# ALAGAPPA CHETTIAR GOVERNMENT COLLEGE OF ENGINEERING AND TECHNOLOGY

**(An Autonomous Institution Affiliated to Anna University, Chennai)**

**KARAIKUDI – 630003**

**PROFESSIONAL READINESS FOR INNOVATION**

**EMPLOYABLITY AND ENTERPRENEURSHIP**

IBM PROJECT REPORT

Submitted by

**Team ID: PNT2022TMID06097**


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In partial fulfillment for the award of the degree

Of

**BACHELOR OF ENGINEERING**

**IN**

**COMPUTER SCIENCE AND ENGINEERING**

**NOVEMBER 2022**

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## KARAIKUDI – 630003

## BONAFIDE CERTIFICATE

Certified that this PROJECT REPORT **"Statistical Machine Learning Approaches to Liver Disease Prediction"** is the bonafide work of KAVIPRIYA R (**91761915021)**, SUSMITHA SV **(91761915041),** GEETHA R **(91761915013),** VISHNU R **(91761915046),** VAITHEESWARI S **(91761915044)** for **IBM NALAIYATHIRAN** in VII semester of B.E., degree course in Computer Science and Engineering branch during the academic year of 2022 - 2023.

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**Head of the Department**

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# ABSTRACT

In this paper we are going discuss how to predict risk of liver disease for a person, based on the blood test report results of the user. In this paper, the risk of liver disease was predicted using various machine learning algorithms.The final output was predicted based on the most accurate machine learning algorithm.Based on the accurate model we designed a system which asks a person to enter the details of his/her blood test report. Then the system uses the most accurate model which is trained to predict, whether a person has risk of liver disease or not.

**Keywords**—Machine learning, Liver disease, Confusion matrix

# 1. INTRODUCTION

## 1.1 Project Overview:

Healthcare is very import aspect for every human, so there is a need to provide medical service that are easily available for everyone. In the human body, liver is considered as the main organ, which plays a major role in several bodily function s like decomposition of red blood cells, etc. In ongoing time liver disease that is any damage in the liver capacity, are exceptionally normal everywhere throughout the world. It has been found that liver disease is discovered more in youthful people as a contrast with other age people. Liver disease refers to any disorder with the liver. This disease contains many conditions like inflammation (hepatitis B, C) from infectious, non-infectious causes (chemical or autoimmune hepatitis), Tumors, malignant and scarring of the liver (Cirrhosis) and Metabolic Disorders. In this paper, three classification algorithms Random Forest, Support Vector Machine and K-nearest Neighbor have been considered for implementation and comparing their results based on the Indian Liver Patient Dataset.

Software's developed for the healthcare plays a crucial role in delivering efficient services to the physicians and ultimately better treatment can be offered to the patients. An efficient healthcare software can assist in several activities like forecasting of the diseases based on the historical data of some another patient, image processing of medical images, a data warehouse for management of the whole institution etc. Proposed work focuses on the development of the software that will help in the prediction of the level diseases based upon the various symptoms. The development stage of the given software includes continuous interaction with the physicians so that more accurate results can be generated.

## 1.2 Purpose:

The liver is a crucial and big organ in the human body, impacts the digestion system. Due to Liver diseases, so many deaths are occurred in worldwide that nearly 2 million deaths per year. The main liver diseases complications are cirrhosis that 11th position in universal deaths, and others hepatocellular carcinoma and viral hepatitis that 16th leading position for global deaths. Fortunately, 3.5% of deaths are occurred due to liver diseases. Issues with liver illnesses are not found until it is regularly past the point of no return as the liver keeps on working in any event, when incompletely harmed. Early determination can conceivably be life sparing. While it is difficult to diagnose even the experienced herbal practitioner, the early signs of these diseases that be identified. Late patient experiences will graciously build up his / her standards of life. Therefore, the findings of this analysis are important from the point of view of both the computer scientist and the medical professional. The capability of an ML approach for controlling liver disease can be identified through their factors, co factors as well as complications respectively. Thus liver-related disease poses more problems for people living and is more important nowadays to recognize the causes, and identification phase. So, for early detection of liver disease, an automated program is needed to build with more accuracy and reliability. Specific machine learning models are developed for this purposeto predict the disease.

# 2. LITERATURE SURVEY

## 2.1 Existing System:

Vasan Durai presented a liver disease prediction based on the machine learning model. The proposed supervised classification algorithm J48 algorithm for prediction. The dataset is collected from the UCI repository dataset. Nazmun proposed liver disease classification by using decision tree classifier. It achieved higher accuracy than other algorithms. Ramalingam proposed the machine learning model for prediction of liver-related diseases. For this work, liver data was collected from UCI which is related to hepatitis and hepatocellular carcinoma liver disease. They proposed the K means algorithm, SVM, LR, RF and Neural Networks for liver disease prediction. Shambel in proposed a data mining technique to predict and analyze the liver disorder. They used SVM, decision tree classifiers. They performed data partitioning based on test set to test the model. Dataset repository UCI is used for prediction. Comparison of the type of liver disease discussed. Ignisha Rajathi proposed the hybrid WOA-SA and ensemble classifier was proposed. They proposed the method got better accuracy, sensitivity and specificity.

## 2.2 References:


1. Vasan Durai, Dinesh, Kalthireddy, "Liver disease prediction using machine learning", International Journal of Advance Research, Ideas and Innovations in Technology, 2017

2. Nazmun Nahar and Ferdous Ara, "Liver disease prediction by using different Decision tree techniques", International Journal of Data Mining & Knowledge Management Process (IJDKP) Vol.8, No.2, March 2018

3. V.V. Ramalingam, A.Pandian, R. Ragavendran, "Machine Learning Techniques on Liver Disease A Survey", International Journal of Engineering & Technology, 7 (4.19) (2018) 485-495

4. Shambel Kefelegn, Pooja Kamat, "Prediction and Analysis of Liver Disorder Diseases by using Data Mining Technique: Survey", International Journal of Pure and Applied Mathematics 2018.

5. G. Ignisha Rajathi 1,* and G. Wiselin Jiji 2, "Chronic Liver Disease Classification Using Hybrid Whale Optimization with Simulated Annealing and Ensemble Classifier", MDPI Journal 2019.

6. E. Brumancia, S. Justin Samuel, R. M. Gomathi and Y. Mistica Dhas,"An Effective Study on Data Fusion Models in Wireless Sensor Networks ", ARPN Journal of Engineering and Applied Sciences, Vol. 13, No. 2, January 2018.

## 2.3 Problem Statement Definition:

Liver disease can cause many deaths in recent years. Liver failure are common among Indians. Such thing alarms the necessary for the early detection of the diseases. Early detection of liver diseases will increase the survival rate of the liver disease patients. Since the population is enormous using predictive model is the best as it is economic and saves time.

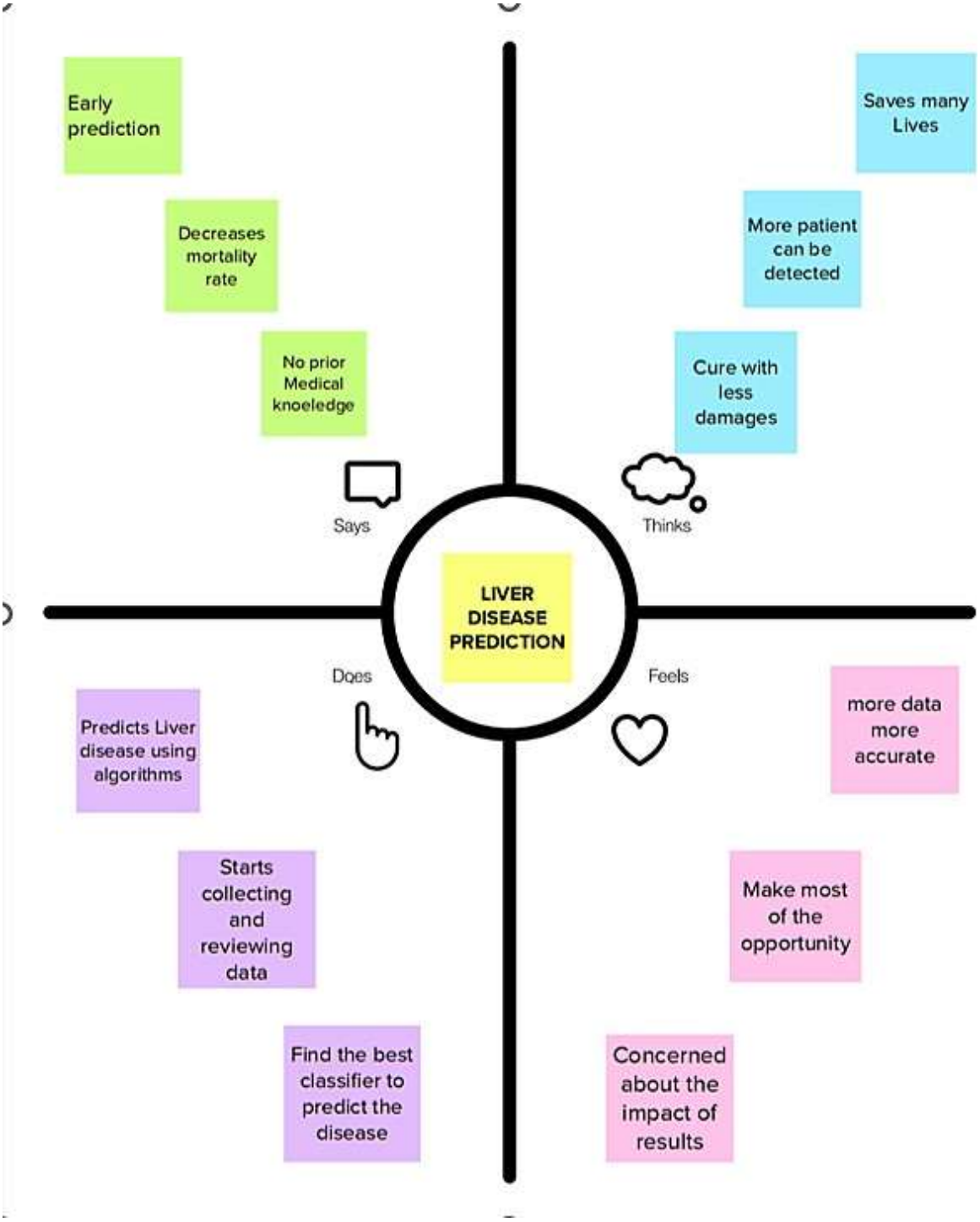
- No medical knowledge is required and the patient can fill only the required details.
- Immediate results are possible there is no need to wait for the doctor.
- Decrease the mortality rate.
- No need to wait for the doctor unlike conventional method

