MACHINE LEARNING

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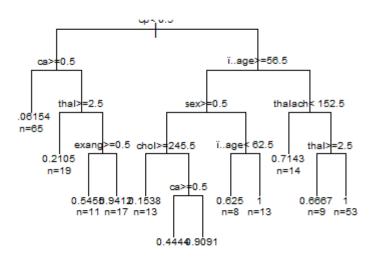
DIGITAL ASSIGNMENT 2

https://www.kaggle.com/ronitf/heart-disease-ucihttps://www.kaggle.com/ronitf/heartdisease-uci

DECISION TREE

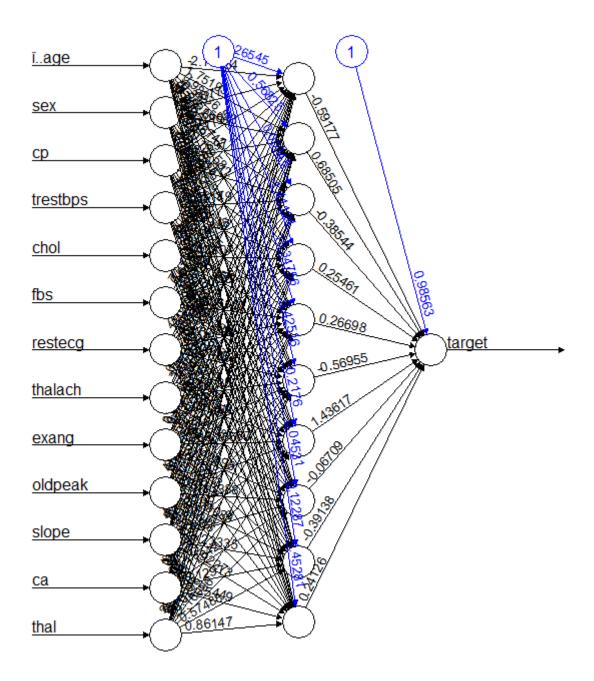
```
> dt=sample(nrow(heart), nrow(heart)*.8)
> heartTrain<- heart[dt,]</pre>
> heartTest<-heart[-dt,]</pre>
> fit <- rpart(target ~ ï..age+sex+cp+trestbps+chol+fbs+restecg+thalach+ex
ang+oldpeak+slope+ca+thal,
               method="anova", data=heartTrain )
> plot(fit, uniform=TRUE,main="Regression Tree for target")
> text(fit, use.n=TRUE, cex = .6)
> predict(fit,heartTest)
                                                      25
0.90909091 0.66666667 0.71428571 1.00000000 0.66666667
        29
                   30
                               31
                                           34
1.00000000 0.71428571 1.00000000 0.71428571 0.66666667
                               57
1.00000000 0.71428571 0.94117647 0.94117647 0.06153846
        67
                   70
                               74
                                           81
0.71428571 0.94117647 0.54545455 1.00000000 0.66666667
                   96
                              103
                                         113
0.94117647 0.21052632 1.00000000 1.00000000 1.00000000
       118
                  125
                              127
                                         131
                                                     134
0.6666667 1.00000000 0.94117647 1.00000000 1.00000000
       136
                  141
                              168
                                         174
                                                     185
0.94117647 1.00000000 0.06153846 0.44444444 0.21052632
       186
                  191
                              195
                                         196
0.06153846 0.21052632 0.90909091 0.21052632 0.06153846
       207
                  209
                              211
                                         215
0.06153846 0.71428571 0.44444444 0.06153846 0.06153846
                   236
                              238
                                          242
0.06153846 0.21052632 0.06153846 0.54545455 0.21052632
                                         259
       249
                  254
                              258
0.66666667 0.06153846 0.21052632 0.54545455 0.06153846
                   264
                              273
                                         278
0.06153846 0.06153846 0.94117647 0.15384615 0.21052632
       300
0.71428571
```

Regression Tree for target



NEURAL NETWORK

```
> plot(model)
> library("neuralnet")
> dt=sample(nrow(heart), nrow(heart)*.8)
> heartTrain<- heart[dt,]
> heartTest<-heart[-dt,]
> model <- neuralnet(target ~ ï..age+sex+cp+trestbps+chol+fbs+restecg+thalach+exang+oldpeak+slope+ca+thal,
+ data=heartTrain ,hidden=10,threshold=0.01)</pre>
```



Support Vector Machine

R code

- > dt=sample(nrow(heart), nrow(heart)*.8)
 > heartTrain<- heart[dt,]</pre>
- > heartTest<-heart[-dt,]</pre>

```
> model <- svm(target ~ ï..age+sex+cp+trestbps+chol+fbs+restecg+thalach+ex</pre>
ang+oldpeak+slope+ca+thal,
                      data=heartTrain )
> pred=predict(model,heartTest)
> pred
                                                    19
                                      15
               1.020409443
 0.522663438
                            0.931675890
                                          0.857341467
           22
                        28
                                       33
 1.072740479
               0.755270687
                             1.043667449
                                           0.782808843
          40
                                       51
                                                    52
                        50
 0.923884317
               1.020954390
                             1.118867435
                                           0.596243733
           58
                        64
                                      69
                                                    77
              0.862133514
 0.930471581
                            1.086894338
                                          0.761669457
```

Logistic Regression

```
> dt=sample(nrow(heart), nrow(heart)*.8)
> heartTrain<- heart[dt,]</pre>
> heartTest<-heart[-dt,]</pre>
> model <- glm(target ~ ï..age+sex+cp+trestbps+chol+fbs+restecg+thalach+ex</pre>
ang+oldpeak+slope+ca+thal,
                      data=heartTrain ,, family=binomial(link="logit"))
> pred=predict(model,heartTest)
> pred
                       9
                                   14
                                                24
                                                             29
 1.96997783
             1.95369473
                           0.13532507
                                       0.06623019
                                                     2.41480209
         39
                      41
                                   42
                                                43
 3.84842931
             1.72074448
                           1.38912504 -2.91576368
                                                     2.16257886
         50
                      54
                                   58
                                                59
                                                             60
 2.75828164
              5.86348356
                           1.44670744
                                        3.98236575
                                                     1.84632870
         61
                      63
                                   64
                                                71
             4.68161696
 3.53780845
                           1.88149477
                                       0.51427780
                                                     0.96102183
         81
                      90
                                   96
                                               109
                                                            124
 3.88070358
             1.12149865 -2.89235596
                                       3.96641538
                                                    4.92985392
        130
                     141
                                               143
                                  142
 0.50006978
             3.87018763
                                       5.66279082 -1.43116757
                          0.69125720
        154
                     157
                                  162
                                               163
                                                            182
 2.68811767
                           3.26829287
              3.54884109
                                        3.51082207 -2.58013883
                                  199
                                               203
        183
                     185
                                                            205
 2.62010243 -3.64763485 -5.28135539 -3.83979269 -5.63335604
                     211
        210
                                  224
                                               228
-0.97917684 -0.06060593 -5.94317505 -2.49650235 -4.78825722
        241
                     251
                                  252
                                               261
-4.07857633 -7.49515819 -4.71988345 -0.96007723 -5.65523995
                                  278
                                               279
        266
                     276
                                                            283
-1.76627383 -0.87349094
                          0.77309688
                                       1.95026392
                                                     0.95380846
        284
                     285
                                  290
                                               297
                                                            299
 1.05271417 -4.02190672 -0.52242199 1.69555149 -0.02519242
        302
-3.15602743
```

```
>
> accuracy(heartTest$target,pred,threshold=0.5)
                AUC omission.rate sensitivity specificity
 threshold
       0.5 0.8153595
                       0.1470588
                                  0.8529412
1
 prop.correct
                Карра
   0.8196721 0.6331329
NAÏVE BAYES
dt=sample(nrow(heart), nrow(heart)*.8)
heartTrain<- heart[dt,]</pre>
heartTest<-heart[-dt,]</pre>
model <- naiveBayes(target ~</pre>
i..aqe+sex+cp+trestbps+chol+fbs+restecq+thalach+exanq+oldpeak+slope+
ca+thal,
             data=heartTrain )
heartTest
pred=predict (model, heartTest)
pred
accuracy (heartTest$target, pred, threshold=0.5)
KNN
> dt=sample(nrow(heart), nrow(heart)*.8)
> heartTrain<- heart[dt,]</pre>
> heartTest<-heart[-dt,]</pre>
> testlabels=heartTest$target
> trainlabels=heartTrain$target
> pred <- knn(train=heartTrain,test=heartTest,cl=trainlabels,k=10)</pre>
> pred
 [59] 1 0 0
Levels: 0 1
> accuracy(heartTest$target,pred,threshold=0.5)
  threshold
                AUC omission.rate sensitivity specificity
       0.5 0.5876344
                       0.2580645
                                  0.7419355
                                            0.4333333
 prop.correct
                Карра
    0.5901639 0.176121
```

Bagging

```
> dt=sample(nrow(heart), nrow(heart)*.8)
> heartTrain<- heart[dt,]</pre>
> heartTest<-heart[-dt,]</pre>
> model <- bagging(target ~ ï..age+sex+cp+trestbps+chol+fbs+restecg+thalac</pre>
h+exang+oldpeak+slope+ca+thal,
                  data=heartTrain ,mfinal=5,
                  control=rpart.control(maxdepth=5, minsplit=15))
> pred=predict(model,heartTest)
> pred
 [1] 0.96217087 0.88132961 0.88846849 0.70100231 0.66247290
0.86246171 0.43213053 0.97324763
 [9] 0.72602135 0.67504257 0.79819194 0.91766163 0.97324763
0.90433516 0.69932280 0.97136964
[17] 0.16688719 0.76030660 0.91436821 0.84672889 0.90077618
0.85465539 0.94470925 0.83760173
[25] 0.50820035 0.94251747 0.91766163 0.96880319 0.96880319
0.72415907 0.73019400 0.64760251
[33] 0.96032739 0.82861027 0.11637102 0.62121631 0.05832085
0.15589307 0.01553802 0.71694160
[41] 0.14825778 0.03191164 0.52911062 0.22358845 0.11294872
0.12573021 0.73227253 0.03760767
[49] 0.03867910 0.79694690 0.06762358 0.64472275 0.85051977
0.49347113 0.54752238 0.16825778
[57] 0.73557266 0.40756672 0.69672520 0.11324437 0.01820468
> accuracy(heartTest$target,pred,threshold=0.5)
                 AUC omission.rate sensitivity specificity prop.correct
 threshold
Kappa
        0.5 0.7854031
                          0.05882353 0.9411765 0.6296296
0.8032787 0.588764
```

RANDOM FOREST

```
In randomForest.default(m, y, ...) :
  The response has five or fewer unique values. Are you sure you want to
do regression?
> pred=predict(model,heartTest)
> pred
                     3
                                                                  15
                                6
0.61480000 0.96197500 0.61836667 0.78856667 0.59586667 0.82644167
        21
                    34
                               35
                                           38
0.35503485 0.59496667 0.39683333 0.64496667 0.65014167 0.76744167
                               73
                                           78
                                                      82
                                                                 102
        64
                    71
0.66713333  0.45940000  0.95333333  0.83983333  0.95430000  0.19700000
       106
                   107
                              112
                                          115
                                                     124
                                                                 127
0.76020000 0.38176667 0.57766667 0.90560000 0.90547500 0.74290000
       128
                   129
                              137
                                          138
                                                     139
                                                                 140
0.91933333  0.97530000  0.72520000  0.63760000  0.26980000  0.11993333
       142
                   146
                              156
                                          160
                                                     178
                                                                 179
0.75238485 0.53746667 0.65793333 0.69616667 0.85443333 0.09753333
       182
                   184
                              185
                                          194
                                                     197
                                                                 206
0.16300000 0.30766667 0.15713333 0.00120000 0.56610000 0.26836667
       210
                   223
                              225
                                          228
                                                     230
                                                                 232
0.26223333 0.55516667 0.03280000 0.08246667 0.27046667 0.08093333
                   248
                                          258
                                                                 264
0.02730000 0.34653333 0.03613333 0.15263333 0.51363333 0.31310000
                              286
                                          289
                                                                 296
       267
                   271
                                                     295
0.24110000 0.36571304 0.06696667 0.05496667 0.34443333 0.07096667
       298
0.09753333
> accuracy(heartTest$target,pred,threshold=0.5)
  threshold
                  AUC omission.rate sensitivity specificity
        0.5 0.8229847
                           0.2058824
                                       0.7941176
  prop.correct
                   Kappa
    0.8196721 0.6386645
1
```

Booosting

```
> library("gbm")
Loaded gbm 2.1.5
Warning message:
package 'gbm' was built under R version 3.5.3
> dt=sample(nrow(heart), nrow(heart)*.8)
> heartTrain<- heart[dt,]</pre>
> heartTest<-heart[-dt,]</pre>
> model <- gbm(target ~ ï..age+sex+cp+trestbps+chol+fbs+restecg+thalach+ex</pre>
ang+oldpeak+slope+ca+thal,
                         data=heartTrain,,distribution = "gaussian",n.trees
= 10000,
                         shrinkage = 0.01, interaction.depth = 4 )
> model
gbm(formula = target ~ i..age + sex + cp + trestbps + chol +
    fbs + restecg + thalach + exang + oldpeak + slope + ca +
    thal, distribution = "gaussian", data = heartTrain,
    n.trees = 10000, interaction.depth = 4, shrinkage = 0.01)
A gradient boosted model with gaussian loss function.
10000 iterations were performed.
```

```
There were 13 predictors of which 13 had non-zero influence.
> pred=predict(model,heartTest)
Error in paste("Using", n.trees, "trees...\n") :
  argument "n.trees" is missing, with no default
> pred
                    3
                                                              15
0.61480000 0.96197500 0.61836667 0.78856667 0.59586667 0.82644167
                   34
                                        38
                             35
0.35503485 0.59496667 0.39683333 0.64496667 0.65014167 0.76744167
       64
                  71
                             73
                                        78
                                                   82
                                                             102
106
                  107
                            112
                                       115
                                                  124
                                                             127
0.76020000 0.38176667 0.57766667 0.90560000 0.90547500 0.74290000
                                                             140
      128
                 129
                            137
                                       138
                                                  139
0.91933333  0.97530000  0.72520000  0.63760000  0.26980000  0.11993333
      142
                 146
                            156
                                       160
                                                  178
                                                             179
0.75238485 0.53746667 0.65793333 0.69616667 0.85443333 0.09753333
      182
                 184
                            185
                                       194
                                                  197
                                                             206
0.16300000 0.30766667 0.15713333 0.00120000 0.56610000 0.26836667
      210
                 223
                            225
                                       228
                                                  230
                                                             232
0.26223333 0.55516667 0.03280000 0.08246667 0.27046667 0.08093333
                  248
                            251
                                        258
                                                  262
                                                             264
0.02730000 0.34653333 0.03613333 0.15263333 0.51363333 0.31310000
                 271
                            286
                                       289
                                                  295
                                                             296
      267
0.24110000 0.36571304 0.06696667 0.05496667 0.34443333 0.07096667
      298
0.09753333
> accuracy(heartTest$target,pred,threshold=0.5)
                 AUC omission.rate sensitivity specificity
  threshold
       0.5 0.8229847
                         0.2058824
                                     0.7941176
                                                 0.8518519
 prop.correct
                  Kappa
    0.8196721 0.6386645
```

