A PROJECT REPORT ON

Exploring Liver Disease with Machine Learning

Submitted To:

DR. SELVA KUMAR S

Submitted By

20BCD7094 RAMPAM GREESHMA GEETHIKA
20BCD7277 VELLALACHERUVU BHANU SANDEEP
20BCE7149 P KUMARA SAI PRADEEP
20BCE7407 T BALA SAI VAMSI
20BCN7071 M SAI NIKHIL CHANDRA

Abstract:

The liver is essential for **digesting food and ridding your body of toxic substances**. Liver disease can be inherited (genetic). Liver problems can also be caused by a variety of factors that damage the liver, such as viruses, alcohol use and obesity. 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.

INTRODUCTION:

With a growing trend of sedentary and lack of physical activities, diseases related to liver have become a common encounter nowadays. In rural areas the intensity is still manageable, but in urban areas, and especially metropolitan areas the liver disease is a very common sighting nowadays. Liver diseases cause millions of deaths every year. Viral hepatitis alone causes 1.34 million deaths every year. Problems with liver patients are not easily discovered in an early stage as it will be functioning normally even when it is partially damaged. An early diagnosis of liver problems will increase patient's survival rate. Liver failures are at high rate of risk among Indians. It is expected that by 2025 India may become the World Capital for Liver Diseases. The widespread occurrence of liver infection in India is contributed due to deskbound lifestyle, increased alcohol consumption and smoking. There are about 100 types of liver infections.

With such alarming figures, it is necessary to have a concern towards tackling these diseases. Afterall, we cannot expect a developed and prosperous nation, with unhealthy youths. In this project we have taken UCI ILPD Dataset which contains 10 variables that are age, gender, total Bilirubin, direct Bilirubin, total proteins, albumin, A/G ratio, SGPT, SGOT and Alkphos and contains 415 as liver disease patients and 167 as non liver disease patients.As we got through the next parts of this paper we will explain what proccess as taken place for the selection of best model and building necccessary sytem for the prediction of liver disease. The major outcomes that can be expected through this project are:

- ➢ Increased convenience for predicting a liver disease
- ➢ Reduction in number of deaths due to liver diseases
- ➢ More accurate diagnosis of liver disease by the doctors.

Objective of the work:

The main objective of the project is to predict whether a person had liver disease or not.

We took the liver disease database. In which they manually assigned labels 1 and 2 indicating whether the disease is present or not.

Define a function that allows us to create a table of missing values in df_liver and their percentages in /descending order

Replace missing values with the mean of feature column Albumin_and_Globulin_Ratio, then check to see that it has been successful, where the sum of missing values should be 0

About data set cleaning (points are noted in code comments)

LITERATURE SURVEY:

Model 1:

Random Forest (simple description of algorithm) is an ensemble learning method for classification, regression and other tasks that operates by constructing a multitude of decision trees at training time. For classification tasks, the output of the random forest is the class selected by most trees.

Model 2:

Logistic Regression : is a process of modeling the probability of a discrete outcome given an input variable.

Model 3:

Decision Tree: is a flowchart-like structure in which each internal node represents a "test" on an attribute (e.g. whether a coin flip comes up heads or tails), each branch represents the outcome of the test, and each leaf node represents a class label (decision taken after computing all attributes).

Model 4:

k neighbours: The k-nearest neighbors (KNN) algorithm is a data classification method for estimating the likelihood that a data point will become a member of one group or another based on what group the data points nearest to it belong to

Detailed system design(architecture):

Familiarizing ourselves with the data

```
# Import the data processing and visualization libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

%matplotlib inline
df_liver = pd.read_csv("/content/sample_data/indian_liver_patient.csv")
from pandas_profiling import ProfileReport
```

```
# Access the first 5 rows of df_liver
df_liver.head()
```

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albumin_and_Globulin_Ratio	Dataset
0	65	Female	0.7	0.1	187	16	18	6.8	3.3	0.90	1
1	62	Male	10.9	5.5	699	64	100	7.5	3.2	0.74	1
2	62	Male	7.3	4.1	490	60	68	7.0	3.3	0.89	1
3	58	Male	1.0	0.4	182	14	20	6.8	3.4	1.00	1
4	72	Male	3.9	2.0	195	27	59	7.3	2.4	0.40	1

