A REVIEW OF LIVER PATIENT ANALYSIS

INTRODUCTION

A group of blood tests called liver function tests can be used to diagnose liver disease. Other blood tests can be done to look for specific liver problems or genetic conditions.Liver is the largest internal organ in the human body,it is essential for digesting food and releasing the

toxic element of the body and plays a major role in metabolism and serving several vital functions. The

liver is the largest glandular organ of the body. It weighs about 3 lb (1.36 kg) .The liver's main job is to

strain the blood coming from the digestive tract, before passing it to the rest of the body. The liver also

detoxifies chemicals and metabolizes drugs. As it does so, the liver hides bile that ends up back in the

intestines. The liver also makes proteins important for blood clotting and other

functions.The liver supports

almost every organ in the body and is vital for our survival

Liver cirrhosis is the biggest health problem posed by alcohol use, with 1.4 lakh deaths every year

purpose

Liver cirrhosis is the biggest health problem posed by alcohol use, with 1.4 lakh deaths ever Cirrhosis isn't curable, but it's treatable. Alcohol abuse, hepatitis, and fatty liver disease are some of the main causes.: Liver Failure is a serious condition and it affects the patient's life time. Disease identification is the most crucial task

for treating any disease. Liver disease can be inherited genetically or caused by a variety of subjects that damage the liver.

Machine learning technique is broadly

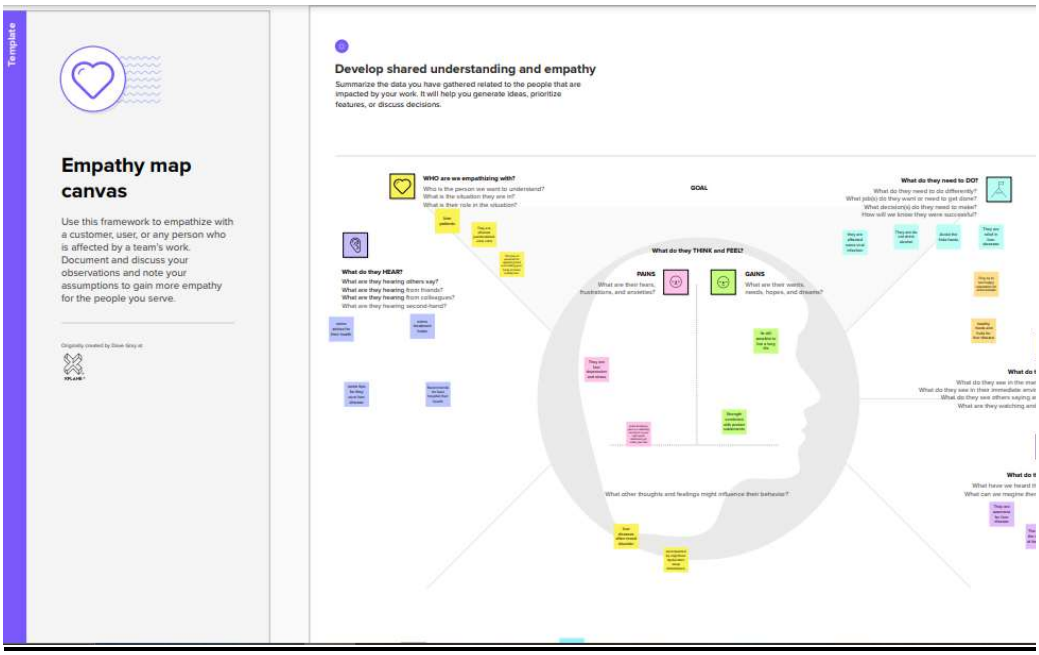
used in various grounds of science and technology. They have been giving out meaningful

information. It also explores in creation and study of algorithms which can learn from data. Data mining in healthcare is an

