IBM PROJECT

Statistical Machine Learning Approaches to Liver Disease Prediction

Team ID	PNT2022TMID52974
	Statistical Machine Learning Approaches to Liver Disease Prediction

TEAM MEMBERS:

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1.INTRODUCTION

1.1 Project Overview

Health is the state of physical, mental and social well-being, Leading a productive life is from having good health i.e., proper functioning of organs that are interconnected. The organ LIVER is crucial organ for one's existence as its one of main functions is detoxification, cleansing blood by eliminating toxins. Liver disease refers to several conditions that badly affects one's health. Liver disease can be predicted/detected by liver function test generally where it takes a day for result and it can go undetected if liver's function may decrease for a while. When undetected for a long time it leads to life threatening condition. So regular health examination is must. The project proposes a model /solution to above problem to predict the liver disease in faster manner using machine learning approaches or methods for early detection .

1.2 Project Purpose

Lets say leading a healthy and happy life is every single beings' motto. Leading a healthy life is by proper functioning of organs. It is said that 40% of Indians suffer from NAFLD(Non-alcoholic fatty liver disease) and 1 among 10 people in America suffer from some sort of liver disease. The cost of liver function tests is affordable by people but when undetected due to SLOW FUNCTIONING of liver leading to critical conditions the cost sums a lot that can't be afforded by all people. The proposed model/solution will be made as an app where a individual can take their own tests by answering some vital questions while not feeling well, and they can consult their doctors regarding their symptoms and taking medications as directed.

1.3 Existing Problems

PROBLEM STATEMENT:

To develop machine learning approaches to predict liver disease by training datasets in existing machine learning methods and the testing the dataset of patient to get the results. This model is made into an user interface app where it is reached to all corners of people effectively.

What does the problem affect? - Health of an individual
What are the boundaries of the problem? - Human life
Why is it important to fix this problem? - "No liver = No life"

2. LITERATURE SURVEY

S.No	Title	Method used	Description	link
1	Supervised machine learning based liver disease prediction approach with LASSO feature selection	1.LASSO feature extraction method 2.10 fold cross validation approach 3.nearly 8 classification algorithms(LR, DT, RF, AdaBoost KNN, LDA,gradient boosting and SVM.)	Reduces overfitting using LASSO. Comparing classification algorithm based on accuracy, sensitivity, precision and f1-scores which help to identify the highest performing algorithm . 10 foldcross validation to split dataset for training and testing. LR has more accuracy than others followed by LDA&SVM.	https://beei. org/index.p hp/EEI/arti cle/view/32 42/2437
2	Intelligent Techniques and Comparative Performance Analysis of Liver Disease Prediction	Bioinfomatics &Random Forest (RF), Multilayer Perceptron (MLP) model, k Nearest Neighbour (kNN), and Support Vector Machine (SVM)	genetic data of patient is known by bioinformatics and drugs are invented into the area of defects in genetic structure. SVM has more accuracy than others	https://kala harijournals .com/resour ces/IJME_ Vol7.1_756 .pdf

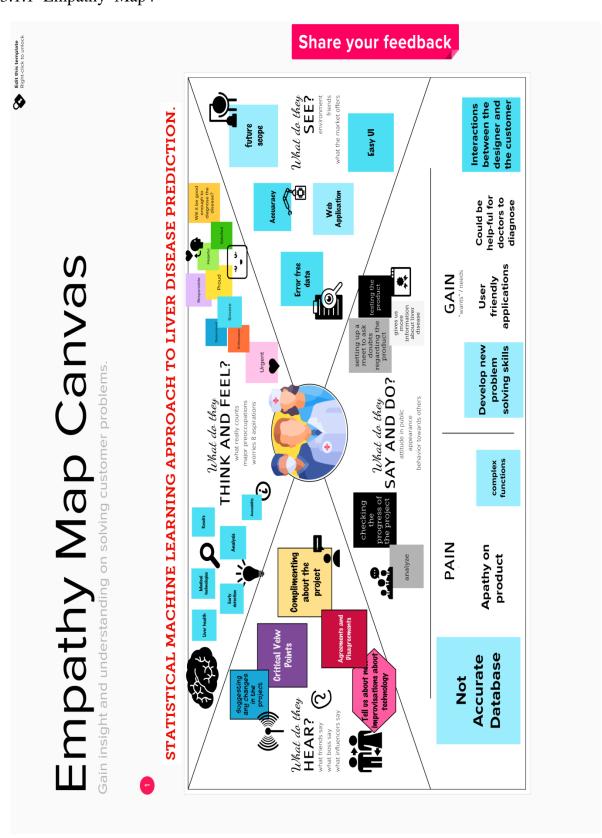
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SSN College Of Engineering