Example:

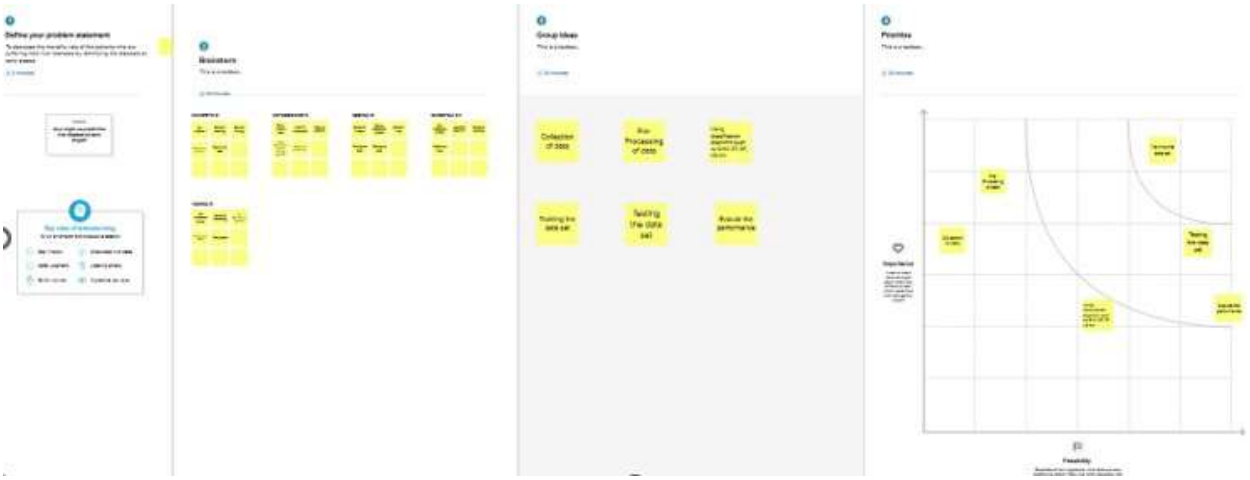
| **Problem Statement(PS)** | **I am (Customer)** | **I'm trying to** | **But** | **Because** | **Which makes me feel** |
|---|---|---|---|---|---|
| PS -1 | Person with busy schedule | Detect the diseases | It takes long time | Run of each and every test is time consuming | Tired and irritated |
| PS - 2 | Person during covid lockdown | Check my health | I can't go out of home | It is a home quarantine | Frustrated |

# 3. IDEATION & PROPOSED SOLUTION

## 3.1 Empathy Map Canvas:



## 3.2 Ideation & Brainstorming:



3

## Group ideas

This is a toolbox...

20 minutes

Collection of data

Pre-Processing of data

Using classification algorithm such as SVM, DT, RF, LG etc.

Training the data set

Testing the data set

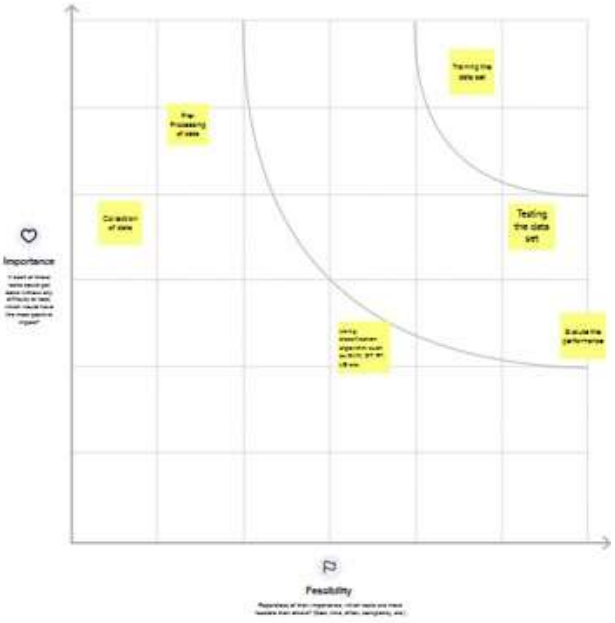
Evalute the performance

4

## Prioritize

This is a toolbox...

