A Review Of Liver Patient Analysis Methods Using Machine Learning

ABSTRACT:

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.

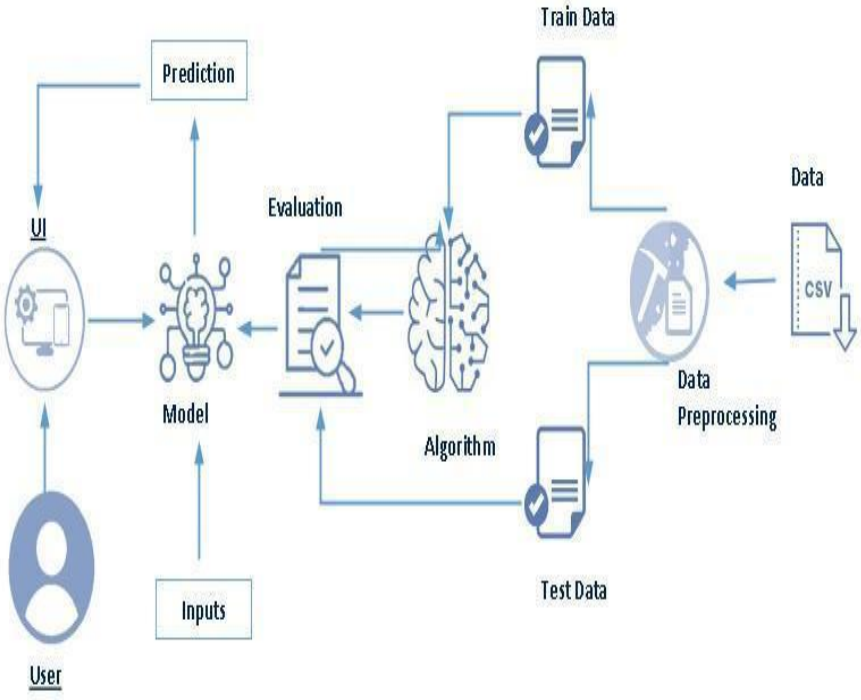
In this project we will analyse the parameters of various classification algorithms and compare their predictive accuracies so as to find out the best classifier for determining the liver disease.

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 the business problem

  - Business requirements

- Literature Survey
- Social or Business Impact.

- Data Collection & Preparation
  - Collect the dataset
  - Data Preparation
- Exploratory Data Analysis
  - Descriptive statistical
  - Visual Analysis
- Model Building

- Training the model in multiple algorithms
- Testing the model

- Performance Testing & Hyperparameter Tuning
  - Testing model with multiple evaluation metrics
  - Comparing model accuracy before & after applying hyperparameter tuning
- Model Deployment
  - Save the best model

- Integrate with Web Framework

- Project Demonstration & Documentation

  - Record explanation Video for project end to end solution

  - Project Documentation-Step by step project development procedure

Milestone – 1:

Define Problem/Problem Understanding:

In this milestone, we will go through the problem understanding.

Specify The Business Problem:

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.

Business Requirements:

Patients with Liver disease have been continuously increasing because of excessive consumption of alcohol, inhale of harmful gases, intake of contaminated food, pickles and drugs and other factors.

This dataset was used to evaluate prediction algorithms in an effort to reduce burden on doctors.

Use these patient records to build a prediction model that will predict which patients have liver disease and which ones do not.

Literature Survey:

With a growing trend of sedentary and lack of physical activities, diseases related to liver have become a common encounter nowadays.

In rural areas the intensity is still manageable, but in urban areas, and especially metropolitan areas the liver disease is a very common sighting nowadays.

Problems with liver patients are not easily discovered in an early stage as it will be functioning normally even when it is partially damaged.

An early diagnosis of liver problems will increase patients survival rate.

There are various algorithms that have been used with varying levels of success. Logistic regression, decision tree, random forest, and neural networks have all been used and have been able to accurately predict liver disease.

Social Or Business Impact:

Social Impact:-Today almost everybody above the age of 12 years has smartphones with them, and so we can incorporate these solutions into an android app or ios app.

Also it can be incorporated into a website and these app and website will be highly beneficial for a large section of society.

Business Model/Impact:- Its now more feasible Blood test centers to give the result. As for this model user don't need to have any deep knowledge of medical science and liver diseases.

User need to do pass the details being asked, which are already present in the blood test report(some like age, gender are already known) and then user will get the results of prediction.

Empathy Map:

Template

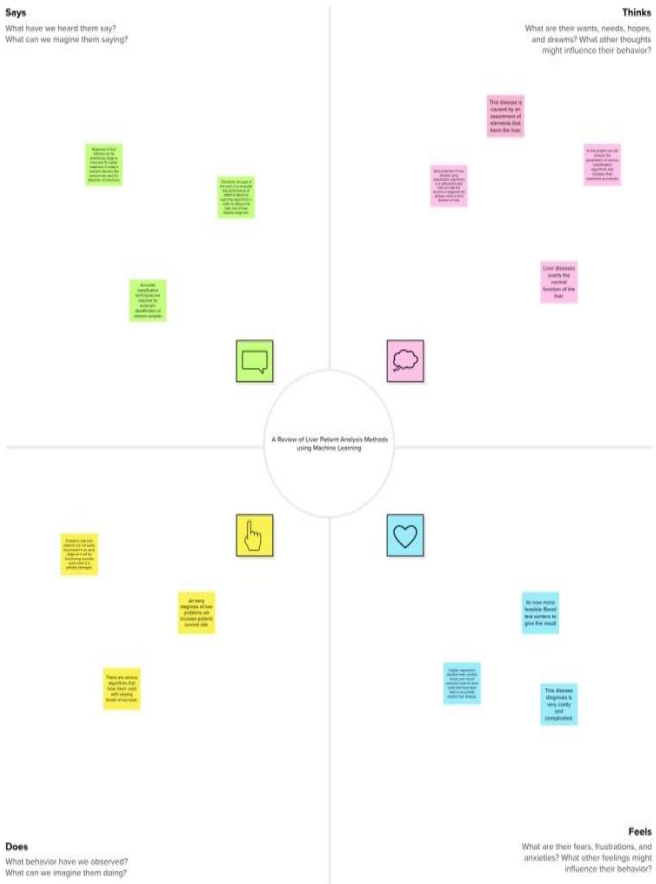
Empathy map

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

Build empathy

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

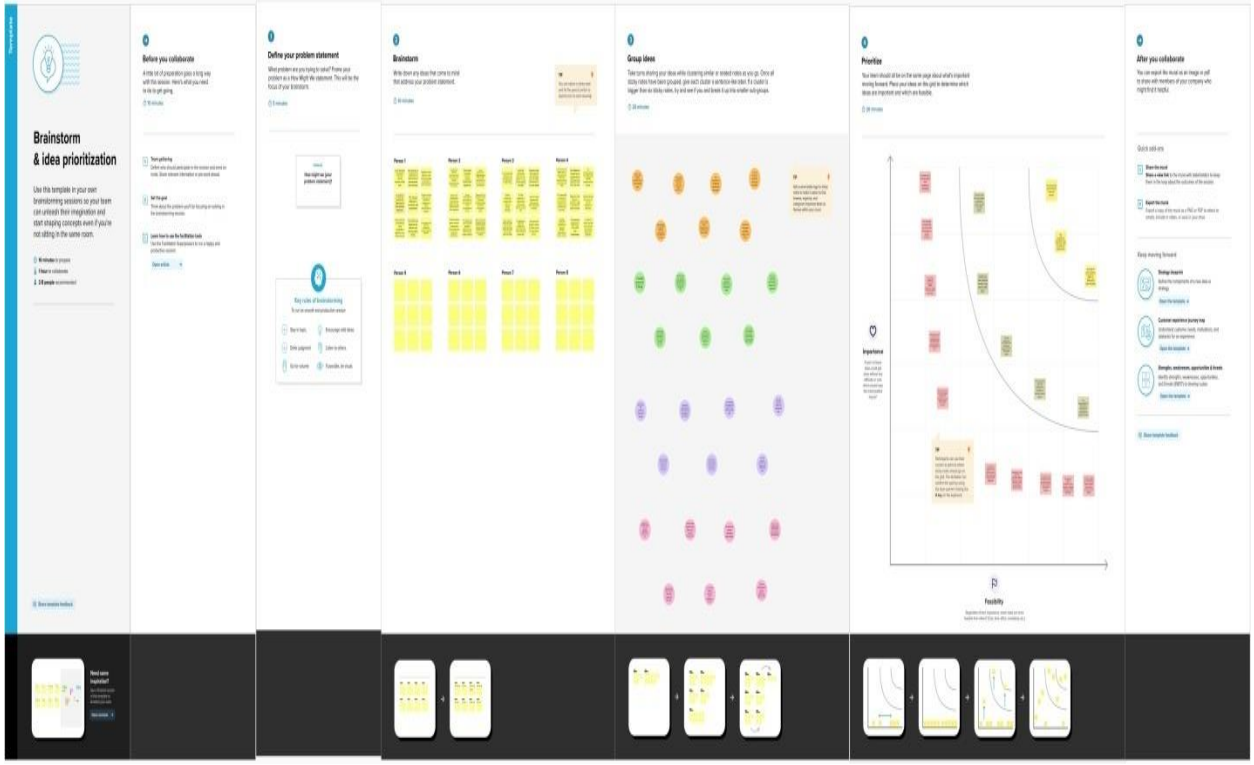


Need some inspiration?

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

Open example →

Brainstorm Map:



Results:

It is a sample of the entire Indian population collected from Andhra Pradesh region. The dataset comprised of 583 instances based on ten biological parameters.

The class value was reported based on these parameters as either yes (416 cases) or no (167 cases) that represent the liver infection. The patients were described as either ‘1’ or ‘2’ on the basis of liver disease.

Advantages:

Diagnoses,Grades and Stages:

- **Hepatitis C**
- **Hepatitis B**
- **Steatohepatitis**
- **Autoimmune hepatitis**

- **Evaluates abnormal liver function tests**
- **Identifies hepatotoxicity**

- **Clarifies uncertain diagnoses**
- **Confirms etiology of liver masses**
- **Defines Extent of necroinflammatory activity**
- **Differentiates fibrosis from cirrhosis**

Liver Transplant:

- **Identifies acute cellular rejection**

- **Defines recurrence of original disease**
- **Identifies progressive fibrosis**
- **Diagnoses other liver processes**

Milestone – 2:

Data Collection & Preparation:

ML depends heavily on data. It is the most crucial aspect that makes algorithm training possible. So this section allows you to download the required dataset.

Collect The Dataset:

There are many popular open sources for collecting the data. Eg: kaggle.com, UCI repository, etc.

In this project we have used .csv data. This data is downloaded from kaggle.com. Please refer to the link given below to download the dataset

Link: https://www.kaggle.com/datasets/uciml/indian-liver-patient-records

As the dataset is downloaded. Let us read and understand the data properly with the help of some visualisation techniques and some analysing techniques.