3	Accurate liver	Modified Principal	The attributes, "Accuracy,	https
	disease prediction	component analysis -	′	://doi.org/1
	system using	preprocessing Score based	_	0.17485/IJS
	convolutional	Artificial Fish Swarm	between modified CNN	T/v14i17.4
	neural network	Algorithm (SAFSA)-	(MCNN) and Multi layer	51
		Optimal feature selection	perceptron neural network	
		Modified CNN-	(MLPNN)	
		classification	MCNN has higher % than	
		Classification	MLPNN	
			IVILI IVIV	
4	Liver Disease	kNN	Datasets are taken from open	https://doi.o
	Prediction Using		source platform and	rg/10.1007/
	Machine Learning	Random Forest	comparison is made between	978-981-
	Algorithm		ML methods	16-0171-
				2_56
5	Evaluation based	SVM	The main objective is to	https://doi.o
	approaches for	N 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	predict tumour or disease with	rg/10.1109/
	Liver disease	LR	respect to data mining	ICCCI5082
	prediction using		techniques. Comparison of	6.2021.940
	Machine learning		evaluation parameters for SVM	2463
	Algorithms		and LR is made	

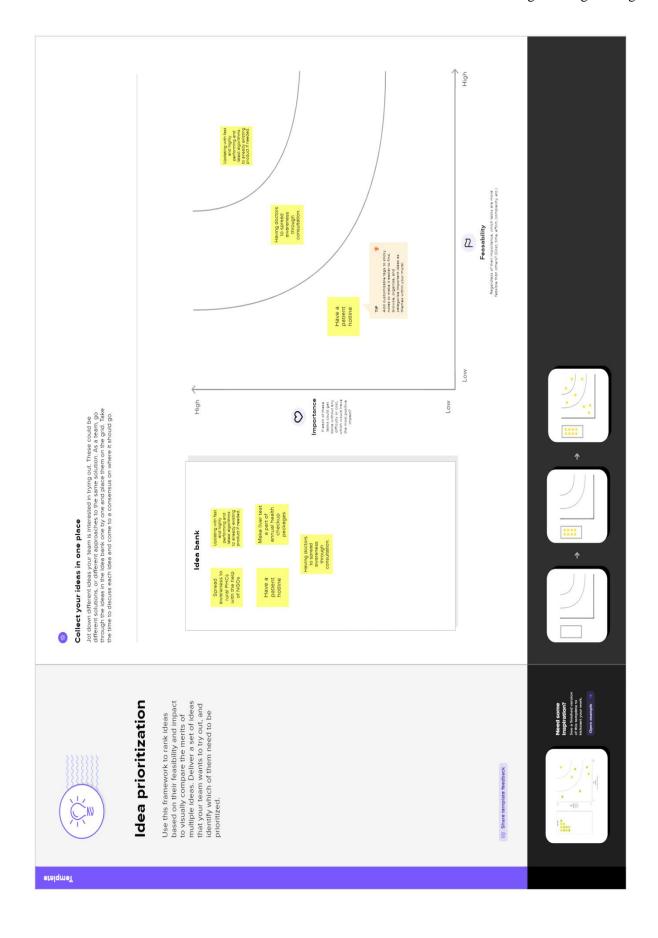
3. PROJECT DESIGN AND PLANNING

- 3.1 Ideation phase
- 3.1.1 Empathy Map:

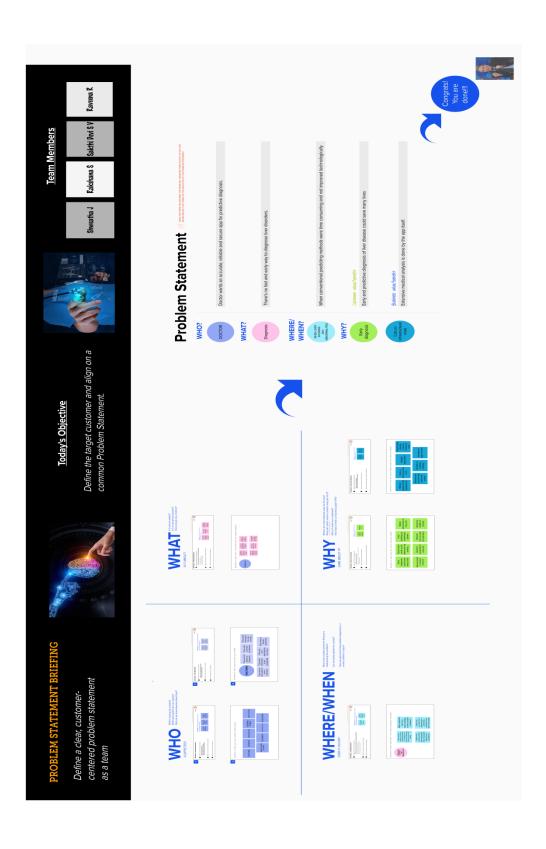


3.1.2 Ideation and Brainstorming





3.1.3 Problem statement



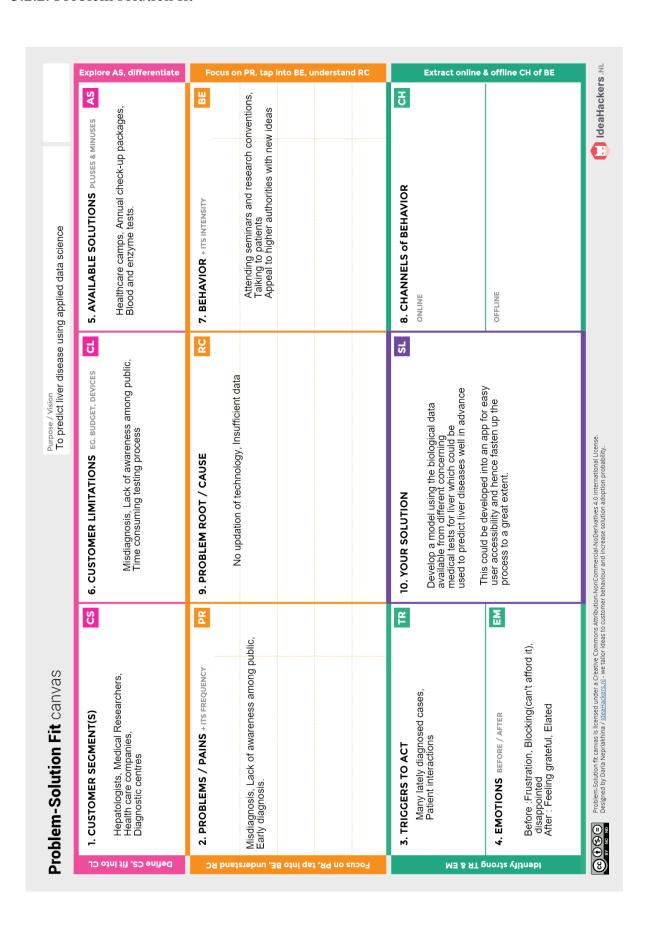
3.2 Project design Phase I

3.2.1. Proposed solution

Project team shall fill the following information in proposed solution template.

S.No.	Parameter	Description
1.	Problem Statement (Problem to besolved)	To develop machine learning approaches topredict liver disease
2.	Idea / Solution description	Testing the data using existing machine learning methods and predicting the solution by giving input samples
3.	Novelty / Uniqueness	The proposed solution takes lesser time than recent testing time(i.e, few hours to day)
4.	Social Impact / Customer Satisfaction	People will get to know about their health condition thereby taking precautionary measures.
5.	Business Model (Revenue Model)	Subscription based health application
6.	Scalability of the Solution	Can be used as app in mobile, web function

3.2.2. Problem solution fit



3.2.3 Solution Architecture

Solution Architecture Diagram:

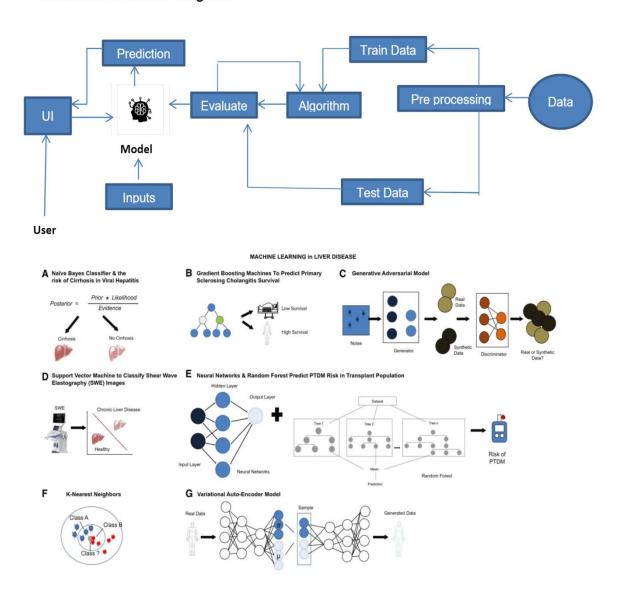
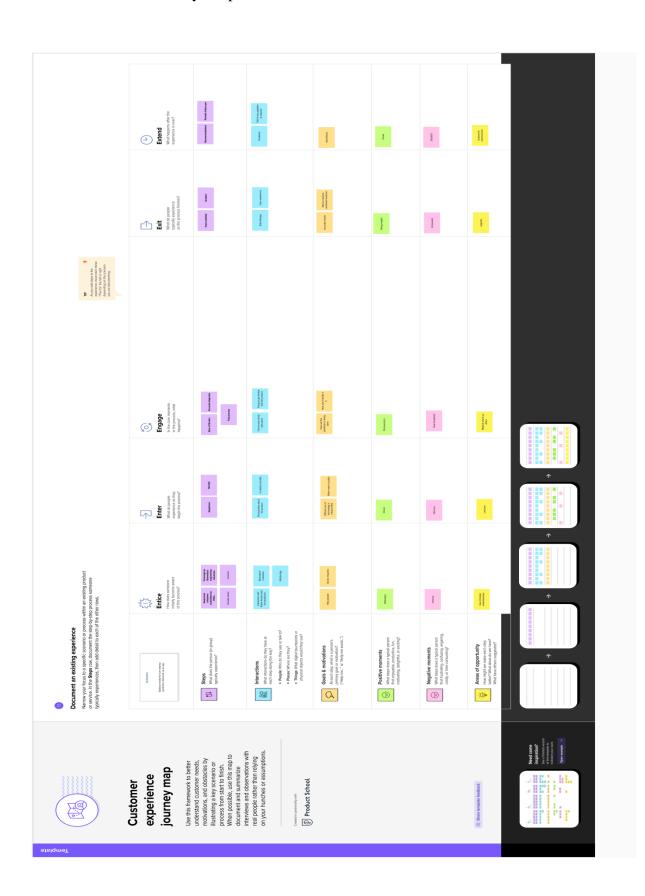


Figure 1: Architecture and data flow of the liver disease prediction system

3.3 Project design Phase II

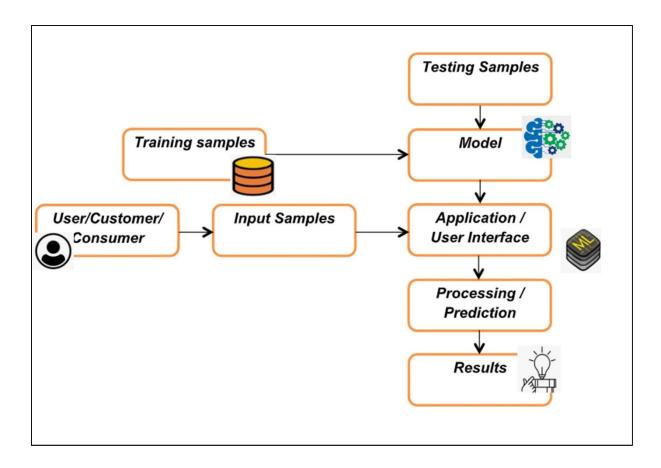
3.3.1 Customer Journey Map



3.3.2 Dataflow diagrams and User stories

A Data Flow Diagram (DFD) is a traditional visual representation of the information flows within a system. A neat and clear DFD can depict the right amount of the system requirement graphically. It shows how data enters and leaves the system, what changes the information, and where data is stored

User Type	Functional Requireme	User Story	User Story /Task	Acceptance criteria	Priority	Release
	nt(Epic)	Number	/ 1 431	Critcria		
Customer (Mobile user)	Installation	USN-1	As a user, I want to easily access the app via	I could easily access the app via app store	High	Sprint 1
	Registration	USN-2	As a user, I should register to the app using my credentials.	I am able to register by providing my credentials.	High	Sprint 1
	Demo	USN-3	As a medical practitioner, I want to easily understand the app via a demo	I am able to learn about the functionalities via a demo.	Low	Sprint 1
	Dashboard	USN-4	As a user, I need a well- built user interface	I am able to efficiently use the dashboard	High	Sprint 1



3.3.3 Solution requirements

Functional Requirements:

Following are the functional requirements of the proposed solution.