ADABOOST

PYTHON

```
Code::
Python-
import numpy as np
import pandas as pd
from sklearn.metrics import confusion matrix,
accuracy_score,r2_score,mean_squared_error
dataset = pd.read_csv('../input/heart.csv')
X = dataset.iloc[:.:-1].values
y = dataset.iloc[:,-1].values
#Encoding Categorical Data
from sklearn.preprocessing import OneHotEncoder
#cp
oneHotEncoder = OneHotEncoder(categorical features=[2], n values='auto')
oneHotEncoder.fit(X)
X = oneHotEncoder.transform(X).toarray()
X = X[:, 1:]
#restecg
oneHotEncoder = OneHotEncoder(categorical_features=[8], n_values='auto')
oneHotEncoder.fit(X)
X = oneHotEncoder.transform(X).toarray()
X = X[:, 1:]
#slope
oneHotEncoder = OneHotEncoder(categorical_features=[13], n_values='auto')
oneHotEncoder.fit(X)
X = oneHotEncoder.transform(X).toarray()
X = X[:, 1:]
#ca
oneHotEncoder = OneHotEncoder(categorical features=[15], n values='auto')
oneHotEncoder.fit(X)
X = oneHotEncoder.transform(X).toarray()
X = X[:, 1:]
#thal
oneHotEncoder = OneHotEncoder(categorical features=[19], n values='auto')
oneHotEncoder.fit(X)
X = oneHotEncoder.transform(X).toarray()
X = X[:, 1:]
from sklearn.preprocessing import StandardScaler
scalerX = StandardScaler()
X = scalerX.fit transform(X)
from sklearn.model_selection import train_test_split
XTrain, XTest, yTrain, yTest = train_test_split(X, y, test_size=0.3, random_state=0)
#Logistic Regression
from sklearn.linear model import LogisticRegression
classifier = LogisticRegression()
classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
```

```
cm = confusion matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
r2 = r2\_score(yTest, yPred)
rmse = mean_squared_error(yTest,yPred)
print("Logistic Regression :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
Logistic Regression:
Accuracy = 0.8461538461538461
R2 = 0.38394584139265
RMSE = 0.15384615384615385
[[34 10]
 [ 4 4311
#K Nearest Neighbors
from sklearn.neighbors import KNeighborsClassifier
classifier = KNeighborsClassifier(n_neighbors=5, p=2, metric='minkowski')
classifier.fit(XTrain,yTrain)
vPred = classifier.predict(XTest)
cm = confusion_matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print("K Nearest Neighbors :")
print("Accuracy = ", accuracy)
print(cm)
K Nearest Neighbors:
Accuracy = 0.8131868131868132
[[32 12]
 [ 5 42]]
#Support Vector Machine
from sklearn.svm import SVC
classifier = SVC(kernel='linear',random_state=0)
classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion_matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print("Support Vector Machine :")
print("Accuracy = ", accuracy)
print(cm)
Support Vector Machine :
Accuracy = 0.8571428571428571
[[35 9]
 [ 4 43]]
```

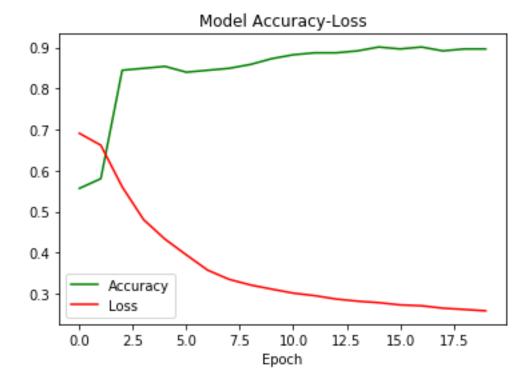
#Gaussian Naive Bayes

```
from sklearn.naive bayes import GaussianNB
classifier = GaussianNB()
classifier.fit(XTrain,yTrain)
vPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print("Gaussian Naive Bayes :")
print("Accuracy = ", accuracy)
print(cm)
Gaussian Naive Bayes:
Accuracy = 0.8131868131868132
[[33 11]
  [ 6 41]]
#Decision Tree Classifier
from sklearn.tree import DecisionTreeClassifier as DT
classifier = DT(criterion='entropy', random_state=0)
classifier.fit(XTrain,yTrain)
vPred = classifier.predict(XTest)
cm = confusion_matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print("Decision Tree Classifier :")
print("Accuracy = ", accuracy)
print(cm)
Decision Tree Classifier:
Accuracy = 0.6813186813186813
[[31 13]
 [16 31]]
#Random Forest Classifier
from sklearn.ensemble import RandomForestClassifier as RF
classifier = RF(n_estimators=10, criterion='entropy', random_state=0)
classifier.fit(XTrain,yTrain)
vPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
accuracy = accuracy score(yTest,yPred)
print("Random Forest Classifier :")
print("Accuracy = ", accuracy)
print(cm)
Random Forest Classifier:
Accuracy = 0.8241758241758241
[[34 10]
 [ 6 41]]
#Artificial Neural Network
from keras.models import Sequential
from keras.layers import Dense
```

```
#Initialising ANN
classifier = Sequential()
#Adding the first hidden layer or the input layer
classifier.add(Dense(activation='relu',
            kernel initializer='uniform',
            input dim=22,
            units=12))
#Adding the second hidden layer
classifier.add(Dense(activation='relu',
            kernel initializer='uniform',
            units=12))
#Adding the output layer
classifier.add(Dense(activation='sigmoid',
            kernel initializer='uniform',
            units=1))
#Compiling the ANN
classifier.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
print(classifier.summary())
#Fitting the ANN
history = classifier.fit(XTrain, yTrain, batch_size=5, epochs=20, verbose=1)
from matplotlib import pyplot as plt
plt.plot(history.history['acc'],'green')
plt.plot(history.history['loss'],'red')
plt.title('Model Accuracy-Loss')
plt.xlabel('Epoch')
plt.legend(['Accuracy','Loss'])
plt.show()
#Predicting the Test set Results
yPred = classifier.predict(XTest)
yPred = (yPred>0.5) #Since output is probability
cm = confusion_matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print("Artificial Neural Network Classifier:")
print("Accuracy = ", accuracy)
print(cm)
Using TensorFlow backend.
Layer (type)
                                             Output Shape
Param #
______
=========
                                              (None, 12)
dense 1 (Dense)
2.76
```

```
dense 2 (Dense)
                    (None, 12)
156
dense 3 (Dense)
                    (None, 1)
13
=========
Total params: 445
Trainable params: 445
Non-trainable params: 0
None
Epoch 1/20
3ms/step - loss: 0.6907 - acc: 0.5566
Epoch 2/20
388us/step - loss: 0.6616 - acc: 0.5802
Epoch 3/20
212/212 [========== ] - 0s
356us/step - loss: 0.5603 - acc: 0.8443
Epoch 4/20
212/212 [========= ] - Os
355us/step - loss: 0.4805 - acc: 0.8491
Epoch 5/20
358us/step - loss: 0.4330 - acc: 0.8538
Epoch 6/20
375us/step - loss: 0.3945 - acc: 0.8396
Epoch 7/20
351us/step - loss: 0.3572 - acc: 0.8443
Epoch 8/20
212/212 [========= ] - Os
373us/step - loss: 0.3349 - acc: 0.8491
Epoch 9/20
```

```
379us/step - loss: 0.3212 - acc: 0.8585
Epoch 10/20
394us/step - loss: 0.3110 - acc: 0.8726
Epoch 11/20
212/212 [======== ] - 0s
390us/step - loss: 0.3014 - acc: 0.8821
Epoch 12/20
212/212 [========= ] - Os
372us/step - loss: 0.2952 - acc: 0.8868
Epoch 13/20
356us/step - loss: 0.2870 - acc: 0.8868
Epoch 14/20
212/212 [======== ] - 0s
375us/step - loss: 0.2818 - acc: 0.8915
Epoch 15/20
212/212 [========== ] - Os
372us/step - loss: 0.2782 - acc: 0.9009
Epoch 16/20
212/212 [========= ] - Os
337us/step - loss: 0.2726 - acc: 0.8962
Epoch 17/20
212/212 [========= ] - Os
341us/step - loss: 0.2706 - acc: 0.9009
Epoch 18/20
375us/step - loss: 0.2647 - acc: 0.8915
Epoch 19/20
212/212 [========== ] - Os
363us/step - loss: 0.2616 - acc: 0.8962
Epoch 20/20
212/212 [========== ] - Os
387us/step - loss: 0.2583 - acc: 0.8962
```



Artificial Neural Network Classifier :
Accuracy = 0.8571428571428571
[[35 9]
 [4 43]]

#Gradient Boosting Classifier

A Gradient Boosting classifier is used for making predictions. This algorithm is the only one that got better results when scaling to the full dataset. The output is a probability representing the likelihood of the presence of heart disease.

Expected Accuray: processed.cleveland.data

The data was tested using a 10-fold cross validation technique.

The results are:

Avg Accuracy Avg Recall Avg Precision Avg ROC_AUC 0.795 0.758 0.800 0.914

Expected Accuray: processed.all.data

The data was randomly shuffled and tested using a 10-fold cross validation technique.

The average results for 5 cross validations are:

Avg Accuracy Avg Recall Avg Precision Avg ROC_AUC

 DATASET: YOUTUBE

RCODE AND RESULTS:

PYTHON CODE AND RESULTS:

Dataset https://www.kaggle.com/mdhrumil/top-5000-youtube-channels-data-from-socialblade

Python:

import numpy as np

import pandas as pd

from sklearn.metrics import confusion_matrix, accuracy_score,r2_score,mean_squared_error

from sklearn.preprocessing import normalize

from sklearn.model_selection import cross_val_score

from sklearn import tree

from sklearn import linear_model

from sklearn import svm

from sklearn.neural_network import MLPClassifier

from sklearn.naive_bayes import MultinomialNB

from sklearn.linear_model import LogisticRegression

from sklearn.neighbors import KNeighborsClassifier

from sklearn.ensemble import BaggingClassifier

from sklearn.ensemble import RandomForestClassifier

from sklearn.ensemble import GradientBoostingClassifier

from sklearn.ensemble import AdaBoostClassifier

import pandas as pd

csv_file = "/content/youtube.csv"

 $dt = pd.read_csv(csv_file)$

```
#REPLACING -- WITH NULL
import numpy as np
dt = dt.replace('--', np.nan, regex=True)
dt["Rank"] = dt["Rank"].replace('th', "", regex=True)
dt["Rank"] = dt["Rank"].replace('rd', "", regex=True)
dt["Rank"] = dt["Rank"].replace('nd', "", regex=True)
dt["Rank"] = dt["Rank"].replace('st', "", regex=True)
dt["Rank"] = dt["Rank"].replace(',', "", regex=True)
#REPIACING OBJECT TYPE WITH FLOAT64
dt["Subscribers"] = pd.to_numeric(dt["Subscribers"])
dt["Video Uploads"] = pd.to_numeric(dt["Video Uploads"])
dt["Video views"] = pd.to_numeric(dt["Video views"])
dt["Rank"] = pd.to_numeric(dt["Rank"])
dt["Average views"] = dt["Video views"] / dt["Video Uploads"]
#INSERTING MEDIAN VALUE TO NULL (in dt_full)
from sklearn.impute import SimpleImputer
sample_incomplete_rows = dt[dt.isnull().any(axis=1)].head()
imputer = SimpleImputer(strategy="median")
dt_num = dt.drop(["Channel name", "Grade"], axis = 1)
imputer.fit(dt_num)
X = imputer.transform(dt_num)
dt_full = pd.DataFrame(X, columns=dt_num.columns)
dt_full.loc[sample_incomplete_rows.index.values]
dt_full = pd.DataFrame(X, columns=dt_num.columns)
```

```
#CATEGORICAL DATA
grade_cat = dt[["Grade"]]
from sklearn.preprocessing import OneHotEncoder
cat_encoder = OneHotEncoder()
dt_cat_1hot = cat_encoder.fit_transform(grade_cat)
dt_one_hot_array = dt_cat_1hot.toarray()
#TRAIN AND TEST DATA
dt_full_train = dt_full[:4000]
dt_full_{test} = dt_full[4000:]
subs_train = dt_full_train["Subscribers"].copy()
#PIPELINES
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler
num_pipeline = Pipeline([
    ('imputer', SimpleImputer(strategy="median")),
    ('std_scaler', StandardScaler()),
  ])
dt_num_tr = num_pipeline.fit_transform(dt_full)
from sklearn.compose import ColumnTransformer
num_attribs = list(dt_full)
cat_attribs = ["Grade"]
full_pipeline = ColumnTransformer([
    ("num", num_pipeline, num_attribs),
```

```
("cat", OneHotEncoder(), cat_attribs)
])
dt_prepared = full_pipeline.fit_transform(dt[:4000])
```

LogisticRegression:

```
lin_reg = LogisticRegression()
lin_reg.fit(dt_prepared, subs_train)

some_data = dt.iloc[:10]

some_labels = subs_train.iloc[:10]

some_data_prepared = full_pipeline.transform(some_data)

dt_predictions = lin_reg.predict(dt_prepared)

rmse = mean_squared_error(subs_train,dt_predictions)

cm = confusion_matrix(subs_train,dt_predictions)

accuracy = accuracy_score(subs_train,dt_predictions)

r2 = r2_score(subs_train,dt_predictions)

print("Logistic Regression :")

print("Accuracy = ", accuracy)

print("R2 = ",r2)

print("RMSE = ",rmse)

print(cm)
```

Output:

```
Logistic Regression:

Accuracy = 0.085

R2 = -0.41283048624407837

RMSE = 23800441219721.88

[[0 0 0 ... 0 0 0]

[0 0 0 ... 0 0 0]

[0 0 0 ... 0 0 0]

...

[0 0 0 ... 1 0 0]

[0 0 0 ... 0 1 0]

[0 0 0 ... 0 0 1]]
```