Note: There are a number of techniques for understanding the data. But here we have used some of it. In an additional way, you can use multiple techniques.

Importing The Libraries:

Import the necessary libraries as shown in the image. (optional) Here we have used visualisation style as fivethirtyeight.

```

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
```

Read The Dataset:

Our dataset format might be in .csv, excel files, .txt, .json, etc. We can read the dataset with the help of pandas.

In pandas we have a function called read_csv() to read the dataset. As a parameter we have to give the directory of the csv file.

```
#import the dataset from specified location
data = pd.read_csv('E:/Datascience/Datasets/indian_liver_patient.csv')
```

```
# showing the data from top 5
data.head()
```

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferas
0	65	Female	0.7	0.1	187	16	18
1	62	Male	10.9	5.5	699	64	100
2	62	Male	7.3	4.1	490	60	68
3	58	Male	1.0	0.4	182	14	20
4	72	Male	3.9	2.0	195	27	59

Data Preparation:

As we have understood how the data is, let's pre-process the collected data.

The download data set is not suitable for training the machine learning model as it might have so much randomness so we need to clean the dataset properly in order to fetch good results.

This activity includes the following steps.

- Handling missing values

- Handling categorical data

Note:

These are the general steps of pre-processing the data before using it for machine learning. Depending on the condition of your dataset, you may or may not have to go through all these steps

Handling Missing Values:

Let's find the shape of our dataset first. To find the shape of our data, the df.shape method is used. To find the

data type, df.info() function is used.

```
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
```

For checking the null values, df.isnull() function is used. To sum those null values we use .sum() function.

```
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
```

We can see that there are null values in the Albumin_and_Globulin_Ration Column.

Let us check how many numbers of null records present in the Closing Value column using sum() function.

```
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
```

From the above code of analysis, we can infer that columns such as Albumin and Globulin Ratio is having the missing values, we need to treat them in a required way.

```python
#checking for the missing data after cleaning data
data['Albumin_and_Globulin_Ratio'] = data.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
```

We will fill in the missing values in the numeric data type using the mean value of that particular column and categorical data type using the most repeated values.

Handling Categorical Values:

As we can see our dataset has categorical data we must convert the categorical data to integer encoding or binary encoding.

To convert the categorical features into numerical features we use encoding techniques. There are several techniques but in our project

we are using manual encoding with the help of list comprehension.

In our project, for Gender, encoding is done.

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

Milestone – 3:

Exploratory Data Analysis:

In this milestone, we will see the exploratory data analysis.

Descriptive Statistical:

Descriptive analysis is to study the basic features of data with the statistical process. Here pandas has a worthy function called describe.

With this describe function we can understand the unique, top and frequent values of categorical features. And we can find mean, std, min, max and percentile values of continuous features.

```
data.describe()
```

	age	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alanine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin
count	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000
mean	44.746141	3.298799	1.486106	290.576329	80.713551	109.910806	6.483190	3.141852
std	16.189833	6.209522	2.808498	242.937989	182.620356	288.918529	1.085451	0.795519
min	4.000000	0.400000	0.100000	63.000000	10.000000	10.000000	2.700000	0.900000
25%	33.000000	0.800000	0.200000	175.500000	23.000000	25.000000	5.800000	2.600000
50%	45.000000	1.000000	0.300000	208.000000	35.000000	42.000000	6.600000	3.100000
75%	58.000000	2.600000	1.300000	298.000000	60.500000	87.000000	7.200000	3.800000
max	90.000000	75.000000	19.700000	2110.000000	2000.000000	4929.000000	9.600000	5.500000

Visual Analysis:

Visual analysis is the process of using visual representations, such as charts, plots, and graphs, to explore and understand data.

It is a way to quickly identify patterns, trends, and outliers in the data, which can help to gain insights and make informed decisions.

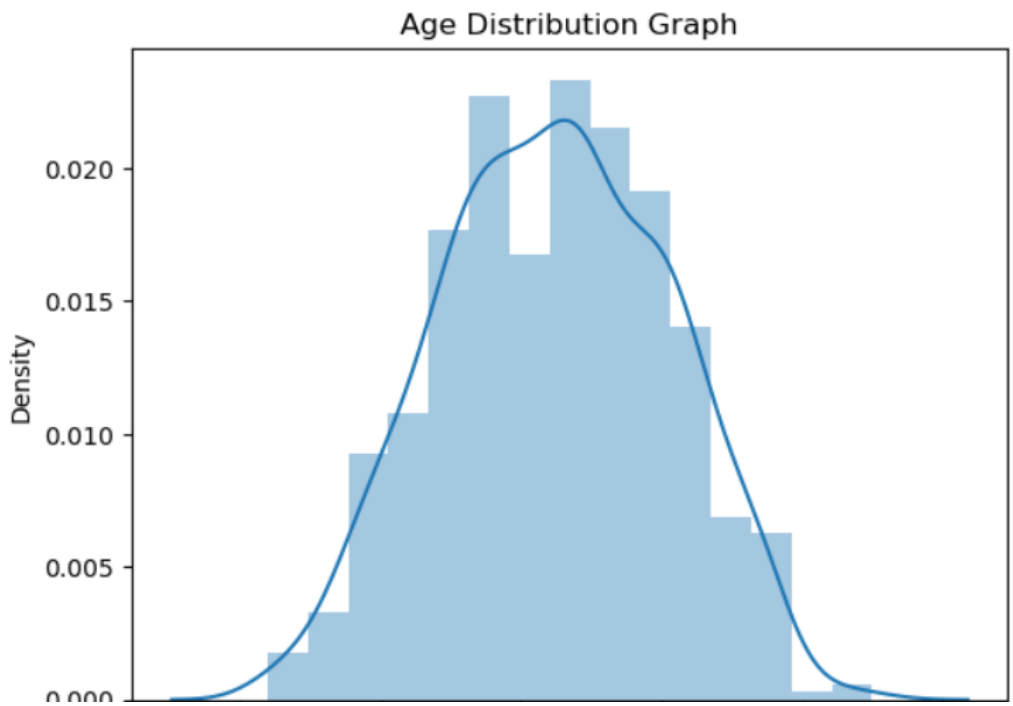
Univariate Analysis:

In simple words, univariate analysis is understanding the data with a single feature. Here we have displayed two different graphs such as distplot and countplot.

The Seaborn package provides a wonderful function distplot. With the help of distplot, we can find the distribution of the feature. To make multiple graphs in a single plot, we use subplot.

```
sns.distplot(data['age'])
plt.title('Age Distribution Graph')
plt.show()
```

```
D:\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a
oved in a future version. Please adapt your code to use either `displot` (a figure-level fun
`histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



In our dataset we have some categorical features. With the count plot function, we are going to count the unique category in those features.

Countplot:-

A count plot can be thought of as a histogram across a categorical, instead of quantitative, variable.

The basic API and options are identical to those for barplot() , so you can compare counts across nested variables.

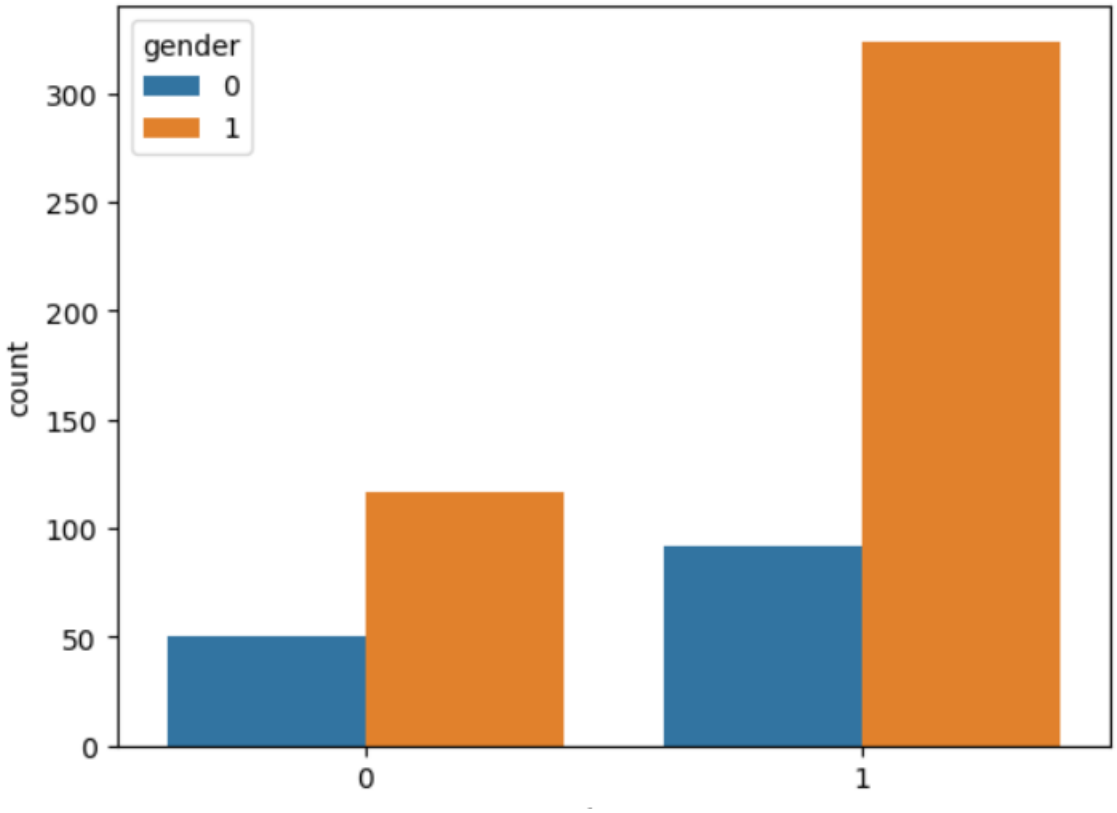
Bivariate Analysis:

```
sns.countplot(data['outcome'], hue=data['gender'])

```

```
D:\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pas
ersion 0.12, the only valid positional argument will be `data`, and passing
sult in an error or misinterpretation.
  warnings.warn(
```

```
<AxesSubplot:xlabel='outcome', ylabel='count'>
```



From the graph we can infer that , gender and outcome is a categorical variables with 2 categories , from gender column we can infer that 1-category is having more weightage than category-0, and outcome with 0,it means healthy is a underclass when compared with category -1, which means liver patient.

Multivariate Analysis:

In simple words, multivariate analysis is to find the relation between multiple features. Here we have used a heat plot from the seaborn package.

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

sns.heatmap(df.corr(),annot=True)
```

```
<AxesSubplot:>
```

Now, the code would be normalising the data by scaling it to have a similar range of values, and then splitting that data into a training set and a test set for training the model and testing its performance, respectively.