CLEANING THE DATA

a) Dealing with missing values

```
[ ] # Define a function that allows us to create a table of missing values in df_liver and their percentages in
    # descending order
    def missing_values(data):
        total = data.isnull().sum().sort_values(ascending=False)
        percentage = (data.isnull().sum()/data.isnull().count()).sort_values(ascending=False)
        percentage_final = (round(percentage, 2) * 100)
        total_percent = pd.concat(objs=[total, percentage_final], axis = 1, keys=['Total', '%'])
        return total_percent
```

```
# Find the total count and % of missing values
missing_values(df_liver)
```

	Total	%
Albumin_and_Globulin_Ratio	4	1.0
Age	0	0.0
Gender	0	0.0
Total_Bilirubin	0	0.0
Direct_Bilirubin	0	0.0
Alkaline_Phosphotase	0	0.0
Alamine_Aminotransferase	0	0.0
Aspartate_Aminotransferase	0	0.0
Total_Protiens	0	0.0
Albumin	0	0.0
Dataset	0	0.0

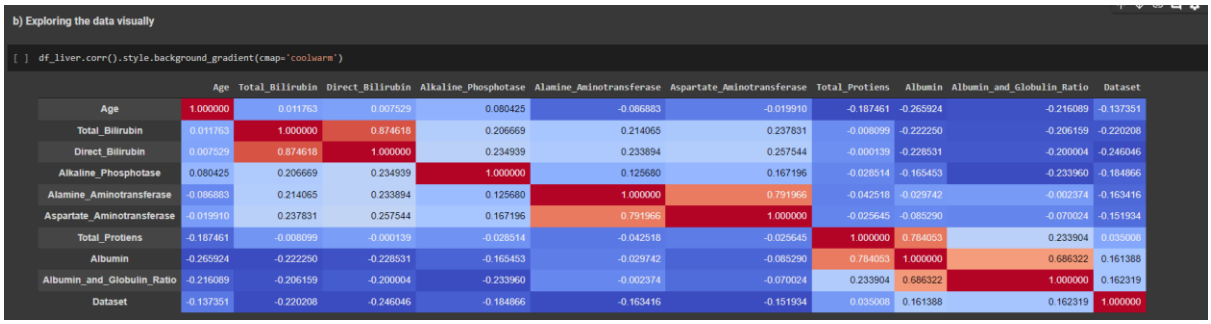
```
[ ] # Replace missing values with the mean of feature column Albumin_and_Globulin_Ratio,
    # then check to see that it has been successfull, where the sum of missig values should be 0
    df_liver['Albumin_and_Globulin_Ratio'].fillna(df_liver['Albumin_and_Globulin_Ratio'].mean(), inplace = True)
    df_liver['Albumin_and_Globulin_Ratio'].isnull().sum()
```

```
0
```

```
# Repeat to see what is the % of missing values
missing_values(df_liver)
```

	Total	%
Age	0	0.0
Gender	0	0.0
Total_Bilirubin	0	0.0
Direct_Bilirubin	0	0.0
Alkaline_Phosphotase	0	0.0
Alamine_Aminotransferase	0	0.0
Aspartate_Aminotransferase	0	0.0
Total_Protiens	0	0.0
Albumin	0	0.0
Albumin_and_Globulin_Ratio	0	0.0
Dataset	0	0.0

b) Exploring the data visually



	Age	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albumin_and_Globulin_Ratio	Dataset
Age	1.000000	0.011763	0.007529	0.080425	-0.086883	-0.019910	-0.187461	-0.265924	-0.216089	-0.137351
Total_Bilirubin	0.011763	1.000000	0.874618	0.206669	0.214065	0.237831	-0.008099	-0.222250	-0.206159	-0.220208
Direct_Bilirubin	0.007529	0.874618	1.000000	0.234939	0.233894	0.257544	-0.000139	-0.228531	-0.200004	-0.246046
Alkaline_Phosphotase	0.080425	0.206669	0.234939	1.000000	0.125680	0.167196	-0.028514	-0.165453	-0.233960	-0.184866
Alamine_Aminotransferase	-0.086883	0.214065	0.233894	0.125680	1.000000	0.791966	-0.042518	-0.029742	-0.002374	-0.163416
Aspartate_Aminotransferase	-0.019910	0.237831	0.257544	0.167196	0.791966	1.000000	-0.025645	-0.085290	-0.070024	-0.151934
Total_Protiens	-0.187461	-0.008099	-0.000139	-0.028514	-0.042518	-0.025645	1.000000	0.784053	0.233904	0.035008
Albumin	-0.265924	-0.222250	-0.228531	-0.165453	-0.029742	-0.085290	0.784053	1.000000	0.686322	0.161388
Albumin_and_Globulin_Ratio	-0.216089	-0.206159	-0.200004	-0.233960	-0.002374	-0.070024	0.233904	0.686322	1.000000	0.162319
Dataset	-0.137351	-0.220208	-0.246046	-0.184866	-0.163416	-0.151934	0.035008	0.161388	0.162319	1.000000

The above correlation heatmap demonstrates strong positive (closer to 1) and negative correlations (closer to -1) but also weak positive and negative correlations (closer to zero).