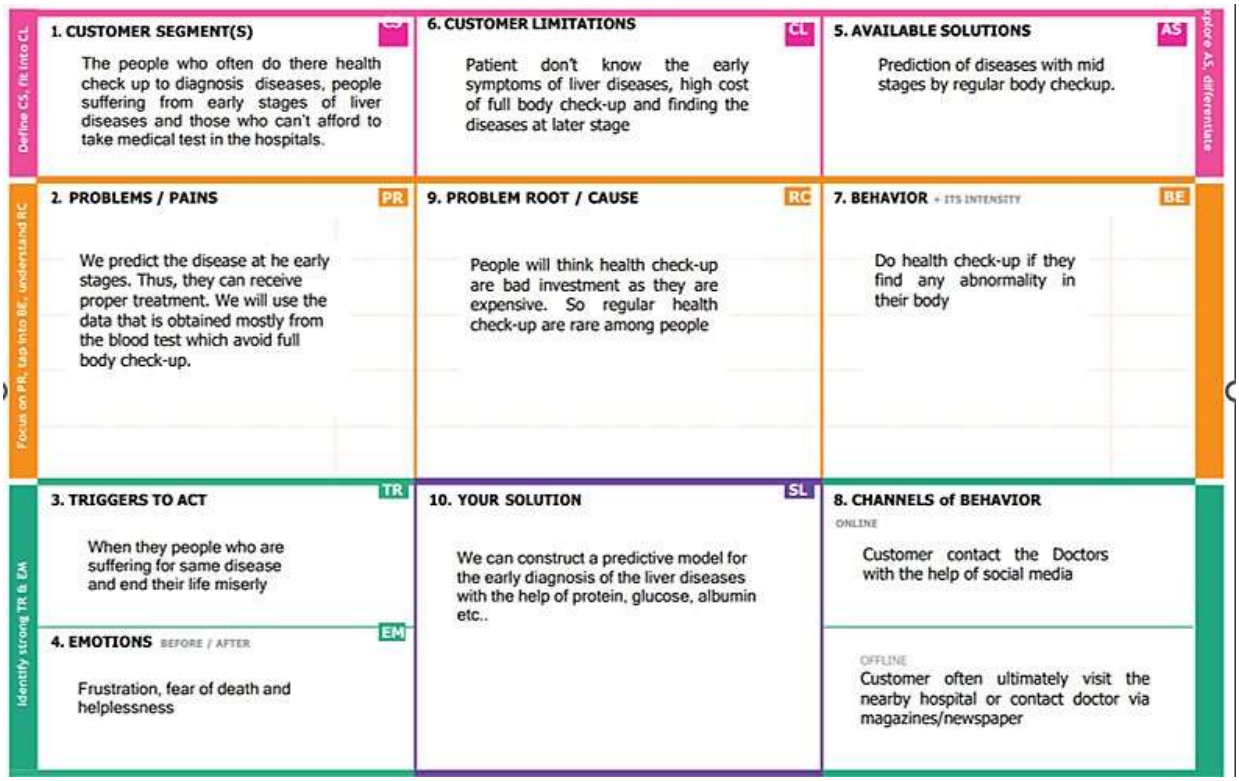
20 minutes



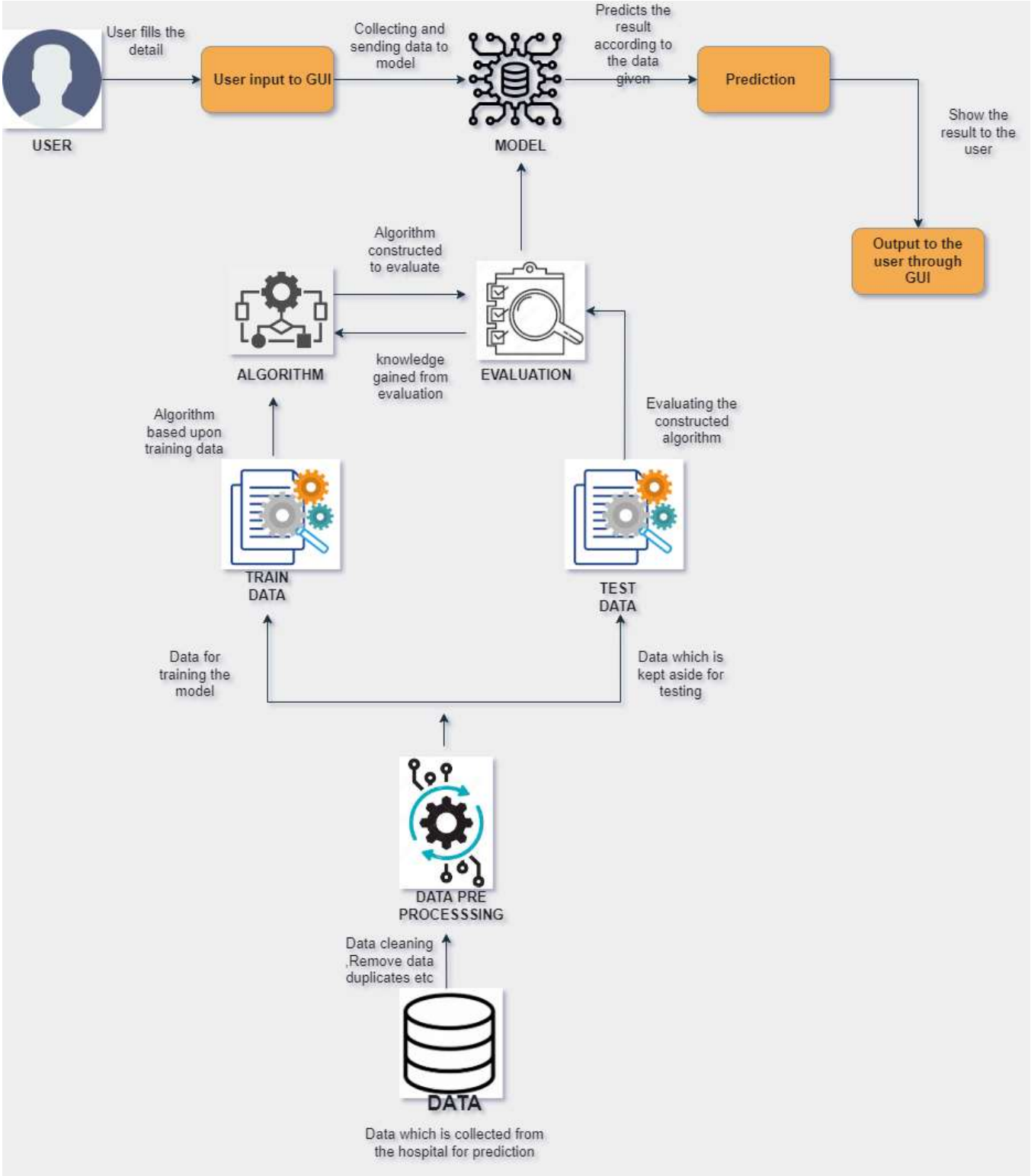
## 3.3 Proposed Solution:

| S.No. | Parameter | Description |
|---|---|---|
| 1. | Problem Statement (Problem to be solved) | To decrease the mortality rate of the patients who are suffering from liverdiseases by identifying the diseases at early stages. |
| 2. | Idea/ Solution description | Applying techniques of Supervised machine-learning algorithms such as Decision tree, Support Vector machine, logistic regression etc,By learning the pattern of the blood content using the above algorithms we can predict the liver disease at the early stage. |
| 3. | Novelty / Uniqueness | Feature selection technique helps to reduce their relevant and redundant data without affecting<br>the accuracy of the prediction model. |
| 4. | Social Impact / CustomerSatisfaction | By predicting the liver disease at the early stages we can reduce the mortality rate, chronic liver failures etc, Patients can take appropriate treatment for their respective liver<br>disease. |
| 5. | Business Model (Revenue Model) | Patients can prolong their lives, reduce medical charges and reduce the side effects. |
| 6. | Scalability of the Solution | This solution works for patients in hospitals. |

## 3.4 Problem Solution fit:



## 3.5 Solution Architecture



# 4. REQUIREMENT ANALYSIS

## 4.1 Functional requirement

Following are the functional requirements of the proposed solution.

| FR No. | Functional Requirement (Epic) | Sub Requirement (Story/ Sub-Task) |
|---|---|---|
| FR-1 | User Input | First the user enters the blood test details in the GUI of the prediction System. |
| FR-2 | Prediction Model | Applying techniques of Supervised machine learning algorithms such as Decision tree, Support Vector machine, logistic regression etc, By learning the pattern of the blood content using the above algorithms it predict the probability whether the person is affected by liver disease or not |
| FR-3 | User Output | The GUI show the predicted output by the model to the user. |

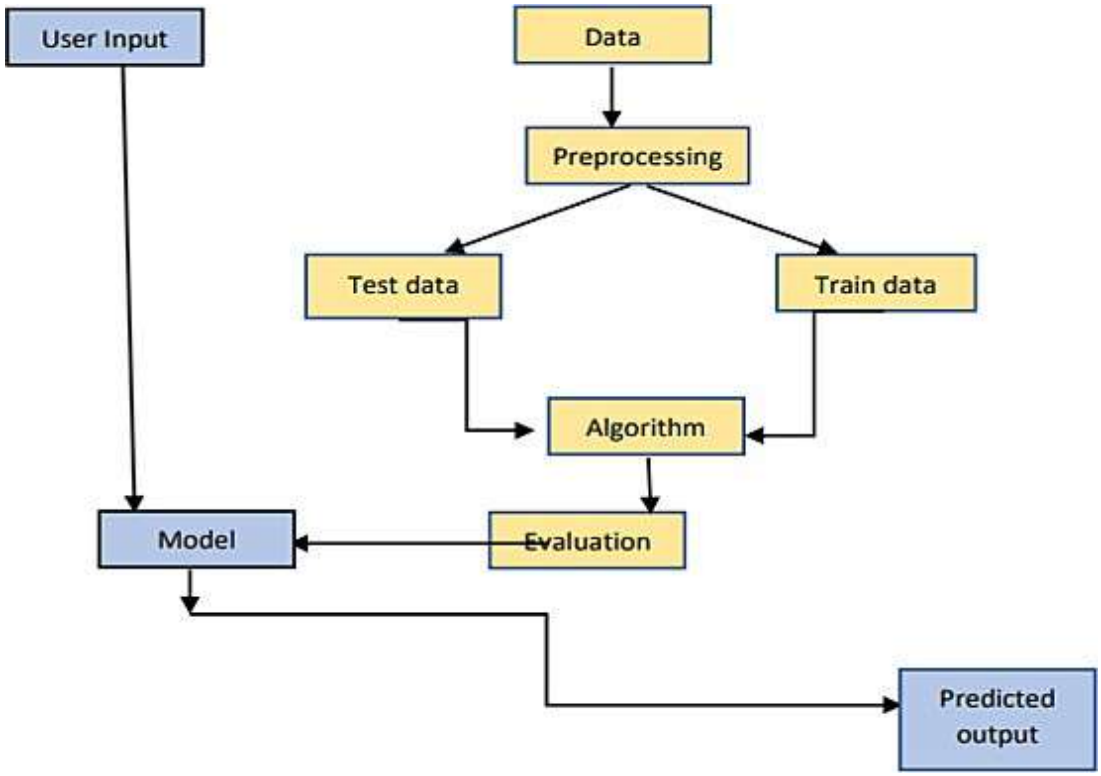
## 4.2 Non-Functional requirements

Following are the non-functional requirements of the proposed solution.

| FR No. | Non-Functional Requirement | Description |
|---|---|---|
| NFR-1 | Usability | The people who can access internet can use this model. |
| NFR-2 | Security | Watson assistant has certifications such as ISO,SOC2,US HIPAA, European Union GDPR,PCIDSS. We use security systems such as TCS/SSL,IPSEC ,Third party CAs, HTTPS, Encrypted file systems, Encrypted storage systems, Key management systems, AES-256bit. |
| NFR-3 | Reliability | Data Type –Dialog Query, Intent etc.Configurations done using small integration Code snippets such as JavaScript, SQL and can also be done using Watson APIs. |
| NFR-4 | Performance | This solution works for patients who don't have time to visit hospitals. |
| NFR-5 | Availability | The Web interface is made available using load balancers, distributed servers etc. |

