ARIGNAR ANNA GOVERNMENT ARTS COLLEGE

VILLUPURAM – 605 602.

DEPARTMENT OF COMPUTER SCIENCE

MACHINE LEARNING WITH PYTHON

**Project Title : ** A Review of Liver Patient Analysis Method using Machine Learning

Team Id :NM2023TMID16681

Team Leader : S.NIVETHA (456B7FA8E1DF64BAAAF409B60C859E49)

Team member: R.NANDHINI(A4FE1E4B1494C8680794BB7E25825C7F)

Team member: P.PARKAVI (209B8E712944981821243F63515DAF4D)

Team member: R.RAJALAKSHMI

(1D2C5EF7695F664A3974153C3F6073D8)

Team member: R.USHA(E378DAD22E1725ABC0340FBD1E504270)

Abstract

Around a million deaths occur due to liver diseases globally.

There are several traditional methods to diagnose liver diseases, but they are expensive. Early prediction of liver disease would

benefit all individuals prone to liver diseases by providing early treatment. As technology is growing in health care, machine learning significantly affects health care for predicting conditions at early stages. This study finds how accurate machine learning is in predicting liver disease.

This present study introduces the liver disease prediction (LDP) method in predicting liver disease that can be utilised by health professionals, stakeholders, students and researchers. Five algorithms, namely Support Vector Machine (SVM), Naïve Bayes, K-Nearest Neighbors (K-NN), Linear Discriminant Analysis (LDA), and Classification and Regression Trees (CART), are selected. The accuracy is compared to uncover the best classification method for predicting liver disease using R and Python. From the results, K-NN obtains the best accuracy with 91.7%, and the autoencoder network achieved 92.1% accuracy, which is above the acceptable level of accuracy and can be considered for liver disease prediction.

Introduction

In this project we will analyse the parameters of various classification algorithms and compare their predictive accuracies so as to find out the best classifier for determining the liver disease. This project compares various classification algorithms such as Random Forest, Logistic Regression, KNN and ANN Algorithm with an aim to identify the best technique. Based on this study, Random Forest with the highest accuracy outperformed the other algorithms and can be further utilised in the prediction of liver disease and can be recommended to the Liver.According to World Health Organization

(WHO) report in 2018, the number of deaths due to liver diseases is around one million and ranked 11th in the world with a critical number of fatalities (World Total Deaths, n.d.). Unnoticed at the initial stages, these symptoms are only visible when the disease turns chronic. However, even though the liver is partially infected, it can still function (Devikanniga et al., 2020).

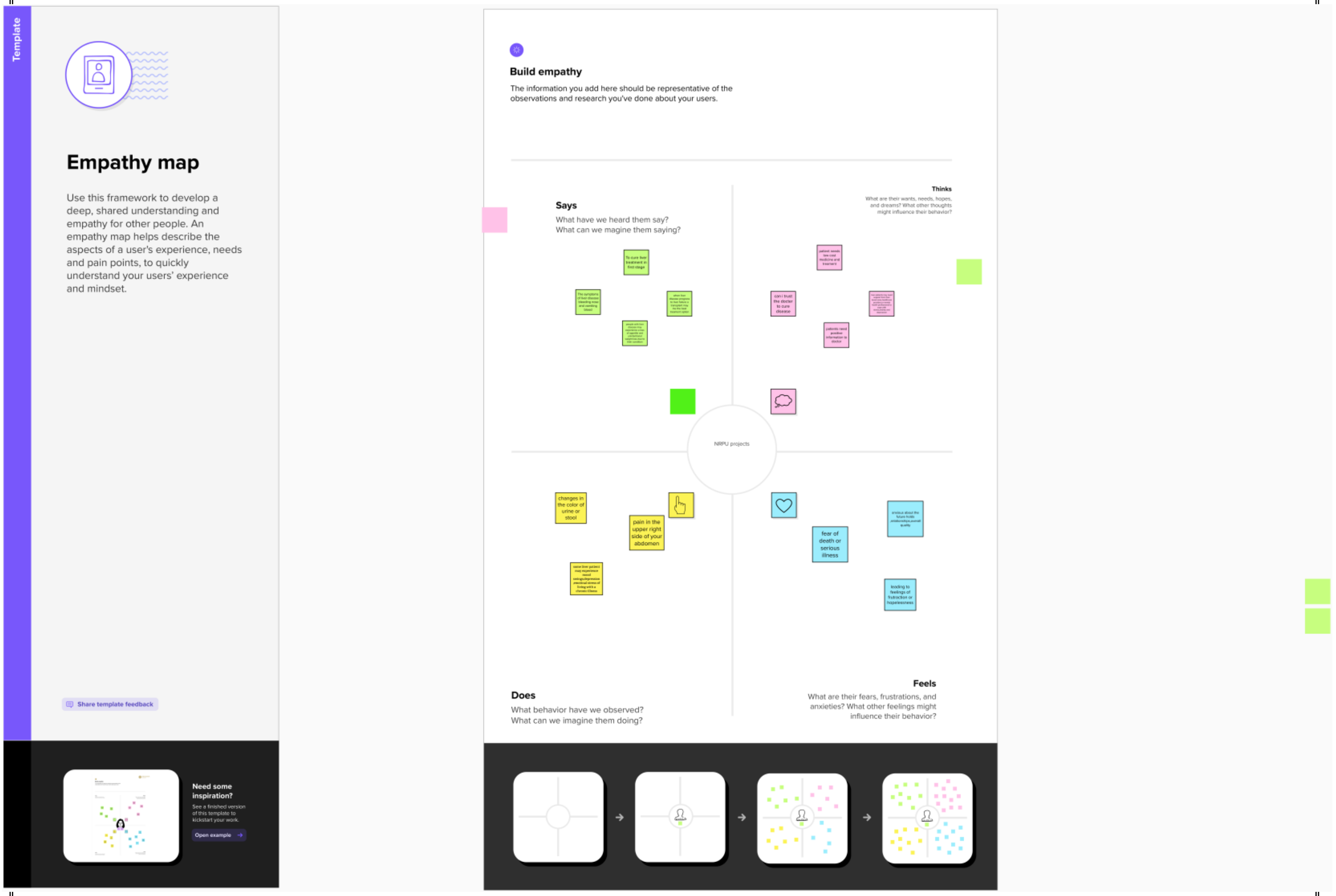
Diagnosis of liver diseases can be divided into three stages i.e., the first stage is liver inflammation, the second is liver scarring (cirrhosis), and the final stage is liver cancer or failure. Since these scenarios are present in liver disease, early prediction is significant to provide better health for New Zealanders. If liver disease is diagnosed early, there will be a chance of early treatment and control of deaths due to liver diseases (Arbain & Balakrishnan, 2019). But when the liver fails to function, few treatments are available except liver transplantation (Shaheamlung et al., 2020), which is very expensive, particularly in New Zealand (Hepatitis C, 2021). Apparently, in New Zealand, 35 - 40% of the population are not diagnosed with Hepatitis C at the early stages because of the asymptomatic behaviour of liver disease. Unfortunately, most of these individuals do not know the risks linked to liver disease. Due to the asymptomatic behaviour and higher costs of liver disease treatment, it is essential to prevent or diagnose early for better treatment.

Purpose

Liver function tests can be used to: Screen for liver infections, such as hepatitis. Monitor the progression of a disease, such as viral or alcoholic hepatitis, and determine how well a treatment is working. Measure the severity of a disease, particularly scarring of the liver (cirrhosis)

Problem Definetion & Design Thinking

Empathy map



Template

Empathy map

Use this framework to develop a deep, shared understanding and empathy for other people. An empathy map helps describe the aspects of a user's experience, needs and pain points, to quickly understand your users' experience and mindset.

Share template feedback

Need some inspiration?

See a finished version of this template to kickstart your work.

Open example

Build empathy

The information you add here should be representative of the observations and research you've done about your users.

Says

What have we heard them say?
What can we magine them saying?

To cure liver treatment in first stage

The symptoms of liver disease (bleeding nose and vomiting blood)

when liver disease progress to liver failure a transplant may be the best treatment option

people with liver disease may experience a loss of appetite and unintentional weight loss due to their condition

Thinks

What are their wants, needs, hopes, and dreams? What other thoughts might influence their behavior?

patient needs low cost medicine and treatment

can i trust the doctor to cure disease

[illegible]

patients need positive information to doctor

NRPU projects

changes in the color of urine or stool

pain in the upper right side of your abdomen

some liver patient may experience mood swings/depression ,emotional stress of living with a chronic illness

Does

What behavior have we observed?
What can we imagine them doing?

fear of death or serious illness

anxious about the future holds ,relationships,overall quality

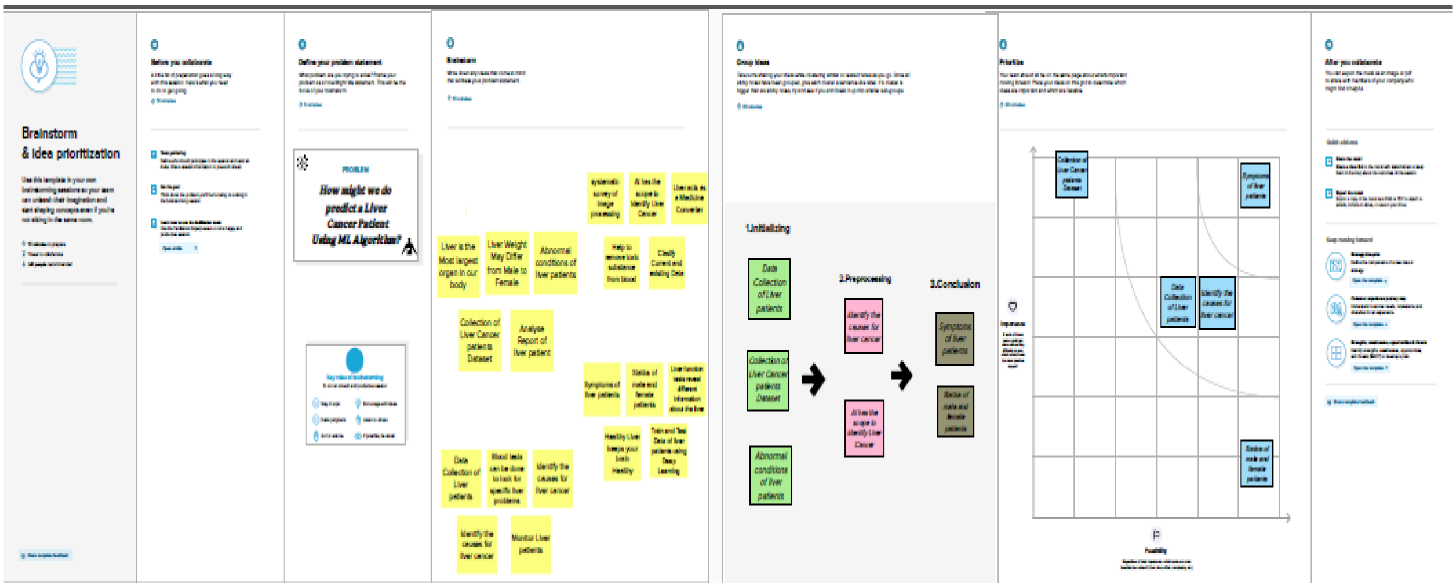
leading to feelings of frustraction or hopelessness

Feels

What are their fears, frustrations, and anxieties? What other feelings might influence their behavior?