Based on the correlative pair plots, we find some interesting results directly.

-Positive correlations:

Total Bilirubin and Direct Bilirubin (vice-versa)

Alamine Aminotransferase and Aspartate Aminotransferase (vice-versa)

Total Protein and Albumin (vice-versa)

Albumin and Globulin Ratio and Albumin (vice-versa)

Total Protein and Albumin and Globulin Ration (vice-versa)

-Negative correlations:

Total Protein and age (vice-versa)

Albumin and age (vice-versa)

Albumin and Globulin Ration and age (vice-versa)

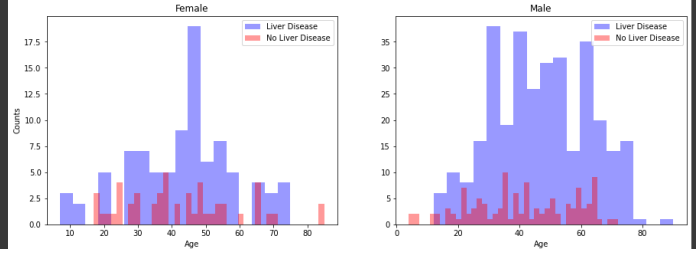
```
[ ]  # Change the current categorical feature Gender to a numerical feature of 0 or 1

     df_liver['Gender'] = df_liver['Gender'].apply(lambda x:1 if x == 'Male' else 0)
     df_liver.head()
```

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albumin_and_Globulin_Ratio	Dataset
0	65	0	0.7	0.1	187	16	18	6.8	3.3	0.90	1
1	62	1	10.9	5.5	699	64	100	7.5	3.2	0.74	1
2	62	1	7.3	4.1	490	60	68	7.0	3.3	0.89	1
3	58	1	1.0	0.4	182	14	20	6.8	3.4	1.00	1
4	72	1	3.9	2.0	195	27	59	7.3	2.4	0.40	1

```
[18]  # Create a table for Dataset (with and without liver disease) and gender
      df_liver_Gender = round(df_liver[['Gender', 'Dataset']].groupby(['Gender'], as_index=False).agg(np.sum), 3)

      # Generate plot to determine the effect of gender on the dataset
      plt.figure(figsize=(10,5))

      sns.barplot(x="Gender", y="Dataset", data=df_liver_Gender, ci=None)
      plt.title("Survival wrt Gender")
      plt.ylim(0, 700)

      (0.0, 700.0)
```

It appears from these plots that men normally have high liver function test results and hence are likely to have liver disease. This is likely because culturally men in NE of Andhra Pradesh in India consume alchohol more than women. Let us now look a dsitribution plot for all the liver function tests in relation to the target feature and gender.

```
# Figure configuration
fig, axes = plt.subplots(1, 2, figsize=(15, 5))

# Visualize the effect of the dataset(with or without disease) based on both Age and Gender.
ld = 'Liver Disease'
no_ld = 'No Liver Disease'
ax = sns.distplot(df_liver[df_liver['Gender'] == 0][df_liver[df_liver['Gender'] == 0]['Dataset'] == 1]['Age'],
                  bins=18, label=ld, ax=axes[0], kde=False, color='blue')
ax = sns.distplot(df_liver[df_liver['Gender'] == 0][df_liver[df_liver['Gender'] == 0]['Dataset'] == 2]['Age'],
                  bins=40, label=no_ld, ax=axes[0], kde=False, color='red')
ax.legend()
ax.set_title('Female')
ax.set_ylabel('Counts')
ax = sns.distplot(df_liver[df_liver['Gender'] == 1][df_liver[df_liver['Gender'] == 1]['Dataset'] == 1]['Age'],
                  bins=18, label=ld, ax=axes[1], kde=False, color='blue')
ax = sns.distplot(df_liver[df_liver['Gender'] == 1][df_liver[df_liver['Gender'] == 1]['Dataset'] == 2]['Age'],
                  bins=40, label=no_ld, ax=axes[1], kde=False, color='red')
ax.legend()
ax.set_title('Male')

/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use eit
  warnings.warn(msg, FutureWarning)
Text(0.5, 1.0, 'Male')
```



This distribution plot shows some interesting things,

1)On average, women tend not to have liver disease than men.