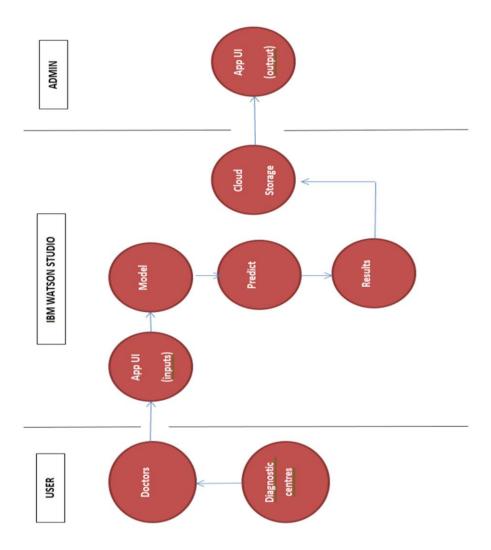
FR No.	Functional Requirement	Sub Requirement (Story / Sub-Task)
	(Epic)	
FR-1	User Registration	Registration through Form
		Registration through Gmail
		Registration through
		LinkedIN
FR-2	User Confirmation	Confirmation via
		Email Confirmation
		via OTP
FR-3	Portal Registration	Registration to common Database
)	

Non-functional Requirements:

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

FR No.	Non-Functional Requirement	Description
NFR-1	Usability	Should User-friendly
NFR-2	Security	Authentication
NFR-3	Reliability	Results should be accurate
NFR-4	Performance	Fast
NFR-5	Availability	Widely available
NFR-6	Scalability	Mobile and Web app

3.3.4 Technology Stack (Architecture & Stack)



3.4 Project Planning

3.4.1 Milestone and Activity list

ASSIGNMENT AND MILESTONE TRACKER

Subject	Assigned to	Status
Pre requisites	Team	Done
Quiz 1	Shweatha	Done
Quiz 2	Sakthi	Done
Quiz 3	Rakshana	Done
Quiz 4	Raveena	Done
Assignment 1	Sakthi	Done
Assignment 2	Shweatha	Done
Assignment 3	Rakshana	Done
Assignment 4	Raveena	Done
Brain storming	Team	Done
Problem statement	Team	Done
Empathy map	Team	Done
Solution Architecture	Team	Done
Problem- solution fit	Team	Done
Solution Requirements	Team	Done
Customer/user journey map	Team	Done
Functional req	Team	Done
Data flow diagrams	Team	Done
Tech arch	Team	Done
Data pre processing	Raveena	Done
Data visualization	Sakthi	Done
Splitting the dataset	Rakshana	Done
Model building	Raveena	Done
Application building	Team	Done
Train on IBM Cloud	Team	Done
Run the application	Team	Done
Report	Team	Done

3.4.2 Sprint delivery plan

Sprint	Functional Requirement	Task	Priority	Team
				Members
Sprint-1	Registration	Register for IBM Cloud Services.	High	Rakshana S
		Install Anaconda navigator and		Raveena R
		necessary packages. Complete design		Sakthi Devi S
		phase and assignments		V
				Shweatha J
Sprint-2	Data processing	Download dataset and process it using	High	Raveena R
		python tools. Visualize the dataset.		Sakthi Devi S
		Split the datasetinto testing and training		V
		dataset.		
Sprint-3	Model Building	Use various machine learning	Medium	Rakshana S
		algorithms to build the model with best		Shweatha J
		accuracy		
Sprint-4	Application & training	Build the web application and train on	Medium	Rakshana S
~F-III		IBM cloudservices.		Raveena R
		in it disaubit vices.		Sakthi Devi S
				VShweatha J

4 PROJECT DEVELOPMENT PHASE

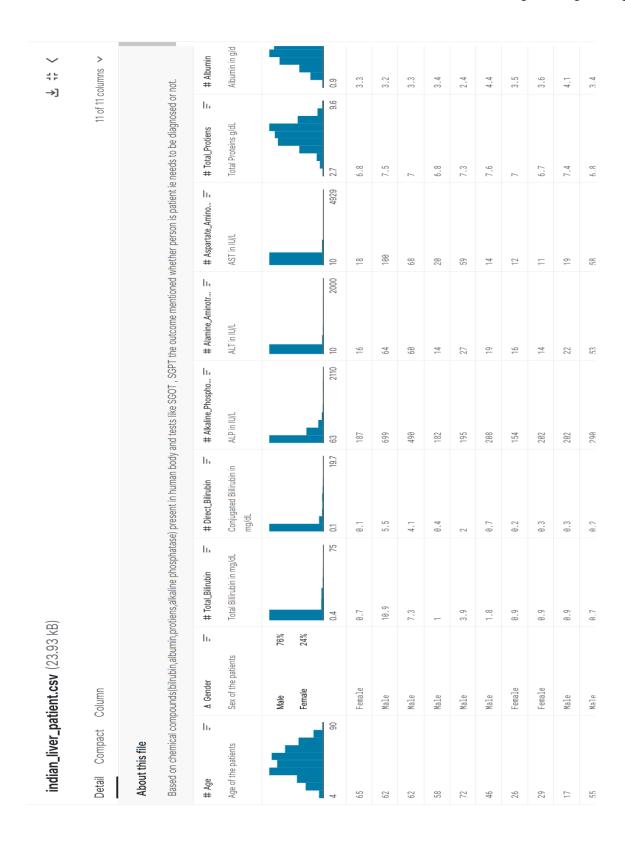
4.1 Dataset Collection

This data set contains 416 liver patient records and 167 non liver patient records collected from North East of Andhra Pradesh, India. The "Dataset" column is a class label used to divide groups into liver patient (liver disease) or not (no disease). This data set contains 441 male patient records and 142 female patient records.