Ideation & brainstorming map

BRAIN STORM AND IDEA PRIORITIZATION



Brainstorm & idea prioritization
PROBLEM
How might we do predict a Liver Cancer Patient Using ML Algorithm?
Liver is the Most largest organ in our body
Liver Weight May Differ from Male to Female
Abnormal conditions of liver patients
Collection of Liver Cancer patients Dataset
Analyse Report of liver patient
Data Collection of Liver patients
Identify the causes for liver cancer
Monitor Liver patients
1.Initializing
2.Preprocessing
3.Conclusion
Symptoms of liver patients
Status of male and female patients
Feasibility
Importance

Result :

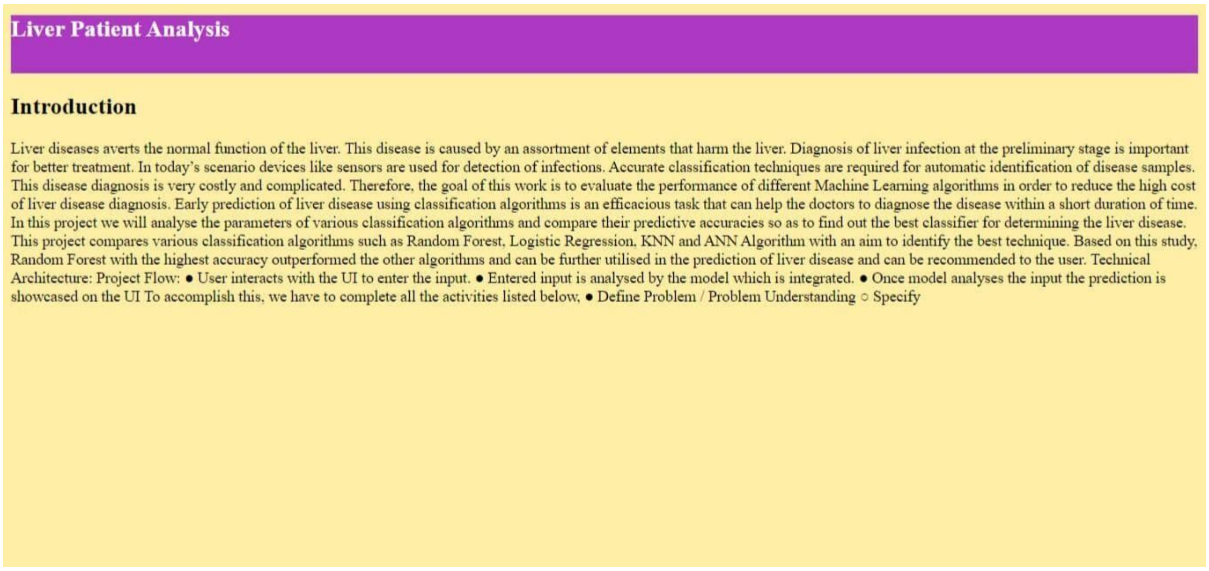
Liver Patients analysis using machine learning can provide accurate and realiable results for the diagnosis, prognosis, and treatment of liver disease. Machine learning algorithm can analyse large amounts of patients data and identify patterns that may be difficult for human experts to detect.

Home.html Source code

```
<!DOCTYPE html>

<html lang="en">

<head>

<title>Bootstrap Example</title>
```

```
<meta charset="utf-8">

<meta name="viewport" content="width=device-width,initial-scale=1">

<link rel="stylesheet" href="https://maxcdn.bootstrapcdn.com/bootstrap/3.4.1/css/bootstrap.min.css">

<style type="text/css">

 body{

 background-color:#ffcf0059;

}

nav{
 background-color:#ad38c2;
 height:60px;
 }
.navbar-brand{
color:white
}
</style>
</head>
<body>


<nav class="navbar">
<div class="containe-field">
<div class="navbar-header">


<a class="navbar-brand"><h1>Liver Patient Analysis</h1></a></nav>
</div>


  <h2>Introduction</h2>


  <p>Liver diseases averts the normal function of the liver. This disease is caused by an assortment of
elements
  that harm the liver. Diagnosis of liver infection at the preliminary stage is important for better treatment.
In
  today’s scenario devices like sensors are used for detection of infections. Accurate classification
  techniques are required for automatic identification of disease samples. This disease diagnosis is very
  costly and complicated. Therefore, the goal of this work is to evaluate the performance of different
Machine
  Learning algorithms in order to reduce the high cost of liver disease diagnosis. Early prediction of liver
  disease using classification algorithms is an efficacious task that can help the doctors to diagnose the
  disease within a short duration of time. In this project we will analyse the parameters of various
  classification algorithms and compare their predictive accuracies so as to find out the best classifier for

  determining the liver disease. This project compares various classification algorithms such as Random

  Forest, Logistic Regression, KNN and ANN Algorithm with an aim to identify the best technique. Based on

  this study, Random Forest with the highest accuracy outperformed the other algorithms and can be
further

  utilised in the prediction of liver disease and can be recommended to the user.

  Technical Architecture:

  Project Flow:

  ● User interacts with the UI to enter the input.

  ● Entered input is analysed by the model which is integrated.

  ● Once model analyses the input the prediction is showcased on the UI

  To accomplish this, we have to complete all the activities listed below,

  ● Define Problem / Problem Understanding

  ○ Specify

</p>

 </div>

 </html>
```

Output :



Liver Patient Analysis

Introduction

Liver diseases averts the normal function of the liver. This disease is caused by an assortment of elements that harm the liver. Diagnosis of liver infection at the preliminary stage is important for better treatment. In today's scenario devices like sensors are used for detection of infections. Accurate classification techniques are required for automatic identification of disease samples. This disease diagnosis is very costly and complicated. Therefore, the goal of this work is to evaluate the performance of different Machine Learning algorithms in order to reduce the high cost of liver disease diagnosis. Early prediction of liver disease using classification algorithms is an efficacious task that can help the doctors to diagnose the disease within a short duration of time. In this project we will analyse the parameters of various classification algorithms and compare their predictive accuracies so as to find out the best classifier for determining the liver disease. This project compares various classification algorithms such as Random Forest, Logistic Regression, KNN and ANN Algorithm with an aim to identify the best technique. Based on this study, Random Forest with the highest accuracy outperformed the other algorithms and can be further utilised in the prediction of liver disease and can be recommended to the user. Technical Architecture: Project Flow: ● User interacts with the UI to enter the input. ● Entered input is analysed by the model which is integrated. ● Once model analyses the input the prediction is showcased on the UI To accomplish this, we have to complete all the activities listed below, ● Define Problem / Problem Understanding ○ Specify