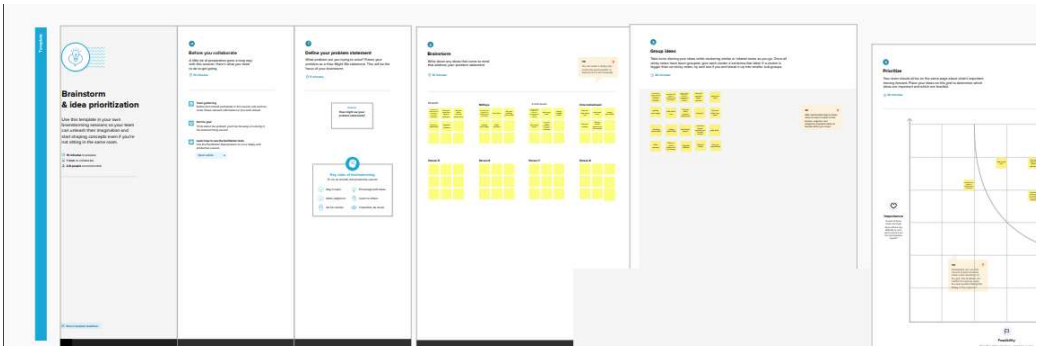
evolving field of high importance for providing diagnosis and a deeper understanding of medical data