Any patient whose age exceeded 89 is listed as being of age "90".

Columns:

- Age of the patient
- Gender of the patient
- Total Bilirubin
- Direct Bilirubin
- Alkaline Phosphotase
- Alamine Aminotransferase
- Aspartate Aminotransferase
- Total Protiens
- Albumin
- Albumin and Globulin Ratio
- Dataset: field used to split the data into two sets (patient with liver disease, or no disease)



4.2 Dataset Pre-processing

Data Pre-processing includes the following main tasks

- 1. Import the Libraries.
- 2. Reading the dataset.
- 3. Analyse the data.
- 4. Taking Care of Missing data.
- 5. Data Visualization.
- 6. Splitting the Dataset into Dependent and Independent variables.
- 7. Splitting Data into Train and Test

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import pickle
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='81NwbGz-
nOfetpoObtERs4vVLTRPbT5SXOohN GSTc4d',
    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 = 'liverhealthmonitor-donotdelete-pr-z7bxt6q1mu2huc'
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
           hasattr(body, " iter "): body. iter
types.MethodType( __iter__, body )
```

```
data = pd.read csv(body)
data.head()
data.tail()
data.info()
data.describe()
data.isnull().any()
data.isnull().sum()
data['Albumin and Globulin Ratio'] = data['Albumin and Globulin
Ratio'].fillna(0)
data.isnull().sum()
sns.countplot(data=data, x='Gender', label='Count')
m,f=data['Gender'].value counts()
print("Number of Males:",m)
print("Number of Females:",f)
sns.countplot(data=data, x='Dataset')
LD, NLD=data['Dataset'].value counts()
print("Liver disease patients:",LD)
print("Non Liver disease patients:", NLD)
x=data.iloc[:,0:-1]
y=data.iloc[:,-1]
from sklearn.model selection import train test split
xtrain, xtest, ytrain, ytest=train test split(x, y, test size=0.2)
xtrain.shape
xtest.shape
```

4.3 Model Building

Predictive modeling is a mathematical approach to create a statistical model to forecast future behavior based on input test data.

Model building includes the following main tasks

- 1. Training and testing the model using classification algorithms
 - Random Forest Classification.
 - Support Vector Machine
 - KNN Classification
- 2. Evaluation of Model
 - To check to see how well our model is performing on the test data.
 - Accuracy Score of 3 algorithms and choose the best out of three.
- 3. Save the model
- 4. Predicting the output using the model

```
#model building
from sklearn.svm import SVC
```

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
le.fit(xtrain['Gender'].astype(str))
xtrain['Gender'] = le.transform(xtrain['Gender'].astype(str))
xtest['Gender'] = le.transform(xtest['Gender'].astype(str))
svm=SVC()
RFmodel=RandomForestClassifier()
KNNmodel=KNeighborsClassifier()
from sklearn.svm import SVC
svm=SVC(gamma='auto')
svm.fit(xtrain,ytrain)
from sklearn.ensemble import RandomForestClassifier
RFmodel=RandomForestClassifier()
RFmodel.fit(xtrain,ytrain)
from sklearn.neighbors import KNeighborsClassifier
KNN=KNeighborsClassifier()
KNN.fit(xtrain,ytrain)
import warnings
warnings.filterwarnings("ignore")
#accuracies
from sklearn.metrics import accuracy score
SVMpred=svm.predict(xtest)
SVMaccuracy=accuracy score(SVMpred,ytest)
print('SVM accuracy:',SVMaccuracy*100)
RFpred=RFmodel.predict(xtest)
RFaccuracy=accuracy score(ytest, RFpred)
print('RFC accuracy:',RFaccuracy*100)
KNNpred=KNN.predict(xtest)
KNNaccuracy=accuracy score(KNNpred,ytest)
print('KNN accuracy:',KNNaccuracy*100)
SVM accuracy: 73.50427350427351
RFC accuracy: 75.21367521367522
```