Index.html Source code

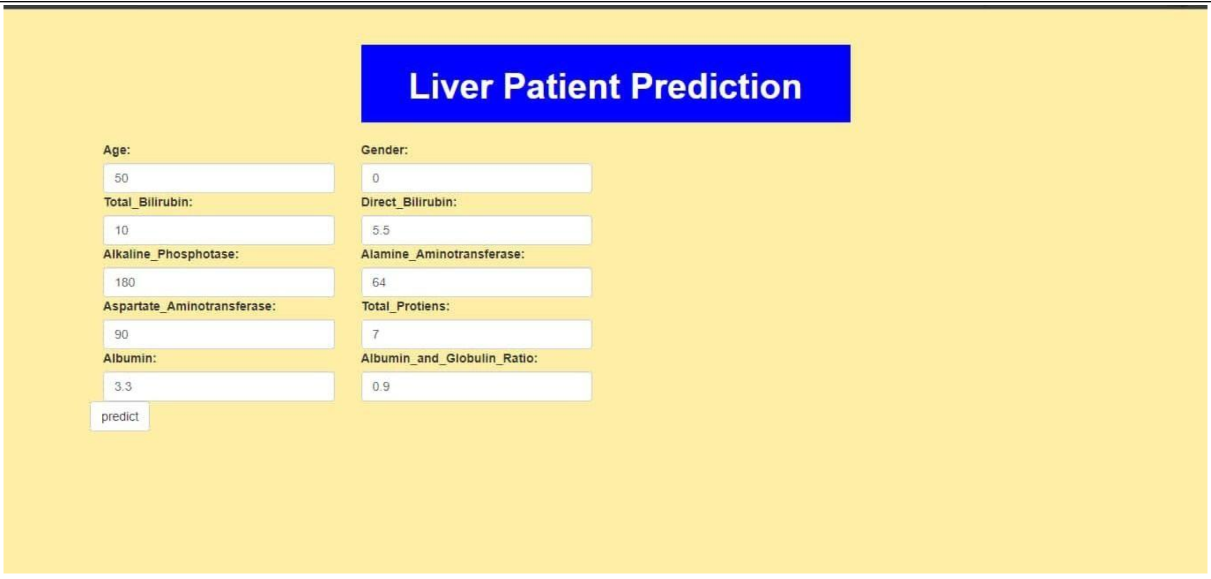
```
<!DOCTYPE html>

<html>

<head>

<title>Liver Patient Analysis</title>

<!-- Latest Compiled and minified CSS -->

<Link rel="stylesheet" href="https://maxcdn.bootstrapcdn.com/bootstrap/3.3.7/css/bootstrap.min.css">

<style type="text/css">

body{

  background-color: #ffcf0059;

    }

.page-header{

  background-color: blue;

  width: 100%;

  height: auto;

  text-align: center;

  padding-top: 5px;

  color: #fff

 }

 h1{

    font-size: 40px;

    font-weight: bold;

    }

</style>

</head>

</body>

    <div class="container">

    <div class="row">

    <div class="col-md-3"></div>

    <div class="col-md-6">
```

```
<div class="page-header">
<h1>Liver Patient Prediction</h1>
</div>
</div>
</div>
</div>
  <div class="container">
  <div class="row">
  <div class="col-mid-3"></div>
  <div class="col-md-6">
  <form action="/data_predict" method="post">
  <div class="row">
  <div class="col-md-6">
  <div class="form-gorup">
  <label for="Age">Age:</label>
  <input type="text" class="form-control" id="age" name="age">
  </div>
 </div>
  <div class="col-md-6">
  <div class="form-gorup">
  <label for="gender">Gender:</label>
  <input type="text" class="form-control" id="gender" name="gender">
  </div>
  </div>
  <div class="col-md-6">
  <div class="form-gorup">
  <label for="tb">Total_Bilirubin:</label>
  <input type="text" class="form-control" id="tb" name="tb">
  </div>
  </div>
```

```html
</div>
<div class="col-md-6">
<div class="form-gorup">
<label for="db">Direct_Bilirubin:</label>
<input type="text" class="form-control" id="db" name="db">
</div>
</div>
<div class="col-md-6">
<div class="form-gorup">
<label for="ap">Alkaline_Phosphotase:</label>
<input type="text" class="form-control" id="ap" name="ap">
</div>
</div>
<div class="col-md-6">
<div class="form-gorup">
<label for="aa1">Alamine_Aminotransferase:</label>
<input type="text" class="form-control" id="aa1" name="aa1">
</div>
</div>
<div class="col-md-6">
<div class="form-gorup">
<label for="aa2">Aspartate_Aminotransferase:</label>
<input type="text" class="form-control" id="aa2" name="aa2">
</div>
</div>
<div class="col-md-6">
<div class="form-gorup">
<label for="tp">Total_Protiens:</label>
<input type="text" class="form-control" id="tp" name="tp">
</div>
```

```
</div>

<div class="col-md-6">

<div class="form-gorup">

<label for="a">Albumin:</label>

<input type="text" class="form-control" id="a" name="a">

</div>

</div>

<div class="col-md-6">

<div class="form-gorup">

<label for="agr">Albumin_and_Globulin_Ratio:</label>

<input type="text" class="form-control" id="agr" name="agr">

</div>

<button type="submit" class="btn btn-default" > predict</button>

</form>

</div>

</div>

</div>

<!-- Latest Compiled and minified javascript -->

<script src="https://maxcdn.bootstrapcdn.com/bootstrap/3.3.7/js/bootstrap.min.js"></script>

</body>

</html>
```

Output :


Liver Patient Prediction

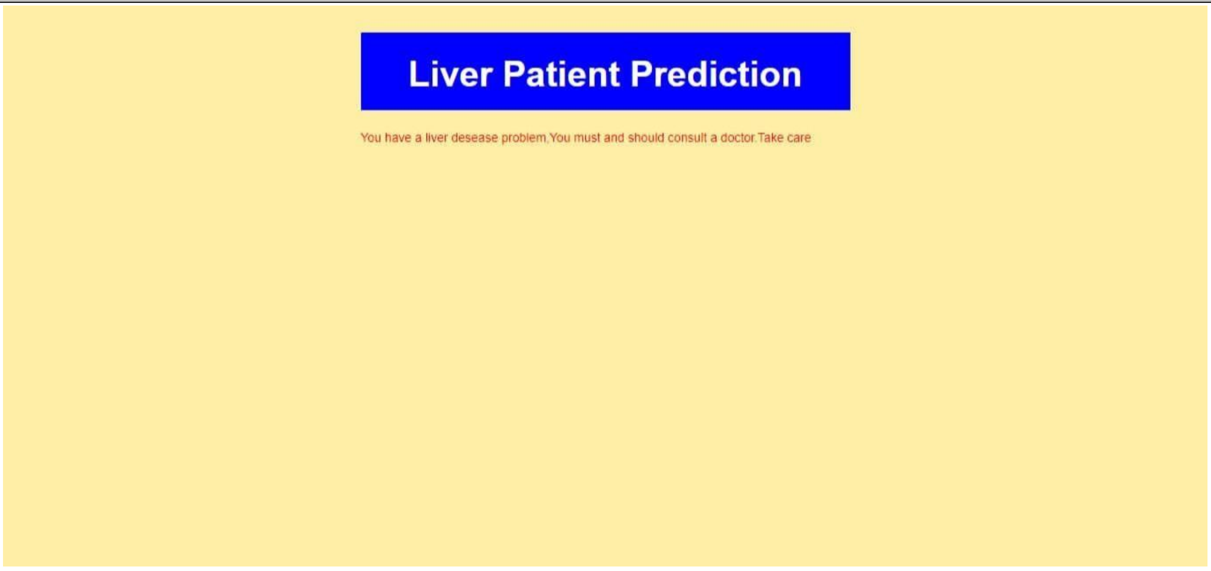
Age: 50
Gender: 0
Total_Bilirubin: 10
Direct_Bilirubin: 5.5
Alkaline_Phosphotase: 180
Alamine_Aminotransferase: 64
Aspartate_Aminotransferase: 90
Total_Protiens: 7
Albumin: 3.3
Albumin_and_Globulin_Ratio: 0.9

<u>No chance.html source code</u>

```
<!DOCTYPE html>

<html>

<head>

  <title>Liver Patient Analysis</title>

  <!-- Latest Compiled and minified CSS -->

  <Link rel="stylesheet" href="https://maxcdn.bootstrapcdn.com/bootstrap/3.3.7/css/bootstrap.min.css">



  <style type="text/css">

    body{

      background-color: #ffcf0059;

    }

    .page-header{

      background-color: blue;

      width: 100%;

      height: auto;

      text-align: center;

      padding-top: 5px;
```

```
        color: #fff;

          }

          h1{

        font-size: 40px;

        font-weight: bold;

     }

  </style>

  </head>

  </body>



    <div class="container">

    <div class="row">

    <div class="col-md-3"></div>

    <div class="col-md-6">

    <div class="page-header">

     <h1>Liver Patient Prediction</h1></div>

    <p style="color:red;">

     You have a liver desease problem,You must and should consult a doctor.Take care</h3></p>

     </style>

     </div>

     </div>

     </div>

    </div>

  <!-- Latest Compiled and minified javascript -->

  <script src="https://maxcdn.bootstrapcdn.com/bootstrap/3.3.7/js/bootstrap.min.js"></script>

</html>
```

Output:


Liver Patient Prediction

You have a liver desease problem,You must and should consult a doctor.Take care

Advantages

General

Diagnoses, grades and stages:

Hepatitis C

Hepatitis B

Steatohepatitis

Autoimmune hepatitis

Evalutes abnormal liver function tests

Identifies hepatotoxicity

Clarifies uncertain diagnoses

Confirms etiology of liver masses

Defines extent of necroinflammatory activity

Differentiates fiabrosis from cirrhosis

Liver transplant

Identifies acute cellular rejection

Defines recurrence of original disease

Identifies progressive fibrosis

Diagnoses other liver processes.

Disadvantage

General

Invasive

Accessibility to the procedure

Need for training

Cost

Sample

Sampling error

Intraobserver and interobserver variations in

Interpretatooin

Specimen length and width

Patient

Site pain

Shoulder pain

Neuralgia

Hypotension

Bleeding

Hemothorax

Hemoblilia

Application :

- Diagnosis: Liver patients analysis can be used to diagnose liver diseases such as cirrhosis, hepatitis, and Livercancer,by analysing various biomarkers such as liver enyzmes, bilirubin, and albumin, doctors can determine the health of the liver and diagnose any underlying diseases.

- Treatment: Liver patients analysis can also to monitor the effectiveness of treatmentsfor liver diseases. By regulary analysing liver function tests and other biomarkers, doctors can achieve optimal results

Conclusion

- pertinent Since the liver disease is not easy to diagnose, given the delicate nature of its signs, this research is in determining the algorithms that have better accuracy in predicting this dreadful disease.
- Once the dataset is selected, the preprocessing step is conducted by replacing the missing values and balancing the dataset.

- After that, using R, five different supervised learning methods are applied (i.e., SVM, Naïve Bayes, K-NN, LDA, and CART), and the accuracy with confusion matrix metrics are recorded.

- In this study, the autoencoder with 3-layers achieved an accuracy of 92.1%, slightly higher than K-NN due to its ability to ascertain overlapping features better than conventional K-NNs. Most of the algorithms are more than the acceptable level of accuracy, which is 75%.

- The results from this study would be able to assist health professionals and relevant stakeholders in the early detection of liver disease.

Future scope

- In this paper ,we proposed and built a machine learning based on a hybrid classifier to be used as a classification model for liver diseases diagnosis to improve performance and experrts to identify the chances of disease and conscious orescription of further treatment healthcare and examination .

- In future work, the use of fast datasets technique like apache hadoop or spark can be incorporated with this technique. In addition to this, we can use distributed refined algorithm like forest tree implement in apache hadoop to increase scalability and efficieny.