Scaling the Data:

Scaling is one the important process, we have to perform on the dataset, because of data measures in different ranges can leads to mislead in prediction

Models such as KNN, Logistic regression need scaled data, as they follow distance based method and Gradient Descent concept

```python
from sklearn.preprocessing import scale
X_scaled=pd.DataFrame (scale(X), columns=X.columns)
```

```python
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

We will perform scaling only on the input values.Once the dataset is scaled, it will be converted into an array and we need to convert it back to a dataframe

Splitting data into train and test:

Now let's split the Dataset into train and test sets

Changes: first split the dataset into x and y and then split the data set

```
X=data.iloc[:,:-1]
y=data.outcome
```

Here x and y variables are created. On x variable, df is passed with dropping the target variable. And on y target variable is passed.

For splitting training and testing data we are using the train_test_split() function from sklearn. As parameters,

we are passing x, y, test_size, random_state.

```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X_scaled,y, test_size=0.2, random_state=42)
```

Handling Imbalance Data:

Data Balancing is one of the most important step, which need to be performed for classification models, because when we train our model on imbalanced dataset, we will get biased results, which means our model is able to predict only one class element

For balancing the data we are using the SMOTE Method.

SMOTE: Synthetic minority over sampling technique, which will create new synthetic data points for under class as per the requirements given by

us using KNN method.

```
pip install imblearn
```

```
Requirement already satisfied: imblearn in d:\anaconda\lib\site-packages
Requirement already satisfied: imbalanced-learn in d:\anaconda\lib\site-
Requirement already satisfied: numpy>=1.17.3 in d:\anaconda\lib\site-pac
Requirement already satisfied: joblib>=1.1.1 in d:\anaconda\lib\site-pac
Requirement already satisfied: scikit-learn>=1.0.2 in d:\anaconda\lib\si
0.2)
Requirement already satisfied: scipy>=1.3.2 in d:\anaconda\lib\site-pack
Requirement already satisfied: threadpoolctl>=2.0.0 in d:\anaconda\lib\s
2.0)
Note: you may need to restart the kernel to use updated packages.
```

```
from imblearn.over_sampling import SMOTE
smote = SMOTE()
```

```
y_train.value_counts()
```

```
1    329
0    137
Name: outcome, dtype: int64
```

```
X_train_smote, y_train_smote = smote.fit_resample(X_train, y_train)
```

```
y_train_smote.value_counts()
```

```
1    329
0    329
Name: outcome, dtype: int64
```

From the above picture, we can infer that,previously our dataset had 329 class 1, and 132 class items, after applying smote technique on the dataset the size has become equal.

Milestone – 4:

Model Building:

In this milestone, we will see model building.

Training The Model In Multiple Algorithms:

Now our data is cleaned and it's time to build the model. We can train our data on different algorithms. For this project we are applying four classification algorithms. The best model is saved based on its performance.

Random Forest Model:

A function named RandomForestClassifier is imported and train and test data are passed as the parameters. Inside the function, RandomForestClassifier algorithm is initialised and training data is passed to the model with .fit() function.

Test data is predicted with .predict() function and saved in a new variable. For evaluating the model, a confusion matrix and classification report is done.

```python
from sklearn.ensemble import RandomForestClassifier
model1=RandomForestClassifier()
model1.fit(X_train_smote, y_train_smote)
y_predict=model1.predict(X_test)
rfc1=accuracy_score(y_test,y_predict)
rfc1
pd.crosstab(y_test, y_predict)
print(classification_report(y_test, y_predict))
```

Decision Tree Model:

A function named DecisionTreeClassifier is imported and train and test data are passed as the parameters. Inside the function, DecisionTreeClassifier algorithm is initialised and training data is passed to the model with the .fit() function.

Test data is predicted with .predict() function and saved in a new variable. For evaluating the model, a

confusion matrix and classification report is done

```
from sklearn.tree import DecisionTreeClassifier
model4=DecisionTreeClassifier()
model4.fit(X_train_smote, y_train_smote)
y_predict=model4.predict(X_test)
dtc1=accuracy_score(y_test,y_predict)
dtc1
pd.crosstab(y_test,y_predict)
print(classification_report(y_test, y_predict))
```

KNN Model:

A function named K KNeighborsClassifier is imported and train and test data are passed as the parameters. Inside the function, KNeighborsClassifier algorithm is initialised and training data is passed to the model with .fit() function.

Test data is predicted with .predict() function and saved in new variable. For evaluating the model,

confusion matrix and classification report is done.

```
from sklearn.neighbors import KNeighborsClassifier
model2=KNeighborsClassifier()
model2.fit(X_train_smote, y_train_smote)
y_predict = model2.predict(X_test)
knn1=(accuracy_score(y_test, y_predict))
knn1
pd.crosstab(y_test,y_predict)
print(classification_report(y_test, y_predict))
```

Logistic Regression Model:

A function named Logistic Regression is imported and train and test data are passed as the parameters.

Inside the function, Logistic Regression algorithm is initialised and training data is passed to the model with .fit() function.

Test data is predicted with .predict() function and saved in new variable.

For evaluating the model, confusion matrix and classification report is done.