# 5. PROJECT DESIGN

## 5.1 Data Flow Diagrams



## 5.2 Solution & Technical Architecture

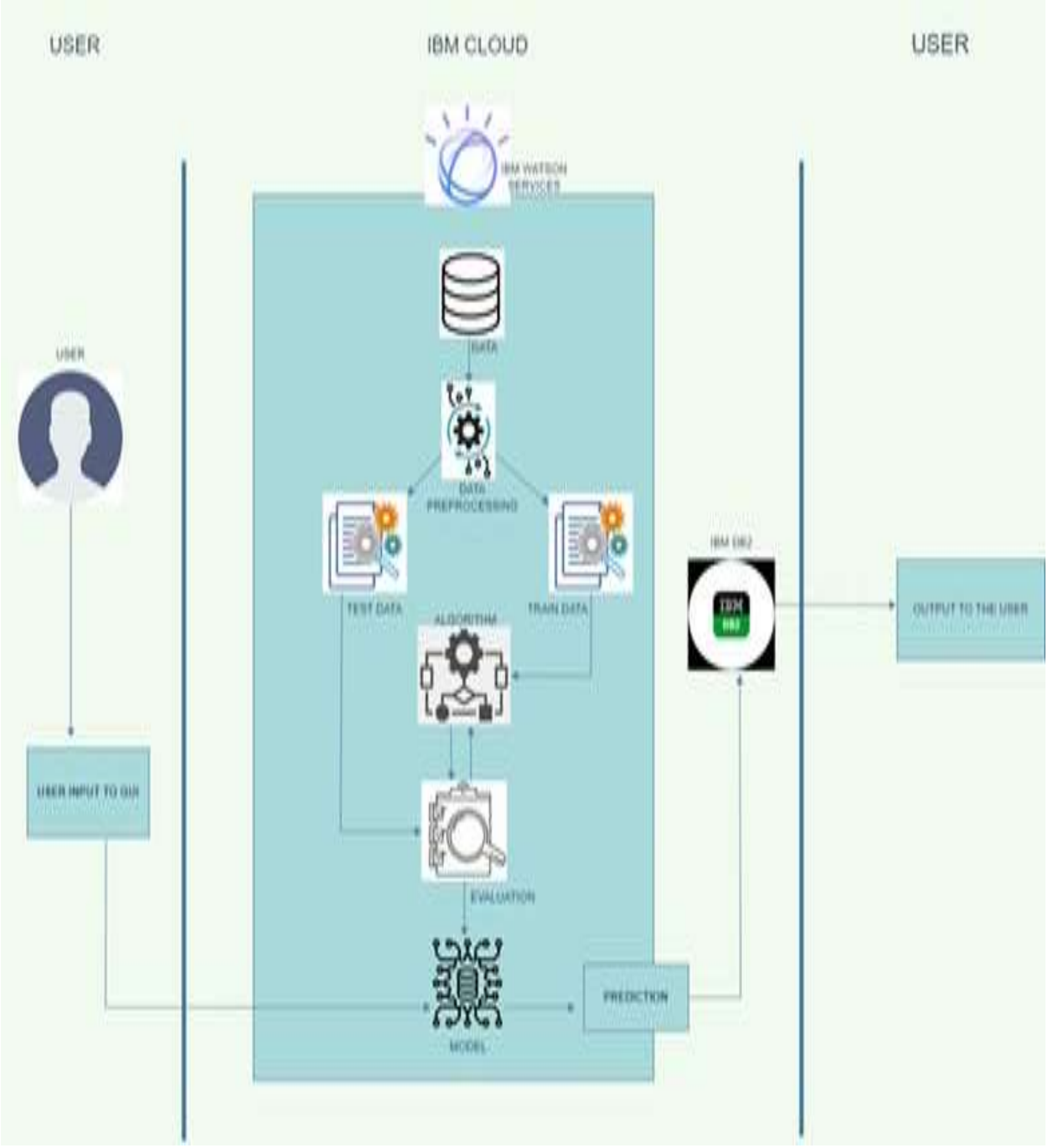


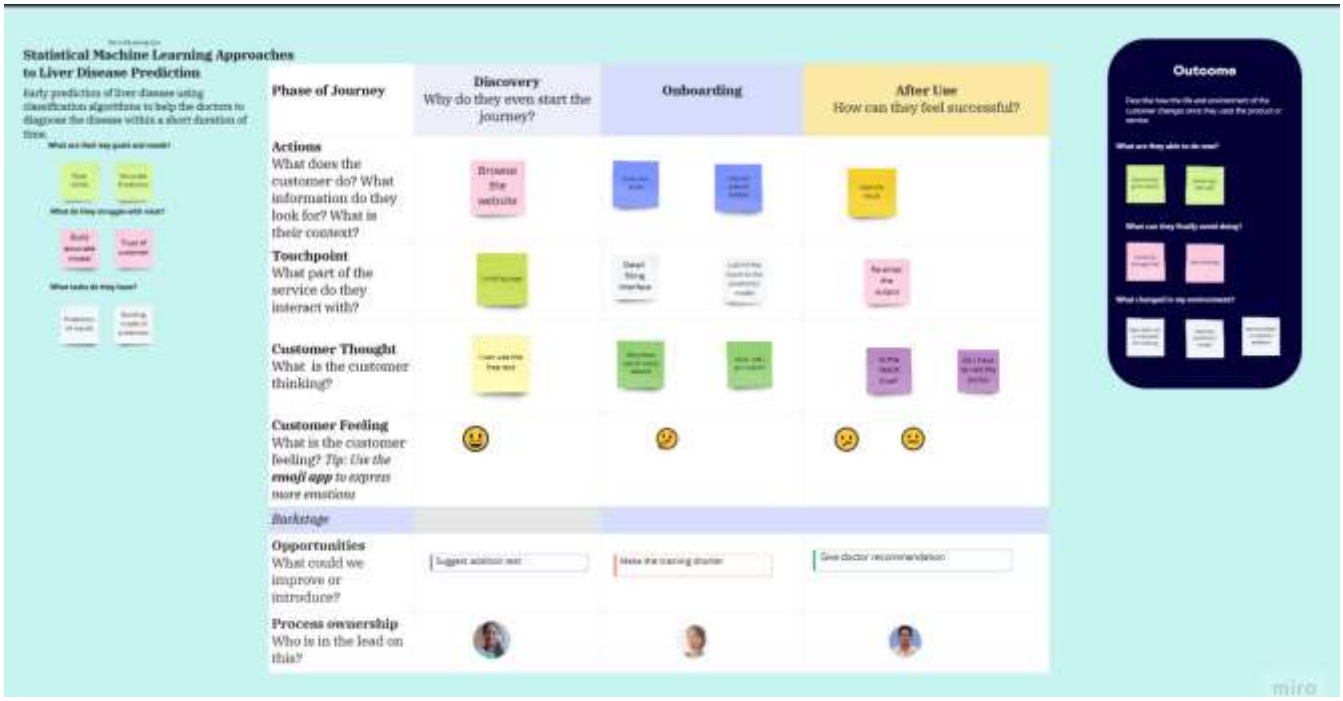
**Table-1 : Components & Technologies:**

| S.No | Component | Description | Technology |
|---|---|---|---|
| 1. | User Interface | Web Interface | HTML, CSS, JavaScript |
| 2. | Application Logic-1 | Prediction Model | Python |
| 3. | Application Logic-2 | Dealing with Dataset | IBM Watson STT service |
| 4. | Application Logic-3 | Training and Building Machine Learning Model | IBM Watson studio |
| 5. | Application Logic-4 | Matching intent /Entities | IBM Watson Assistant ,IBM Watson Studio, Knowledge Base/Studio |
| 6. | Application Logic-5 | Deployment | Python Flask |
| 7. | Database | Data Type –Dialog Query, Intent etc.Configurations done using small integration Code snippets such as Javascript , SQL and can also be done using Watson APIs. | MySQL or IBMDB2 |
| 8. | Cloud Database | Database Service on Cloud | IBM DB2, IBM Cloudant etc. |
| 9. | File Storage | For storing datasets | IBM Block Storage Service or Local Filesystem, IBM cloud, IBM Watson studio |
| 10. | Machine LearningModel | Liver Disease detection model and other machine learning models | IBM Watson studio etc. |
| 11. | Infrastructure(Server / Cloud) | On cloud server we will be deploying the web interface using flask in the web page | Python Flask |

**Table-2: Application Characteristics:**

| S.No | Characteristics | Description | Technology |
|---|---|---|---|
| 1. | Open-SourceFrameworks | Open-source frameworks used is IBM Watson | Technology of Opensource framework<br>IBM Watson |
| 2. | Security Implementations | IBM cloud | Watson assistant has certifications such as ISO,SOC2,US HIPAA, European Union GDPR,PCI DSS.We use securitysystems such as TCS/SSL,IPSEC,Third party CAs, HTTPS, Encrypted file systems, Encrypted storage systems, Key management systems, AES -256 bit. |
| 3. | ScalableArchitecture | Web interface architecture consist offour pillars. They are intents, entities ,data flow, scripts (3 – tier architecture Micro-services architecture) | Technology used - IBM Watson Assistant |
| 4. | Availability | The Web interface is made available using load balancers,<br>distributed servers etc. | Technology used- IBM Watson Assistant |
| 5. | Performance | IBM Watson<br>–automate processes, The deep learning model is trained using IBM Watson studio for better performance, Cache, CDN's, etc. | Technology used-IBM Watson |

## 5.3 Customer Journey Map



| User Type | Functional Requirement (Epic) | User Story Number | User Story / Task | Acceptance criteria | Priority | Release |
|---|---|---|---|---|---|---|
| Customer (Mobile user) | User Input | USN-1 | As a user, Ican enter the level of blood contents as an input | The levelmust be in perfect units | High | Sprint-4 |
| Customer (Web user) | Access ofresource | USN-2 | The user canget the result from his blood report through this platform | The levelmust be in perfect units | High | Sprint-3 |
| Administrator | Manipulationof dataset | USN-3 | Can do modification or updation and storing of data | Modify, Update,store | High | Sprint-4 |

# 6. PROJECT PLANNING & SCHEDULING

## 6.1 Sprint Planning & Estimation

| Sprint | Functional Requirement (Epic) | User Story Number | User Story/ Task | Story Points | Priority | Team Members |
|---|---|---|---|---|---|---|
| **Sprint-1** | Dataset reading and Pre-processing | USN-1 | Cleaning the dataset and splitting to dependent and independent variables | 2 | High | R.Kavipriya, S.Vaitheeswari, R.Geetha |
| **Sprint-2** | Building the model | USN-2 | Choosing the appropriate model for building and saving the model as Pickle file | 1 | High | R.Kavipriya, S.Vaitheeswari, R.Vishnu |
| **Sprint-3** | Application Building | USN-3 | Using flask deploying the ML model | 2 | Medium | R.Kavipriya, SV.Susmitha, R.Geetha |
| **Sprint-4** | Train the model in IBM | USN-4 | Finally train the model on IBM cloud and deploy the application | 2 | Medium | R.Kavipriya, S.Vaitheeswari, R.Vishnu, SV.Susmitha |