KNN accuracy: 75.21367521367522

```
#confusion matrix
from sklearn.metrics import confusion_matrix
cm1=confusion_matrix(ytest,SVMpred)
cm2=confusion_matrix(ytest,RFpred)
cm3=confusion_matrix(ytest,KNNpred)
print('SVM Confusion matrix',cm1)
print('RFC Confusion matrix',cm2)
print('KNN Confusion matrix',cm3)

SVM Confusion matrix [[86 0]
   [31 0]]
RFC Confusion matrix [[73 13]
   [16 15]]
KNN Confusion matrix [[69 17]
   [12 19]]
```

4.4 Application Building

Application Building involves following steps

- 1. Create an HTML file
- 2. Build a Python Code
- 3. Run the app

Create an HTML File:

```
<!DOCTYPE html>
<html>
<head>
<title>
Liver patient analysis
</title>
<meta name="viewport" content="width=device-width, initial-</pre>
scale=1">
<style>
font-family: Calibri, Helvetica, sans-serif;
background-color: DarkRed;
.container {
padding: 300px;
padding-top: 25px;
background-color:DarkSalmon ;
input[type=number] {
```

```
width: 100%;
  padding: 15px;
margin: 5px 0 22px 0;
display: block;
border: none;
background: #f1f1f1;
input[type=number]:focus {
background-color: orange;
outline: none;
}
div {
         padding: 10px 0;
.predictbtn {
  background-color: #20B2AA;
  color: white;
  padding: 15px;
  margin: 5px 0 22px 0;
  border: center;
  cursor: pointer;
  width: 104%;
  opacity: 0.9;
}
.predictbtn:hover {
opacity: 1;
}
</style>
</head>
<body>
<div class="container">
<center> <h1> LIVER HEALTH MONITOR</h1> </center>
<form action="home.html" method="post">
<label> Age </label>
<input type="number" step=0.01 name="Age" placeholder= "Age"</pre>
size="15" required />
<label> Gender: </label>
             type="number" step=0.01 name="Gender"
Gender (0 for male, 1 for female)"
<input
placeholder="Gender
size="15"required />
<label>
Total bilirubin :
</label>
         type="number" step=0.01 name="Total bilirubin"
placeholder="Total bilirubin" size="10" required>
<label>
```

```
Direct bilirubin :
</label>
       type="number" step=0.01 name="Direct bilirubin"
<input
placeholder="Direct bilirubin" size="10" required>
<label>
Alkaline Phosphotase :
</label>
<input type="number" step=0.01 name="Alkaline Phosphotase"</pre>
placeholder="Alkaline_Phosphotase" size="10" required>
<label>
Alamine aminotransferase :
</label>
<input type="number" step=0.01 name="Alamine aminotransferase"</pre>
placeholder="Alamine aminotransferase" size="10" required>
<label>
Aspartate aminotransferase :
</label>
<input
                       type="number"
                                                     step=0.01
name="Aspartate aminotransferase"
placeholder="Aspartate aminotransferase" size="10" required>
<label>
Total proteins :
</label>
         type="number" step=0.01 name="Total proteins"
<input
placeholder="Total proteins" size="10" required>
<label>
Albumin:
</label>
<input type="number" step=0.01 name="Albumin"</pre>
placeholder="Albumin" size="10" required>
<label>
Albumin and Globulin Ratio:
</label>
<input
                       type="number"
                                                     step=0.01
name="Albumin and Globulin Ratio"
placeholder="Albumin and Globulin Ratio" size="10" required>
<button type="submit" class="predictbtn">Predict</button>
</form>
<br><h4 align="center"<b>{{pred}}</b></h4>
<br>
</div>
</body>
```

Web Design using HTML

Age 60 Gender: 0 Total_bilirubin: 0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.0 Albumin_and_Globulin_Ratio: 0.37	Gender: 0 Total_bilirubin: 0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase:
Gender: 0 Total_bilirubin: 0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.0 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	Gender: 0 Total_bilirubin: 0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase:
Total_bilirubin: 0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.0 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	Total_bilirubin: 0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase:
Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase:
Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	0.5 Direct_bilirubin: 0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase:
0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase:
0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	0.1 Alkaline_Phosphotase: 500 Alamine_aminotransferase:
Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	Alamine_aminotransferase:
Alamine_aminotransferase: 20 Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	Alamine_aminotransferase:
Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	
Aspartate_aminotransferase: 34 Total_proteins: 5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	20
Total_proteins: 5.9 Albumin: 16 Albumin_and_Globulin_Ratio: 0.37	
Total_proteins: 5.9 Albumin: 16 Albumin_and_Globulin_Ratio: 0.37	
5.9 Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	34
Albumin: 1.6 Albumin_and_Globulin_Ratio: 0.37	
1.6 Albumin_and_Globulin_Ratio:	59
Albumin_and_Globulin_Ratio: 0.37	
0.37	
Predict	
	Predict