```python
from sklearn.linear_model import LogisticRegression
model5=LogisticRegression()
model5.fit(X_train_smote, y_train_smote)
y_predict=model5.predict(X_test)
logi1=accuracy_score(y_test, y_predict)
logi1
pd.crosstab(y_test,y_predict)
print(classification_report(y_test, y_predict))
```

ANN Model:

Building and training an Artificial Neural Network (ANN) using the Keras library with TensorFlow as the backend.

The ANN is initialised as an instance of the Sequential class, which is a linear stack of layers.

Then, the input layer and two hidden layers are added to the model using the Dense class, where the number of units and activation function are specified.

The output layer is also added using the Dense class with a sigmoid activation function.

The model is then compiled with the Adam optimizer, binary cross-entropy loss function, and accuracy metric.

Finally, the model is fit to the training data with a batch size of 100, 20% validation split, and 100 epochs

```python
import tensorflow.keras
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense

```

```python
# Initialising the ANN
classifier = Sequential()
```

```python
# Adding the input layer and the first hidden layer
classifier.add(Dense(units=100, activation='relu', input_dim=10))
```

```python
# Adding the second hidden layer
classifier.add(Dense(units=50, activation='relu'))
```

```python
# Adding the output layer
classifier.add(Dense(units=1, activation='sigmoid'))
```

```python
# Compiling the ANN
classifier.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
```

```python
# Fitting the ANN to the Training set
model_history = classifier.fit(X_train, y_train, batch_size=100, validation_split=0.2, epochs=100)
```

```
Epoch 1/100
4/4 [==============================] - 2s 133ms/step - loss: 0.6497 - accuracy: 0.6532 - val_loss: 0.6394 - val_accuracy: 0.7
234
Epoch 2/100
4/4 [==============================] - 0s 21ms/step - loss: 0.6112 - accuracy: 0.7070 - val_loss: 0.6062 - val_accuracy: 0.72
34
Epoch 3/100
4/4 [==============================] - 0s 20ms/step - loss: 0.5901 - accuracy: 0.7016 - val_loss: 0.5800 - val_accuracy: 0.72
34
Epoch 4/100
4/4 [==============================] - 0s 20ms/step - loss: 0.5743 - accuracy: 0.7016 - val_loss: 0.5592 - val_accuracy: 0.72
34
Epoch 5/100
4/4 [==============================] - 0s 21ms/step - loss: 0.5619 - accuracy: 0.7016 - val_loss: 0.5437 - val_accuracy: 0.72
34
```

Testing The Model:

```
#Age	Gender	Total_Bilrubin	Direct_Bilrubin	Alkaline_Phosphotase	Alanin_Aminotransferase	Asparate_Aminotrans
model4.predict([[50,1,1.2,0.8,150,70,80,7.2,3.4,0.8]])
```

```
D:\Anaconda\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClass
ifier was fitted with feature names
  warnings.warn(
```

```
array([1], dtype=int64)
```

```
#Age	Gender	Total_Bilrubin	Direct_Bilrubin	Alkaline_Phosphotase	Alanin_Aminotransferase	Asparate_Aminotrans
model1.predict([[50,1,1.2,0.8,150,70,80,7.2,3.4,0.8]])
```

```
D:\Anaconda\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClass
ifier was fitted with feature names
  warnings.warn(
```

```
array([1], dtype=int64)
```

```
#Age	Gender	Total_Bilrubin	Direct_Bilrubin	Alkaline_Phosphotase	Alanin_Aminotransferase	Asparate_Aminotrans
model2.predict([[50,1,1.2,0.8,150,70,80,7.2,3.4,0.8]])
```

```
D:\Anaconda\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but KNeighborsClassif
ier was fitted with feature names
  warnings.warn(
D:\Anaconda\lib\site-packages\sklearn\neighbors\_classification.py:228: FutureWarning: Unlike other reduction functions
(e.g. `skew`, `kurtosis`), the default behavior of `mode` typically preserves the axis it acts along. In SciPy 1.11.0, thi
s behavior will change: the default value of `keepdims` will become False, the `axis` over which the statistic is taken wi
ll be eliminated, and the value None will no longer be accepted. Set `keepdims` to True or False to avoid this warning.
  mode, _ = stats.mode(_y[neigh_ind, k], axis=1)
```

```
array([1], dtype=int64)
```

```
#Age	Gender	Total_Bilrubin	Direct_Bilrubin	Alkaline_Phosphotase	Alanin_Aminotransferase	Asparate_Aminotrans
model5.predict([[42,0,1.2,0.8,240,70,80,7.2,3.4,0.8]])
```

```
D:\Anaconda\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but LogisticRegressio
n was fitted with feature names
  warnings.warn(
```

```
array([1], dtype=int64)
```

```
y_pred = (y_pred > 0.5)
y_pred
```

```
y([[ True],
   [ True],
   [ True],
   [ True],
```

This code defines a function named "predict_exit" which takes in a sample_value as an input.

The function then converts the input sample_value from a list to a numpy array.

It reshapes the sample_value array as it contains only one record.

Then, it applies feature scaling to the reshaped sample_value array using a scaler object 'scale' that should have been previously defined and fitted.

Finally, the function returns the prediction of the classifier on the scaled sample_value.

```python
def predict_exit(sample_value):