Problem Definition &Design Thinking

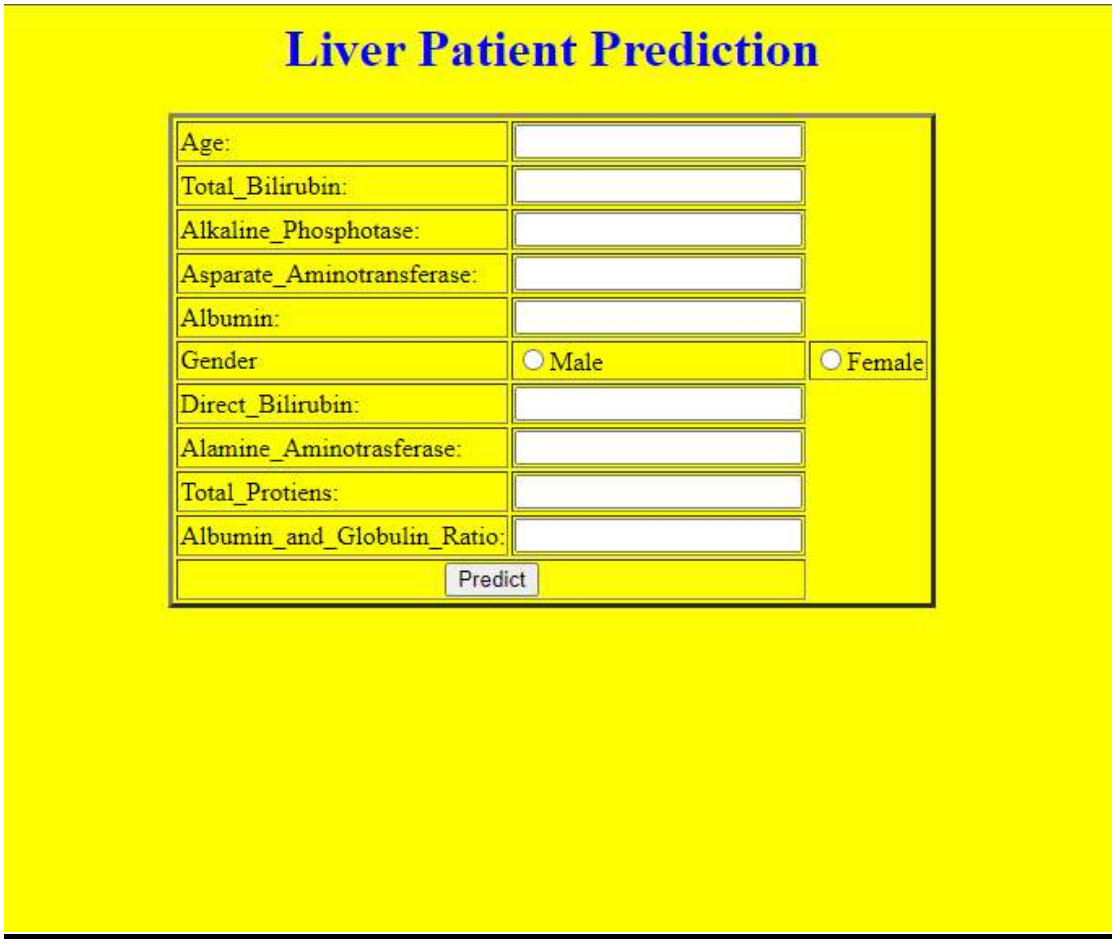
Empathy map

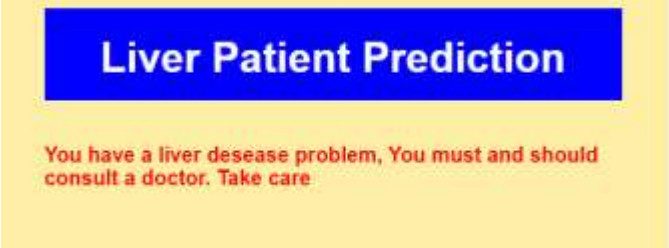


ideation&Brainstroming Map



RESULT





Advantages

Liver function tests, also known as liver chemistries, help determine the health of your liver by measuring the levels of proteins, liver enzymes, and bilirubin in your blood. They can also monitor the progression or treatment of an existing disease.

Disadvantages

Heavy alcohol use.

Obesity.

Type 2 diabetes.

Tattoos or body piercings.

Injecting drugs using shared needles.

Blood transfusion before 1992.

Exposure to other people's blood and body fluids.

Unprotected sex.

APPLICATION

Classification algorithms

Classification algorithm is one of the greatest significant and applicable data mining techniques used to

apply in disease prediction. Classification algorithm is the most common in several automatic medical

health diagnoses. Many of them show good classification accuracy. Different data mining algorithms like

Naïve Bayes, Decision Tree, Logistic Regression, Random forest and Support vectormachine (SVM) were

implemented. The algorithms are briefly discussed below

CONCLUSION

Cirrhosis is the pathogenic consequence of a remarkably conserved response to injury within the liver, characterized by progressive fibrosis tissue deposition and eventual disruption of normal hepatic architecture. The hallmark of liver injury is activation of the hepatic stellate cell, which mediates the development of fibrous tissue and change in the composition of the extracellular matrix. Inflammation and immune responses are the driving forces behind the transition of the quiescent hepatic stellate cell to an activated

phenotype. Additionally, liver response to injury includes changes in cellular proliferation and apoptosis that may explain the premalignant potential of cirrhosis. Although remarkably consistent in its development, cirrhosis can arise from many diverse causes, is often difficult to diagnose, and once established is often difficult to treat. Unfortunately, it is clear that better pharmaceutical agents are needed to alter the natural history of fibrosis and subsequent development of cirrhosis. Importantly, the promise of genomics approaches is now being realized, as these technologies are being used to better understand liver disease pathogenesis, and determine response to treatment and susceptibility to progression, as well enabling the development of novel therapies. Consequently, individualized patient assessment and tailored therapy will be possible in liver disease due to genomics approacheCommon Hepatic Duct: A tube that carries bile out of the liver. It is formed from the intersection of the right and left hepatic ducts.

FUTURE SCOPE

Falciform Ligament: A thin, fibrous ligament that separates the two lobes of the liver and connects it to the abdominal wall.

Glisson's Capsule: A layer of loose connective

tissue that surrounds the liver and its related arteries and ducts.

Hepatic Artery: The main blood vessel that supplies the liver with oxygenated blood.

Hepatic Portal Vein: The blood vessel that carries blood from the gastrointestinal tract, gallbladder, pancreas, and spleen to the liver.

The anatomical sections of the liver.

Lobules: Microscopic building blocks of the liver.