## 6.1 Sprint Delivery Schedule

| Sprint | TotalStory Points | Duration | Sprint Start Date | Sprint End Date (Planned) | Story Points Completed (as on Planned End Date) | Sprint Release Date (Actual) |
|---|---|---|---|---|---|---|
| **Sprint-1** | 15 | 5 Days | 24 Oct 2022 | 29 Oct 2022 | 15 | 29 Oct 2022 |
| **Sprint-2** | 15 | 5 Days | 31 Oct 2022 | 05 Nov 2022 | 15 | 05 Nov 2022 |
| **Sprint-3** | 15 | 5 Days | 07 Nov 2022 | 12 Nov 2022 | 15 | 12 Nov 2022 |
| **Sprint-4** | 15 | 5 Days | 14 Nov 2022 | 19 Nov 2022 | 15 | 1 Nov 2022 |

## 6.2 Reports from JIRA

# 7.CODING & SOLUTIONING

## Importing libraries

```
from __future__import print_function
import numpy as np
import pandas as pd

import matplotlib.pyplot as plt
import seaborn as sns
import pickle

from sklearn.metrics import classification_report
from sklearn import metrics
from sklearn import tree
import warnings
warnings.filterwarnings('ignore')
```

## Reading the dataset

```
import os, types
import pandas as pd
from botocore.client import Config
import ibm_boto3
def __iter__(self): return 0
# @hidden_cell
# The following code accesses a file in your IBM Cloud Object Storage. It includes your credentials.
# You might want to remove those credentials before you share the notebook.
cos_client = ibm_boto3.client(service_name='s3',
    ibm_api_key_id='S99NLHOje_E5Woi1838p4ky6uiswjO73jrW5jkU1scRn',
    ibm_auth_endpoint="https://iam.cloud.ibm.com/oidc/token",
    config=Config(signature_version='oauth'),
    endpoint_url='https://s3.private.us.cloud-object-storage.appdomain.cloud')
bucket = 'liverdiseaseprediction-donotdelete-pr-ktrgtkel8a8ktv'
object_key = 'indian_liver_patient.csv'
body = cos_client.get_object(Bucket=bucket,Key=object_key)['Body']

# add missing __iter__method, so pandas accepts body as file-like object

if not hasattr(body, "__iter__"): body.__iter__= types.MethodType(__iter__, body )


df= pd.read_csv(body)
df.head()
df.tail(10)
df.info()
```

```
df.describe()
df.shape
df['Gender'] = df['Gender'].apply(lambda x:1 if x=='Male' else 0)
df.head(10)
df.describe()
```

## Checking and handling null values

```
df.isnull().any()
```

## Checking misssing data

```
df.isnull().sum()
df['Albumin_and_Globulin_Ratio'].mean()
df = df.fillna(0.9474)
df.isnull().sum()
```

## Data visualization

```
sns.pairplot(df,hue='Gender')
cor =df.corr()
plt.figure(figsize=(20,10))
sns.heatmap(cor,annot=True,cmap="Blues")
```

## Counting patients who are male and female

```
sns.countplot(data=df, x ='Gender')
M,F= df['Gender'].value_counts()
print("No of males:",M)
print("No of females: ",F)
sns.countplot(data=df, x ='Dataset')
LD,NLD = df['Dataset'].value_counts()
print("Liver disease patients:",LD)
print("Non-Liver disease patients:",NLD)
```

## Splitting the dataser into dependent and independent variable

```
#independent variable as x
x=df.iloc[:,0:-1]
#dependent variable as y
y=df.iloc[:,-1]
from sklearn.model_selection import train_test_split
xtrain,xtest,ytrain,ytest=train_test_split(x,y,test_size=0.2,random_state=3)
xtrain.shape
ytrain.shape
xtest.shape
```

## Train and Test the model

```
from sklearn.svm import SVC

from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
acc =[]
model =[]
```

## Support vector machine

```
from sklearn.svm import SVC
svm = SVC()
svm.fit(xtrain,ytrain)
#Evalution model

svmpred =svm.predict(xtest)
x=metrics.accuracy_score(ytest,svmpred) acc.append(x)
model.append("SVM") print("SVM Accuracy is : ",x*100)
print(classification_report(ytest,svmpred))
svmcm = metrics.confusion_matrix(svmpred,ytest) svmcm
```

## Random Forest

```
from sklearn.ensemble import RandomForestClassifier
RF = RandomForestClassifier()
RF.fit(xtrain,ytrain)


#Evalution model
RFpred =RF.predict(xtest)
x=metrics.accuracy_score(ytest,RFpred)
acc.append(x)
model.append("RF")


print("RF Accuracy is : ",x*100)
print(classification_report(ytest,RFpred))
RFcm = metrics.confusion_matrix(RFpred,ytest)
RFcm
```