  # Convert list to numpy array
    sample_value = np.array(sample_value)

  # Reshape because sample_value contains only 1 record
    sample_value = sample_value.reshape(1, -1)

  # Feature Scaling
    sample_value = scale(sample_value)

    return classifier.predict(sample_value)
```

```python
#Age	Gender	Total_Bilrubin	Direct_Bilrubin	Alkaline_Phosphotase	A
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
```

Milestone – 5:

Performance Testing & Hyperparameter Tuning:

In this milestone, we will see performance testing and hyperparameter turning.

Testing Model With Multiple Evaluation Metrics:

Multiple evaluation metrics means evaluating the model's performance on

a test set using different performance measures.

This can provide a more comprehensive understanding of the model's strengths and weaknesses.

We are using accuracy, score to compare between models

Compare The Model:

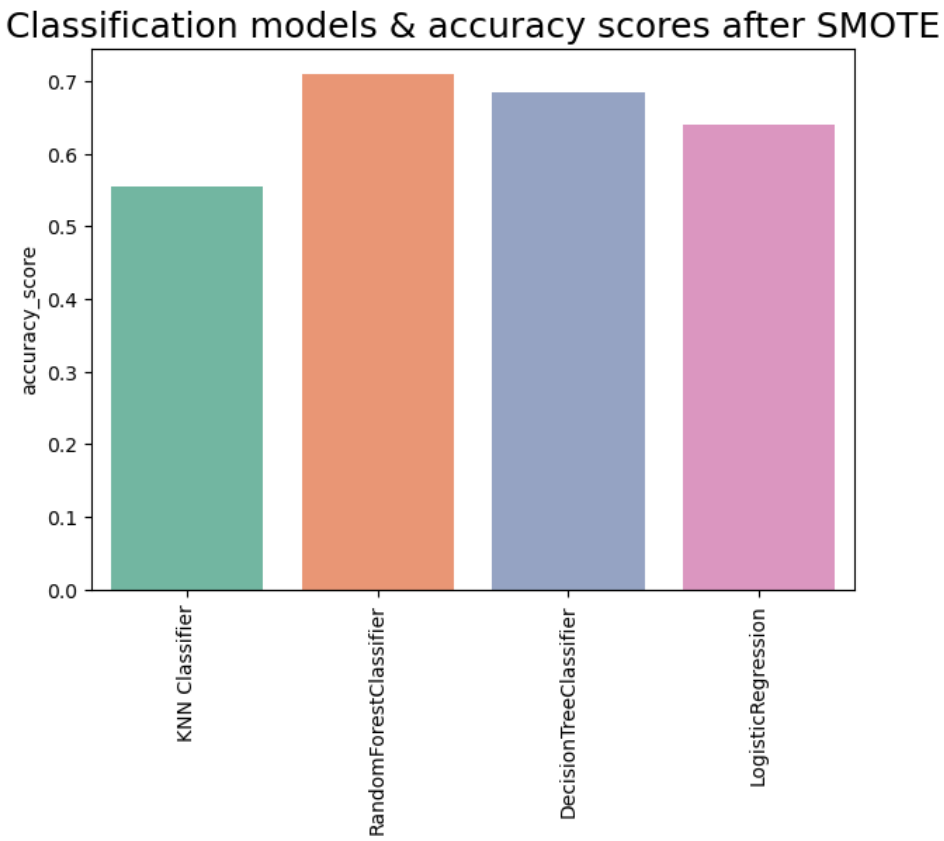
For comparing the above four models, the Accuracy function is defined.

```
acc_smote= [['KNN Classifier', knn1],  ['RandomForestClassifier', rfc1],
              ['DecisionTreeClassifier', dtc1],['LogisticRegression',logi1]]
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")
```

```
<AxesSubplot:title={'center':'Classification models & accuracy scores after SMOTE'}, xlabel='classification
l='accuracy_score'>
```



After calling the function, the results of models are displayed as output.

From the five models Random Forest Classifier is performing well.

From the above image, We can see the accuracy of the model.

Random Forest Classifer is giving the accuracy of 70 percent.

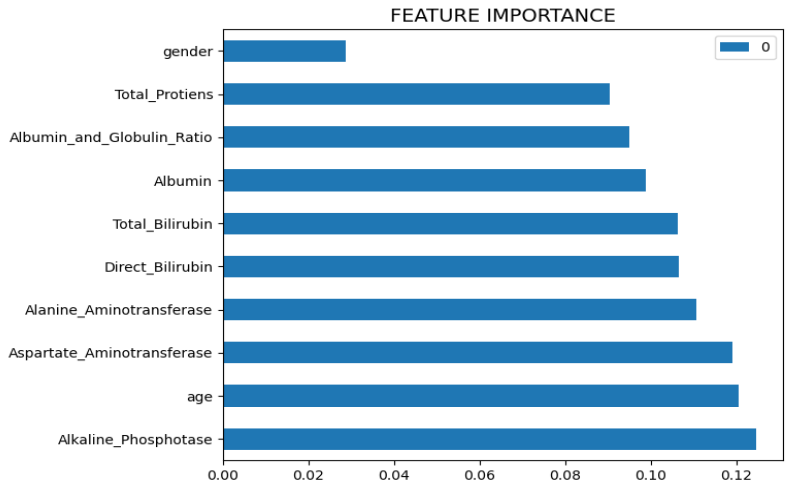
Identifying Important Features:

10 attributes are passed to predict the actucal outcome, Its necessary to identify the l important feature to determin the output.

Here we are using function called feature_importance to identify the important features among the available attributes and understand with a visualization.

```
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

Milestone – 6:

Model Deployment:

In this milestone, we will see the model deployement

Save The Best Model:

Saving the best model after comparing its performance using different evaluation metrics means selecting the model with the highest performance and saving its weights and configuration.

This can be useful in avoiding the need to retrain the model every time it is needed and also to be able to use it in the future.

```
import joblib
joblib.dump(model1, 'ETC.pkl')
```

```
['ETC.pkl']
```

Integrate With Web Framework:

In this section, we will be building a web application that is integrated to the model we built.

A UI is provided for the uses where he has to enter the values for predictions.

The enter values are given to the saved model and prediction is showcased on the UI.

This section has the following tasks

- Building HTML Pages

- Building server side script
- Run the web application

Building Html Pages:

For this project create two HTML files namely

- home.html
- predict.html

and save them in the templates folder.