2)The greatest number of women without liver disease were about 38 yrs old.

3)Girls around the age of 10 had liver disease, this may be a genetic link.

4)Men are more prone to liver disease (may be due to alcoholism).

5)The greatest number of men without liver diseae were about 38 yrs old.

Applying machine learning approaches to liver disease

I will employ the following supervised machine learning models, whilst evaluating the mean accuracy of each of them by a stratified kfold cross validation procedure.

```
[19] # Machine learning libraries in sklearn

     from sklearn.ensemble import RandomForestClassifier
     from sklearn.preprocessing import MinMaxScaler
     from sklearn.metrics import accuracy_score

     from sklearn.model_selection import StratifiedKFold, train_test_split, cross_val_score

     from sklearn.linear_model import LogisticRegression
     from sklearn.neighbors import KNeighborsClassifier
     from sklearn.tree import DecisionTreeClassifier
```

```
[20] K_fold = StratifiedKFold(n_splits=10)
```

```
# Separate train features and response
X = df_liver.drop(["Dataset"],axis = 1)
Y = df_liver["Dataset"]



# Scale the data
scaler=MinMaxScaler()
scaled_values=scaler.fit_transform(X)
X.loc[:,:]=scaled_values

# Create the Train and Test sets
# Splitting the train and test into 70% training and 30% testing
X_train, X_test, Y_train, Y_test=train_test_split(X,Y,stratify=Y, test_size=0.3,random_state=42)


# Find the shape of all sets
X_train.shape, Y_train.shape, X_test.shape, Y_test.shape
```

```
((408, 10), (408,), (175, 10), (175,))
```

- **Logistic regression**

Logistic regression models the probabilities for classification problems with two possible outcomes. Furthermore, this models is an extension of the linear regression model but for classification problems.

```
# Logistic Regression
model_logreg = LogisticRegression()
model_logreg.fit(X_train,Y_train)
y_pred = model_logreg.predict(X_test)

scores = cross_val_score(model_logreg, X_train, Y_train, cv=K_fold, n_jobs=4, scoring='accuracy')

print(scores)
score_logreg = round(np.mean(scores) * 100, 3)
print("Score: {}".format(score_logreg))
acc_logreg = round(np.mean(accuracy_score(Y_test, y_pred)) * 100, 3)
print("Accuracy: {}".format(acc_logreg))
```

```
[0.73170732 0.73170732 0.70731707 0.68292683 0.70731707 0.68292683
 0.70731707 0.73170732 0.725      0.725     ]
Score: 71.329
Accuracy: 72.0
```

- **KNeighborsClassifier**

This is a test that searches for the K nearest measurements of the training data and draws a Euclidean distance. It then votes based on that information of how to classify the data.

```
[23] # K-Neighbors
     model_knn = KNeighborsClassifier(n_neighbors=5)
     model_knn.fit(X_train, Y_train)
     y_pred = model_knn.predict(X_test)

     scores = cross_val_score(model_knn, X_train, Y_train, cv=K_fold, n_jobs=4, scoring='accuracy')

     print(scores)
     score_knn = round(np.mean(scores) * 100, 3)
     print("Score: {}".format(score_knn))
     acc_knn = round(np.mean(accuracy_score(Y_test, y_pred)) * 100, 3)
     print("Accuracy: {}".format(acc_knn))
```

```
[0.73170732 0.70731707 0.70731707 0.58536585 0.56097561 0.75609756
 0.63414634 0.70731707 0.725      0.6       ]
Score: 67.152
Accuracy: 65.143
```

- **Decision Tree Classifier**

The data is continously split according to a certain parameter, in this case we are basing it on the features.

```
[24] # Decision Tree
     model_dtc = DecisionTreeClassifier()
     model_dtc.fit(X_train, Y_train)
     y_pred = model_dtc.predict(X_test)

     scores = cross_val_score(model_dtc, X_train, Y_train, cv=K_fold, n_jobs=4, scoring='accuracy')

     print(scores)
     score_dtc = round(np.mean(scores) * 100, 3)
     print("Score: {}".format(score_dtc))
     acc_dtc = round(np.mean(accuracy_score(Y_test, y_pred)) * 100, 3)
     print("Accuracy: {}".format(acc_dtc))
```

```
[0.70731707 0.68292683 0.70731707 0.70731707 0.6097561  0.56097561
 0.70731707 0.58536585 0.675      0.675     ]
Score: 66.183
Accuracy: 65.143
```