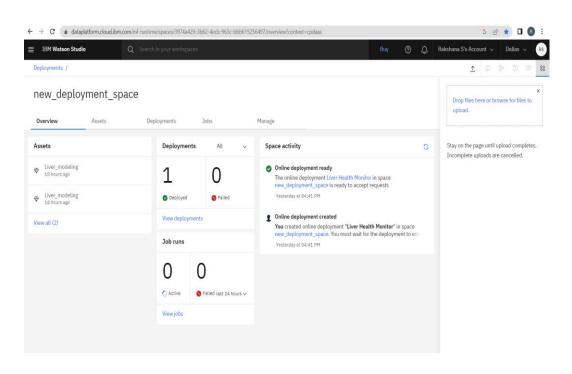
Build a Python code:

```
from flask import Flask, render template, request
import pickle
app = Flask( name )
@app.route('/')
def bot():
    return render template('home.html')
@app.route('/predict', methods=["POST"])
def predict():
    Age=request.form['Age']
    gender=request.form['Gender']
    tb=request.form['Total bilirubin']
    db=request.form['Direct bilirubin']
    ap=request.form['Alkaline Phosphotase']
    aa1=request.form['Alamine aminotransferase']
    aa2=request.form['Aspartate aminotransferase']
    tp=request.form['Total_proteins']
    a=request.form['Albumin']
    agr=request.form['Albumin and Globulin Ratio']
data=[[float(Age),float(gender),float(tb),float(db),float(ap),
float(aa1),float(aa2),float(tp),float(a),float(agr)]]
   model=pickle.load(open('liver analysis.pkl','rb'))
    print(data)
   prediction=model.predict(data)
    if (prediction==1):
        output="You have liver disease."
    else:
        output="You do not have liver disease"
    return render template('home.html',prediction text=output)
if name ==' main ':
    app.run (debug=True)
```

4.5 Train the model on IBM

To build a Machine Learning Model and deploy it on the IBM Cloud

```
!pip install ibm watson machine learning
from ibm watson machine learning import APIClient
wml credentials={"url":"https://us-
south.ml.cloud.ibm.com", "apikey": "eJqAgq9PC4DNCsDnTj0pfeO4-
Rk0jXwNWF61-LDwFYDL"}
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']
item['entity']["name"] == space name)['metadata']['id'])
space uid=guid from space name(client,'new deployment space')
print("Space UID ="+space uid)
client.set.default space(space uid)
client.software specifications.list()
software spec uid=client.software specifications.get uid by na
me("runtime-22.1-py3.9")
software spec uid
model details
client.repository.store model(model=svm, meta props={
    client.repository.ModelMetaNames.NAME:"Liver modeling",
    client.repository.ModelMetaNames.TYPE: "scikit-learn 1.0",
client.repository.ModelMetaNames.SOFTWARE SPEC UID:software sp
ec uid})
model id = client.repository.get model uid(model details)
```



5. RESULTS

LIVER HEALTH MONITOR
Age
Age
Gender:
Gender (0 for male, 1 for female)
Total_bilirubin :
Tota[_bilirubin
Direct_bilirubin :
Direct_bilirubin
Alkaline_Phosphotase :
Alkaline_Phosphotase
Alamine_aminotransferase :
Alamine_aminotransferase
Aspartate_aminotransferase :
Aspartate_aminotransferase
Total_proteins :
Total_proteins
Albumin:
Albumin
Albumin_and_Globulin_Ratio:
Albumin_and_Globulin_Ratio
Prodict
You have liver disease

6. FUTURE SCOPE

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.

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 algorithms like Forest Tree implemented in Apache Hadoop to increase scalability and efficiency.

7. CONCLUSION

Liver disease is one such critical disease that can be treated when detected early and it will become a life threating condition when undetected . There are many approaches and method for predicting liver disease like logistic regression Decision Tree, Random Forest, AdaBoost, k-Nearest Neighbour, convolution neural network, Multilayer perceptron and Support Vector Machine. Out of which we compared the accuracy of SVM ,KNN and random forest methods using various packages such as NumPy, Matplotlib, Pandas, Seaborn and so and resulted that Support Vector Machine has more accuracy compared to others. Also the proposed is made into an user interface app for well being of people.

APPENDIX

Demo link

https://vimeo.com/772712483

Github project page link

https://github.com/IBM-EPBL/IBM-Project-19384-1659697109