Appenix

Source code

Mliestone 2:

```
import pandas as pd
import numpy as np

import seaborn as sns

import matplotlib.pyplot as plt

from matplotlib import rcParams

from scipy import stats

import warnings

warnings.filterwarnings('ignore')

from sklearn.tree import DecisionTreeClassifier

from sklearn.ensemble import RandomForestClassifier

from sklearn.model_selection import train_test_split

from sklearn.metrics import classification_report,confusion_matrix


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

data.head()
```

```
data.info()

<class 'pandas.core.frame.DataFrame'>

RangeIndex: 583 entries, 0 to 582

Data columns (total 11 columns):

 #    Column                      Non-Null Count       Dtype

---   -------                      ----------------     ------

 0    Age                          583 non-null         int64

 1    Gender                       583 non-null         object

 2    Total_Bilirubin              583 non-null         float64

 3    Direct_Bilirubin             583 non-null         float64

 4    Alkaline_Phosphotase         583 non-null         int64
 5    Alamine_Aminotransferase          583 non-null             int64
 6    Aspartate_Aminotransferase        583 non-null             int64
 7    Total_Protiens                    583 non-null             float64
 8    Albumin                           583 non-null             float64
 9    Albumin_and_Globulin_Ratio        579 non-null             float64
 10   Dataset                           583 non-null             int64
dtypes: float64(5), int64(5), object(1)
memory usage: 50.2+ KB
```

```
data.isnull().any()
Age                           False
Gender                        False
Total_Bilirubin               False
Direct_Bilirubin              False
Alkaline_Phosphotase          False
Alamine_Aminotransferase      False
Aspartate_Aminotransferase    False
Total_Protiens                False
Albumin                       False
Albumin_and_Globulin_Ratio    True
Dataset                       False
dtype: bool
```

```
data.isnull().sum()
Age                           0
Gender                        0
Total_Bilirubin               0
Direct_Bilirubin              0
Alkaline_Phosphotase          0
Alamine_Aminotransferase      0
```

```
Aspartate_Aminotransferase          0
Total_Protiens                      0
Albumin                             0
Albumin_and_Globulin_Ratio          4
Dataset                             0
dtype: int64
```

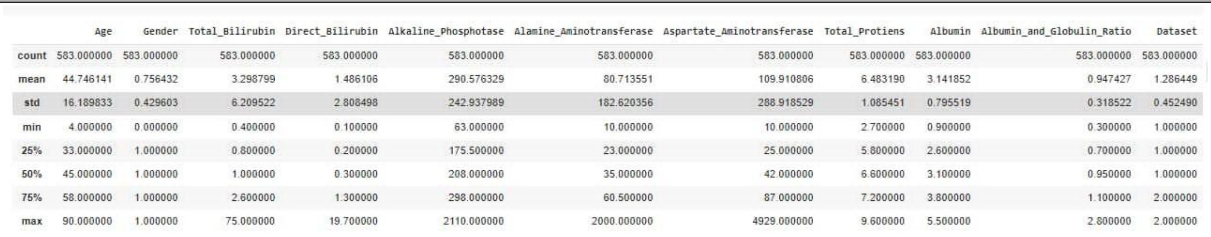
```
data['Albumin_and_Globulin_Ratio'] =
data['Albumin_and_Globulin_Ratio'].fillna(data['Albumin_and_Globulin_Ratio'].mode()[0])
data.isnull().sum()
```

```
Age                                 0
Gender                              0
Total_Bilirubin                     0
Direct_Bilirubin                    0
Alkaline_Phosphotase                0
Alamine_Aminotransferase            0
Aspartate_Aminotransferase          0
Total_Protiens                      0
Albumin                             0
Albumin_and_Globulin_Ratio          0
Dataset                             0
dtype: int64
```

```
from sklearn.preprocessing import LabelEncoder
lc = LabelEncoder()
data['Gender'] = lc.fit_transform(data['Gender'])
```

<u>Milestone 3:</u>

```
data.describe()
```

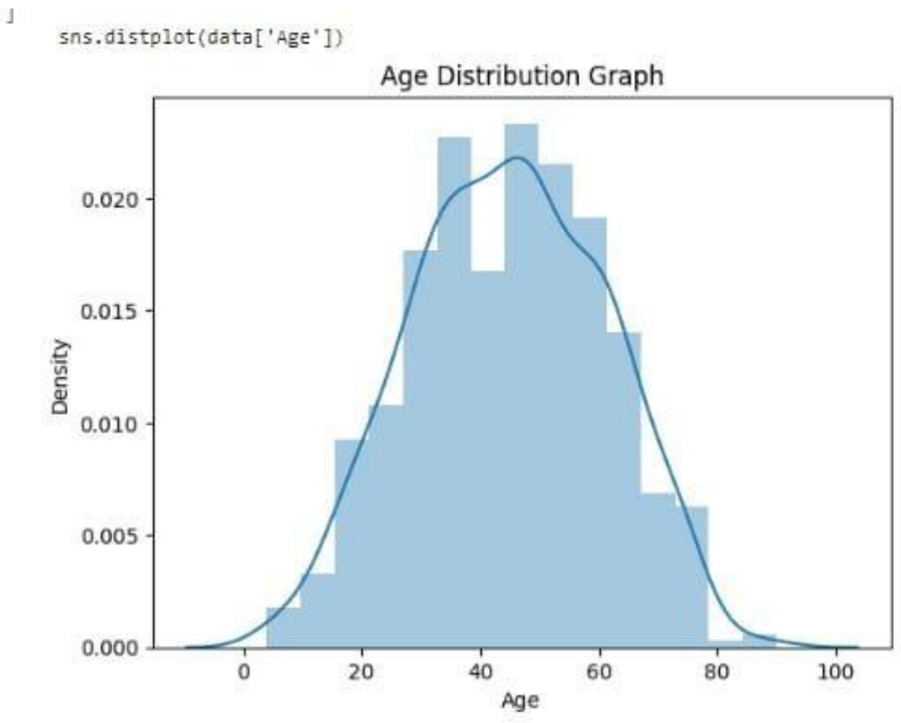


	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albumin_and_Globulin_Ratio	Dataset
count	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000
mean	44.746141	0.756432	3.298799	1.486106	290.576329	80.713551	109.910806	6.483190	3.141852	0.947427	1.286449
std	16.189833	0.429603	6.209522	2.808498	242.937989	182.620356	288.918529	1.085451	0.795519	0.318522	0.452490
min	4.000000	0.000000	0.400000	0.100000	63.000000	10.000000	10.000000	2.700000	0.900000	0.300000	1.000000
25%	33.000000	1.000000	0.800000	0.200000	175.500000	23.000000	25.000000	5.800000	2.600000	0.700000	1.000000
50%	45.000000	1.000000	1.000000	0.300000	208.000000	35.000000	42.000000	6.600000	3.100000	0.950000	1.000000
75%	58.000000	1.000000	2.600000	1.300000	298.000000	60.500000	87.000000	7.200000	3.800000	1.100000	2.000000
max	90.000000	1.000000	75.000000	19.700000	2110.000000	2000.000000	4929.000000	9.600000	5.500000	2.800000	2.000000

sns.distplot(data['Age'])

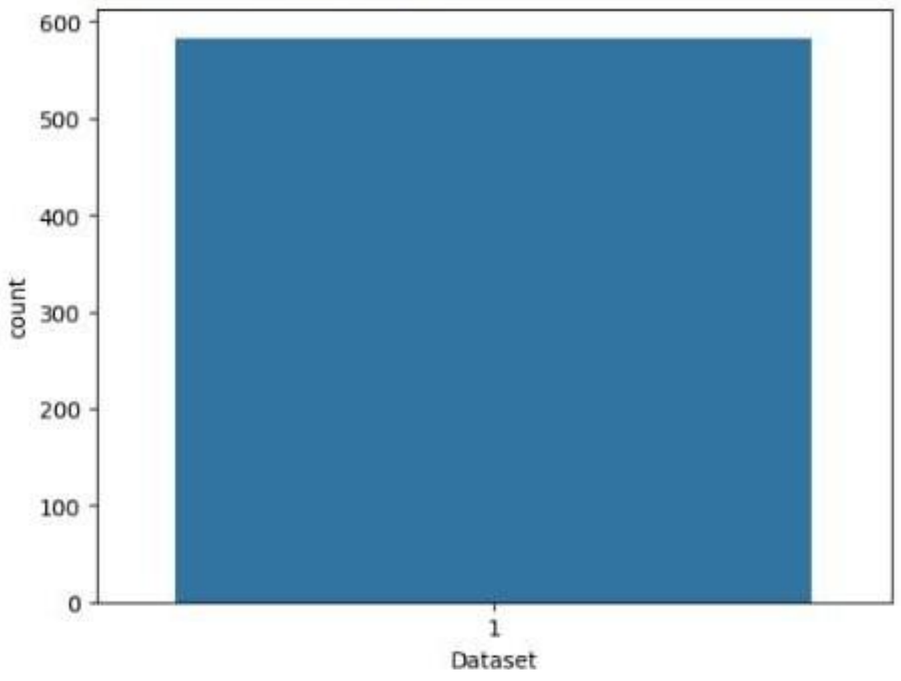
plt.title('Age Distribution Graph')