Peritoneum: A membrane covering the liver that forms the extet.

APPENDIX

```
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


from google.colab import drive

drive.mount('/content/drive')


with open('/content/drive/My Drive/Colab
```

```
Notebooks/indian_liver_patient.csv', 'r') as
dataset:
  data = pd.read_csv(dataset)


data.head()

data.info()

data.isnull().any()

data.isnull().sum()


#data['Albumin_and_Globulin_Rati'o]=
data.fillna(data['Albumin_and_Globulin_Ratio'
].mode()[0])

data.isnull().sum()


from sklearn.preprocessing import
LabelEncoder

lc=LabelEncoder()

#data['gender']=lc.fit_transform(data['gender'
])



 #data.describe()

#sns.distplot(data['age'])
```

```
#plt.title('Age Distribution Graph')

#plt.show()

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

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

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

from sklearn.preprocessing import scale

#X_scaled=pd.DataFrame(scale(X),columns=
x.columns)

#X_scaled.head()

#X=data.iloc[:,;-1]

#y=data.outcome

from sklearn.model_selection import
train_test_split

#_train,x_test,y_train,y_test=train_test_split

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

#pip install imblearn

from imblearn.over_sampling import SMOTE

smote= SMOTE()

#Y_train.value_counts()

#X_train.smote,y_train_smote
=smote.fit_resmple(X_train,y_train)
```

#y_train-smote.value_counts()

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))

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))

#model2=KNeighborsClassifier()

#model2=.fit(X-train-smote,Y-train-smote)

#y-predict=models5.predict(x-test)

#logil=accuracy-score(y-test,y-predict)

logil

pd.crosstab(y-test,y-predict)

print(classificatoin-report(y-test,y-predict))

import tensorflow.keras

from tensorflow.keras.models import sequential

from tensorflow.keras.layers import Dense

```
# initialising the ANN

Classifier=sequential()

# Adding the input Layer and the first hidden layer

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

# Adding the second hidden Layer

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

# Adding the output Layer

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

# compiling the ANN

classifier.compile(optimizer='adam',l oss='binnary_crossentropy',metrics=[' accuracy'])

# Fitting the ANN to the Training set

model_history=classifier.fit(X_train,Y_ train,batch_size=100,validation_split= 0.2, epochs=100)

model14.predict([[50,1,1.2,0.8,150,70
```

```
,80,7.2,3.4,0.8]])
array([1],dtype=int64)
model11.predict([[50,1,1.2,0.8,150,70
,80,7.2,3.4,0.8]])
classifier.save("liver.h5")
y_pred=classifier.predict(x_test)
y_pred
def predict_exit(sample_value):

sample_value=np.array(samble_value
)

sample_value=sample_value.reshape(
1,-1)
 sample_value=scale(sample_value)
 return
classifier.predict(sample_value)

sample_value=[[50,1,1.2,0.8,150,70,80
,7.2,3.4,0.8]]
 if predict_exit(sample_value)>0.5:
```

```
    print('prediction:Liver patient')
  else:
    print('prediction:Healthy')


import joblib
joblib.dump(model,'ETC.pkl')
@app.route('/data_predict',method=['POST'])
def predict():
  age=request.form['age']
  gender=request.form['gender']
  tb=request.form['tb']
  dp=request.form['dp']
  ap=request.form['ao']
  aa1=request.form['aa1']
  aa2=request.form['aa2']
  tb=request.form['tb']
  a=request.form['a']
  agr=request.form['agr']
```

```
data=[[float(age),float(gender),float(tb),float(dp),float(ap),float(ap),float(aa1),float(aa2),float(tb)


model=pickle.load(open('liver_analysis.pkl','rb'))
 prediction=model.predict(data)[0]
 if(prediction==1):
  return render_template('noChance.html',prediction='You have aliver deasese problem,you must and:
 else:
  return render_template('chance.html',prediction='You dont have a liver deasease problem')
if _name_=='_main_':
 app.run()
if _name_ =='_main_':
 app.run()
```