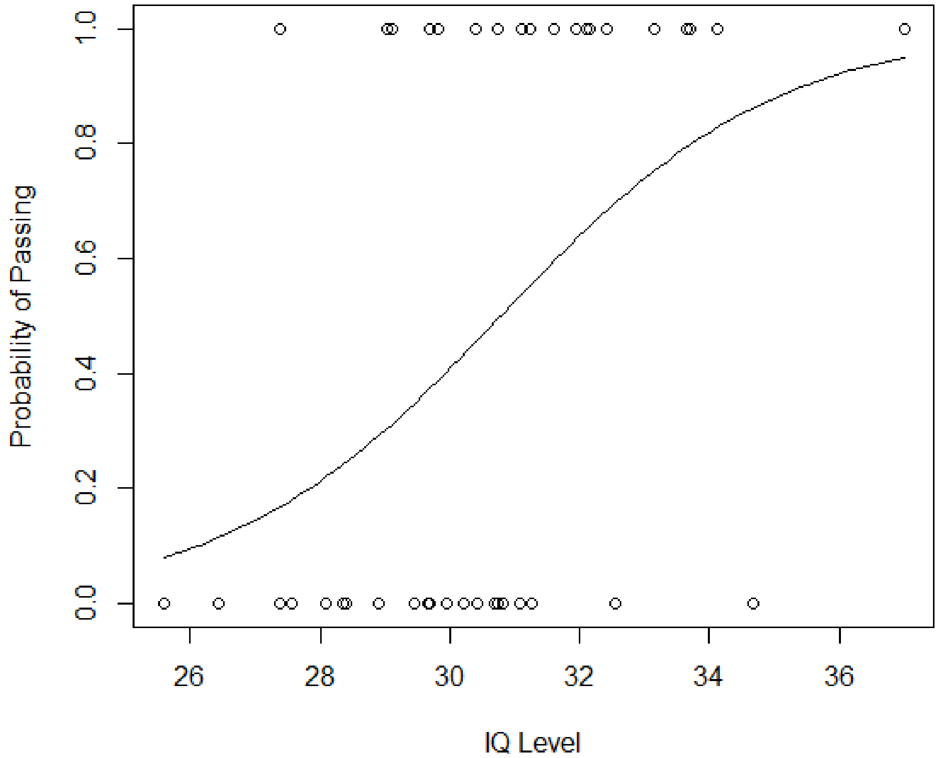
```
> df <- as.data.frame(cbind(IQ, result))
> print(df)
         IQ result
1  25.58824      0
2  26.43200      0
3  27.37083      0
4  27.37898      1
5  27.56671      0
6  28.08275      0
7  28.35637      0
8  28.41538      0
9  28.89752      0
10 29.03158      1
11 29.12386      1
12 29.46181      0
13 29.66945      0
14 29.68934      0
15 29.69886      1
16 29.80735      1
17 29.95326      0
18 30.21428      0
19 30.39298      1
20 30.43421      0
21 30.67802      0
22 30.72653      0
23 30.74974      1
24 30.82265      0
25 31.07116      0
26 31.11633      1
27 31.24740      1
28 31.25662      0
29 31.60194      1
30 31.93038      1
```

```
> png(file="LogisticRegressionGFG.png")
```

```
> plot(IQ, result, xlab = "IQ Level",
+ ylab = "Probability of Passing")
> g = glm(result~IQ, family=binomial, df)
```




```
> curve(predict(g, data.frame(IQ=x), type="resp"), add=TRUE)
> points(IQ, fitted(g), pch=30)
```




```
> summary(g)

Call:
glm(formula = result ~ IQ, family = binomial, data = df)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9877  -0.9804  -0.4502   0.9731   1.8898

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -14.4934     5.8835  -2.463   0.0138 *
IQ            0.4708     0.1922   2.450   0.0143 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 55.352  on 39  degrees of freedom
Residual deviance: 47.090  on 38  degrees of freedom
AIC: 51.09

Number of Fisher Scoring iterations: 4
```

```
> dev.off()
null device
          1
```

PRACTICAL NO : 7

Aim: **Write a Program showing clustering.**

Description:

 # In this Program we understand about K-Mean Clustering #

What Does K-Means Clustering Mean?

- K-means clustering is a simple unsupervised learning algorithm that is used to solve clustering problems.
- It follows a simple procedure of classifying a given data set into a number of clusters, defined by the letter "k," which is fixed beforehand.
- The clusters are then positioned as points and all observations or data points are associated with the nearest cluster, computed, adjusted and then the process starts over using the new adjustments until a desired result is reached.

We Understand in different Steps :

Step 1: Apply kmeans to *newiris*, and store the clustering result in *kc*. The cluster number is set to 3.