Artificial Neural Network:

```
lin_reg = MLPClassifier()
lin_reg.set_params(hidden_layer_sizes =(100,100), max_iter = 1000,alpha = 0.01, momentum = 0.7)
lin_reg.fit(dt_prepared, subs_train)

some_data = dt.iloc[:10]
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)

dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
accuracy = accuracy_score(subs_train,dt_predictions)
r2 = r2_score(subs_train,dt_predictions)
```

```
print("Artificial Neural Network :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT
Artificial Neural Network:
Accuracy = 0.72875
R2 = 0.993882156273152
RMSE = 103060757415.6885
[[1 0 0 ... 0 0 0]
 [0 0 0 ... 0 0 0]
 [0 0 0 ... 0 0 0]
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
```

Support Vector Machine

```
rom sklearn.svm import SVC
lin_reg = SVC(kernel='linear',random_state=0)
lin_reg.fit(dt_prepared, subs_train)
```

```
some_data = dt.iloc[:10]
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)
dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
accuracy = accuracy_score(subs_train,dt_predictions)
r2 = r2\_score(subs\_train,dt\_predictions)
print("Support Vector Machine :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
Naive Bayes
from sklearn.naive_bayes import GaussianNB
lin_reg = GaussianNB()
lin_reg.fit(dt_prepared, subs_train)
some_data = dt.iloc[:10]
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)
dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
accuracy = accuracy_score(subs_train,dt_predictions)
r2 = r2\_score(subs\_train,dt\_predictions)
print("Gaussian Naive Bayes :")
print("Accuracy = ", accuracy)
```

```
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)

OUTPUT::

Gaussian Naive Bayes :
Accuracy = 1.0

R2 = 1.0

RMSE = 0.0

[[1 0 0 ... 0 0 0]
        [0 1 0 ... 0 0 0]
        [0 0 1 ... 0 0 0]
        [0 0 0 ... 1 0 0]
        [0 0 0 ... 1 0 0]
        [0 0 0 ... 0 0 1]
```

K nearest neighbour

```
from sklearn.neighbors import KNeighborsClassifier
```

```
lin_reg = KNeighborsClassifier(n_neighbors=5, p=2, metric='minkowski')
lin_reg.fit(dt_prepared, subs_train)

some_data = dt.iloc[:10]
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)

dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
accuracy = accuracy_score(subs_train,dt_predictions)
```

```
r2 = r2\_score(subs\_train,dt\_predictions)
print("K nearest neighbour :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
K nearest neighbour :
Accuracy = 0.1495
R2 = 0.8962040635132252
RMSE = 1748538914790.0137
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 [0 0 0 ... 0 0 0]
 [0 0 0 ... 0 0 0]
 [0 0 0 ... 0 0 0]]
```

Bagging

```
lin_reg = BaggingClassifier()
lin_reg.set_params(n_estimators = 30,max_samples = 1000)
lin_reg.fit(dt_prepared, subs_train)

some_data = dt.iloc[:10]
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)

dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
```

```
accuracy = accuracy_score(subs_train,dt_predictions)
r2 = r2_score(subs_train,dt_predictions)
print("Bagging :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
Bagging :
Accuracy = 0.93575
R2 = 0.9894947501109713
RMSE = 176970687507.60474
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
```

Random Forest:

```
lin_reg = RandomForestClassifier()
lin_reg.set_params(n_estimators = 100, max_depth = 10)
lin_reg.fit(dt_prepared, subs_train)

some_data = dt.iloc[:10]
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)
```

```
dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
accuracy = accuracy_score(subs_train,dt_predictions)
r2 = r2_score(subs_train,dt_predictions)
print("Random Forest :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
Random Forest :
Accuracy = 0.713
R2 = 0.9199350282485733
RMSE = 1348768781875.8728
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 . . .
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
```

Gradient Boosting

```
lin_reg = GradientBoostingClassifier()
lin_reg.set_params(n_estimators = 30,learning_rate = 1)
lin_reg.fit(dt_prepared, subs_train)
some_data = dt.iloc[:10]
```

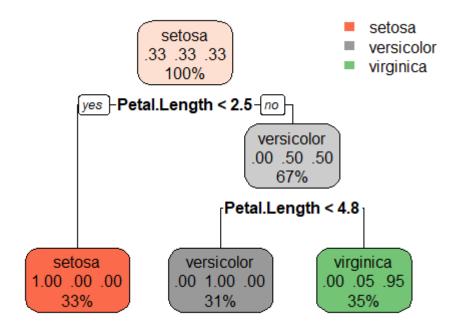
```
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)
dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
accuracy = accuracy_score(subs_train,dt_predictions)
r2 = r2\_score(subs\_train,dt\_predictions)
print("Gradient Boosting :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
lin_reg = AdaBoostClassifier()
lin_reg.set_params(n_estimators = 10, learning_rate = 1)
lin_reg.fit(dt_prepared, subs_train)
some_data = dt.iloc[:10]
some_labels = subs_train.iloc[:10]
some_data_prepared = full_pipeline.transform(some_data)
dt_predictions = lin_reg.predict(dt_prepared)
rmse = mean_squared_error(subs_train,dt_predictions)
cm = confusion_matrix(subs_train,dt_predictions)
accuracy = accuracy_score(subs_train,dt_predictions)
r2 = r2_score(subs_train,dt_predictions)
print("AdaBoost :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
```

```
DATASET: IRIS
RCODE AND RESULTS:
Decision Tree
library("caTools")
library(rpart)
install.packages("rpart.plot")
library(rpart.plot)
data("iris")
# Split data into Train and test
set.seed(123)
split <- sample.split(iris$Species,SplitRatio = 0.7)</pre>
# split using subsetsubset(
train <- subset(iris, split==TRUE)</pre>
test <- subset(iris, split==FALSE)</pre>
#Build the model
Sptree <- rpart (Species ~., train, method ="class")
#Plot the model
rpart.plot(Sptree)
```

#Predict using the test data set
pptree <- predict(Sptree, test, type ="class")</pre>

#Confusion matrix

table(test[,5],pptree)



- > #Confusion matrix
- > table(test[,5],pptree)

pptree

setosa versicolor virginica setosa 15 0 0 versicolor 0 11 4 virginica 0 1 14

LOGISTIC REGRESSION

library(datasets)

ir_data<- iris

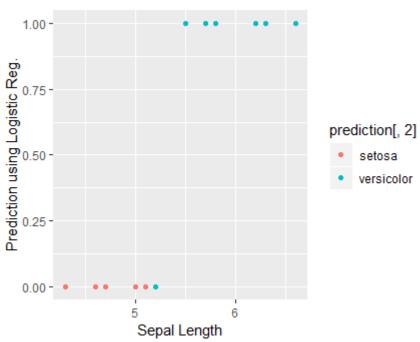
head(ir_data)

str(ir_data)

levels(ir_data\$Species)

sum(is.na(ir_data))

```
ir_data<-ir_data[1:100,]</pre>
set.seed(100)
samp<-sample(1:100,80)
ir_test<-ir_data[samp,]</pre>
ir_ctrl<-ir_data[-samp,]</pre>
library(ggplot2); library(GGally)
ggpairs(ir_test)
y<-ir_test$Species; x<-ir_test$Sepal.Length
glfit < -glm(y \sim x, family = 'binomial')
summary(glfit)
newdata<- data.frame(x=ir_ctrl$Sepal.Length)</pre>
predicted_val<-predict(glfit, newdata, type="response")</pre>
prediction<-data.frame(ir_ctrl$Sepal.Length, ir_ctrl$Species,predicted_val)</pre>
prediction
qplot(prediction[,1], round(prediction[,3]), col=prediction[,2], xlab = 'Sepal Length', ylab = 'Prediction
using Logistic Reg.')
```



SVM

library("e1071")

head(iris,5)

```
attach(iris)
x <- subset(iris, select=-Species)</pre>
y <- Species
svm_model <- svm(Species ~ ., data=iris)</pre>
summary(svm_model)
svm_model1 <- svm(x,y)</pre>
summary(svm_model1)
pred <- predict(svm_model1,x)</pre>
system.time(pred <- predict(svm_model1,x))</pre>
table(pred,y)
svm_tune <- tune(svm, train.x=x, train.y=y,</pre>
         kernel="radial", ranges=list(cost=10^(-1:2), gamma=c(.5,1,2)))
print(svm_tune)
svm_model_after_tune <- svm(Species ~ ., data=iris, kernel="radial", cost=1, gamma=0.5)
summary(svm_model_after_tune)
pred <- predict(svm_model_after_tune,x)</pre>
system.time(predict(svm_model_after_tune,x))
table(pred,y)
OUTPUT:
Confusion Matrix:
> table(pred,y)
pred
                 setosa versicolor virginica
  setosa
                                                    0
                      50
                                      0
  versicolor
                       0
                                     48
                                                   2
  virginica
                        0
# load libraries
library(mlbench)
library(caret)
# load data
data("iris")
# rename dataset to keep code below generic
```

```
dataset <- iris
control <- trainControl(method="repeatedcv", number=10, repeats=3)</pre>
seed <- 7
metric <- "Accuracy"
preProcess=c("center", "scale")
# Logistic Regression
set.seed(seed)
fit.glm <- train(iris~., data=dataset, method="glm", metric=metric, trControl=control)
# SVM Radial
set.seed(seed)
fit.svmRadial <- train(iris~., data=dataset, method="svmRadial", metric=metric, preProc=c("center",
"scale"), trControl=control, fit=FALSE)
# kNN
set.seed(seed)
fit.knn <- train(iris~., data=dataset, method="knn", metric=metric, preProc=c("center", "scale"),
trControl=control)
# Naive Bayes
set.seed(seed)
fit.nb <- train(iris~., data=dataset, method="nb", metric=metric, trControl=control)
# Bagged CART
set.seed(seed)
fit.treebag <- train(iris~., data=dataset, method="treebag", metric=metric, trControl=control)
# Random Forest
set.seed(seed)
fit.rf <- train(iris~., data=dataset, method="rf", metric=metric, trControl=control)
# Stochastic Gradient Boosting (Generalized Boosted Modeling)
set.seed(seed)
fit.gbm <- train(iris~., data=dataset, method="gbm", metric=metric, trControl=control,
verbose=FALSE)
results <- resamples(list(lda=fit.lda, logistic=fit.glm, glmnet=fit.glmnet,
              svm=fit.svmRadial, knn=fit.knn, nb=fit.nb, cart=fit.cart, c50=fit.c50,
```

```
bagging=fit.treebag, rf=fit.rf, gbm=fit.gbm))
```

Table comparison

summary(results)

OUTPUT:

Models: logistic, svm, knn, nb, bagging, rf, gbm

Number of resamples: 30

Accuracy

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's logistic 0.6842 0.7639 0.7713 0.7781 0.8019 0.8701 0 svm 0.6711 0.7403 0.7582 0.7651 0.7890 0.8961 0 knn 0.6753 0.7115 0.7386 0.7465 0.7785 0.8961 0 nb 0.6316 0.7305 0.7597 0.7569 0.7869 0.8571 0 bagging 0.6883 0.7246 0.7451 0.7530 0.7792 0.8571 0 rf 0.6711 0.7273 0.7516 0.7617 0.7890 0.8571 0 gbm 0.6974 0.7273 0.7727 0.7708 0.8052 0.8831 0

PYTHON CODE AND RESULTS:

import pandas as pd

import numpy as np

from sklearn.preprocessing import normalize

from sklearn.model_selection import cross_val_score

data = pd.read_csv("Iris.csv")

train =data.sample(frac = 0.7)

test = data.loc[~data.index.isin(train.index)]

train

 $from\ sklearn.metrics\ import\ confusion_matrix,\ accuracy_score, r2_score, mean_squared_error$

from sklearn import tree

```
from sklearn import linear_model
from sklearn import svm
from sklearn.neural_network import MLPClassifier
from sklearn.naive_bayes import MultinomialNB
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import BaggingClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.ensemble import AdaBoostClassifier
x_train = train[train.columns[1:5]]
y_train = train[train.columns[5]]
x_test = test[test.columns[1:5]]
y_test = test[test.columns[5]]
#logistic regression
classifier = LogisticRegression()
classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
cm = confusion_matrix(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
print("Logistic Regression :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT:
Accuracy = 0.977777777777777
R2 = 0.9654907975460123
```

```
RMSE = 0.022222222222223
[[15 0 0]
[0 16 0]
[0 1 13]]
#Neural Network
classifier = MLPClassifier()
classifier.set_params(hidden_layer_sizes =(100,100), max_iter = 1000,alpha = 0.01, momentum =
0.7)
classifier = classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
cm = confusion_matrix(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
print("Artificial Neural Network :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT:
Accuracy = 1.0
R2 = 1.0
RMSE = 0.0
[[15 0 0]
[0 16 0]
[0 0 14]]
#Support Vector Machine
from sklearn.svm import SVC
classifier = SVC(kernel='linear',random_state=0)
classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
```

```
cm = confusion_matrix(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
print("Support Vector Machine :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT:
Accuracy = 1.0
R2 = 1.0
RMSE = 0.0
[[15 0 0]
[0 16 0]
[0 0 14]]
#Gaussian Naive Bayes
from sklearn.naive_bayes import GaussianNB
classifier = GaussianNB()
classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
cm = confusion_matrix(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
print("Gaussian Naive Bayes :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT:
```

```
Accuracy = 0.977777777777777
R2 = 0.9654907975460123
RMSE = 0.022222222222223
[[15 0 0]
[0151]
[0 0 14]]
#K-Nearest Neighbours
from sklearn.neighbors import KNeighborsClassifier
classifier = KNeighborsClassifier(n_neighbors=5, p=2, metric='minkowski')
classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
cm = confusion_matrix(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
print("K nearest neighbour :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT:
Accuracy = 0.977777777777777
R2 = 0.9654907975460123
RMSE = 0.022222222222223
[[15 0 0]
[0151]
[0 0 14]]
#Bagging
classifier = BaggingClassifier()
classifier.set_params(n_estimators = 30,max_samples = 1000)
classifier = classifier.fit(x_train,y_train)
```

```
yPred = classifier.predict(x_test)
cm = confusion_matrix(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
print("Bagging :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
#Random Forest
classifier = RandomForestClassifier()
classifier.set_params(n_estimators = 100, max_depth = 10)
classifier = classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
cm = confusion_matrix(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
print("Random Forest :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT:
Accuracy = 0.977777777777777
R2 = 0.9654907975460123
RMSE = 0.022222222222223
[[15 0 0]
[0151]
```

```
[0 0 14]]
```

```
#Boosting
classifier = GradientBoostingClassifier()
classifier.set_params(n_estimators = 30,learning_rate = 1)
classifier = classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
cm = confusion_matrix(y_test,yPred)
r2 = r2_score(y_test,yPred)
rmse = mean_squared_error(y_test,yPred)
accuracy = accuracy_score(y_test,yPred)
print("Gradient Boosting :")
print("Accuracy = ", accuracy)
print("R2 = ",r2)
print("RMSE = ",rmse)
print(cm)
OUTPUT:
Accuracy = 0.977777777777777
R2 = 0.9654907975460123
RMSE = 0.022222222222223
[[15 0 0]
[0151]
[0 0 14]]
#AdaBoost.
classifier = AdaBoostClassifier()
classifier.set_params(n_estimators = 10, learning_rate = 1)
classifier = classifier.fit(x_train,y_train)
yPred = classifier.predict(x_test)
```