Build Python Code:

Import the libraries

```
from flask import Flask, render_template, request
import numpy as np
import pickle
```

Importing the flask module in the project is mandatory. An object of Flask class is our WSGI application.

Flask constructor takes the name of the current module (__name__) as argument. And render HTML page:

```
app=Flask(__name__) # our flask app

@app.route('/') # rendering the html template
def home():
    return render_template('home.html')
@app.route('/predict') # rendering the html template
def index() :
    return render_template("index.html")
```

Here we will be using a declared constructor to route to the HTML page which we have created earlier.

In the above example, ‘/’ URL is bound with the home.html function. Hence, when the home page of the web server is opened in the browser, the html page will be rendered.

Whenever you enter the values from the html page the values can be retrieved using POST Method.

Retrieves the value from UI:

```python
@app.route('/data_predict', methods=['POST']) # route for our prediction
def predict():
    age = request.form['age'] # requesting for age data
    gender = request.form['gender'] # requesting for gender data
    tb = request.form['tb'] # requesting for Total_Bilirubin data
    db = request.form['db'] # requesting for Direct_Bilirubin data
    ap = request.form['ap'] # requesting for Alkaline_Phosphotase data
    aa1 = request.form['aa1'] # requesting for Alamine_Aminotransferase data
    aa2 = request.form['aa2'] # requesting for Aspartate_Aminotransferase data
    tp = request.form['tp'] # requesting for Total_Protiens data
    a = request.form['a'] # requesting for Albumin data
    agr = request.form['agr'] # requesting for Albumin_and_Globulin_Ratio data

    # coverting data into float format
    data = [[float(age), float(gender), float(tb), float(db), float(ap), float(aa1), float(aa2), float(tp),

    # loading model which we saved
    model = pickle.load(open('liver_analysis.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 :
    else:
        return render_template('chance.html', prediction='You dont have a liver desease problem')

if __name__ == '__main__':
    app.run()
```

Here we are routing our app to predict() function. This function retrieves all the values from the HTML page using Post request.

That is stored in an array. This array is passed to the model.predict() function.

This function returns the prediction. And this prediction value will be

rendered to the text that we have mentioned in the submit.html page earlier.

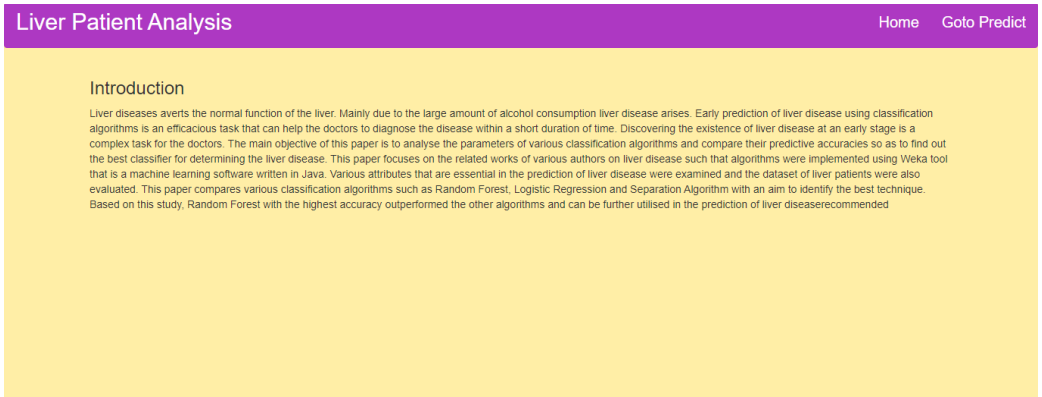
```
if __name__ == '__main__':
    app.run()
```

Run The Web Application:

- Open anaconda prompt from the start menu
- Navigate to the folder where your python script is.
- Now type “python app.py” command
- Navigate to the localhost where you can view your web page.
- Click on the predict button from the top left corner, enter the inputs, click on the submit button, and see the result/prediction on the web.

```
base) D:\TheSmartBridge\Projects\2. DrugClassification\Drug c
* Serving Flask app "app" (lazy loading)
* Environment: production
  WARNING: This is a development server. Do not use it in a p
  Use a production WSGI server instead.
* Debug mode: off
* Running on http://127.0.0.1:5000/ (Press CTRL+C to quit)
```

Now,Go the web browser and write the localhost url (http://127.0.0.1:5000) to get the below result



Now,when you click Go to predict the button from the banner you will get redirected to the prediction page.

Inputs- Now, the user will give inputs to get the predicted page after giving details user has to click on Predict Button to get the result.

Liver Patient Prediction

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

Conclusion:

Initially, the dataset was explored and made ready to be fed into the classifiers.

This was achieved by removing some rows containing null values, transforming some columns which were showing skewness and using appropriate methods (Label Encoding) to convert the labels so that they can be useful for classification purposes.

Performance metrics on which the models would be evaluated were

decided. The dataset was then split into a training and testing set.

Firstly, a naive predictor and a benchmark model ('Logistic Regression') were run on the dataset to determine the benchmark value of accuracy.

The greatest difficulty in the execution of this project was faced in two areas- determining the algorithms for training and choosing proper parameters for fine-tuning.

Initially, I found it very vexing to decide upon 3 or 4 techniques out of

the numerous options available in sklearn.

This exercise made me realize that parameter tuning is not only a very interesting but also a very important part of machine learning.

I think this area can warrant further improvement, if we are willing to invest a greater amount of time as well as computing power.