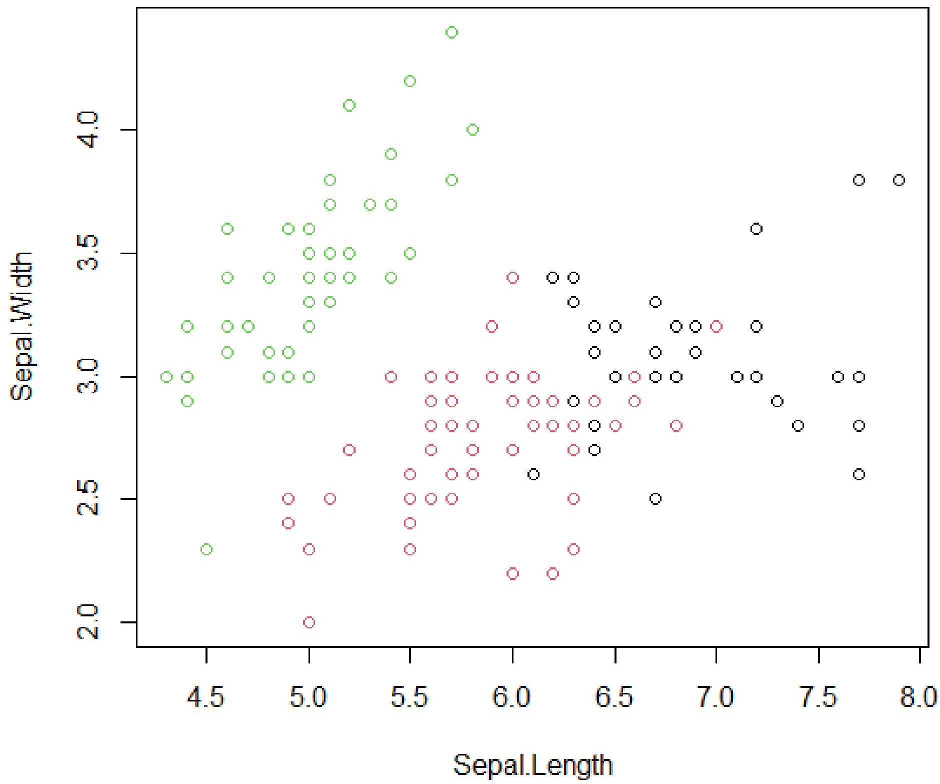
```
> newiris <- iris
> newiris$Species <- NULL
> (kc <- kmeans(newiris, 3))
K-means clustering with 3 clusters of sizes 38, 62, 50

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

Clustering vector:
  [1] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
 [35] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 [69] 2 2 2 2 2 2 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 2
[103] 1 1 1 1 2 1 1 1 1 1 1 2 2 1 1 1 1 2 1 2 1 2 1 1 2 2 1 1 1 1 1 2 1 1
[137] 1 1 2 1 1 1 2 1 1 1 2 1 1 2

Within cluster sum of squares by cluster:
[1] 23.87947 39.82097 15.15100
 (between_SS / total_SS =  88.4 %)

Available components:

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

Step 2: Compare the Species label with the clustering result

```
> table(iris$Species, kc$cluster)

              1  2  3
  setosa      0  0 50
  versicolor  2 48  0
  virginica  36 14  0
```

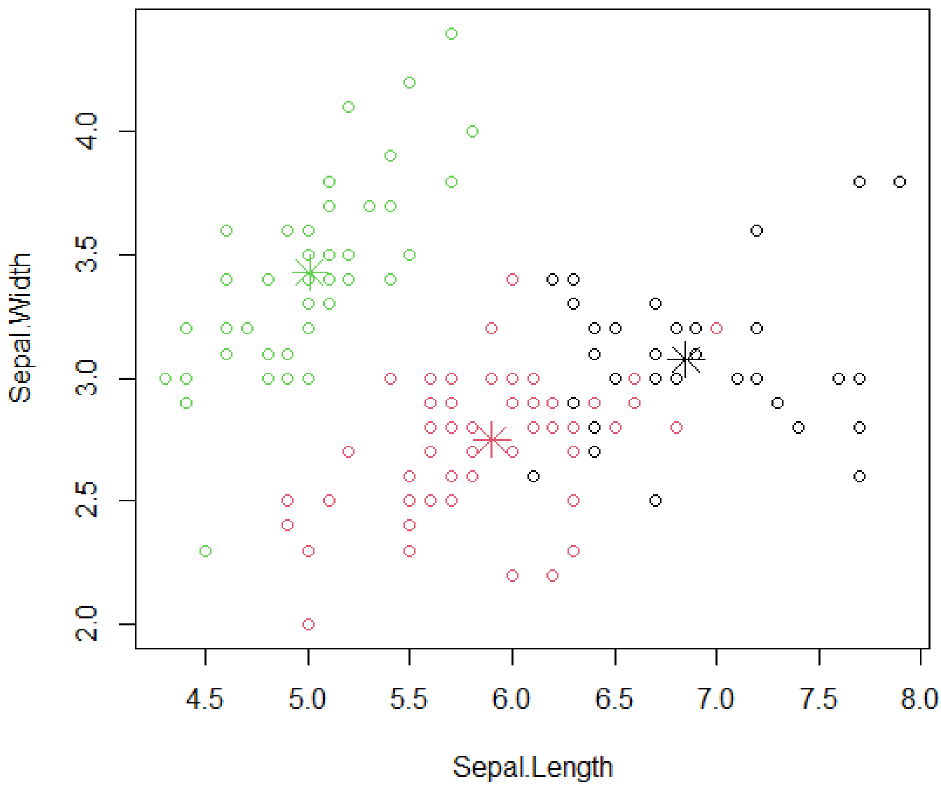
Step 3 : Plot the clusters and their centres. Note that there are four dimensions in the data and that only the first two dimensions are used to draw the plot below.

```
> plot(newiris[c("Sepal.Length", "Sepal.Width")], col=kc$cluster)
```



Step 4: Some black points close to the green centre (asterisk) are actually closer to the black centre in the four dimensional space.

```
> points(kc$centers[,c("Sepal.Length", "Sepal.Width")], col=1:3, pch=8, cex=2)
```


Sepal.Width
2.0
2.5
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.0
Sepal.Length