









GOVERNMENT OF TAMILNADU

Naan Mudhalvan - Project-Based Experiential Learning

A Review of Liver Patient Analysis Methods Using Machine Learning

Submitted by

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M.V.MUTHIAH GOVERNMENT ARTS COLLEGE FOR WOMEN

(Affiliated to Mother Teresa Women's University, Kodaikanal)
Reaccredited with 'A' Grade by NAAC **DINDIGUL-624001.**

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PG & RESEARCH DEPARTMENT OF COMPUTER SCIENCE

BONAFIDE CERTIFICATE

This is to certify that this is a bonafide record of the project entitled, A REVIEW OF LIVER PATIENT ANALYSIS METHODS USING MACHINE LEARNING done by AAFRIN. A (20326ER001), ABINAYA. K (20326ER002), BOOMIKA. A (20326ER003), DEEPA. K (20326ER004). This is submitted in partial fulfillment for the award of the degree of Bachelor of Science in Computer Science in M.V.MUTHIAH GOVERNMENT ARTS COLLEGE FOR WOMEN, DINDIGUL during the period of December 2022 to April 2023.

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INTRODUCTION

1.1 OVERVIEW

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, Decision Tree, 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.

1.2 PURPOSE

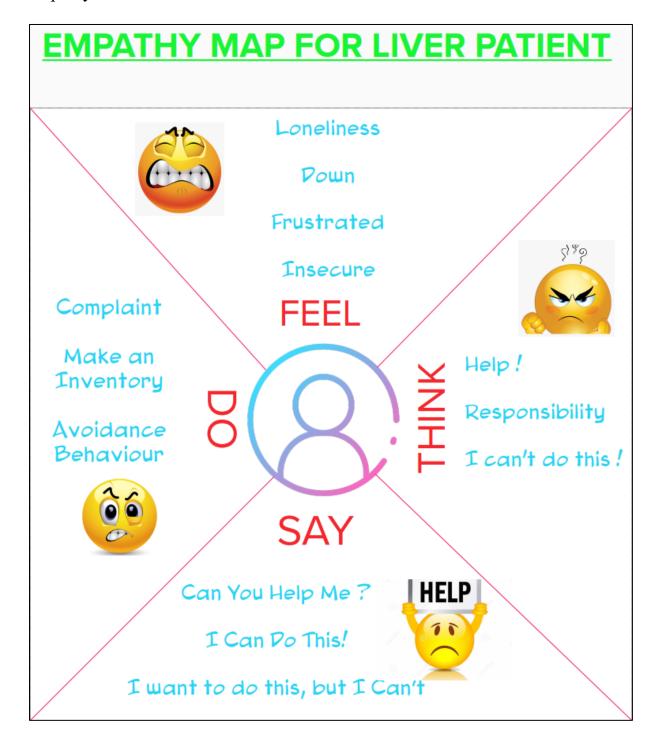
The Purpose of this Project includes,

- Reduce the high cost of liver disease diagnosis
- It detects patterns of specific Liver diseases
- It can alert clinicians to any irregularities to assess a patient's health based on knowledge collected from large data sets.
- It shows improved accuracy, efficiency, and decision-making.
- It helps physicians to identify best treatment for particular Liver disease.
- It can produce fast analysis report, operational efficiency and reduce operational cost.

PROBLEM DEFINITION & DESIGN THINKING

2.1 EMPATHY MAP

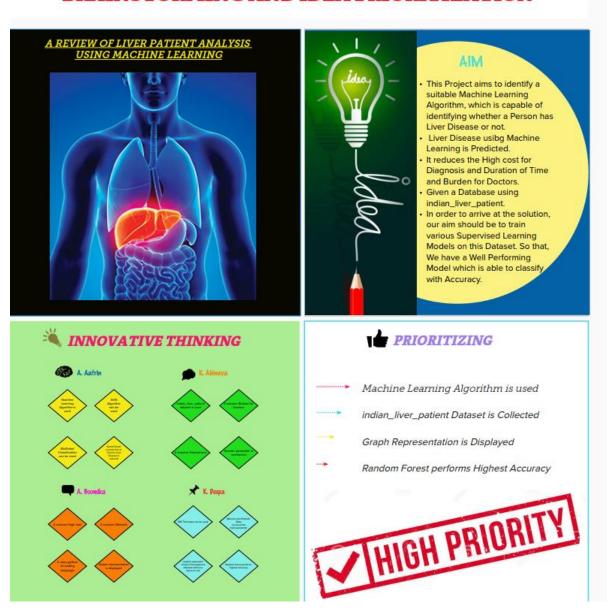
A Template that organizes User's Behaviors and feelings to create sense of empathy between the User and Admin.