cm = confusion_matrix(y_test,yPred)

r2 = r2_score(y_test,yPred)

```
Logistic Regression :
Accuracy = 0.977777777777777
R2 = 0.9654907975460123
RMSE = 0.022222222222223
[[15 0 0]
 [ 0 16 0]
[0 1 13]]
In [5]: classifier = MLPClassifier()
   ...: classifier.set_params(hidden_layer_sizes
=(100,100), max_iter = 1000,alpha = 0.01, momentum = 0.7)
   ...: classifier = classifier.fit(x_train,y_train)
   ...: yPred = classifier.predict(x_test)
   ...: cm = confusion_matrix(y_test,yPred)
   ...: accuracy = accuracy score(y test,yPred)
  ...: r2 = r2_score(y_test,yPred)
   ...: rmse = mean_squared_error(y_test,yPred)
  ...: print("Artificial Neural Network :")
   ...: print("Accuracy = ", accuracy)
   ...: print("R2 = ",r2)
   ...: print("RMSE = ",rmse)
   ...: print(cm)
Artificial Neural Network :
Accuracy = 1.0
R2 = 1.0
RMSE = 0.0
[[15 0 0]
 [ 0 16 0]
IPython console
              History log
```

```
...: print(cm)
Support Vector Machine :
Accuracy = 1.0
R2 = 1.0
RMSE = 0.0
[[15 0 0]
 [ 0 16 0]
[ 0 0 14]]
In [7]: from sklearn.naive bayes import GaussianNB
   ...: classifier = GaussianNB()
   ...: classifier.fit(x_train,y_train)
  ...: yPred = classifier.predict(x_test)
  ...: cm = confusion_matrix(y_test,yPred)
  ...: r2 = r2_score(y_test,yPred)
  ...: rmse = mean_squared_error(y_test,yPred)
  ...: accuracy = accuracy_score(y_test,yPred)
  ...: print("Gaussian Naive Bayes :")
  ...: print("Accuracy = ", accuracy)
  ...: print("R2 = ",r2)
  ...: print("RMSE = ",rmse)
  ...: print(cm)
Gaussian Naive Bayes :
Accuracy = 0.977777777777777
R2 = 0.9654907975460123
RMSE = 0.022222222222223
[[15 0 0]
[ 0 15 1]
```

DATASET: CAR EVALUATION

RCODE AND RESULTS:

#load the data

Code:

```
car_eval = read.csv("F:/ML DA/carsevaluation.csv")
colnames(car_eval)<-c("buying","maint","doors","persons","lug_boot","safety","class")
head(car_eval)</pre>
```

```
> #load the data
> car_eval = read.csv("F:/ML DA/carsevaluation.csv")
> colnames(car_eval)<-c("buying","maint","doors","persons","lug_boot","saf</pre>
ety", "class")
> head(car_eval)
 buying maint doors persons lug_boot safety class
1 vhigh vhigh
                  2
                      2
                               small
                                        low unacc
2 vhigh vhigh
                  2
                          2
                               small
                                        med unacc
3 vhigh vhigh
                  2
                         2
                               small
                                       high unacc
4 vhigh vhigh
                  2
                         2
                                med
                                       low unacc
5 vhigh vhigh
                  2
                         2
                                med
                                        med unacc
6 vhigh vhigh
                         2
                                 med
                                       high unacc
```

#Exploratory Data Analysis

Code:

summary(car_eval)
str(car_eval)

```
> #Exploratory Data Analysis
> summary(car_eval)
                           doors
                                                  lug_boot
                                                              safety
  buying
               maint
                                      persons
                                                                           C
lass
high :432
             high :432
                         2
                              :432
                                          :576
                                                 big :576
                                                             high:576
                                                                         acc
: 384
low:432
             low:432
                         3
                              :432
                                          :576
                                                 med :576
                                                             low:576
                                                                        goo
d: 69
med :432
             med :432
                              :432
                                      more:576
                                                 small:576
                                                             med :576
                                                                        una
cc:1210
             vhigh:432
                         5more:432
vhigh:432
                                                                        vgo
od: 65
> str(car_eval)
'data.frame': 1728 obs. of 7 variables:
$ buying : Factor w/ 4 levels "high","low","med",..: 4 4 4 4 4 4 4 4 4 4
           : Factor w/ 4 levels "high", "low", "med", ...: 4 4 4 4 4 4 4 4 4 4 4
$ maint
 $ doors
           : Factor w/ 4 levels "2", "3", "4", "5more": 1 1 1 1 1 1 1 1 1 1 1 .
 $ persons : Factor w/ 3 levels "2","4","more": 1 1 1 1 1 1 1 1 1 2 ...
 $ lug_boot: Factor w/ 3 levels "big", "med", "small": 3 3 3 2 2 2 1 1 1 3 .
$ safety : Factor w/ 3 levels "high","low","med": 2 3 1 2 3 1 2 3 1 2 ...
$ class
           : Factor w/ 4 levels "acc", "good", "unacc", ...: 3 3 3 3 3 3 3 3 3
3 ...
```

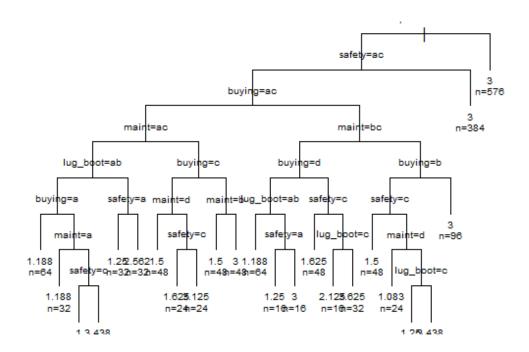
#Decision Tree

Code:

```
library(rpart)
#Build the model
model<-rpart(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval, method =
'anova')
plot(model, uniform=TRUE,main="Cars Evaluation")
text(model, use.n=TRUE,cex=.6)
printcp(model)</pre>
```

```
#Classification and Regression Trees(CART) decision tree
> library(rpart)
> #Build the model
> model<-rpart(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval ,</pre>
method = 'anova')
> plot(model, uniform=TRUE, main="Cars Evaluation")
> text(model, use.n=TRUE, cex=.6)
> printcp(model)
Regression tree:
rpart(formula = class ~ buying + maint + doors + persons + lug_boot +
    safety, data = car_eval, method = "anova")
Variables actually used in tree construction:
[1] buying
              lug_boot maint
                                     persons safety
Root node error: 1325.1/1728 = 0.76684
n = 1728
         CP nsplit rel error
                                  xerror
                                                xstd
                        1.00000 1.00101 0.029822
1 0.162675
                   0
2
7
2 0.028817
                       0.67465 0.67744 0.026490
3 0.020675
                       0.51971 0.42688 0.023983
                       0.45769 0.36828 0.024915
                  10
4 0.018112
                       0.43958 0.35263 0.025713
5 0.017121
                  11
6 0.016555
                  13
                       0.40533 0.33491 0.024881
                       0.32256 0.32139 0.024957
0.28992 0.28363 0.023593
7 0.016320
                  18
8 0.013376
                  20
9 0.010000
                  23
                       0.24391 0.25830 0.022847
```

Cars Evaluation



Neural Network:

Code:

```
library(nnet)
#Build the model
model<-
nnet(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval,size
= 4,decay = 0.0001,maxit = 500)
model</pre>
```

```
> library(nnet)
> #Build the model
> model<-nnet(class~buying+maint+doors+persons+lug_boot+safety,data=car_ev
al, size = 4, decay = 0.0001, maxit = 500)
# weights:
            84
initial value 2876.941690
     10 value 664.833515
iter
      20 value 351.146192
iter
      30 value 196.097581
iter
      40 value 127.153784
iter
      50 value 102.124774
iter
      60 value 88.106953
iter
      70 value 84.409178
iter
     80 value 79.814165
iter
iter 90 value 76.168802
```

```
iter 100 value 71.391408
iter 110 value 69.587460
iter 120 value 68.422438
iter 130 value 67.685459
iter 140 value 65.735973
iter 150 value 63.069165
iter 160 value 55.646582
iter 170 value 50.902625
iter 180 value 49.089001
iter 190 value 47.556182
iter 200 value 47.287091
iter 210 value 46.161999
iter 220 value 45.420187
iter 230 value 44.774950
iter 240 value 43.499987
iter 250 value 41.604496
iter 260 value 39.896982
iter 270 value 39.628078
iter 280 value 39.195841
iter 290 value 36.451245
iter 300 value 34.717002
iter 310 value 33.000447
iter 320 value 31.840266
iter 330 value 31.122663
iter 340 value 30.502133
iter 350 value 30.290285
iter 360 value 30.193979
iter 370 value 30.071046 iter 380 value 29.969224 iter 390 value 29.820713
iter 400 value 29.725851
iter 410 value 29.643706
iter 420 value 29.601526
iter 430 value 29.581857
iter 440 value 29.556836
iter 450 value 29.532638
iter 460 value 29.519943
iter 470 value 29.519535
iter 480 value 29.518424
iter 490 value 29.516032
iter 500 value 29.512283
final value 29.512283
stopped after 500 iterations
> model
a 15-4-4 network with 84 weights
inputs: buyinglow buyingmed buyingvhigh maintlow maintmed maintvhigh doors
3 doors4 doors5more persons4 personsmore lug_bootmed lug_bootsmall safetyl
ow safetymed
output(s): class
options were - softmax modelling decay=1e-04
```

#Support Vector Machine

Code:

library(kernlab)
#Build the model
model<ksvm(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval)
model

Output:

```
> #Support Vector Machine
> library(kernlab)
> #Build the model
> model<-ksvm(class~buying+maint+doors+persons+lug_boot+safety,data=car_ev al)
> model
Support Vector Machine object of class "ksvm"

SV type: C-svc (classification)
   parameter : cost C = 1

Gaussian Radial Basis kernel function.
   Hyperparameter : sigma = 0.1805555555556

Number of Support Vectors : 790

Objective Function Value : -86.159 -269.3608 -63.2354 -66.9172 -40.5667 -5 0.3608
Training error : 0.03125
```

#Summarize the model

summary(model)

#NaiveBayes

Code:

```
library(e1071)
#Build the model
model<-
naiveBayes(class~buying+maint+doors+persons+lug boot+safety,data=car eva
I,k=5)
model
```

Output:

```
> #NaiveBayes
> library(e1071)
> #Build the model
> model<-naiveBayes(class~buying+maint+doors+persons+lug_boot+safety,data=</pre>
car_eval, k=5
> model
Naive Bayes Classifier for Discrete Predictors
naiveBayes.default(x = X, y = Y, laplace = laplace, k = 5)
A-priori probabilities:
                 good
                                      vgood
                           unacc
       acc
0.2222222 0.03993056 0.70023148 0.03761574
Conditional probabilities:
       buying
                                  med
                        low
             high
                                           vhigh
        0.2812500 0.2317708 0.2994792 0.1875000
  acc
  good 0.0000000 0.6666667 0.3333333 0.0000000
  unacc 0.2677686 0.2132231 0.2214876 0.2975207
  vgood 0.0000000 0.6000000 0.4000000 0.0000000
       maint
             high
                        low
                                  med
                                           vhigh
        0.2734375 0.2395833 0.2994792 0.1875000
  acc
  good 0.0000000 0.6666667 0.3333333 0.0000000
  unacc 0.2595041 0.2214876 0.2214876 0.2975207
  vgood 0.2000000 0.4000000 0.4000000 0.0000000
       doors
        0.2109375 0.2578125 0.2656250 0.2656250
  acc
  good 0.2173913 0.2608696 0.2608696 0.2608696
  unacc 0.2694215 0.2479339 0.2413223 0.2413223
  vgood 0.1538462 0.2307692 0.3076923 0.3076923
       persons
                2
        0.0000000 0.5156250 0.4843750
  acc
  good 0.0000000 0.5217391 0.4782609
```

unacc 0.4760331 0.2578512 0.2661157

```
vgood 0.0000000 0.4615385 0.5384615
     lug_boot
            big
                      med
      0.3750000 0.3515625 0.2734375
acc
good 0.3478261 0.3478261 0.3043478
unacc 0.3041322 0.3239669 0.3719008
vgood 0.6153846 0.3846154 0.0000000
     safety
           high
                      low
      0.5312500 0.0000000 0.4687500
good 0.4347826 0.0000000 0.5652174
unacc 0.2289256 0.4760331 0.2950413
vgood 1.0000000 0.0000000 0.0000000
```

#Summarize the model

summary(model)

#k-Nearest Neighbors

Code:

library(caret)
#Build the model
model<knn3(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval,k=5)

Output:

model

```
> #k-Nearest Neighbors
> library(caret)
> #Build the model
> model<-knn3(class~buying+maint+doors+persons+lug_boot+safety,data=car_ev al,k=5)
> model
5-nearest neighbor model
Training set outcome distribution:
    acc good unacc vgood
    384 69 1210 65
```

#Summarize the model

summary(model)

#Bagging

Code:

library(ipred)

#Build the model

model<-

bagging(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval) model

Output:

```
> #Bagging CART
> library(ipred)
> #Build the model
> model<-bagging(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval)
> model

Bagging classification trees with 25 bootstrap replications

Call: bagging.data.frame(formula = class ~ buying + maint + doors + persons + lug_boot + safety, data = car_eval)
```

#Summarize the model

summary(model)

#Random Forest

Code:

```
library(randomForest)
#Build the model
model<-
randomForest(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval)
```

model

Output:

```
> #Random Forest
> library(randomForest)
> #Build the model
> model<-randomForest(class~buying+maint+doors+persons+lug_boot+safety,dat</pre>
a=car_eval)
> model
call:
 randomForest(formula = class ~ buying + maint + doors + persons +
                                                                         ٦u
g_boot + safety, data = car_eval)
               Type of random forest: classification
                     Number of trees: 500
No. of variables tried at each split: 2
        OOB estimate of error rate: 3.07%
Confusion matrix:
      acc good unacc vgood class.error
acc
      375
             4
                   3
                         2 0.02343750
            54
good
       8
                   0
                         7 0.21739130
```

0 0.01652893

56 0.13846154

#Summarize the model

0 1190

0

summary(model)

unacc 20

vgood

- > #Summarize the model
- > summary(model)

	Length	class	Mode
call	3	-none-	call
type	1	-none-	character
predicted	1728	factor	numeric
err.rate	2500	-none-	numeric
confusion	20	-none-	numeric
votes	6912	matrix	numeric
oob.times	1728	-none-	numeric
classes	4	-none-	character
importance	6	-none-	numeric
importanceSD	0	-none-	NULL
localImportance	0	-none-	NULL
proximity	0	-none-	NULL
ntree	1	-none-	numeric
mtry	1	-none-	numeric
forest	14	-none-	list
У	1728	factor	numeric
test	0	-none-	NULL
inbag	0	-none-	NULL
terms	3	terms	call

#Gradient Boosted Machine

Code:

library(gbm)
#Build the model
model<-

gbm(class~buying+maint+doors+persons+lug_boot+safety,data=car_eval,distribution="multinomial")

model

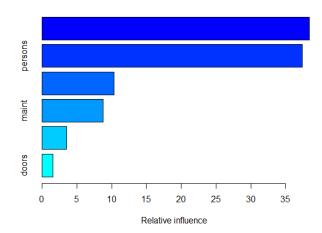
#Summarize the model

summary(model)

```
> #Summarize the model
```

> summary(model)

```
var rel.inf
safety safety 38.430954
persons persons 37.395453
buying buying 10.328409
maint maint 8.769498
lug_boot lug_boot 3.536240
doors doors 1.539447
```



PYTHON CODE AND RESULTS:

DATASET: CERVICAL CANCER

This dataset focuses on the prediction of indicators/diagnosis of cervical cancer. The features cover demographic information, habits, and historic medical records.