- **Random Forest Classifier**

Random forest classifier creates decision trees on randomly selected data samples. The model obtains prediction from each tree and subsequently selects the best solution by means of voting. Furthermore, random forest classfier also provides a very good indicator of the feature importance.

```
# Random Forest
model_rfc = RandomForestClassifier(n_estimators=50)
model_rfc.fit(X_train, Y_train)
y_pred = model_rfc.predict(X_test)

scores = cross_val_score(model_rfc, X_train, Y_train, cv=K_fold, n_jobs=4, scoring ='accuracy')

print(scores)
score_rfc = round(np.mean(scores) * 100, 3)
print("Score: {}".format(score_rfc))
acc_rfc = round(np.mean(accuracy_score(Y_test, y_pred)) * 100, 3)
print("Accuracy: {}".format(acc_rfc))
```

```
[0.6097561  0.73170732 0.68292683 0.82926829 0.75609756 0.65853659
 0.7804878  0.63414634 0.75       0.75       ]
Score: 71.829
Accuracy: 66.286
```

Which is the best model?

```
results = pd.DataFrame({'Model': ['Logistic Regression','KNeighbor',
                                  'Decision Tree ', 'Random Forest ',
                                  ],
                        'Accuracy': [acc_logreg, acc_knn,  acc_dtc, acc_rfc,
                                  ],
                        'Score': [score_logreg, score_knn, score_dtc, score_rfc,
                             ],})
df_results = results.sort_values(by='Score', ascending=False)
df_results = df_results.set_index('Score')
df_results
```

Score	Model	Accuracy
71.329	Logistic Regression	72.000
70.610	Random Forest	67.429
67.152	KNeighbor	65.143
66.183	Decision Tree	65.143

```
[31] accuracy = [acc_logreg, acc_knn,  acc_dtc, acc_rfc]
     x1 = [1,3,5,7]
     score = [score_logreg, score_knn, score_dtc, score_rfc]
```

```
plt.bar(x1, accuracy, label="Green Bar", color='g')
plt.plot()
plt.xlabel("")
plt.ylabel("bar height")
plt.title(" Acccuracy of different algorithms in order logistic regression,knn, ID3,random forest")
plt.legend()
plt.show()
```

```
[34] plt.bar(x1, score, label="Green Bar", color='g')
     plt.plot()
     plt.xlabel("")
     plt.ylabel("bar height")
     plt.title(" scores of  algorithms in order logistic regression,knn, ID3,random forest")
     plt.legend()
     plt.show()
```

- **RESULTS :**

Descript scores and accuracy

	Model	Accuracy
Score		
72.317	Random Forest	68.571
71.329	Logistic Regression	72.000
67.152	KNeighbor	65.143
66.427	Decision Tree	61.714

- **Drawbacks:**

Accuracy is not 100%, hence we cannot completely rely on these predictions. We cannot predict what type of liver disease is present, we can only predict whether a person has disease or not

- **Conclusion:**

  Through the above project We can predict whether a person had liver disease or not.We can see that the most accurate ML Model is Logistic Regression, and the least is the decision tree. Furthermore, we can also see the random forest ML model has Highest score and decision tree ML has the least score.

- **References:**

[1] Biomarkers for prediction of liver fibrosis in patients with chronic alcoholic liver disease written by Sylvie Naveau and Bruno Runyard.
[2] Strategic analysis in prediction of liver disease using classification algorithms written by Piyush Kr Shukla andBinish Khan.
[3] Software based prediction of liver disease with feature selection and classification techniques witten Jagdeep Singh, Sandeep Bagga and Ranjodh Kaur.
[4] Liver disease prediction using SVM and Naïve Bayes algorithm written by S Dhayanand.
[5] Prediction and analysis of liver diseases using data mining written Shambel Kefelgen, Pooja Kamat

- **Acknowledgements :**

It is my pleasure to express with deep sense of gratitude to Dr. S Selva Kumar, SCOPE, VIT-AP, for his constant guidance, continual encouragement, understanding; more than all, he taught us patience in our endeavour.