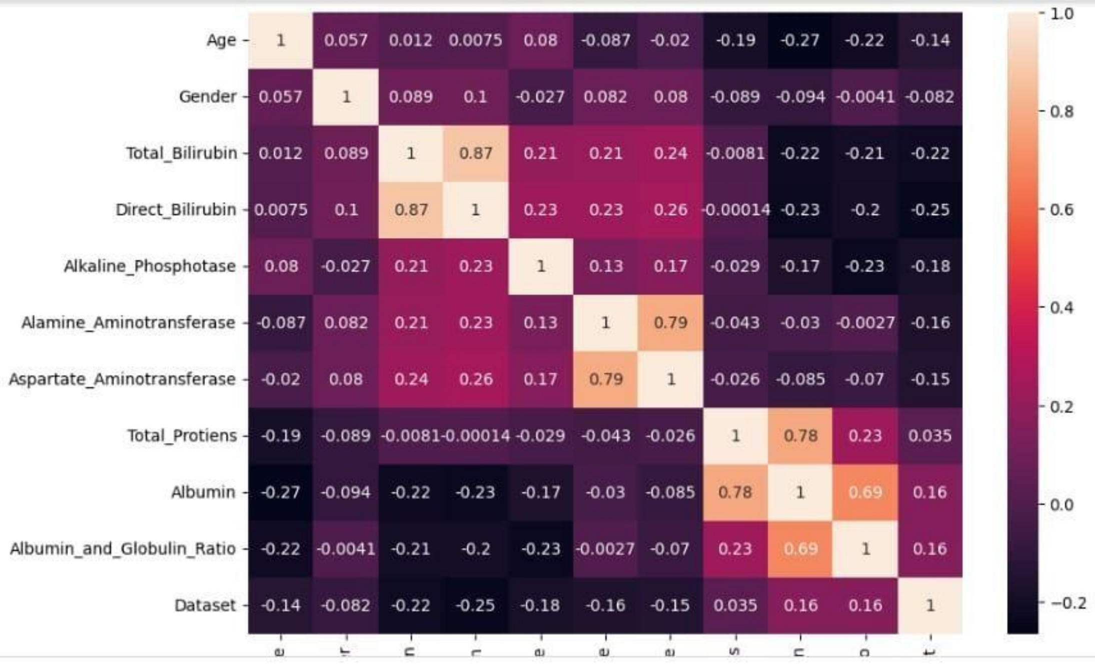
plt.show()



```
sns.distplot(data['Age'])
```

```
<Axes: xlabel='Dataset', ylabel='count'>
```





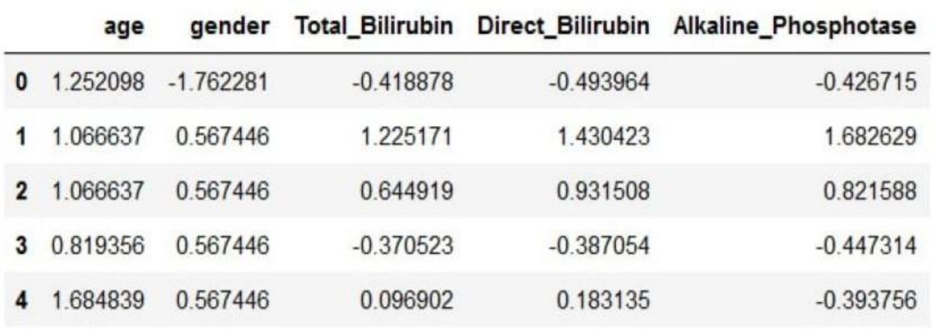
Age	1	0.057	0.012	0.0075	0.08	-0.087	-0.02	-0.19	-0.27	-0.22	-0.14
Gender	0.057	1	0.089	0.1	-0.027	0.082	0.08	-0.089	-0.094	-0.0041	-0.082
Total_Bilirubin	0.012	0.089	1	0.87	0.21	0.21	0.24	-0.0081	-0.22	-0.21	-0.22
Direct_Bilirubin	0.0075	0.1	0.87	1	0.23	0.23	0.26	-0.00014	-0.23	-0.2	-0.25
Alkaline_Phosphotase	0.08	-0.027	0.21	0.23	1	0.13	0.17	-0.029	-0.17	-0.23	-0.18
Alamine_Aminotransferase	-0.087	0.082	0.21	0.23	0.13	1	0.79	-0.043	-0.03	-0.0027	-0.16
Aspartate_Aminotransferase	-0.02	0.08	0.24	0.26	0.17	0.79	1	-0.026	-0.085	-0.07	-0.15
Total_Protiens	-0.19	-0.089	-0.0081	-0.00014	-0.029	-0.043	-0.026	1	0.78	0.23	0.035
Albumin	-0.27	-0.094	-0.22	-0.23	-0.17	-0.03	-0.085	0.78	1	0.69	0.16
Albumin_and_Globulin_Ratio	-0.22	-0.0041	-0.21	-0.2	-0.23	-0.0027	-0.07	0.23	0.69	1	0.16
Dataset	-0.14	-0.082	-0.22	-0.25	-0.18	-0.16	-0.15	0.035	0.16	0.16	1

sns.countplot(data['Dataset'],x=data['Gender'])

plt.figure(figsize=(10,7))

sns.heatmap(data.corr(),annot=True)

```
from sklearn.preprocessing import scale

x=pd.DataFrame (scale(x),columns=x.columns)

x_scaled.head()
```

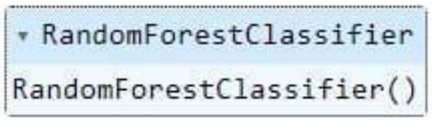


	age	gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase
0	1.252098	-1.762281	-0.418878	-0.493964	-0.426715
1	1.066637	0.567446	1.225171	1.430423	1.682629
2	1.066637	0.567446	0.644919	0.931508	0.821588
3	0.819356	0.567446	-0.370523	-0.387054	-0.447314
4	1.684839	0.567446	0.096902	0.183135	-0.393756

```
x=data.iloc[:,:-1]

y=data.Dataset


from sklearn.model_selection import train_test_split

x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=42)


from imblearn.over_sampling import SMOTE

smote = SMOTE()

y_train.value_counts()

   1 329

  2    137

Name: Dataset, dtype: int64

x_train_smote, y_train_smote = smote.fit_resample(x_train,y_train)

y_train_smote.value_counts()

1    329

2    329

Name: Dataset, dtype: int64
```

Milestone 4:

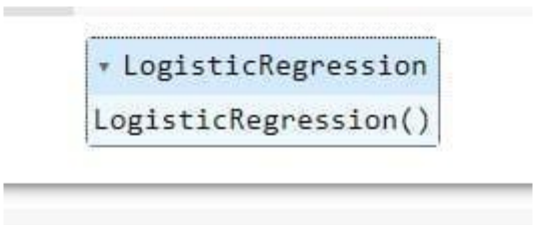
```
from sklearn.ensemble import RandomForestClassifier

RFmodel=RandomForestClassifier()

RFmodel.fit(x_train,y_train)
```



```
▾ RandomForestClassifier
RandomForestClassifier()
```

```
RFpred=RFmodel.predict(x_test)

RFaccuracy=accuracy_score(RFpred,y_test)

RFaccuracy

0.7521367521367521

RFcm=confusion_matrix(RFpred,y_test)

RFcm

array([[75, 17],
      [12, 13]])

from sklearn.neighbors import KNeighborsClassifier

KNN=KNeighborsClassifier()

KNN.fit(x_train,y_train)

KNNpred=KNN.predict(x_test)

KNNaccuracy=accuracy_score(KNNpred,y_test)

KNNaccuracy

0.6837606837606838

KNNcm=confusion_matrix(KNNpred,y_test)

KNNcm

array([[69, 19],
      [18, 11]])

from sklearn.tree import DecisionTreeClassifier
```

```
DTC=DecisionTreeClassifier()

DTC.fit(x_train,y_train)
```



```
▾ LogisticRegression
LogisticRegression()
```

```
DTCpred=DTC.predict(x_test)

DTCaccuracy=accuracy_score(DTCpred,y_test)

DTCaccuracy

0.717948717948718

DTCcm=confusion_matrix(DTCpred,y_test)

DTCcm

array([[66, 12],

      [21, 18]])

from sklearn.linear_model import LogisticRegression

LR=LogisticRegression()


LRpred=LR.predict(x_test)

LRaccuracy=accuracy_score(LRpred,y_test)

LRaccuracy

0.7435897435897436

LRcm=confusion_matrix(LRpred,y_test)

LRcm

array([[82, 25],

      [ 5,  5]])

import tensorflow.keras

from tensorflow.keras.models import Sequential

from tensorflow.keras.layers import Dense
```

```
classifier = Sequential()

classifier.add(Dense(units=100,activation='relu',input_dim=10))

classifier.add(Dense(units=50,activation='relu'))

classifier.add(Dense(units=1,activation='sigmoid'))

classifier.compile(optimizer='adam',loss='binary_crossentropy',metrics=['accuracy'])

RFmodel_history=classifier.fit(x_train,y_train,batch_size=100,validation_split=0.2,epochs=100)

Epoch 1/100

4/4 [==============================] - 0s 80ms/step - loss: -658367.8125 - accuracy: 0.7016 - val_loss: -593204.0625 - val_accuracy: 0.7234

Epoch 2/100

4/4 [==============================] - 0s 37ms/step - loss: -667815.0000 - accuracy: 0.7016 - val_loss: -601997.3125 - val_accuracy: 0.7234

Epoch 3/100

4/4 [==============================] - 0s 53ms/step - loss: -677944.8750 - accuracy: 0.7016 - val_loss: -610722.8125 - val_accuracy: 0.7234

Epoch 4/100

4/4 [==============================] - 0s 51ms/step - loss: -687855.5625 - accuracy: 0.7016 - val_loss: -619532.7500 - val_accuracy: 0.7234

Epoch 5/100

4/4 [==============================] - 0s 43ms/step - loss: -697299.9375 - accuracy: 0.7016 - val_loss: -628574.0000 - val_accuracy: 0.7234

Epoch 6/100

4/4 [==============================] - 0s 41ms/step - loss: -707700.5000 - accuracy: 0.7016 - val_loss: -637505.2500 - val_accuracy: 0.7234

Epoch 7/100

4/4 [==============================] - 0s 41ms/step - loss: -717873.1875 - accuracy: 0.7016 - val_loss: -646466.5625 - val_accuracy: 0.7234

Epoch 8/100

4/4 [==============================] - 0s 52ms/step - loss: -727852.1250 - accuracy: 0.7016 - val_loss: -655572.5625 - val_accuracy: 0.7234

Epoch 9/100
```

```
4/4 [==============================] - 0s 29ms/step - loss: -738061.7500 - accuracy: 0.7016 - val_loss: -664791.8125 - val_accuracy: 0.7234

Epoch 10/100

4/4 [==============================] - 0s 24ms/step - loss: -748137.7500 - accuracy: 0.7016 - val_loss: -674201.8125 - val_accuracy: 0.7234

Epoch 11/100

4/4 [==============================] - 0s 37ms/step - loss: -759247.3125 - accuracy: 0.7016 - val_loss: -683482.2500 - val_accuracy: 0.7234

Epoch 12/100

4/4 [==============================] - 0s 26ms/step - loss: -769670.8750 - accuracy: 0.7016 - val_loss: -692927.8125 - val_accuracy: 0.7234

Epoch 13/100

4/4 [==============================] - 0s 19ms/step - loss: -780058.7500 - accuracy: 0.7016 - val_loss: -702565.5625 - val_accuracy: 0.7234

Epoch 14/100

4/4 [==============================] - 0s 36ms/step - loss: -790572.3125 - accuracy: 0.7016 - val_loss: -712313.8125 - val_accuracy: 0.7234

Epoch 15/100

4/4 [==============================] - 0s 25ms/step - loss: -801802.5000 - accuracy: 0.7016 - val_loss: -721993.8125 - val_accuracy: 0.7234

Epoch 16/100

4/4 [==============================] - 0s 30ms/step - loss: -812847.3750 - accuracy: 0.7016 - val_loss: -731739.5625 - val_accuracy: 0.7234

Epoch 17/100

4/4 [==============================] - 0s 42ms/step - loss: -823909.3125 - accuracy: 0.7016 - val_loss: -741573.6875 - val_accuracy: 0.7234

Epoch 18/100

4/4 [==============================] - 0s 43ms/step - loss: -834615.9375 - accuracy: 0.7016 - val_loss: -751650.8125 - val_accuracy: 0.7234

Epoch 19/100

4/4 [==============================] - 0s 20ms/step - loss: -846041.3125 - accuracy: 0.7016 - val_loss: -761723.0000 - val_accuracy: 0.7234

Epoch 20/100
```

```
4/4 [==============================] - 0s 27ms/step - loss: -857278.9375 - accuracy: 0.7016 - val_loss:
-771933.6875 - val_accuracy: 0.7234

Epoch 21/100

4/4 [==============================] - 0s 20ms/step - loss: -868970.2500 - accuracy: 0.7016 - val_loss:
-782164.2500 - val_accuracy: 0.7234

Epoch 22/100

4/4 [==============================] - 0s 33ms/step - loss: -880613.0000 - accuracy: 0.7016 - val_loss:
-792485.2500 - val_accuracy: 0.7234

Epoch 23/100

4/4 [==============================] - 0s 67ms/step - loss: -891858.9375 - accuracy: 0.7016 - val_loss:
-803042.0625 - val_accuracy: 0.7234

Epoch 24/100

4/4 [==============================] - 0s 57ms/step - loss: -903902.8750 - accuracy: 0.7016 - val_loss:
-813523.7500 - val_accuracy: 0.7234

Epoch 25/100

4/4 [==============================] - 0s 56ms/step - loss: -915529.8750 - accuracy: 0.7016 - val_loss:
-824129.3750 - val_accuracy: 0.7234

Epoch 26/100

4/4 [==============================] - 0s 55ms/step - loss: -927790.4375 - accuracy: 0.7016 - val_loss:
-834718.0625 - val_accuracy: 0.7234

Epoch 27/100

4/4 [==============================] - 0s 53ms/step - loss: -939390.9375 - accuracy: 0.7016 - val_loss:
-845578.3750 - val_accuracy: 0.7234

Epoch 28/100

4/4 [==============================] - 0s 20ms/step - loss: -951746.6875 - accuracy: 0.7016 - val_loss:
-856461.6250 - val_accuracy: 0.7234

Epoch 29/100

4/4 [==============================] - 0s 13ms/step - loss: -964017.0625 - accuracy: 0.7016 - val_loss:
-867335.2500 - val_accuracy: 0.7234

Epoch 30/100

4/4 [==============================] - 0s 14ms/step - loss: -976092.1875 - accuracy: 0.7016 - val_loss:
-878283.5625 - val_accuracy: 0.7234

Epoch 31/100
```

```
4/4 [==============================] - 0s 18ms/step - loss: -988350.1875 - accuracy: 0.7016 - val_loss: -889272.2500 - val_accuracy: 0.7234

Epoch 32/100

4/4 [==============================] - 0s 16ms/step - loss: -1000706.9375 - accuracy: 0.7016 - val_loss: -900362.7500 - val_accuracy: 0.7234

Epoch 33/100

4/4 [==============================] - 0s 19ms/step - loss: -1013206.9375 - accuracy: 0.7016 - val_loss: -911565.0000 - val_accuracy: 0.7234

Epoch 34/100

4/4 [==============================] - 0s 21ms/step - loss: -1026137.4375 - accuracy: 0.7016 - val_loss: -922823.0000 - val_accuracy: 0.7234

Epoch 35/100

4/4 [==============================] - 0s 19ms/step - loss: -1037931.1875 - accuracy: 0.7016 - val_loss: -934481.6250 - val_accuracy: 0.7234

Epoch 36/100

4/4 [==============================] - 0s 14ms/step - loss: -1051233.7500 - accuracy: 0.7016 - val_loss: -945996.4375 - val_accuracy: 0.7234

Epoch 37/100

4/4 [==============================] - 0s 19ms/step - loss: -1064053.8750 - accuracy: 0.7016 - val_loss: -957543.7500 - val_accuracy: 0.7234

Epoch 38/100

4/4 [==============================] - 0s 19ms/step - loss: -1077281.3750 - accuracy: 0.7016 - val_loss: -969030.5625 - val_accuracy: 0.7234

Epoch 39/100

4/4 [==============================] - 0s 19ms/step - loss: -1090125.3750 - accuracy: 0.7016 - val_loss: -980694.3125 - val_accuracy: 0.7234

Epoch 40/100

4/4 [==============================] - 0s 25ms/step - loss: -1103089.1250 - accuracy: 0.7016 - val_loss: -992526.8125 - val_accuracy: 0.7234

Epoch 41/100

4/4 [==============================] - 0s 19ms/step - loss: -1116665.6250 - accuracy: 0.7016 - val_loss: -1004365.9375 - val_accuracy: 0.7234

Epoch 42/100
```

```
4/4 [==============================] - 0s 14ms/step - loss: -1129659.7500 - accuracy: 0.7016 -
val_loss: -1016444.1875 - val_accuracy: 0.7234

Epoch 43/100

4/4 [==============================] - 0s 13ms/step - loss: -1143343.8750 - accuracy: 0.7016 -
val_loss: -1028518.8125 - val_accuracy: 0.7234

Epoch 44/100

4/4 [==============================] - 0s 20ms/step - loss: -1156914.8750 - accuracy: 0.7016 -
val_loss: -1040690.8750 - val_accuracy: 0.7234

Epoch 45/100

4/4 [==============================] - 0s 17ms/step - loss: -1170839.7500 - accuracy: 0.7016 -
val_loss: -1052845.2500 - val_accuracy: 0.7234

Epoch 46/100

4/4 [==============================] - 0s 20ms/step - loss: -1184115.1250 - accuracy: 0.7016 -
val_loss: -1065299.1250 - val_accuracy: 0.7234

Epoch 47/100

4/4 [==============================] - 0s 19ms/step - loss: -1198001.7500 - accuracy: 0.7016 -
val_loss: -1077800.1250 - val_accuracy: 0.7234

Epoch 48/100

4/4 [==============================] - 0s 19ms/step - loss: -1212449.0000 - accuracy: 0.7016 -
val_loss: -1090211.3750 - val_accuracy: 0.7234

Epoch 49/100

4/4 [==============================] - 0s 19ms/step - loss: -1226363.3750 - accuracy: 0.7016 -
val_loss: -1102746.2500 - val_accuracy: 0.7234

Epoch 50/100

4/4 [==============================] - 0s 20ms/step - loss: -1240148.2500 - accuracy: 0.7016 -
val_loss: -1115452.1250 - val_accuracy: 0.7234

Epoch 51/100

4/4 [==============================] - 0s 15ms/step - loss: -1254514.6250 - accuracy: 0.7016 -
val_loss: -1128213.5000 - val_accuracy: 0.7234

Epoch 52/100

4/4 [==============================] - 0s 19ms/step - loss: -1268405.0000 - accuracy: 0.7016 -
val_loss: -1141175.3750 - val_accuracy: 0.7234

Epoch 53/100
```

```
4/4 [==============================] - 0s 13ms/step - loss: -1283378.7500 - accuracy: 0.7016 -
val_loss: -1153975.8750 - val_accuracy: 0.7234

Epoch 54/100

4/4 [==============================] - 0s 13ms/step - loss: -1297842.6250 - accuracy: 0.7016 -
val_loss: -1166885.2500 - val_accuracy: 0.7234

Epoch 55/100

4/4 [==============================] - 0s 19ms/step - loss: -1313219.6250 - accuracy: 0.7016 -
val_loss: -1179737.3750 - val_accuracy: 0.7234

Epoch 56/100

4/4 [==============================] - 0s 14ms/step - loss: -1327222.6250 - accuracy: 0.7016 -
val_loss: -1193090.7500 - val_accuracy: 0.7234

Epoch 57/100

4/4 [==============================] - 0s 19ms/step - loss: -1341815.2500 - accuracy: 0.7016 -
val_loss: -1206648.1250 - val_accuracy: 0.7234

Epoch 58/100

4/4 [==============================] - 0s 19ms/step - loss: -1356829.8750 - accuracy: 0.7016 -
val_loss: -1220226.7500 - val_accuracy: 0.7234

Epoch 59/100

4/4 [==============================] - 0s 14ms/step - loss: -1372226.3750 - accuracy: 0.7016 -
val_loss: -1233714.5000 - val_accuracy: 0.7234

Epoch 60/100

4/4 [==============================] - 0s 13ms/step - loss: -1387510.3750 - accuracy: 0.7016 -
val_loss: -1247228.3750 - val_accuracy: 0.7234

Epoch 61/100

4/4 [==============================] - 0s 14ms/step - loss: -1402555.0000 - accuracy: 0.7016 -
val_loss: -1260871.1250 - val_accuracy: 0.7234

Epoch 62/100

4/4 [==============================] - 0s 23ms/step - loss: -1417701.6250 - accuracy: 0.7016 -
val_loss: -1274690.7500 - val_accuracy: 0.7234

Epoch 63/100

4/4 [==============================] - 0s 14ms/step - loss: -1433544.1250 - accuracy: 0.7016 -
val_loss: -1288476.2500 - val_accuracy: 0.7234

Epoch 64/100
```

```
4/4 [==============================] - 0s 19ms/step - loss: -1449153.0000 - accuracy: 0.7016 -
val_loss: -1302399.7500 - val_accuracy: 0.7234

Epoch 65/100

4/4 [==============================] - 0s 13ms/step - loss: -1464224.3750 - accuracy: 0.7016 -
val_loss: -1316549.5000 - val_accuracy: 0.7234

Epoch 66/100

4/4 [==============================] - 0s 12ms/step - loss: -1479801.0000 - accuracy: 0.7016 -
val_loss: -1330783.8750 - val_accuracy: 0.7234

Epoch 67/100

4/4 [==============================] - 0s 13ms/step - loss: -1496706.6250 - accuracy: 0.7016 -
val_loss: -1344791.1250 - val_accuracy: 0.7234

Epoch 68/100

4/4 [==============================] - 0s 14ms/step - loss: -1512144.8750 - accuracy: 0.7016 -
val_loss: -1359089.2500 - val_accuracy: 0.7234

Epoch 69/100

4/4 [==============================] - 0s 14ms/step - loss: -1528065.8750 - accuracy: 0.7016 -
val_loss: -1373541.0000 - val_accuracy: 0.7234

Epoch 70/100

4/4 [==============================] - 0s 19ms/step - loss: -1544517.3750 - accuracy: 0.7016 -
val_loss: -1388008.6250 - val_accuracy: 0.7234

Epoch 71/100

4/4 [==============================] - 0s 13ms/step - loss: -1561332.0000 - accuracy: 0.7016 -
val_loss: -1402453.5000 - val_accuracy: 0.7234

Epoch 72/100

4/4 [==============================] - 0s 19ms/step - loss: -1577190.0000 - accuracy: 0.7016 -
val_loss: -1417268.3750 - val_accuracy: 0.7234

Epoch 73/100

4/4 [==============================] - 0s 14ms/step - loss: -1594071.0000 - accuracy: 0.7016 -
val_loss: -1432073.5000 - val_accuracy: 0.7234

Epoch 74/100

4/4 [==============================] - 0s 13ms/step - loss: -1610046.1250 - accuracy: 0.7016 -
val_loss: -1447196.8750 - val_accuracy: 0.7234

Epoch 75/100
```

```
4/4 [==============================] - 0s 20ms/step - loss: -1627160.6250 - accuracy: 0.7016 -
val_loss: -1462295.5000 - val_accuracy: 0.7234

Epoch 76/100

4/4 [==============================] - 0s 14ms/step - loss: -1644354.2500 - accuracy: 0.7016 -
val_loss: -1477444.3750 - val_accuracy: 0.7234

Epoch 77/100

4/4 [==============================] - 0s 19ms/step - loss: -1661460.2500 - accuracy: 0.7016 -
val_loss: -1492718.0000 - val_accuracy: 0.7234

Epoch 78/100

4/4 [==============================] - 0s 19ms/step - loss: -1679104.5000 - accuracy: 0.7016 -
val_loss: -1508000.1250 - val_accuracy: 0.7234

Epoch 79/100

4/4 [==============================] - 0s 14ms/step - loss: -1695154.1250 - accuracy: 0.7016 -
val_loss: -1523874.7500 - val_accuracy: 0.7234

Epoch 80/100

4/4 [==============================] - 0s 19ms/step - loss: -1713723.8750 - accuracy: 0.7016 -
val_loss: -1539401.7500 - val_accuracy: 0.7234

Epoch 81/100

4/4 [==============================] - 0s 20ms/step - loss: -1730503.8750 - accuracy: 0.7016 -
val_loss: -1555277.7500 - val_accuracy: 0.7234

Epoch 82/100

4/4 [==============================] - 0s 20ms/step - loss: -1748175.6250 - accuracy: 0.7016 -
val_loss: -1571173.1250 - val_accuracy: 0.7234

Epoch 83/100

4/4 [==============================] - 0s 22ms/step - loss: -1766677.6250 - accuracy: 0.7016 -
val_loss: -1586805.2500 - val_accuracy: 0.7234

Epoch 84/100

4/4 [==============================] - 0s 14ms/step - loss: -1784156.8750 - accuracy: 0.7016 -
val_loss: -1602683.8750 - val_accuracy: 0.7234

Epoch 85/100

4/4 [==============================] - 0s 14ms/step - loss: -1801669.3750 - accuracy: 0.7016 -
val_loss: -1618731.8750 - val_accuracy: 0.7234

Epoch 86/100
```

```
4/4 [==============================] - 0s 20ms/step - loss: -1819357.3750 - accuracy: 0.7016 - val_loss: -1634839.8750 - val_accuracy: 0.7234

Epoch 87/100

4/4 [==============================] - 0s 20ms/step - loss: -1838195.5000 - accuracy: 0.7016 - val_loss: -1650720.6250 - val_accuracy: 0.7234

Epoch 88/100

4/4 [==============================] - 0s 14ms/step - loss: -1855447.3750 - accuracy: 0.7016 - val_loss: -1667040.0000 - val_accuracy: 0.7234

Epoch 89/100

4/4 [==============================] - 0s 20ms/step - loss: -1874518.3750 - accuracy: 0.7016 - val_loss: -1683222.5000 - val_accuracy: 0.7234

Epoch 90/100

4/4 [==============================] - 0s 18ms/step - loss: -1891730.3750 - accuracy: 0.7016 - val_loss: -1699956.3750 - val_accuracy: 0.7234

Epoch 91/100

4/4 [==============================] - 0s 19ms/step - loss: -1910361.5000 - accuracy: 0.7016 - val_loss: -1716632.1250 - val_accuracy: 0.7234

Epoch 92/100

4/4 [==============================] - 0s 20ms/step - loss: -1929668.5000 - accuracy: 0.7016 - val_loss: -1733106.0000 - val_accuracy: 0.7234

Epoch 93/100

4/4 [==============================] - 0s 13ms/step - loss: -1948571.8750 - accuracy: 0.7016 - val_loss: -1749683.3750 - val_accuracy: 0.7234

Epoch 94/100

4/4 [==============================] - 0s 14ms/step - loss: -1966975.2500 - accuracy: 0.7016 - val_loss: -1766571.7500 - val_accuracy: 0.7234

Epoch 95/100

4/4 [==============================] - 0s 14ms/step - loss: -1985814.0000 - accuracy: 0.7016 - val_loss: -1783625.3750 - val_accuracy: 0.7234

Epoch 96/100

4/4 [==============================] - 0s 19ms/step - loss: -2004937.6250 - accuracy: 0.7016 - val_loss: -1800817.8750 - val_accuracy: 0.7234

Epoch 97/100
```