Data Set Characteristics:	Multivariate	Number of Instances:	858	Area:	Life
Attribute Characteristics:	Integer, Real	Number of Attributes:	36	Date Donated	2017-03-03
Associated Tasks:	Classification	Missing Values?	Yes	Number of Web Hits:	76618

Attribute Information:

(int) Age

(int) Number of sexual partners

(int) First sexual intercourse (age)

(int) Num of pregnancies

(bool) Smokes

(bool) Smokes (years)

(bool) Smokes (packs/year)

(bool) Hormonal Contraceptives

(int) Hormonal Contraceptives (years)

(bool) IUD

(int) IUD (years)

(bool) STDs

(int) STDs (number)

(bool) STDs:condylomatosis

(bool) STDs:cervical condylomatosis

(bool) STDs:vaginal condylomatosis

(bool) STDs:vulvo-perineal condylomatosis

(bool) STDs:syphilis

(bool) STDs:pelvic inflammatory disease

(bool) STDs:genital herpes

(bool) STDs:molluscum contagiosum

(bool) STDs:AIDS

(bool) STDs:HIV

(bool) STDs:Hepatitis B

(bool) STDs:HPV

(int) STDs: Number of diagnosis

(int) STDs: Time since first diagnosis

(int) STDs: Time since last diagnosis

(bool) Dx:Cancer

(bool) Dx:CIN

(bool) Dx:HPV

```
(bool) Dx
(bool) Hinselmann: target variable
(bool) Schiller: target variable
(bool) Cytology: target variable
(bool) Biopsy: target variable
RCODE AND RESULTS:
> library(dplyr)
> library(readr)
> library(tidyverse)
> library(mlr)
> library(ggplot2)
> library(gridExtra)
> library(gmodels)
> library(GGally)
> library(cowplot)
> library(tidyr)
> library(magrittr)
> library(moments)
> library(purrr)
> library(data.table)
> library(latex2exp)
> library(caret)
> library(robustHD)
> library(spFSR)
> library(rjson)
> library(party)
> library(knitr)
> library(kableExtra)
> library(stringr)
> library(mlbench)
> library(e1071)
> library(MASS)
> set.seed(999)
> dataCancer <- read_csv("C:/Users/hp/Desktop/risk_factors_cervical_cancer</pre>
.csv", col_names = TRUE, na = "?", trim_ws = TRUE)
> kable(dataCancer %>% head(), caption = "Table 1. Cervical Cancer Dataset
") %>% kable_styling(bootstrap_options = c("condensed"), full_width = TRUE
 font_size = 10
auto; margin-right: auto;">
<caption style="font-size: initial !important;">Table 1. Cervical Cancer D
ataset</caption>
<thead>
  Age 
   First_sexual_intercourse 
   Num_of_pregnancies 
   Smokes 
   Smokes (years) 
   Smokes (packs/year) 
   Hormonal Contraceptives (years) 
   IUD 
   IUD (years)
```

STDs

```
 STDs (number) 

style="text-align:right;"> STDs_condylomatosis 

style="text-align:right;"> STDs_cervical_condylomatosis 

style="text-align:right;"> STDs_valvo_perineal_condylomatosis 

style="text-align:right;"> STDs_valvo_perineal_condylomatosis 

style="text-align:right;"> STDs_syphilis 

style="text-align:right;"> STDs_pelvic_inflammatory_disease 

style="text-align:right;"> STDs_pelvic_inflammatory_disease 

style="text-align:right;"> STDs_pelvic_inflammatory_disease 

style="text-align:right;"> STDs_molluscum_contagiosum 

style="text-align:right;"> STDs_AIDS 

style="text-align:right;"> STDs_AIDS 

style="text-align:right;"> STDS_HIV 

style="text-align:right;"> STDS_HEPATITIS_B 

style="text-align:right;"> STDS_HEPATITIS_B 

style="text-align:right;"> STDS_Number_of_diagnosis 

style="text-align:right;"> STDS_Time_since_first_diagnosis 

style="text-align:right;"> STDS_Time_since_first_diagnosis 

style="text-align:right;"> Dx_Cancer 

style="text-align:right;"> Dx_Cancer 

style="text-align:right;"> Dx_Cancer 

style="text-align:right;"> Dx_HPV 

sth style="text-align:right;"> Dx_HPV 

sth style="text-align:right;"> SX SIDS_Time_since_first_diagnosis 

sth style="text-align:right;"> Dx_CIN 

sth style="text-align:right;"> Dx_HPV 

sth style="text-align:right;"> Biopsy 

sth style="text-align:right;"> Biopsy 

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Table 1. Cervical Cancer Dataset

Age	Number_of_sexual_partners	First_sexual_intercourse	Num_of_pregnancies	Sn
18	4	15	1	
15	1	14	1	
34	1	NA	1	
52	5	16	4	
46	3	21	4	
42	3	23	2	

```
> dim(dataCancer)
[1] 858 36
> kable(dataCancer %>% summarizeColumns(), caption = "Table 2. Statistical
Summary") %>% kable_styling(bootstrap_options = c("condensed"), full_width
= TRUE, font_size = 10)
<table class="table table-condensed" style="font-size: 10px; margin-left:
auto; margin-right: auto;">
<caption style="font-size: initial !important;">Table 2. Statistical Summa
ry</caption>
<thead>
  name 
  type 
  na 
  mean 
 disp 
  median 
  mad 
  min 
  max 
  nlevs 
 </thead>
 Age 
  numeric
```

```
 0 
  0 
 Number_of_sexual_partners 
 numeric 
  26 
  First_sexual_intercourse 
style="text-align:left;"> numeric 
  numeric 
 7 
 16.9952996 
 2.8033554 
 17.0 
<<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td><<td>
 11 
   0 
 13 
  0.1455621 

 0.1455621 

 0.3528756 

 0.0 

 0.0000 

 0 

 1 

   0 
 Smokes (years) 
   numeric 
  13 

 1.2197214
```

```
 4.0890169 
 4.0690169 </
<td style="text-align:right;"> 0.0 
 0.0000 
 0 
 37 
 0 

 Smokes (packs/year) 
 numeric 
 numeric 
 13 
 0.4531440 
 0.22266098 
 0.0 
 0.0000 
 0 
 37 
 37 
 0 

 Hormonal_Contraceptives style="text-align:left;"> numeric 
 0 
 0 
 IUD  
 0.0 

 0.0000 

 0 

 0 

 1 

 0 
 IUD (years) 
 numeric 
 117 
 0.0
```

```
 0.0000 
 0 

 19 

 0 

 STDs 
 numeric 
 numeric 
 105 
 0.1049137 
 0.3066458 
 0.0 
 0.0000 
 0 
 0 
 1 
 0 

 STDs (number) 
 numeric 
 numeric 
 105 
 0.1766268 
 0.5619928 
 0.0 
 0.0000 
 0 
 0 
 0 
 0 
 0 

 0 
 numeric 
 105 
 0.0584329 
 0.2347162 
 0.0 
 0.0000 
 0 
 0 
 1 
 1 

 0 
 0 
 0 
 STDs_vaginal_condylomatosis 
 numeric 
 105 
 0.0053121 

 0.0053121 

 0.0727385 

 0.0 

 0.0000 

 0
```

```
 1 
 0 
 STDs_vulvo_perineal_condylomatosis 
 numeric 
 0 
 STDs_syphilis 
 numeric 
 numeric 
 105 
 0.0239044 
 0.1528528 
 0.0 
 0.0000 
 0 
 0 
 1 
 0 

 numeric 
 105 
 0.0013280 
 0.0364420 
 0.0 
 0.0000 
 0.0000 
 0 
 1 
 0 

 0 
 STDs_genital_herpes 
style="text-align:left;"> numeric 
 numeric 

 0.0013280 

 0.0364420 

 0.0000 

 0 

 1 

 1 

 0 
 105 
 0.0013280 

 0.0364420 

 0.0 

 0.0 

 0.0000 

 0
```

```
 STDs_AIDS 
 numeric 
 numeric 
 105 
 0.0000000 
 0.0000000 
 0.0 
 0.0000 
 0 
 0 
 0 
 0 
 0 

 STDs_HIV 
 numeric 
 numeric 
 105 
 0.0239044 
 0.1528528 
 0.0 
 0.0000 
 0 
 0 
 1 
 0 

 STDs_Hepatitis_B 
 numeric 
 105 
 0.0013280 
 0.0364420 
 0.0 
 0.0000 
 0 
 0 
 1 
 0 
 0 

 0 
 STDs_HPV 
style="text-align:left;"> numeric 

 105 

 0.0026560 

 0.0515025 

 0.0515025 

 0.0

 0.0000 

 0 

 1 

 0 
 STDs_Number_of_diagnosis  numeric 
 0 

 0.0874126 

 0.3025447 

 0.0 

 0 
 3 
 0
```

```
 STDs_Time_since_first_diagnosis 
 numeric 
 numeric 
 787 
 6.1408451 
 5.8950240 
 4.0 
 4.4478 
 1 
 22 
 22 

 STDs_Time_since_last_diagnosis 
 numeric 
 numeric 
 787 
 5.8169014 
 5.7552705 
 3.0 
 2.9652 
 1 
 2 
 2 

 Dx_Cancer 
 numeric 
 numeric 
 0 
 0.0209790 
 0.1433976 
 0.0 
 0.0000 
 0 
 0 
 1 
 0 

 0 
 0 
 0 

 0.0104895 

 0.1019392 

 0.0 

 0 
 Dx_HPV 
 numeric 
 0 
 0 
 1 
 0 
 Dx 
 numeric
```

```
 0 
 0 
 Hinselmann 
  numeric 
 numeric 
 0 
 0.0407925 
 0.1979246 
 0.0 
 0.0000 
 0 
 0 
 1 
 0 

 Schiller 
 numeric 
 Citology 
style="text-align:left;"> numeric 
 1 
  0 
 Biopsy 
  0 
 0.0641026 

 0.0641026 

 0.2450784 

 0.0 

 0.0000 

 0 

 1 

  0
```

Ta	h۱	2 ر د	Stat	tisti	cal	Sum	nma	rv
ICI	$\mathbf{v}_{\mathbf{i}}$		J.(a)	usu	Cal	Jun	HHC	ΙУ

name	type	na	mean	disp	mediai
Age	numeric	0	26.8205128	8.4979481	25.
Number_of_sexual_partners	numeric	26	2.5276442	1.6677605	2.0
First_sexual_intercourse	numeric	7	16.9952996	2.8033554	17.
Num_of_pregnancies	numeric	56	2.2755611	1.4474141	2.0
Smokes	numeric	13	0.1455621	0.3528756	0.0
Smokes (years)	numeric	13	1.2197214	4.0890169	0.0
Smokes (packs/year)	numeric	13	0.4531440	2.2266098	0.0
Hormonal_Contraceptives	numeric	108	0.6413333	0.4799292	1.)
Hormonal Contraceptives (years)	numeric	108	2.2564192	3.7642535	0.
IUD	numeric	117	0.1120108	0.3155928	0.0
IUD (years)	numeric	117	0.5148043	1.9430885	0.0
<					>

```
> dataCancer <- subset(dataCancer, select = -STDs_cervical_condylomatosis)</pre>
> dataCancer <- subset(dataCancer, select = -STDs_vaginal_condylomatosis)</pre>
> dataCancer <- subset(dataCancer, select = -STDs_pelvic_inflammatory_dise</pre>
ase)
> dataCancer <- subset(dataCancer, select = -STDs_genital_herpes)</pre>
> dataCancer <- subset(dataCancer, select = -STDs_molluscum_contagiosum)</pre>
> dataCancer <- subset(dataCancer, select = -STDs_Hepatitis_B)</pre>
> dataCancer <- subset(dataCancer, select = -STDs_HPV)</pre>
> dataCancer <- subset(dataCancer, select = -STDs_AIDS)</pre>
> dataCancer <- subset(dataCancer, select = -STDs_Time_since_first_diagnos</pre>
is)
> dataCancer <- subset(dataCancer, select = -STDs_Time_since_last_diagnosi</pre>
s)
> length(which(is.na(dataCancer)))
[1] 1208
> kable(colSums(is.na(dataCancer)), caption = "Table 3. Number of Missing
Values in Each Column") %>% kable_styling(bootstrap_options = c("condensed
"), full_width = TRUE, font_size = 10)
<table class="table table-condensed" style="font-size: 10px; margin-left:
auto; margin-right: auto;">
<caption style="font-size: initial !important;">Table 3. Number of Missing
Values in Each Column</caption>
<thead>
  x 
 </thead>
 Age 
   0 
  Number_of_sexual_partners 
   26
```