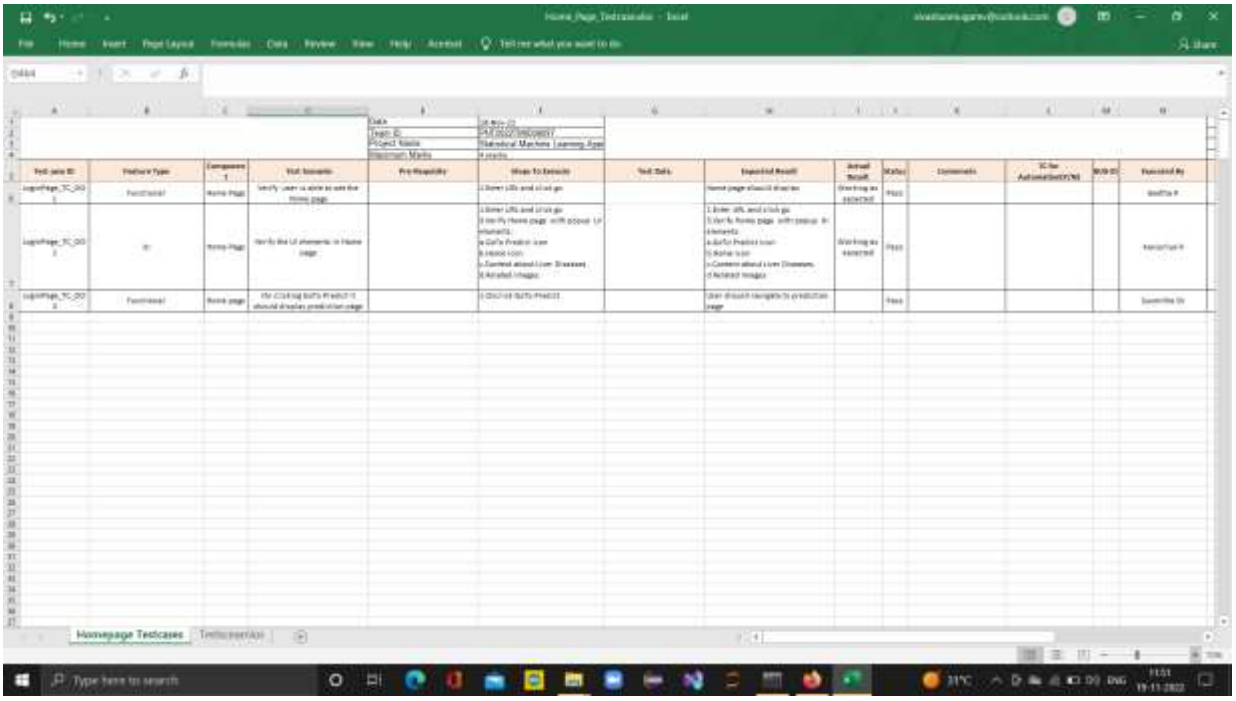
## K -Neighbors

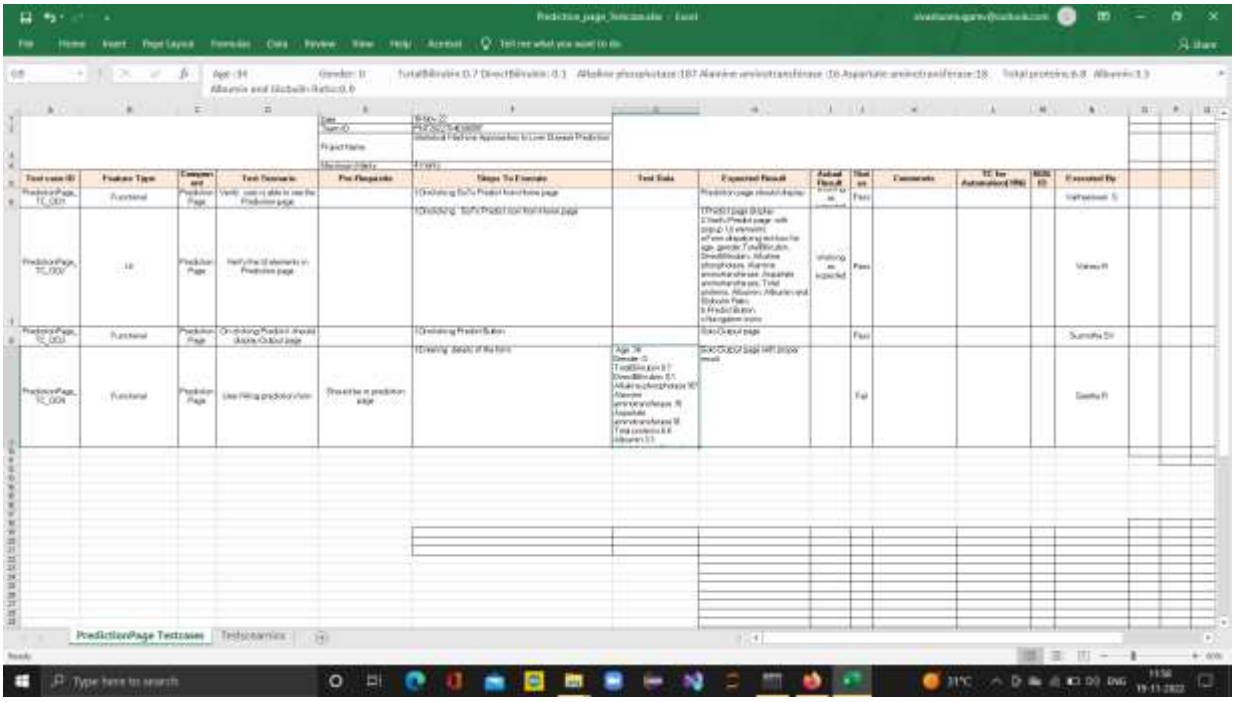
```
from sklearn.neighbors import KNeighborsClassifier
KNN = KNeighborsClassifier()
KNN.fit(xtrain,ytrain) #Evalution model
KNNpred=KNN.predict(xtest)
x=metrics.accuracy_score(ytest,KNNpred)
acc.append(x)
model.append("KNN") print("KNN Accuracy is :
```

```
",x*100)
print(classification_report(ytest,KNNpred))

KNNcm =
metrics.confusion_matrix(KNNpred,ytest)


KNNcm


# Comparsion Accuracy plt.figure(figsize=[10,5],dpi
= 100) plt.title('Accuracy Comparison')
plt.xlabel('Accuracy') plt.ylabel('Algorithm')
sns.barplot(x = acc,y = model,palette='dark')
accuracy_models = dict(zip(model, acc))
for k, v in accuracy_models.items():
   print (k, '-->', v)


!pip install ibm_watson_machine_learning


from ibm_watson_machine_learning import APIClient
import json
wml_credentials={


   "url":"https://us-south.ml.cloud.ibm.com",
   "apikey":"93CJYdbuZo_81MXVlqD41jwkevyGqn9W6IXR-t1p16Fd"}
client=APIClient(wml_credentials)
def guid_from_space_name(client,space_name):
  space= client.spaces.get_details()
  return(next(item for item in space['resources']if

item['entity']["name"]==space_name)['metadata']['id'])
```

# 8.TESTING

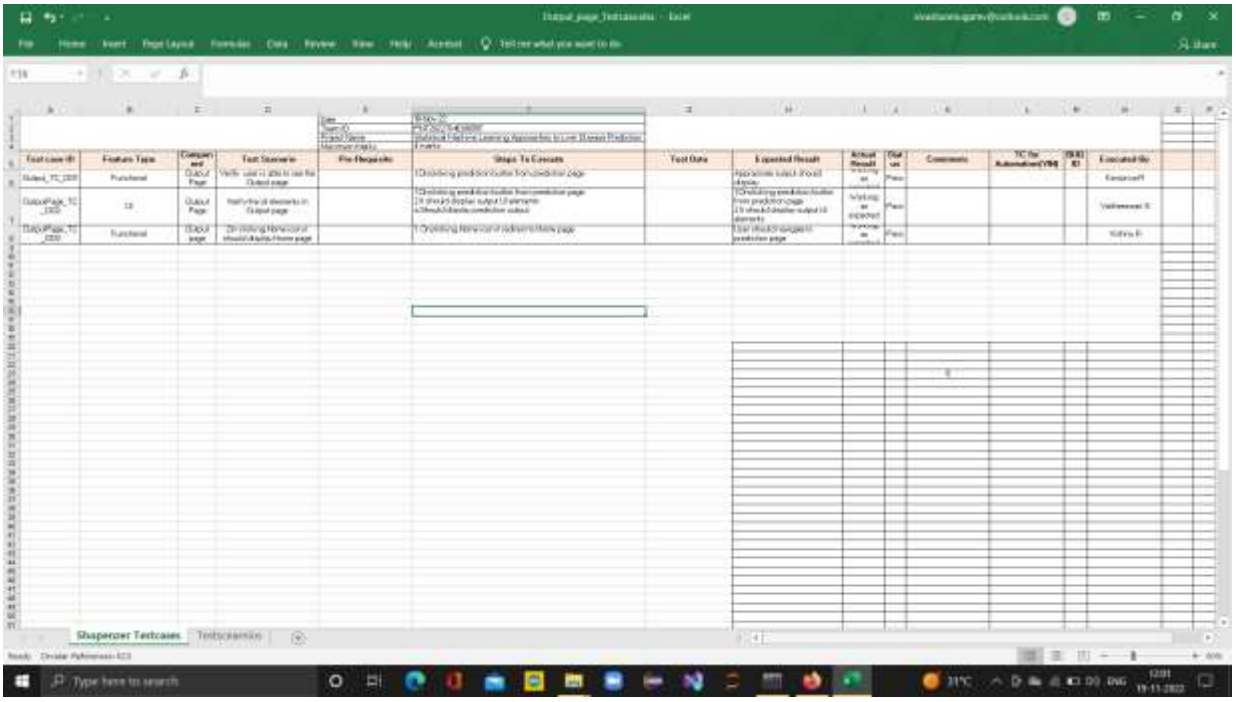
## 8.1 User Acceptance Testing





| Test case ID | Feature Type | Component | Test Scenario | Pre-Requisite | Steps To Execute | Test Data | Expected Result | Actual Result | Status | Comments | TC for Automation? (Y/N) | BUG ID | Executed By |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PredictionPage_TC_001 | Functional | Prediction Page | Verify user is able to see the Prediction page | | 1)Clicking 'Go' to Predict from home page | | Prediction page should display | | Pass | | | | Vaitheeswari. S |
| PredictionPage_TC_002 | UI | Prediction Page | Verify the UI elements in Prediction page | | 1)Clicking 'Go' to Predict from Home page | | 1)Predict page should be:<br>i)Check i)Predict page with proper UI elements<br>ii)From should have the age, gender, Total Bilirubin, Direct Bilirubin, Alkaline phosphatase, Alanine aminotransferase, Aspartate aminotransferase, Total proteins, Albumin, Albumin and Globulin Ratio<br>iii)Predict Button<br>iv)Navigation icons | Working as expected | Pass | | | | Vishnu R |
| PredictionPage_TC_003 | Functional | Prediction Page | On clicking Predict it should display Output page | | 1)Clicking Predict Button | | Must Output page | | Pass | | | | Sumitha SV |
| PredictionPage_TC_004 | Functional | Prediction Page | User Filling prediction form | Should be in prediction page | 1)Clicking 'Predict' button of the form | Age: 34<br>Gender: 0<br>Total Bilirubin: 0.7<br>Direct Bilirubin: 0.1<br>Alkaline phosphatase: 187<br>Alanine aminotransferase: 16<br>Aspartate aminotransferase: 18<br>Total proteins: 6.8<br>Albumin: 3.3 | Must Output page with proper result | | Fail | | | | Geetha R |