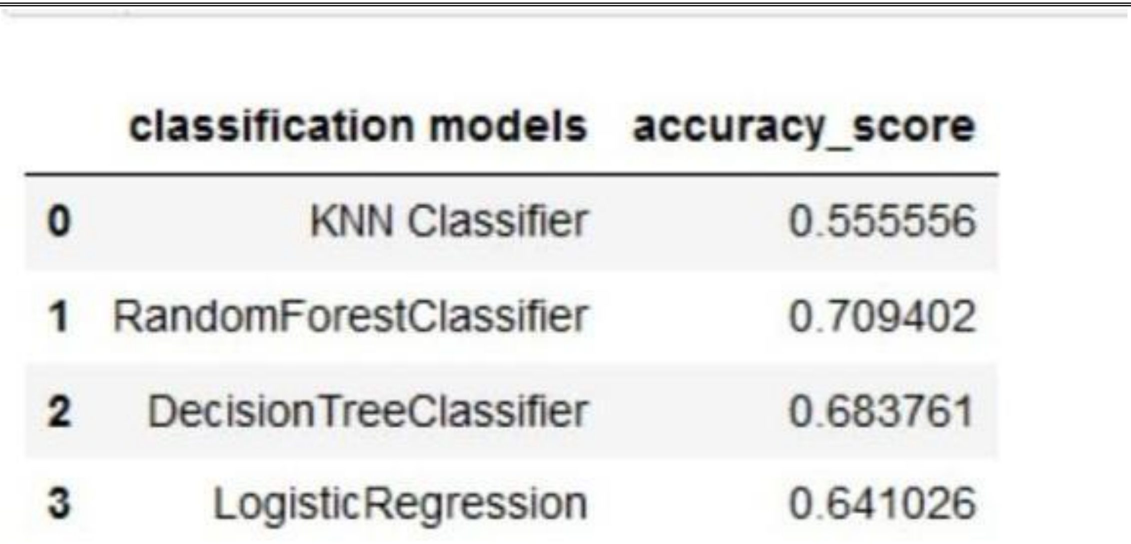
```
4/4 [==============================] - 0s 13ms/step - loss: -2024367.1250 - accuracy: 0.7016 -
val_loss: -1818068.7500 - val_accuracy: 0.7234

Epoch 98/100

4/4 [==============================] - 0s 14ms/step - loss: -2043511.3750 - accuracy: 0.7016 -
val_loss: -1835457.7500 - val_accuracy: 0.7234

Epoch 99/100

4/4 [==============================] - 0s 19ms/step - loss: -2062323.6250 - accuracy: 0.7016 -
val_loss: -1853025.7500 - val_accuracy: 0.7234

Epoch 100/100

4/4 [==============================] - 0s 19ms/step - loss: -2082436.8750 - accuracy: 0.7016 -
val_loss: -1870389.7500 - val_accuracy: 0.7234

DTC.predict([[50,1,1.2,0.8,150,70,80,7.2,3.4,0.8]])

array([2])

RFmodel.predict([[50,1,1.2,0.8,150,70,80,7.2,3.4,0.8]])

array([1])

classifier.save("liver.h5")

y_test =(y_test>0.5)

y_test

355    True

407    True

90     True

402    True

268    True

      ...

516    True

305    True

167    True

312    True

329    True

Name: Dataset, Length: 117, dtype: bool
```

```
def predict_exit(sample_value):

 sample_value =np.array(sample_value)

 sample_value =sample_value.reshape(1,-1)

 sample_value =scale(sample_value)

 return classifier.predict(sample_value)


sample_value=[[50,1,1.2,0.8,150,70,80,7.2,3.4,0.8]]

if predict_exit(sample_value)>0.5:

print('Prediction: Liver Patient')

else:

  print('Prediction: Healthy')
```

```
1/1 [==============================] - 0s 105ms/step

Prediction: Liver Patient

1/1 [==============================] - 0s 24ms/step

Prediction: Liver Patient
```