```
 First_sexual_intercourse 
 7 
 Num_of_pregnancies 
 56 
 Smokes 
 13 
 Smokes (years) 
 13 
 Smokes (packs/year) 
 13 
 Hormonal_Contraceptives 
 108 
 Hormonal Contraceptives (years) 
 108 
 IUD 
 117 
 IUD (years) 
 117 
 STDs 
 105 
 STDs (number) 
 105 
 STDs_condylomatosis 
 105 
 STDs_vulvo_perineal_condylomatosis 
 105 
 STDs_syphilis 
 105 
 STDs_HIV 
 105
```

```
 STDs_Number_of_diagnosis 
  0 
  Dx_Cancer 
  0 
  Dx_CIN 
  0 
  Dx_HPV 
  0 
  Dx 
  0 
  Hinselmann 
  0 
  Schiller 
  0 
  Citology 
  0 
  Biopsy 
  0 
 Table 3. Number of Missing Values in Each Column
Age
                         0
Number_of_sexual_partners
                         26
First sexual intercourse
Num_of_pregnancies
                         56
Smokes
                         13
                         13
Smokes (years)
                         13
Hormonal_Contraceptives
                         108
Hormonal Contraceptives (vears)
                         108
                         117
IUD (years)
STDs
                         105
> dataCancer <- dataCancer[!is.na(dataCancer$Smokes),]</pre>
> dataCancer <- dataCancer[!is.na(dataCancer$First_sexual_intercourse),]</pre>
> dataCancer <- dataCancer[!is.na(dataCancer$STDs),]</pre>
```

> prop_NA <- function(x) { mean(is.na(x))}
> missingData <- sapply(dataCancer, prop_NA)</pre>

```
> missingData <- data.frame(Variables = names(missingData), Proportion = m</pre>
issingData, Completude = 1 - missingData)
> dataCancer$Num_of_pregnancies[is.na(dataCancer$Num_of_pregnancies)] <- 0</pre>
 summary(dataCancer)
                 Number_of_sexual_partners First_sexual_intercourse Num_of
      Age
_pregnancies
                 Smokes
Min.
       :13.00
                 Min.
                         : 1.000
                                             Min.
                                                    :10.00
                                                                       Min.
: 0.000
            Min.
                   :0.0000
 1st Qu.:21.00
                 1st Qu.: 2.000
                                             1st Qu.:15.00
                                                                       1st Qu
.: 1.000
             1st Qu.:0.0000
                 Median : 2.000
                                             Median :17.00
                                                                       Median
Median :26.00
: 2.000
            Median :0.0000
Mean
        :27.22
                 Mean
                       : 2.512
                                             Mean
                                                    :17.09
                                                                       Mean
: 2.182
            Mean
                   :0.1438
                                             3rd Qu.:18.00
 3rd Qu.:33.00
                 3rd Qu.: 3.000
                                                                       3rd Qu
.: 3.000
             3rd Qu.:0.0000
Max.
       :84.00
                 Max.
                         :28.000
                                             Max.
                                                    :32.00
                                                                       Max.
:11.000
            Max.
                    :1.0000
                 NA's
                         :13
 Smokes (years)
                   Smokes (packs/year) Hormonal_Contraceptives Hormonal Con
traceptives (years)
                                       Min.
Min.
        : 0.000
                  Min.
                          : 0.0000
                                               :0.0000
                                                                 Min.
                                                                        : 0.0
00
                  1st Qu.: 0.0000
                                        1st Qu.:0.0000
 1st Qu.: 0.000
                                                                 1st Qu.: 0.0
00
                  Median : 0.0000
Median : 0.000
                                       Median :1.0000
                                                                 Median: 0.5
00
Mean
        : 1.222
                  Mean
                          : 0.4606
                                       Mean
                                               :0.6405
                                                                 Mean
                                                                        : 2.2
34
                   3rd Qu.: 0.0000
 3rd Qu.: 0.000
                                        3rd Qu.:1.0000
                                                                 3rd Qu.: 3.0
00
Max.
        :37.000
                  Max.
                          :37.0000
                                       Max.
                                               :1.0000
                                                                 Max.
                                                                        :22.0
00
                                        NA's
                                               :11
                                                                 NA's
                                                                         :11
                                                       STDs (number)
      IUD
                   IUD (years)
                                           STDs
                                                                         STDS
_condylomatosis
Min.
       :0.0000
                  Min.
                          : 0.0000
                                     Min.
                                             :0.0000
                                                       Min.
                                                               :0.0000
                                                                         Min.
:0.00000
 1st Qu.:0.0000
                   1st Qu.: 0.0000
                                     1st Qu.:0.0000
                                                       1st Qu.:0.0000
                                                                         1st
Qu.:0.00000
Median :0.0000
                  Median : 0.0000
                                     Median :0.0000
                                                       Median :0.0000
                                                                         Medi
an :0.00000
Mean
        :0.1122
                  Mean
                        : 0.5173
                                     Mean
                                             :0.1031
                                                       Mean
                                                               :0.1723
                                                                         Mean
:0.05699
 3rd Qu.:0.0000
                   3rd Qu.: 0.0000
                                     3rd Qu.:0.0000
                                                       3rd Qu.:0.0000
                                                                         3rd
Qu.:0.00000
        :1.0000
                          :19.0000
                                             :1.0000
                                                               :4.0000
Max.
                  Max.
                                     Max.
                                                       Max.
                                                                         Max.
:1.00000
                  NA's
 NA's
        :15
                          :15
 STDs_vulvo_perineal_condylomatosis STDs_syphilis
                                                           STDs_HIV
                                                                           ST
Ds_Number_of_diagnosis
        :0.00000
                                     Min.
                                             :0.00000
                                                        Min.
                                                                :0.00000
Min.
                                                                           Μi
     :0.0000
1st Qu.:0.00000
                                     1st Qu.:0.00000
                                                        1st Qu.:0.00000
                                                                           1s
t Qu.:0.00000
                                     Median :0.00000
Median :0.00000
                                                        Median :0.00000
                                                                           Me
dian :0.00000
        :0.05563
Mean
                                     Mean
                                             :0.02307
                                                        Mean
                                                                :0.02307
                                                                           Me
an
    :0.09634
```

```
3rd Qu.:0.00000
                                      3rd Qu.:0.00000
                                                         3rd Qu.:0.00000
                                                                            3r
d Qu.:0.00000
Max.
      :1.00000
                                      Max.
                                             :1.00000
                                                         Max.
                                                                :1.00000
                                                                            Ма
     :3.00000
   Dx_Cancer
                        DX_CIN
                                           Dx_HPV
                                                                Dx
Hinselmann
Min.
        :0.00000
                    Min.
                           :0.00000
                                       Min.
                                              :0.00000
                                                          Min.
                                                                  :0.00000
                                                                             Μ
in.
      :0.00000
                    1st Qu.:0.00000
1st Qu.:0.00000
                                       1st Qu.:0.00000
                                                          1st Qu.:0.00000
                                                                             1
st Qu.:0.00000
                    Median :0.00000
                                       Median :0.00000
                                                          Median :0.00000
Median :0.00000
edian :0.00000
Mean
        :0.02307
                    Mean
                           :0.01085
                                       Mean
                                              :0.02307
                                                          Mean
                                                                  :0.02985
                                                                             Μ
ean
      :0.04613
 3rd Qu.:0.00000
                    3rd Qu.:0.00000
                                       3rd Qu.:0.00000
                                                          3rd Qu.:0.00000
                                                                             3
rd Qu.:0.00000
Max.
        :1.00000
                    Max.
                           :1.00000
                                       Max.
                                              :1.00000
                                                          Max.
                                                                  :1.00000
ax.
      :1.00000
    Schiller
                       Citology
                                           Biopsy
       :0.00000
                           :0.00000
                                              :0.00000
 Min.
                    Min.
                                       Min.
 1st Qu.:0.00000
                    1st Qu.:0.00000
                                       1st Qu.:0.00000
 Median :0.00000
                    Median :0.00000
                                       Median :0.00000
 Mean
        :0.09634
                    Mean
                           :0.05427
                                       Mean
                                              :0.07056
 3rd Qu.:0.00000
                    3rd Qu.:0.00000
                                       3rd Qu.:0.00000
 Max.
        :1.00000
                    Max.
                           :1.00000
                                       Max.
                                              :1.00000
> dataCancer$Cancer <- dataCancer$Biopsy + dataCancer$Citology + dataCance</pre>
r$Schiller + dataCancer$Hinselmann
> dataCancer$Cancer[dataCancer$Cancer == 2] <- 1</pre>
> dataCancer$Cancer[dataCancer$Cancer == 3] <- 1</pre>
> dataCancer$Cancer[dataCancer$Cancer == 4] <- 1</pre>
> dataCancer$Cancer <- factor(dataCancer$Cancer, levels = c("0", "1"))</pre>
> dataCancer <- subset(dataCancer, select = -Biopsy)</pre>
> dataCancer <- subset(dataCancer, select = -Citology)</pre>
> dataCancer <- subset(dataCancer, select = -Schiller)</pre>
> dataCancer <- subset(dataCancer, select = -Hinselmann)</pre>
> #DECISION TREE
> library(rpart)
> model1<-rpart(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sexua</pre>
1_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer)
> summary(model1)
Call:
rpart(formula = Cancer ~ Age + First_sexual_intercourse + Smokes +
    Number_of_sexual_partners + Hormonal_Contraceptives + IUD +
    STDs, data = dataCancer)
  n = 737
           CP nsplit rel error xerror xstd
1 0.007894737
Node number 1: 737 observations
  predicted class=0 expected loss=0.1289009 P(node) =1
    class counts:
                     642
                            95
   probabilities: 0.871 0.129
```

```
> x<-dataCancer[,1:12]</pre>
> y<-dataCancer[,23]</pre>
> dataCancer$pred_cart<-predict(model1,x,type="class")</pre>
> mtab<-table(dataCancer$pred_cart,dataCancer$Cancer)</pre>
> confusionMatrix(mtab)
Confusion Matrix and Statistics
      0
          1
         95
  0 642
     0
          0
               Accuracy : 0.8711
                 95% CI: (0.8447, 0.8944)
    No Information Rate: 0.8711
    P-Value [Acc > NIR] : 0.5273
                  Kappa: 0
 Mcnemar's Test P-Value : <2e-16
            Sensitivity: 1.0000
            Specificity: 0.0000
         Pos Pred Value: 0.8711
         Neg Pred Value:
             Prevalence: 0.8711
         Detection Rate: 0.8711
   Detection Prevalence: 1.0000
      Balanced Accuracy: 0.5000
       'Positive' Class: 0
> #NEURAL NETWORK
> library(nnet)
> model2<-nnet(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sexual</pre>
_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer,size = 4.decay
= 0.0001, maxit = 500)
# weights: 37
initial value 506.212925
    10 value 273.377416
    20 value 270.305858
iter
    30 value 267.169796
iter
     40 value 267.098009
iter
     50 value 266.963554
iter
     60 value 266.925369
iter
     70 value 266.907812
iter
iter 80 value 266.854842
final value 266.840591
converged
> summary(model2)
a 7-4-1 network with 37 weights
options were - entropy fitting decay=1e-04
 b->h1 i1->h1 i2->h1 i3->h1 i4->h1 i5->h1 i6->h1 i7->h1
 -0.04
       -3.36 -1.41 -0.08 -0.31 -0.05
                                           -0.18 - 0.04
 b->h2 i1->h2 i2->h2 i3->h2 i4->h2 i5->h2 i6->h2 i7->h2
 0.10 - 1.15 - 0.64
                      0.16 - 0.19
                                     0.07
                                            0.08 - 0.16
 b->h3 i1->h3 i2->h3 i3->h3 i4->h3 i5->h3 i6->h3 i7->h3
 13.18
       7.89 -17.07 27.61 -28.74 22.04 -3.72 -2.16
 b->h4 i1->h4 i2->h4 i3->h4 i4->h4 i5->h4 i6->h4 i7->h4
  0.01 - 0.42 - 0.35
                       0.12
                              0.09 - 0.04 - 0.08
```

```
b->o h1->o h2->o h3->o h4->o
 -2.01
         0.19
               -2.82
                       1.48
                             -0.05
> dataCancer$pred_nnet<-predict(model2,x,type="class")</pre>
> mtab<-table(dataCancer$pred_nnet,dataCancer$Cancer)</pre>
> confusionMatrix(mtab)
> #SVM
> library(kernlab)
> model3<-ksvm(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sexual</pre>
_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer)
> summary(model3)
Length Class
                Mode
         ksvm
                  S4
> dataCancer$pred_svm<-predict(model3,x,type="response")</pre>
> mtab<-table(dataCancer$pred_svm,dataCancer$Cancer)</pre>
> confusionMatrix(mtab)
> #LOGISTIC REGRESSION
> library(VGAM)
> model4<-vqlm(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sexual</pre>
_partners+Hormonal_Contraceptives+IUD+STDs,family = "multinomial",data=dat
aCancer)
> summary(model4)
call:
vglm(formula = Cancer ~ Age + First_sexual_intercourse + Smokes +
    Number_of_sexual_partners + Hormonal_Contraceptives + IUD +
    STDs, family = "multinomial", data = dataCancer)
Pearson residuals:
                      Min
                               1Q Median
                                                  Max
log(mu[,1]/mu[,2]) -3.593 0.3209 0.3445 0.3771 0.889
Coefficients:
                            Estimate Std. Error z value Pr(>|z|)
(Intercept)
                            1.362857
                                       0.803878
                                                  1.695
                                                          0.09001
Age
                           -0.006423
                                       0.014219
                                                 -0.452
                                                          0.65147
First_sexual_intercourse
                           0.045422
                                       0.046617
                                                  0.974
                                                          0.32987
Smokes
                           -0.485906
                                       0.303670
                                                 -1.600
                                                          0.10957
Number_of_sexual_partners 0.080258
                                       0.087716
                                                  0.915
                                                          0.36020
Hormonal_Contraceptives
                           0.009675
                                       0.236581
                                                  0.041
                                                          0.96738
IUD
                           -0.538483
                                       0.331836
                                                 -1.623
                                                          0.10465
                           -0.855076
                                                 -2.734
                                                         0.00626 **
STDS
                                       0.312771
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Name of linear predictor: log(mu[,1]/mu[,2])
Residual deviance: 531.6312 on 699 degrees of freedom
Log-likelihood: -265.8156 on 699 degrees of freedom
Number of Fisher scoring iterations: 5
No Hauck-Donner effect found in any of the estimates
Reference group is level 2 of the response
> probability<-predict(model4,x,type="response")</pre>
```