2.2 IDEATION & BRAINSTORMING MAP

- ➤ Ideation is the process of forming ideas from Conception to Implementation in a Business Testing
- > Brainstorming Map is a technique that can be used to organize Thoughts and Idea

BRAINSTORMING AND IDEA PRIORITIZATION



RESULT

Liver Patient Analysis

Home

Goto Predict

Introduction

Liver diseases averts the normal function of the liver. Mainly due to the large amount of alcohol consumption liver disease arises. 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. Discovering the existence of liver disease at an early stage is a complex task for the doctors. The main objective of this paper is to 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 paper focuses on the related works of various authors on liver disease such that algorithms were implemented using Weka tool that is a machine learning software written in Java. Various attributes that are essential in the prediction of liver disease were examined and the dataset of liver patients were also evaluated. This paper compares various classification algorithms such as Random Forest, Logistic Regression and Separation 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 diseaserecommended

Age:	Gender:
	Enter 0 as male, 1 as female
Total_Bilirubin:	Direct_Bilirubin:
Alkaline_Phosphotase:	Alamine_Aminotransferase:
Aspartate_Aminotransferase:	Total_Protiens:
Albumin:	Albumin_and_Globulin_Ratio:

Liver Patient Prediction

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

ADVANTAGES & DISADVANTAGES

ADVANTAGES

- Reduce the high cost of liver disease diagnosis
- It detects patterns of specific Liver diseases
- It can alert clinicians to any irregularities to assess a patient's health based on knowledge collected from large data sets.
- It shows improved accuracy, efficiency, and decision-making.
- It helps physicians to identify best treatment for particular Liver disease.
- It can produce fast analysis report, operational efficiency and reduce operational cost.

DISADVANTAGES

- Acquisition in Data
- Human Interface is Eliminated
- Nature of the Jobs in being replaced by Machines

APPLICATIONS

- Liver Disease Monitoring
- Liver Disease Risk Prediction
- Discoveries in Disease
- Diagnosis and Detection of Disease
- Epidemic Outbreak Prediction
- Medical Research
- Image Analysis
- EMR Scans

. CHAPTER - 6

CONCLUSION

Liver disease is a serious condition that threatens human life and requires urgent medical attention. Health professionals are based on pathological methods to make a medical report concerning a patient's condition. ML models, such as Random Forest, Decision Tree, Logistic Regression, KNN and ANN, were evaluated in terms of Accuracy, Precision, Recall, F-Measure and AUC, in order to predict liver disease occurrence. From the experimental results, 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.

FUTURE SCOPE

In future work, we aim to re-consider the liver disease manifestation methodology following, first, the ROPE (region of practical equivalence) analysis to test whether a feature is significant (in the sense of important enough for the liver disease risk prediction) and, secondly, extend the machine learning framework by using deep learning methods and comparing the results on the aforementioned metrics.

APPENDIX

8.1 SOURCE CODE

```
import pandas as pd
import numpy as np
import seaborn as sns
import sklearn
import matplotlib.pyplot as plt
from matplotlib import rcParams
from scipy import stats
from pandas import DataFrame
import pip
data=pd.read csv('/indian liver patient.csv')
data.head()
data.info()
data.isnull().any()
data.isnull().sum()
#checking for the missing data after cleansing data(
data['Albumin and Globulin Ratio'].fillna(data['Albumin and Globulin Ratio'
].median(),inplace=True)
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 ['Dataset'],
hue=data['Gender'])
plt.figure(figsize=(10,7))
sns.heatmap(data.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.Dataset
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)
pip install imblearn
from imblearn.over sampling import SMOTE
smote = SMOTE()
y train.value counts()
X train smote, y train smote = smote.fit resample(X train, y train)
y train smote.value counts()
from sklearn.metrics import classification report, confusion matrix
from sklearn.metrics import accuracy score
from sklearn.ensemble import RandomForestClassifier
model1=RandomForestClassifier()
model1.fit(X train smote, y train smote)
rf 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.metrics import classification report, confusion matrix
from sklearn.metrics import accuracy score
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))
from sklearn.metrics import classification report, confusion matrix
from sklearn.metrics import accuracy score
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))
from sklearn.metrics import classification_report,confusion matrix
from sklearn.metrics import accuracy score
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))
import tensorflow.keras
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
#intialising 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', loss='binary 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)
model4.predict([[50,1,1,2,0.8,150,70,80,7.2,3.4,0.8]])
model1.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(sample value)
```

```
sample value = sample value.reshape(1,-1)
sample value = scale(sample value)
return classifier.predict(sample value)
sample value = [[50,1,1.2,0.8,150,70,80,7.2,3.4,0.8]]
if predict exit(sample value)>0.5:
print('prediction:liver patient')
else:
print('prediction:healthy')
acc smote= [['KNN classifier',knn1],['RandomForestClassifier',rfc1],
['DecisionTreeClassifier',dtc1],['LogisticRegression',logi1]]
Liverpatient pred= pd.DataFrame(acc smote, columns=['classification
models', 'accuracy score']
Liverpatient pred
from sklearn.metrics import classification report, confusion matrix
from sklearn.metrics import accuracy score
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)
from sklearn.ensemble import ExtraTreesClassifier
model=ExtraTreesClassifier()
model.fit(X,y)
model.feature importances
dd=pd.DataFrame(model.feature importances ,index=X.columns).sort values(
0,ascending=False)
dd
dd.plot(kind='barh',figsize=(7,6))
```

plt.title("FEATURE IMPORTANCE",fontsize=14)
import joblib
joblib.dump(model1, 'ETC.pk1')