PredictionPage Testcases | Testscenarios

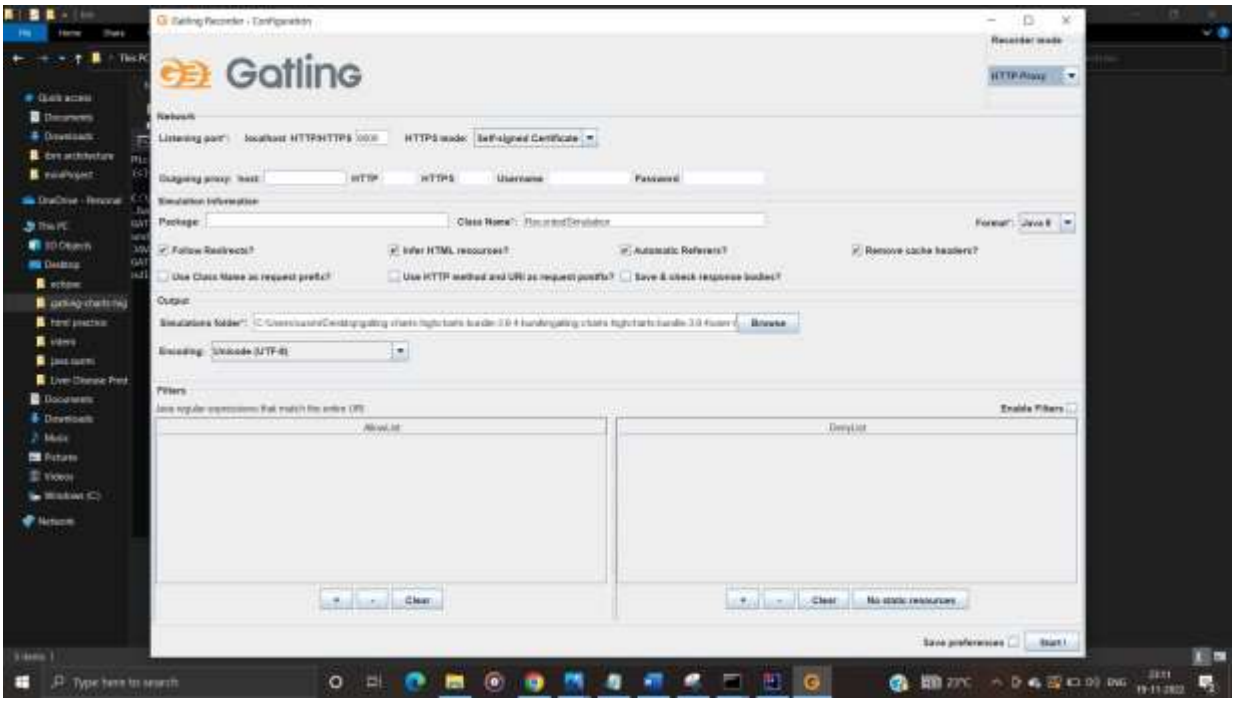


| Test case ID | Feature Type | Component | Test Scenario | Pre-Requisite | Steps To Execute | Test Data | Expected Result | Actual Result | Status | Comments | TC for Automation? (Y/N) | BUG ID | Executed By |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Output_TC_000 | Functional | Output Page | Verify user is able to see the Output page | | 1)Clicking prediction button from prediction page | | Appropriate output should display | | Pass | | | | Kanaiyan R |
| OutputPage_TC_001 | UI | Output Page | Verify the UI elements in Output page | | 1)Clicking prediction button from prediction page<br>2) It should display output UI elements<br>a)Result b)Alcoholic cirrhosis or not | | 1)Clicking prediction button from prediction page<br>2) It should display output UI elements | Working as expected | Pass | | | | Vaitheeswari. S |
| OutputPage_TC_002 | Functional | Output page | On clicking Home icon it should display Home page | | 1) Clicking Home icon in redirect to Home page | | 1) UI should navigate to prediction page | | Pass | | | | Vishnu R |

Shapezer Testcases | Testscenarios

# 9 RESULTS

## 9.1 Performance Metrics:



# 10 ADVANTAGES & DISADVANTAGES

## 10.1 ADVANTAGES:

- Improving the business operations for seamless hospital management.
- Predictive analytics in healthcare insurance has led to the patients, hospitals, and insurance companies working in tandem to process claims and avoid complications.
- Lowers the risk of error and increases customer satisfaction.
- Identifying the right target audiences to promote.
- Predicting and analyzing the risk of outbreaks and pandemics.
- Analyzing and controlling the deterioration of patients health.

## 10.2 DISADVANTAGES:

- Prediction results is may not accurate.
- May influence customer-purchasing patterns when anticipating human behavior.
- Initial implementation of predictive analytics is expensive in terms of hiring specialists who can manage data.

# 11.CONCLUSION

In this worK, the different machine learning algorithms is evaluated for the prediction of liver disease. Due to the subtle nature of its symptoms, liver disease is particularly difficult to diagnose. Liver disease prediction followed the step of preparing data in that data was collected from the public database preprocessing of data for -1 value replacement. Data division into the entire array of data split into training and research. Eventually, quantitative measurement metrics such as precision, accuracy and recall are measured over various machine learning models.

# 12.FUTURE SCOPE

In future we can apply the efficient feature selection algorithms and deep learning algorithms to improve the accuracy in liver disease classifications.

# APPENDIX

**Source code:**

**HTML pages:**

**Home page:**

```
<!DOCTYPE html>
<html lang="en">

<head>
   <!-- Required meta tags always come first -->
      <meta charset="utf-8">
      <meta name="viewport" content="width=device-width, initial-scale=1, shrink-to-fit=no">
      <meta http-equiv="x-ua-compatible" content="ie=edge">

      <!-- Bootstrap CSS -->
      <link rel="stylesheet" href="{{
url_for('Static',filename='node_modules/bootstrap/dist/css/bootstrap.min.css') }} ">
      <link rel="stylesheet" href= "{{ url_for('Static',filename='node_modules/font-awesome/css/font-
awesome.min.css') }}">
      <link rel="stylesheet" href="{{ url_for('Static',filename='node_modules/bootstrap-social/bootstrap-
social.css') }}">
      <link rel="stylesheet" href="{{ url_for('Static',filename='Static/css/ibmcss.css') }} ">

   <title>Liver disease prediction</title>

</head>
<body>
   <nav class="navbar navbar-dark navbar-expand-sm  fixed-top" style="background-color:#9575CD;">
      <div class="container">
         <h1 style="color: floralwhite">Liver Disease Prediction</h1>
         <button class="navbar-toggler" type="button" data-toggle="collapse" data-target="#Navbar">
            <span class="navbar-toggler-icon"></span>
         </button>

         <div class="collapse navbar-collapse" id="Navbar">

            <ul class="navbar-nav ml-auto">
               <li class="nav-item "><a class="nav-link" href="#"><span class="fa fa-home fa-
lg"></span>Home</a></li>
               <li class="nav-item active"><a class="nav-link" href="/predict" ><span class="fa fa-info fa-
lg"></span>Goto predict</a> </li>

            </ul>
```

```
        </div>

      </div>

  </nav>
<header class="jumbotron" >
  <div class="container">
    <div class="row row-header" style="padding-top: 60px;">
      <div class="col-12 col-sm-8">
        <h1>Liver Disease</h1>
        <p>There are many types of liver disease, which can be caused by infections, inherited conditions, obesity and misuse of alcohol. Over time, liver disease may lead to scarring and more serious complications. Early treatment can help heal the damage and prevent liver failure.</p>
      </div>
      <div class="ml-auto">
        <img src="static/img/liver.jpg" class="img-fluid" style="width:270px; height: 180px;">
      </div>
    </div>
  </div>
</header>



  <div class="container">



      <div class="row row-content ">
        <div class=" col-sm-8">
          <h2>What is Liver Disease?</h2>
          <p>Your liver is your body’s second-largest organ (after the skin). It sits just under your ribcage on the right side and is about the size of a football. The liver separates nutrients and waste as they move through your digestive system. It also produces bile, a substance that carries toxins out of your body and aids in digestion.The term “liver disease” refers to any of several conditions that can affect and damage your liver. Over time, liver disease can cause cirrhosis (scarring). As more scar tissue replaces healthy liver tissue, the liver can no longer function properly. Left untreated, liver disease can lead to liver failure and liver cancer.</p>
          <h2>What causes different type of liver disease ?</h2>
          <p>Different types of liver disease result from different causes. Liver disease may result from:</p>
          <ul>
          <li><p>Viral infections: Hepatitis A, hepatitis B and hepatitis C are diseases caused by a viral infection.</p></li>
          <li><p>Problems with your immune system: When your immune system mistakenly attacks your liver, it can cause autoimmune liver diseases. These include primary biliary cholangitis and autoimmune hepatitis.</p></li>
          <li><p>Inherited diseases: Some liver problems develop because of a genetic condition (one you inherit from your parents). Inherited liver diseases include Wilson disease and hemochromatosis.</p></li>
          <li><p>Cancer: When abnormal cells multiply in your liver, you may develop tumors. These tumors may be benign (noncancerous) or malignant (liver cancer).</p></li>
          <li><p>Consuming too many toxins: Alcohol-related fatty liver disease is the result of alcohol use. Non-alcohol related fatty liver disease (NAFLD) results from consuming too much fat. NAFLD is becoming
```

more common as rates of obesity and diabetes rise. </li></ul>
<h2>What are the symptoms of liver disease?</h2>
Some types of liver disease (including non-alcohol fatty liver disease) rarely cause symptoms. For other conditions, the most common symptom is jaundice — a yellowing of your skin and the whites of your eyes. Jaundice develops when your liver can't clear a substance called bilirubin.
Other signs of liver disease may include:
<ul>
<li> Abdominal (belly) pain (especially on the right side). </li>
<li> Bruising easily. </li>
<li> Changes in the color of your urine or stool. </li>
<li> Fatigue. </li>
<li> Nausea or vomiting. </li>
<li> Swelling in your arms or legs (edema). </li>
</ul>
<h2>What are the complications of liver disease?</h2>
Some types of liver disease can increase your risk of developing liver cancer. Others, if left untreated, continue to damage your liver. Cirrhosis (scarring) develops.
Over time, a damaged liver won't have enough healthy tissue to function. Liver disease that isn't treated can eventually lead to liver failure

<dl>

<img src="static/img/liver1.jpg" class="img-fluid" style="width:300px">
</dl>

<blockquote class="blockquote">
"Your liver is your vital detoxification organ, and if it becomes overloaded with toxins from the food, drink, or medications you're consuming, you'll have more toxins circulating throughout your body, damaging your organs and glands. Detoxing your liver will help it work more efficiently and help you slim your waistline."