```
> mtab<-table(dataCancer$pred_log_reg,dataCancer$Cancer)</pre>
> confusionMatrix(mtab)
> #NAIVE BAYES
> model5<-naiveBayes(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_</pre>
sexual_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer,k=5)
> summary(model5)
          Length Class Mode
                  table numeric
apriori
          2
                  -none- list
tables
          7
                  -none- character
-none- logical
levels
          2
isnumeric 7
call
                  -none- call
> dataCancer$pred_naive<-predict(model5,x)</pre>
> mtab<-table(dataCancer$pred_naive.dataCancer$Cancer)</pre>
> confusionMatrix(mtab)
Confusion Matrix and Statistics
      0
          1
  0 581
         74
     61
         21
                Accuracy : 0.8168
                  95% CI: (0.787, 0.8441)
    No Information Rate : 0.8711 P-Value [Acc > NIR] : 1.0000
                   Kappa : 0.1338
 Mcnemar's Test P-Value: 0.3017
            Sensitivity: 0.9050
            Specificity: 0.2211
         Pos Pred Value : 0.8870
         Neg Pred Value: 0.2561
              Prevalence: 0.8711
         Detection Rate: 0.7883
   Detection Prevalence: 0.8887
      Balanced Accuracy: 0.5630
       'Positive' Class: 0
> #KNN
> model6<-knn3(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sexual
_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer,k=5)
> summary(mode16)
          Length Class Mode
                  -none- list
learn
           2
                  -none- numeric
k
           1
                  terms call
-none- list
terms
           3
xlevels
           0
                  -none- list
theDots
           0
na.action 30
                  omit
                         numeric
> dataCancer$pred_knn<-predict(model6,x,type="class")</pre>
> mtab<-table(dataCancer$pred_knn,dataCancer$Cancer)</pre>
> confusionMatrix(mtab)
Confusion Matrix and Statistics
```

> dataCancer\$pred_log_reg<-apply(probability,1,which.max)</pre>

```
0
         1
         74
  0 581
    61
         21
                Accuracy : 0.8168
                  95% CI: (0.787, 0.8441)
    No Information Rate : 0.8711 P-Value [Acc > NIR] : 1.0000
                   Kappa : 0.1338
 Mcnemar's Test P-Value: 0.3017
             Sensitivity: 0.9050
         Specificity: 0.2211
Pos Pred Value: 0.8870
         Neg Pred Value: 0.2561
              Prevalence: 0.8711
         Detection Rate: 0.7883
   Detection Prevalence: 0.8887
      Balanced Accuracy: 0.5630
       'Positive' Class: 0
> library(ipred)
> model7<-bagging(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sex</pre>
ual_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer)
> summary(model7)
attr(,"class")
   class
"sclass"
$00B
[1] FALSE
$comb
[1] FALSE
$call
bagging.data.frame(formula = Cancer ~ Age + First_sexual_intercourse +
    Smokes + Number_of_sexual_partners + Hormonal_Contraceptives +
    IUD + STDs, data = dataCancer)
attr(,"class")
[1] "summary.bagging"
> dataCancer$pred_bagging<-predict(model7,x)</pre>
> mtab<-table(dataCancer$pred_bagging,dataCancer$Cancer)</pre>
> confusionMatrix(mtab)
Confusion Matrix and Statistics
      0
          1
```

0 640 19

Accuracy : 0.9715

95% CI: (0.9568, 0.9823)

No Information Rate: 0.8711 P-Value [Acc > NIR] : < 2.2e-16

Kappa: 0.8626

Mcnemar's Test P-Value: 0.0004803

Sensitivity: 0.9969 Specificity: 0.8000 Pos Pred Value: 0.9712 Neg Pred Value: 0.9744 Prevalence: 0.8711 Detection Rate: 0.8684

Detection Prevalence: 0.8942 Balanced Accuracy: 0.8984

'Positive' Class: 0

> #RANDOM FOREST

- > library(randomForest)
- > mode18<-randomForest(Cancer~Age+First_sexual_intercourse+Smokes+Number_o</pre>

f_sexual_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer)

- > summary(mode18)
- > dataCancer\$pred_randomforest<-predict(model8.x)</pre>
- > mtab<-table(dataCancer\$pred_randomforest,dataCancer\$Cancer)</pre>
- > confusionMatrix(mtab)

Confusion Matrix and Statistics

0 1 0 640 19 2 76

Accuracy: 0.9715 95% CI: (0.9568, 0.9823)

No Information Rate : 0.8711 P-Value [Acc > NIR] : < 2.2e-16

Kappa: 0.8626

Mcnemar's Test P-Value: 0.0004803

Sensitivity: 0.9969 Specificity: 0.8000 Pos Pred Value: 0.9712 Neg Pred Value: 0.9744 Prevalence: 0.8711 Detection Rate: 0.8684

Detection Prevalence: 0.8942 Balanced Accuracy: 0.8984

'Positive' Class: 0

> #BOOSTING

> library(gbm)

```
> model9<-gbm(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sexual_
partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer,distribution="mu
ltinomial")
> summary(mode19)
                                                 var
                                                       rel.inf
                                                 Age 42.716009
First_sexual_intercourse First_sexual_intercourse 15.449944
                                                STDs 10.369832
Number_of_sexual_partners Number_of_sexual_partners 10.180619
Smokes
                                              Smokes 8.195943
                            Hormonal_Contraceptives
Hormonal_Contraceptives
                                                     6.558022
                                                 IUD 6.529631
> probability<-predict(model9,x,n.trees=1)</pre>
> dataCancer$pred_gbm<-colnames(probability)[apply(probability,1,which.max</pre>
> mtab<-table(dataCancer$pred_gbm,dataCancer$Cancer)</pre>
> mtab
      0
         1
  0 642
        95
> confusionMatrix(mtab)
> #ADABOOST
> library(C50)
> model10<-C5.0(Cancer~Age+First_sexual_intercourse+Smokes+Number_of_sexua</pre>
l_partners+Hormonal_Contraceptives+IUD+STDs,data=dataCancer,trials=10)
> summary(model10)
call:
C5.0.formula(formula = Cancer ~ Age + First_sexual_intercourse + Smokes +
Number_of_sexual_partners
 + Hormonal_Contraceptives + IUD + STDs, data = dataCancer, trials = 10)
C5.0 [Release 2.07 GPL Edition]
                                      Wed Mar 27 21:33:39 2019
Class specified by attribute `outcome'
Read 737 cases (8 attributes) from undefined.data
---- Trial 0: ----
Decision tree:
0 (737/95)
---- Trial 1: ----
Decision tree:
0 (737/231.7)
*** boosting reduced to 1 trial since last classifier is very inaccurate
*** boosting abandoned (too few classifiers)
Evaluation on training data (737 cases):
           Decision Tree
```

```
Size
         Errors
   1
      95(12.9%)
```

Time: 0.0 secs

- > dataCancer\$pred_c50<-predict(model10,x)</pre>
- > mtab<-table(dataCancer\$pred_c50,dataCancer\$Cancer)</pre>
- > confusionMatrix(mtab)

Confusion Matrix and Statistics

0 1 0 642 95 0 0

Accuracy : 0.8711 95% CI : (0.8447, 0.8944)

No Information Rate : 0.8711 P-Value [Acc > NIR] : 0.5273

Kappa: 0

Mcnemar's Test P-Value : <2e-16

Sensitivity : 1.0000 Specificity: 0.0000 Pos Pred Value: 0.8711 Neg Pred Value : Prevalence: 0.8711 Detection Rate: 0.8711

Detection Prevalence: 1.0000 Balanced Accuracy: 0.5000

'Positive' Class: 0

PYTHON CODE AND RESULTS:

import numpy as np

import pandas as pd

import matplotlib.pyplot as plt

import scikitplot as skplt

from sklearn.model selection import train test split

from sklearn import preprocessing

from sklearn.preprocessing import Imputer

from pandas.plotting import scatter_matrix

from sklearn import svm

%matplotlib inline

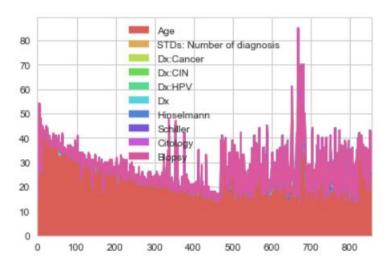
seed = 42

df=pd.read_csv("kag_risk_factors_cervical_cancer.csv")
len(df)

858

df.plot.area()

<matplotlib.axes._subplots.AxesSubplot at 0x123cfcb70>



#Replace ?s with -1 to represent missing values

df=df.replace("?", 0)

imp = Imputer(missing_values="?", strategy='most_frequent', axis=0)

```
# imp.fit(df)
# df = imp.transform(df)
#Split data into training and testing setsy=df["Biopsy"]X=df.drop(["Biopsy"], axis=1)#20% of dataset
goes to test setX_train, X_test, y_train, y_test=train_test_split(X, y, test_size=0.2,
random_state=seed)
#Standardize the data
X_scaled = preprocessing.scale(X_train)
X_scaled.mean()
-1.4389896095932891e-17
X_scaled.std()
0.9561828874675149
#Train the random forest classifier using training data
from sklearn.ensemble import RandomForestClassifier
rfc=RandomForestClassifier(random_state=seed)
rfc.fit(X_train, y_train)
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gini',
      max_depth=None, max_features='auto', max_leaf_nodes=None,
      min_impurity_split=1e-07, min_samples_leaf=1,
      min_samples_split=2, min_weight_fraction_leaf=0.0,
      n_estimators=10, n_jobs=1, oob_score=False, random_state=42,
      verbose=0, warm_start=False)
#Evaluating the classifier using training set
from sklearn.metrics import accuracy_score
y_pred=rfc.predict(X_test)
accuracy_score(y_pred, y_test)
```

0.94186046511627908

#Evaulating which features the classifier finds important for making its decisions

feats = rfc.feature_importances_

#Create new instance of dataframe

feat_importances=pd.DataFrame()

#set columns in datafram to features and their importances

feat_importances["feature"]=X.columns

feat_importances["rfc"]=feats

#Display data

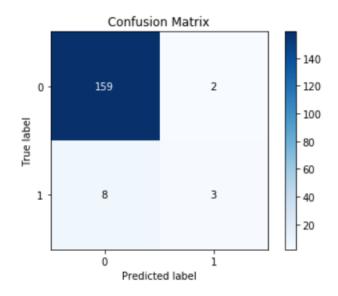
feat_importances

feature	rfc			
0	Age 0.108359			
1	Number of sexual partners 0.043818			
2	First sexual intercourse 0.090490			
3	Num of pregnancies 0.043802			
4	Smokes 0.000732			
5	Smokes (years) 0.0084			
6	Smokes (packs/year) 0.0123			
7	Hormonal Contraceptives 0.01878			
8	Hormonal Contraceptives (years) 0.073255			
9	IUD	0.007286		
10	IUD (years)	0.014674		
11	STDs 0.002097			
12	STDs (number) 0.004735			
13	STDs:condylomatosis 0.002229			

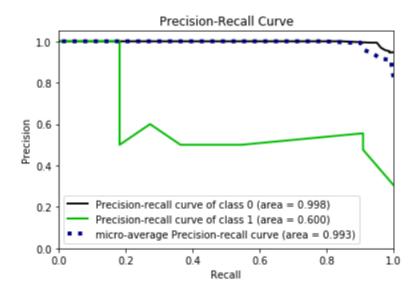
14	STDs:cervical condylomatosis	0.000000		
15	STDs:vaginal condylomatosis 0.000000			
16	STDs:vulvo-perineal condylomatosis 0.005680			
17	STDs:syphilis	0.000113		
18	STDs:pelvic inflammatory disease	0.000000		
19	STDs:genital herpes	0.029498		
20	STDs:molluscum contagiosum	0.000000		
21	STDs:AIDS	0.000000		
22	STDs:HIV 0.005			
23	STDs:Hepatitis B 0.000000			
24	STDs:HPV 0.000068			
25	STDs: Number of diagnosis 0.002572			
26	STDs: Time since first diagnosis 0.01331			
27	STDs: Time since last diagnosis 0.009971			
28	Dx:Cancer 0.003834			

29	Dx:CIN	0.015490
30	Dx:HPV	0.014051
31	Dx	0.015054
32	Hinselmann	0.123566
33	Schiller	0.278592
34	Citology	0.051970

skplt.metrics.plot_confusion_matrix(y_true=y_test, y_pred=y_pred)
plt.show()



 $np.sum(y_test.values==1), np.sum(y_test.values==0) \\ skplt.metrics.plot_precision_recall_curve(y_true=y_test, y_probas=rfc.predict_proba(X_test)) \\ plt.show()$



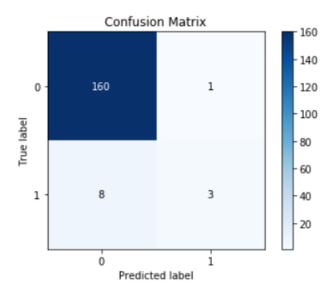
from sklearn.metrics import classification_report print(classification_report(y_test, y_pred))

support	f1-score	recall	precision	
161 11	0.97	0.99	0.95	0
	0.37	0.27	0.60	1
172	0.93	0.94	0.93	avg / total

#Train the random forest classifier using training data from sklearn.ensemble import RandomForestClassifier rfcw=RandomForestClassifier(random_state=seed, class_weight={0:20, 1:0.5}) rfcw.fit(X_train, y_train)

```
rfcw_pred = rfcw.predict(X_test)
print(classification_report(y_test, rfcw_pred))
skplt.metrics.plot_confusion_matrix(y_true=y_test, y_pred=rfcw_pred)
plt.show()
```

support	f1-score	recall	precision	
161 11	0.97 0.40	0.99 0.27	0.95 0.75	0 1
172	0.94	0.95	0.94	avg / total



from sklearn.metrics import accuracy_score
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier, VotingClassifier
from sklearn.neural_network import MLPClassifier
from sklearn.svm import SVC
import numpy as np