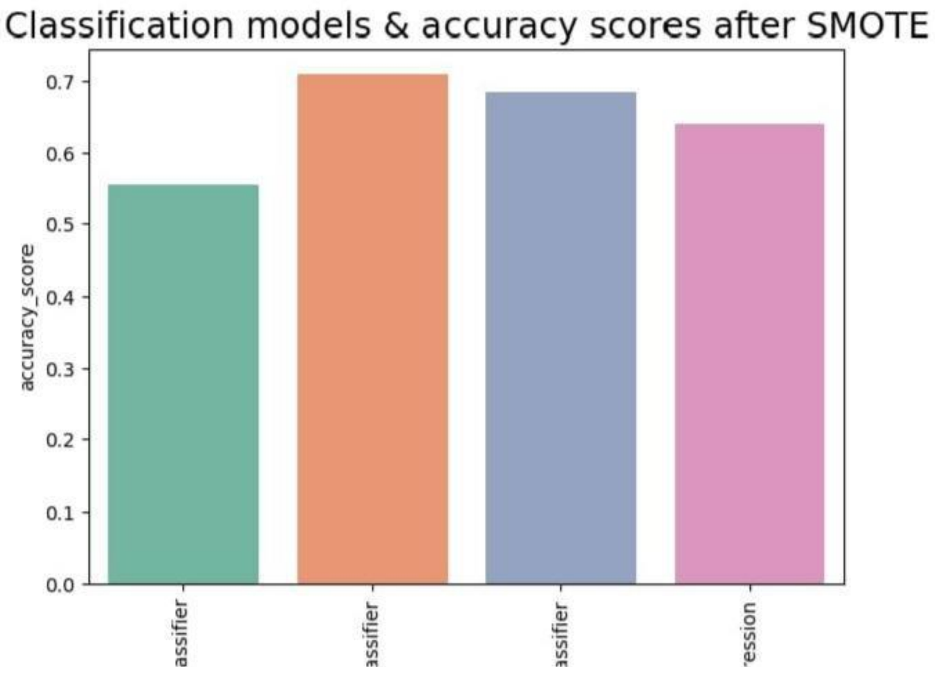
Milestone 5:

```
acc_smote=[['KNN Classifier',KNN],['RandomForestClassifier',RFaccuracy],['DecisionTreeClassifier',DTCaccuracy],['LogisticRegression',LRaccuracy]]

Liverpatient_pred=pd.DataFrame(acc_smote,columns=['classification models','accuracy_score'])

Liverpatient_pred
```



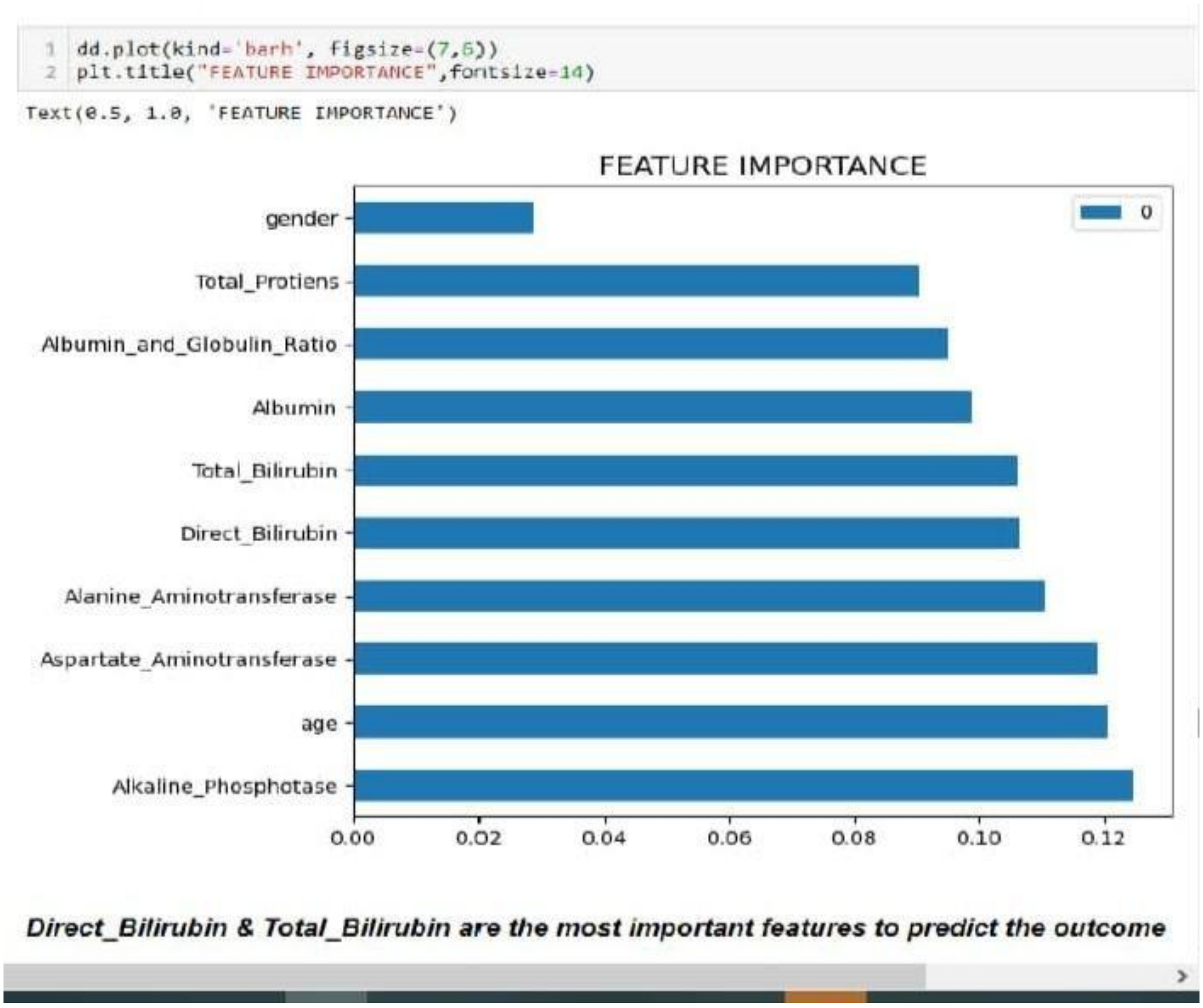
	classification models	accuracy_score
0	KNN Classifier	0.555556
1	RandomForestClassifier	0.709402
2	DecisionTreeClassifier	0.683761
3	LogisticRegression	0.641026

```
plt.figure(figsize=(7,5))
plt.xticks(rotation=90)
plt.title('Classification models & accuracy scores after SMOTE',fontsize=18)
sns.barplot(x="classification models",y="accuracy_score",data=Liverpatient_pred,palette="Set2")
```



```
from sklearn.ensemble import ExtraTreesClassifier
model1=ExtraTreesClassifier()
model1.fit(x,y)
```

```
model1.feature_importances

array([0.13287739, 0.01991026, 0.09463777, 0.08566328, 0.14577484,

      0.13219089, 0.12830574, 0.09378994, 0.09210753, 0.07474237])

dd.pd.DataFrame(model1.feature_importances_,index=x.columns).sort_values(0,ascending=False)

dd

data.plot(kind='barh',figsize=(7,6))

plt.title("FEATURE IMPORTANCE",fontsize=14)
```



```
dd.plot(kind='barh', figsize=(7,6))
plt.title("FEATURE IMPORTANCE",fontsize=14)
```

```
Text(0.5, 1.0, 'FEATURE IMPORTANCE')
```

Direct_Bilirubin & Total_Bilirubin are the most important features to predict the outcome

```
import joblib

joblib.dump(RFmodel,'liver_analysis_1.pkl')
```

```
['liver_analysis_1.pkl']
```

```
data.plot(kind='barh',figsize=(6,5))

plt.title("FEATURE IMPORTANCE",fontsize=14)
```

Milestone6

```
import numpy as np

import  pickle

import os

app=Flask(_name_)

@app.route('/')

def home():

  return render_template('home.html')

@app.route('/predict')

def index():

 return render_template("index.html")

@app.route('/data_predict',methods=['POST'])

def predict():

    age = request.form['age']

    gender=request.form['gender']

    tb = request.form['tb']

    db = request.form['db']

    ap = request.form['ap']

    aa1 = request.form['aa1']
    aa2 = request.form['aa2']

    tp = request.form['tp']

    a = request.form['a']

    agr = request.form['agr']

    data = [[float(age),float(gender),float(db),float(ap),float(aa1),float(aa2),float(tp),float(a),float(agr)]

    model=pickle.load(open(os.path.join('c:Users/91630/Desktop/liver patient/Liver Patient Analysis/Flask
app,pkl_objects','liver_analysis_1.pkl'),'rb'))

    prediction= model.predict(data)[0]

    if (prediction == 1):

      return render_template('noChance.html',prediction='You have a liver desease problem,You must and should
consult a doctor.Take care')

    else:

      return render_template('chance.html', prediction='You dont have a liver desease problem')

if___name___=='_main_':

    app.run(debug=True)
```