<footer class="blockquote-footer">Suzanne Somers
</footer>
</blockquote>

<!-- jQuery first, then Popper.js, then Bootstrap JS. -->
<script src="{{ url_for('Static',filename='node_modules/jquery/dist/jquery.slim.min.js') }} "></script>
<script src="{{ url_for('Static',filename='node_modules/popper.js/dist/umd/popper.min.js') }}"></script>

```
        <script src="{{ url_for('Static',filename='node_modules/bootstrap/dist/js/bootstrap.min.js') }}"></script>

    </body>

</html>
```

**Prediction page:**

```
<!DOCTYPE html>
<html lang="en">
<head>
    <!-- Required meta tags always come first -->
    <meta charset="utf-8">
    <meta name="viewport" content="width=device-width, initial-scale=1, shrink-to-fit=no">
    <meta http-equiv="x-ua-compatible" content="ie=edge">

    <!-- Bootstrap CSS -->
    <link rel="stylesheet" href="{{
url_for('Static',filename='node_modules/bootstrap/dist/css/bootstrap.min.css') }} ">
    <link rel="stylesheet" href="{{ url_for('Static',filename='node_modules/font-awesome/css/font-
awesome.min.css') }}">
    <link rel="stylesheet" href="{{ url_for('Static',filename='node_modules/bootstrap-social/bootstrap-
social.css') }}">
    <link rel="stylesheet" href="{{ url_for('Static',filename='Static/css/ibmcss.css') }}">
  <title>Liver disease predication</title>


</head>

<body>
  <nav class="navbar navbar-dark navbar-expand-sm  fixed-top" style="background: #9575CD;">
    <div class="container">
      <h1 style="color: floralwhite">Liver disease prediction</h1>
      <button class="navbar-toggler" type="button" data-toggle="collapse" data-target="#Navbar">
        <span class="navbar-toggler-icon"></span>
      </button>
      <a class="navbar-brand mr-auto" href="./index.html"></a>
      <div class="collapse navbar-collapse" id="Navbar">

        <ul class="navbar-nav ml-auto">
          <li class="nav-item active "><a class="nav-link" href="./"><span class="fa fa-home fa-
lg"></span>Home</a></li>
          <li class="nav-item "><a class="nav-link" href="#"><span class="fa fa-info fa-lg"></span>Goto
predict</a></li>

        </ul>

      </div>

    </div>

  </nav>
```

```
<form action='/data_predict' method="post">

   <div class="offset-sm-1 col-sm-10 align-self-center"  style="padding-top:100px">
      <div class="card" >

         <h3 class="card-header bg-warning text-white"  >
           <a name="Prediction"> Details for Prediction</a>
          </h3>
          <div class="card-body" >


             <dl class="row">
                <dt class="col-sm-3">Age</dt>

                    <div class=" col-sm-2 ">
                    <input type="text"  id="age" name="age"  required></input>
                  </div>
                  <dt class="offset-sm-1 col-sm-3">Gender</dt>
                  <div class="offset-sm-0 col-sm-1">
                    <input type="text"  id="gender" name="gender" placeholder="For male 1 female
0"required ></input>
                  </div>

             </dl>
         <dl class="row">
            <dt class="col-sm-3">Total_Bilirubin</dt>

                <div class=" col-sm-2 ">
                <input type="text"  id="tb" name="tb" required></input>
             </div>
             <dt class="offset-sm-1 col-sm-3">Direct_Bilirubin</dt>
             <div class="offset-sm-0 col-sm-1">
                <input type="text"  id="db" name="db" required></input>
             </div>

          </dl>
          <dl class="row">
             <dt class="col-sm-3">AlkalinePhosphotase</dt>

                <div class=" col-sm-2 ">
                <input type="text"  id="ap" name="ap" required></input>
             </div>
             <dt class="offset-sm-1 col-sm-3">AlamineAminotransferase</dt>
             <div class="offset-sm-0 col-sm-1">
                <input type="text"  id="aa1" name="aa1" required></input>
             </div>

          </dl>
          <dl class="row">
             <dt class="col-sm-3">AspartateAminotransferase</dt>
```

```
                    <div class=" col-sm-2 ">
                    <input type="text"  id="aa2" name="aa2" required ></input>
                  </div>
                  <dt class="offset-sm-1 col-sm-3">Total_Proteins</dt>
                  <div class="offset-sm-0 col-sm-1">
                    <input type="text"  id="tp" name="tp" required></input>
                  </div>

                </dl>
                <dl class="row">
                  <dt class="col-sm-3">Albumin</dt>

                    <div class=" col-sm-2 ">
                    <input type="text"  id="a" name="a" required></input>
                  </div>
                  <dt class="offset-sm-1 col-sm-3">AlbuminGlobulin_Ratio</dt>
                  <div class="offset-sm-0 col-sm-1">
                    <input type="text"  id="agr" name="agr" required></input>
                  </div>

                </dl>
        <div class="offset-sm-4 col-sm-6 align-self-center" style="padding: 40px;">
          <button class="btn btn-info" type="submit" style="width: 200px;" >Predict</button>
        </div>

        </div>

      </div>
    </div>
    </form>
    <br></br>


    <!-- jQuery first, then Popper.js, then Bootstrap JS. -->
    <script src="{{ url_for('Static',filename='node_modules/jquery/dist/jquery.slim.min.js') }} "></script>
    <script src="{{ url_for('Static',filename='node_modules/popper.js/dist/umd/popper.min.js') }}"></script>
    <script src="{{ url_for('Static',filename='node_modules/bootstrap/dist/js/bootstrap.min.js') }}"></script>

    </script>

</body>

</html>
```

**Output Page:**

```
<!DOCTYPE html>
<html lang="en">
<head>
    <!-- Required meta tags always come first -->
    <meta charset="utf-8">
    <meta name="viewport" content="width=device-width, initial-scale=1, shrink-to-fit=no">
    <meta http-equiv="x-ua-compatible" content="ie=edge">

    <!-- Bootstrap CSS -->
    <link rel="stylesheet" href="{{ url_for('Static',filename='node_modules/bootstrap/dist/css/bootstrap.min.css') }} ">
    <link rel="stylesheet" href="{{ url_for('Static',filename='node_modules/font-awesome/css/font-awesome.min.css') }}">
    <link rel="stylesheet" href="{{ url_for('Static',filename='node_modules/bootstrap-social/bootstrap-social.css') }}">
    <link rel="stylesheet" href="{{ url_for('Static',filename='Static/css/ibmcss.css') }}">
  <title>Liver disease predication</title>


</head>

<body>
  <nav class="navbar navbar-dark navbar-expand-sm  fixed-top"  style="background-color:#9575CD;">
    <div class="container">
      <h1 style="color: floralwhite">Liver disease prediction</h1>
      <button class="navbar-toggler" type="button" data-toggle="collapse" data-target="#Navbar">
        <span class="navbar-toggler-icon"></span>
      </button>

      <div class="collapse navbar-collapse" id="Navbar">

        <ul class="navbar-nav ml-auto">
          <li class="nav-item active "><a class="nav-link" href="./"><span class="fa fa-home fa-lg"></span>Home</a></li>
          <li class="nav-item "><a class="nav-link" href="#"><span class="fa fa-info fa-lg"></span>Goto predict</a> </li>

        </ul>

      </div>

    </div>

  </nav>



  <div class="offset-sm-1 col-sm-10" style="padding: 80px;" >
    <div class="card">
      <h3 class="card-header bg-warning text-white"  >
        <a name="Prediction"> PREDICTION RESULT</a>

        <div class="card-body">
          <dl>
            {{prediction}}
          </dl>
```

```
        </div>

      </div>
   </div>
   <br></br>


   <!-- jQuery first, then Popper.js, then Bootstrap JS. -->
   <script src="{{ url_for('Static',filename='node_modules/jquery/dist/jquery.slim.min.js') }} "></script>
   <script src="{{ url_for('Static',filename='node_modules/popper.js/dist/umd/popper.min.js') }}"></script>
   <script src="{{ url_for('Static',filename='node_modules/bootstrap/dist/js/bootstrap.min.js') }}"></script>


   </script>

</body>

</html>
```

**Flask integration code:**

```
import requests

import flask
from flask import render_template,request
from flask_cors import CORS

# NOTE: you must manually set API_KEY below using information retrieved from your IBM Cloud account.
API_KEY = "mEN1R-IypcevD8OJ3TmLAuEF69C53deaLliQClu7Qg-m"
token_response = requests.post('https://iam.cloud.ibm.com/identity/token', data={"apikey":
 API_KEY, "grant_type": 'urn:ibm:params:oauth:grant-type:apikey'})
mltoken = token_response.json()["access_token"]

header = {'Content-Type': 'application/json', 'Authorization': 'Bearer ' + mltoken}

app = flask.Flask(__name__,static_url_path='')
CORS(app)

@app.route('/',methods =['GET','POST'])
def home():
   return render_template('Home.html')


@app.route('/predict',methods =['GET','POST'])
def index():
   return render_template('Prediction.html')

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

def predict():
   age =float(request.form['age'])
   gender =float(request.form['gender'])
```

```
    tb =float(request.form['tb'])
    db =float(request.form['db'])
    ap =float(request.form['ap'])
    aa1 =float(request.form['aa1'])
    aa2 =float(request.form['aa2'])
    tp =float(request.form['tp'])
    a =float(request.form['a'])
    agr =float(request.form['agr'])

    X=[[age,gender,tb,db,ap,aa1,aa2,tp,a,agr]]

# NOTE: manually define and pass the array(s) of values to be scored in the next line
    payload_scoring = {"input_data": [{"field": [['age','gender','tb','db','ap','aa1','aa2','tp','a','agr']], "values": X}]}

    response_scoring = requests.post('https://us-south.ml.cloud.ibm.com/ml/v4/deployments/58fa0711-e9d9-4847-adca-
ce45c5a43f93/predictions?version=2022-11-18', json=payload_scoring,
    headers={'Authorization': 'Bearer ' + mltoken})
    predictions = response_scoring.json()
    predict = predictions['predictions'][0]['values'][0][0]
    if(predict == 1):
        return render_template('Output.html',prediction ='You have a liver disease and you must take treatment')
    else :
        return render_template('Output.html',prediction ='You have dont have liver')


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

**GITHUB LINK:**

https://github.com/IBM-EPBL/IBM-Project-39320-1660406217

**DEMO LINK:**

https://drive.google.com/file/d/15W2yLWnr4pkGJx-2XyF-xPXDVEcKG5It/view?usp=sharing