```
classifiers = [
   KNeighborsClassifier(3),
   SVC(kernel="linear", C=0.025),
```

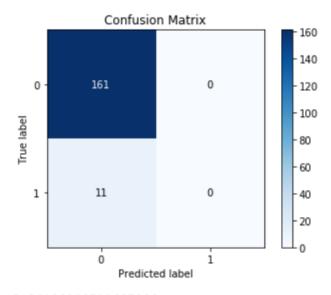
```
SVC(gamma=2, C=1),
  RandomForestClassifier(max_depth=5, n_estimators=10, max_features=1, random_state=42),
  MLPClassifier(alpha=1),
  GradientBoostingClassifier(random_state=42)
 ]
names = ["KNC", "Linear SVC", "SVC", "RFC", "MLP", "GBC"]
clfs = list(zip(classifiers, names))
for clf, n in clfs:
  clf.fit(X_train, y_train)
  preds = np.rint(clf.predict(X_test))
  print(n, accuracy_score(y_test, preds))
vclf = VotingClassifier(estimators=clfs, voting="hard")
KNC 0.93023255814
Linear SVC 0.936046511628
SVC 0.936046511628
RFC 0.941860465116
MLP 0.953488372093
GBC 0.953488372093
from sklearn.decomposition import PCA
from sklearn.gaussian_process.kernels import Product
from itertools import product
pca = PCA(n_components=2)
```

```
pca.fit(X_train)
X_train2d = pca.transform(X_train)
# Plotting decision regions
x_{min}, x_{max} = X_{train2d}[:, 0].min() - 1, X_{train2d}[:, 0].max() + 1
y_min, y_max = X_train2d[:, 1].min() - 1, X_train2d[:, 1].max() + 1
xx, yy = np.meshgrid(np.arange(x_min, x_max, 0.1),
            np.arange(y_min, y_max, 0.1))
f, axarr = plt.subplots(2, 2, sharex='col', sharey='row', figsize=(10, 8))
for idx, clf, tt in zip(product([0, 1], [0, 1]),
              classifiers,
              names):
  clf.fit(X_train2d, y)
  Z = clf.predict(np.c_[xx.ravel(), yy.ravel()])
  Z = Z.reshape(xx.shape)
  axarr[idx[0], idx[1]].contourf(xx, yy, Z, alpha=0.4)
  axarr[idx[0], idx[1]].scatter(X[:, 0], X[:, 1], c=y,
                   s=20, edgecolor='k')
  axarr[idx[0], idx[1]].set_title(tt)
plt.show()
svmc=svm.SVC()
svmc.fit(X_train, y_train)
SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
```

decision_function_shape=None, degree=3, gamma='auto', kernel='rbf', max_iter=-1, probability=False, random_state=None, shrinking=True, tol=0.001, verbose=False)

svmc_pred = svmc.predict(X_test)
print(classification_report(y_test, svmc_pred))
skplt.metrics.plot_confusion_matrix(y_true=y_test, y_pred=svmc_pred)
plt.show()#Evaluating the classifier using training set
from sklearn.metrics import accuracy_score
y_pred=rfc.predict(X_test)
accuracy_score(y_pred, y_test)

support	f1-score	recall	precision	
161	0.97	1.00	0.94	0
11	0.00	0.00	0.00	1
172	0.91	0.94	0.88	avg / total



0.94186046511627908

from sklearn.metrics import accuracy_score
y_pred=rfc.predict(X_test)
accuracy_score(y_pred, y_test)

0.94186046511627908 def make_meshgrid(x, y, h=.02): """Create a mesh of points to plot in **Parameters** x: data to base x-axis meshgrid on y: data to base y-axis meshgrid on h: stepsize for meshgrid, optional Returns xx, yy: ndarray $x_{min}, x_{max} = x.min() - 1, x.max() + 1$ $y_{min}, y_{max} = y.min() - 1, y.max() + 1$ xx, yy = np.meshgrid(np.arange(x_min, x_max, h), np.arange(y_min, y_max, h)) return xx, yy def plot_contours(ax, clf, xx, yy, **params): """Plot the decision boundaries for a classifier. **Parameters**

ax: matplotlib axes object

xx: meshgrid ndarray

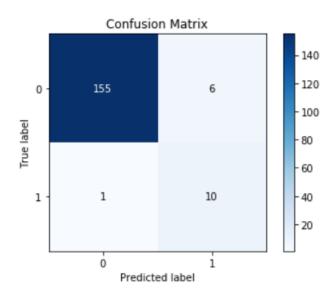
clf: a classifier

```
yy: meshgrid ndarray
  params: dictionary of params to pass to contourf, optional
  Z = clf.predict(np.c_[xx.ravel(), yy.ravel()])
  Z = Z.reshape(xx.shape)
  out = ax.contourf(xx, yy, Z, **params)
  return out
# we create an instance of SVM and fit out data. We do not scale our
# data since we want to plot the support vectors
C = 1.0 # SVM regularization parameter
models = (svm.SVC(kernel='linear', C=C),
     svm.LinearSVC(C=C),
     svm.SVC(kernel='rbf', gamma=0.7, C=C),
     svm.SVC(kernel='poly', degree=3, C=C))
models = (clf.fit(X_train, y_train) for clf in models)
# title for the plots
titles = ('SVC with linear kernel',
     'LinearSVC (linear kernel)',
     'SVC with RBF kernel',
     'SVC with polynomial (degree 3) kernel')
# Set-up 2x2 grid for plotting.
fig, sub = plt.subplots(2, 2)
plt.subplots_adjust(wspace=0.4, hspace=0.4)
X0, X1 = X_train[:, 0], X_train[:, 1]
xx, yy = make_meshgrid(X0, X1)
```

```
for clf, title, ax in zip(models, titles, sub.flatten()):
  plot_contours(ax, clf, xx, yy,
         cmap=plt.cm.coolwarm, alpha=0.8)
  ax.scatter(X0, X1, c=y_test, cmap=plt.cm.coolwarm, s=20, edgecolors='k')
  ax.set_xlim(xx.min(), xx.max())
  ax.set_ylim(yy.min(), yy.max())
  ax.set_xlabel('Sepal length')
  ax.set_ylabel('Sepal width')
  ax.set_xticks(())
  ax.set_yticks(())
  ax.set_title(title)
plt.show()
from sklearn.ensemble import GradientBoostingClassifier
gbc = GradientBoostingClassifier(max_depth=1)
gbc.fit(X_train, y_train)
GradientBoostingClassifier(criterion='friedman_mse', init=None,
       learning_rate=0.1, loss='deviance', max_depth=1,
       max_features=None, max_leaf_nodes=None,
       min_impurity_split=1e-07, min_samples_leaf=1,
       min_samples_split=2, min_weight_fraction_leaf=0.0,
       n_estimators=100, presort='auto', random_state=None,
       subsample=1.0, verbose=0, warm_start=False)
from sklearn.metrics import accuracy_score
gbcy_pred=gbc.predict(X_test)
accuracy_score(gbcy_pred, y_test)
```

0.95930232558139539

skplt.metrics.plot_confusion_matrix(y_true=y_test, y_pred=gbcy_pred)
plt.show()

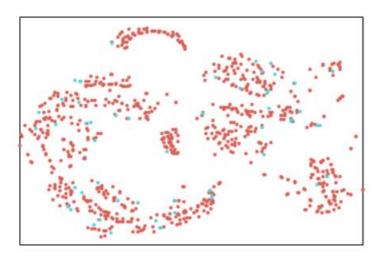


from sklearn import datasets

import hypertools as hyp

hyp.plot(X, '.', reduce='TSNE', group=y, ndims=2)

hyp.plot(X, '.', reduce='TSNE', n_clusters=10, ndims=2)



DATASET: CHRONIC KIDNEY DISEASE

RCODE AND RESULTS:

PYTHON CODE AND RESULTS:

import pandas as pd
import numpy as np
from IPython.display import display
from scipy.stats import mode
import matplotlib.pyplot as plt

csv_file = "/content/kidney_disease.csv"
data = pd.read_csv(csv_file)

#No of people with chronic kidney disease
n_ckd = len(data[data['classification']=='ckd'])

#No of people without chronic kidney disease
n_notckd = len(data[data['classification']=='notckd'])

```
#Filling missing value with most frequent for nominal and median for numerical
```

```
X = pd.DataFrame(data)
fill = pd.Series([X[c].value_counts().index[0]
    if X[c].dtype == np.dtype('O') else X[c].median() for c in X],
    index=X.columns)
new_data=X.fillna(fill)
from sklearn import preprocessing
le = preprocessing.LabelEncoder()
data=new_data.copy()
for items in data:
  if data[items].dtype == np.dtype('O'):
    data[items]=le.fit_transform(data[items])
from sklearn.preprocessing import StandardScaler, RobustScaler
target_class = data['classification']
features = data.drop('classification', axis = 1)
data_robust = pd.DataFrame(RobustScaler().fit_transform(features), columns=features.columns)
from sklearn.decomposition import PCA
pca = PCA()
data_pca = pd.DataFrame(pca.fit_transform(data_robust), columns=data_robust.columns)
pca = PCA(n_components=11)
pca.fit(data_robust)
reduced_data = pca.transform(data_robust)
reduced data = pd.DataFrame(reduced data, columns =
['dim1','dim2','dim3','dim4','dim5','dim6','dim7','dim8','dim9','dim10','dim11'])
from sklearn.model_selection import train_test_split
XTrain, XTest, yTrain, yTest = train_test_split(reduced_data,target_class, test_size=0.25,
random_state=42)
from sklearn.metrics import confusion_matrix, accuracy_score,r2_score,mean_squared_error
from sklearn import tree
```

```
from sklearn import linear_model
from sklearn import svm
from sklearn.neural_network import MLPClassifier
from sklearn.naive_bayes import MultinomialNB
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import BaggingClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.ensemble import AdaBoostClassifier
```

#Logistic Regression from sklearn.linear_model import LogisticRegression classifier = LogisticRegression() classifier.fit(XTrain,yTrain) yPred = classifier.predict(XTest) cm = confusion_matrix(yTest,yPred) accuracy = accuracy_score(yTest,yPred) r2 = r2_score(yTest,yPred) rmse = mean_squared_error(yTest,yPred) print"Logistic Regression:" print"Accuracy = ", accuracy print"R2 = ",r2 print"RMSE = ",rmse print cm

Output:

```
Logistic Regression :
```

```
Accuracy = 0.99
R2 = 0.9560439560439561
RMSE = 0.04
[[64 1]
 [ 0 35]]
K Nearest Neighbors
#K Nearest Neighbors
from sklearn.neighbors import KNeighborsClassifier
classifier = KNeighborsClassifier(n_neighbors=5, p=2,
metric='minkowski')
classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion_matrix(yTest,yPred)
accuracy = accuracy score(yTest,yPred)
print"K Nearest Neighbors :"
print"Accuracy = ", accuracy
print cm
output:
K Nearest Neighbors :
Accuracy = 0.97
[[62 3]
 [ 0 35]]
Support Vector Machine
#Support Vector Machine
from sklearn.svm import SVC
classifier = SVC(kernel='linear', random state=0)
classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
```

```
cm = confusion matrix(yTest,yPred)
accuracy = accuracy score(yTest,yPred)
print "Support Vector Machine :"
print "Accuracy = ", accuracy
print cm
Support Vector Machine :
Accuracy = 1.0
[[65 0]
 [ 0 35]]
Gaussian Naive Bayes
#Gaussian Naive Bayes
from sklearn.naive bayes import GaussianNB
classifier = GaussianNB()
classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion_matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print"Gaussian Naive Bayes :"
print"Accuracy = ", accuracy
print cm
Output:
Gaussian Naive Bayes :
Accuracy = 0.96
[[61 4]
 [ 0 35]]
Decision Tree Classifier
#Decision Tree Classifier
```

```
from sklearn.tree import DecisionTreeClassifier as DT
classifier = DT(criterion='entropy', random state=0)
classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
accuracy = accuracy score(yTest,yPred)
print "Decision Tree Classifier :"
print "Accuracy = ", accuracy
print cm
Decision Tree Classifier :
Accuracy = 0.93
[[63 2]
 [ 5 30]]
#Random Forest Classifier
from sklearn.ensemble import RandomForestClassifier as RF
classifier = RF(n estimators=10, criterion='entropy', random state=0)
classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print"Random Forest Classifier :"
print"Accuracy = ", accuracy
print cm
Output:
Random Forest Classifier :
Accuracy = 0.97
[[64 1]
 [ 2 33]]
Artificial Neural Network
```

```
classifier.set params(hidden layer sizes = (100,100), max iter =
1000, alpha = 0.01, momentum = 0.7)
classifier = classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
accuracy = accuracy score(yTest,yPred)
r2 = r2 score(yTest,yPred)
rmse = mean squared error(yTest,yPred)
print"Artificial Neural Network :"
print"Accuracy = ", accuracy
print"R2 = ",r2
print"RMSE = ",rmse
print cm
Output:
Artificial Neural Network:
Accuracy = 1.0
R2 = 1.0
RMSE = 0.0
[[65 0]
 [ 0 35]]
Bagging
classifier = BaggingClassifier()
#classifier.set params(n estimators = 30,max samples = 1000)
classifier = classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
r2 = r2 score(yTest,yPred)
rmse = mean squared error(yTest,yPred)
accuracy = accuracy score(yTest,yPred)
```

classifier = MLPClassifier()

```
print"Bagging :"
print"Accuracy = ", accuracy
print"R2 = ",r2
print"RMSE = ",rmse
print cm
Output:
Bagging :
Accuracy = 0.94
R2 = 0.7362637362637362
RMSE = 0.24
[[64 1]
[ 5 30]]
Gradient Boosting
classifier = GradientBoostingClassifier()
classifier.set_params(n_estimators = 30,learning_rate = 1)
classifier = classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
r2 = r2_score(yTest, yPred)
rmse = mean_squared_error(yTest,yPred)
accuracy = accuracy_score(yTest,yPred)
print"Gradient Boosting :"
print"Accuracy = ", accuracy
print"R2 = ",r2
print"RMSE = ",rmse
print cm
Output:
Gradient Boosting :
```

```
Accuracy = 0.96
R2 = 0.8241758241758241
RMSE = 0.16
[[64 1]
[ 3 32]]
AdaBoost
classifier = AdaBoostClassifier()
classifier.set params(n estimators = 10, learning rate = 1)
classifier = classifier.fit(XTrain,yTrain)
yPred = classifier.predict(XTest)
cm = confusion matrix(yTest,yPred)
r2 = r2_score(yTest,yPred)
rmse = mean squared error(yTest,yPred)
accuracy = accuracy score(yTest,yPred)
print"AdaBoost :"
print"Accuracy = ", accuracy
print"R2 = ",r2
print"RMSE = ",rmse
print cm
Output:
AdaBoost :
Accuracy = 0.82
R2 = 0.20879120879120872
RMSE = 0.72
[[65 0]
 [18 17]]
```