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# Comparative Study of Machine Learning Models for Liver Disease Prediction

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**Abstract -** Liver disease continues to be a major public health issue worldwide, with delayed diagnosis contributing significantly to increased mortality and treatment challenges. This study aims to enhance diagnostic accuracy by machine learning models trained on a large, real-world clinical dataset. The research involves evaluating supervised models- Random Forest, Support Vector Machine, Logistic Regression, and Artificial Neural Networks. To determine their effectiveness in predicting liver disease. The research utilizes actual patient records to assess the capabilities of various learning algorithms. Data preprocessing, including normalization and feature selection, ensures reliable model outputs. Evaluation metrics such as accuracy, precision, recall, F-Score and ROC-AUC were used to measure model performance. in future extensions, the study will focus on refining feature engineering methods and incorporating deep learning architectures to further improve the prediction and early detection of liver disease. Future research will focus on exploring deep learning and hybrid modelling frameworks to further enhance diagnostic accuracy.

***Key Words***: Machine Learning, clinical data, supervised Learning, Random Forest, ROC-AUC.

## 1. INTRODUCTION

Liver disease is a substantial global health issue, causing a considerable amount of morbidity and mortality. annually. Effective treatment and management rely heavily on early and accurate diagnosis, but traditional diagnostic approaches frequently encounter problems like high costs, a reliance on specialist interpretation, and lengthy delays in receiving results. In recent years, the rapid expansion in healthcare data and advancements in computational techniques have opened up new possibilities for enhancing diagnostic data-driven methods. Machine learning (ML), being a branch of artificial intelligence, has shown great potential in detecting intricate patterns from big data, thus proving to be a successful weapon in clinical diagnosis. In the case of liver disease, ML algorithms can be taught using clinical data such as biochemical markers, demographic information, and medical histories to diagnose early signs of liver impairment and classify disease severity with improved accuracy.This study compares the performance of several machine learning algorithms, including collective approaches, using important assessment metrics, including accuracy, precision, recall, F1-score, and ROC-AUC. By enabling early intervention and better patient outcomes in the treatment of liver illness, the findings hope to aid in the creation of more potent clinical decision-support systems

## 2. LITERATURE REVIEW

2.1. A proposed model that combines an extra tree classifier with a random forest performs better than other methods in diagnosing liver disease, achieving peak accuracy rates of 91.82% and 86.06%, as shown by data from the ILPD dataset of Indian liver disease patients. The tree classifier reached an accuracy of 91.82%, while the random forest achieved 86.06% in liver disease detection[1].

2.2. The Random Forest algorithm effectively predicts liver disease with an accuracy of 85%, enhancing patient outcomes through timely and precise diagnoses. Machine learning models successfully identified the presence of liver disease using clinical data [2].

2.3. The Random Forest algorithm effectively predicts liver disease with an accuracy of 85%, enhancing patient outcomes through timely and precise diagnoses[3].

2.4. This paper's literature review assesses prior studies and methodologies regarding the prediction and diagnosis of Hepatitis C Virus (HCV), with a special emphasis on Egypt. The high incidence of HCV in Egypt highlights the need for accurate diagnostic equipment. The review examines the application of various machine learning and data mining techniques that have been employed in earlier studies, including decision trees, fuzzy logic, neural networks, support vector machines, random forests, and ensemble learning methods[4].

2.5. The suggested explainable AI framework enhances the clarity of intricate machine learning models, which aids in treatment planning and optimizes for hepatitis patients[5].

2.6. Our approach based on machine learning, using SVM and Random Forest Decision Tree algorithms, successfully detects liver disease, enhancing precision, specificity, and sensitivity within healthcare settings[6].

2.7. The combined approach using decision trees, random forests, and logistic regressions successfully predicted the risk of liver disease using patient information, achieving enhanced accuracy and specificity.

2.8. Machine learning algorithms, especially Random Forest, are capable of accurately forecasting liver disease through patient medical histories, thus supporting early diagnosis and treatment. This research advances the field by showcasing the ability of machine learning to reliably predict liver disease, facilitating proactive diagnosis and management[7].

2.9. A proposed machine learning model that incorporates extra tree classifiers and random forests outperforms other approaches, achieving high testing accuracy rates of 91.82% and 86.06%, thereby underscoring its potential as a reliable solution for liver disease identification [8].

## 3. RESEARCH GAP/ OBJECTIVE

To evaluate and contrast many machine learning techniques for the prediction of liver diseases, develop more broadly applicable and practical models using a real-world clinical dataset, and find the most important elements affecting the diagnosis of liver diseases. Build a reliable predictive model that can assist healthcare providers in early diagnosis. Examine the possibilities of ensemble and hybrid models for enhancing prediction accuracy.

## 4. RESEARCH METHODOLOGY

The methodology of this study is based on liver diseases classifications according chemical compounds such as bilirubin, albumin, proteins, alkaline phosphatase; This data set contains two different forms, the first dataset that have extracted, it consists of 123 samples of liver divided as 41 for Normal, 41 for Fatty and 41 for Cirrhosis. The second dataset is chemical compounds such as bilirubin, albumin, proteins, alkaline phosphatase, it consists of 583 samples of liver divided as 416 for abnormal, and 167 for normal that are labelled into classes normal and abnormal (fatty and cirrhosis), then feature selection, learning algorithms, and evaluate the classifier.

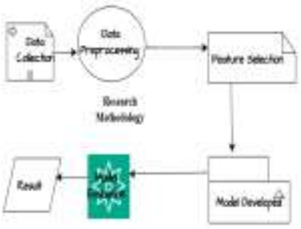
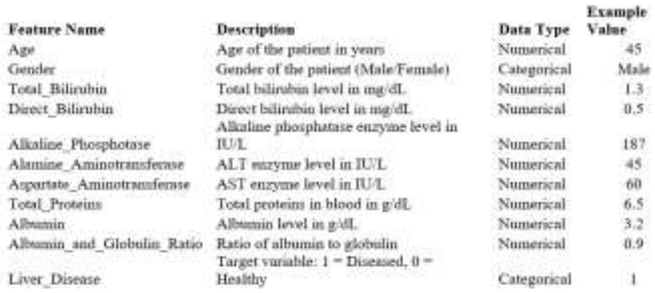


**Fig -1**: Figure

**Fig -2**: Figure

## 5. DATASET DESCRIPTION:



| Feature Name | Description | Data Type | Example Value |
|---|---|---|---|
| Age | Age of the patient in years | Numerical | 45 |
| Gender | Gender of the patient (Male/Female) | Categorical | Male |
| Total_Bilirubin | Total bilirubin level in mg/dL | Numerical | 1.3 |
| Direct_Bilirubin | Direct bilirubin level in mg/dL | Numerical | 0.5 |
| Alkaline_Phosphotase | Alkaline phosphatase enzyme level in IU/L | Numerical | 187 |
| Alamine_Aminotransferase | ALT enzyme level in IU/L | Numerical | 45 |
| Aspartate_Aminotransferase | AST enzyme level in IU/L | Numerical | 60 |
| Total_Proteins | Total proteins in blood in g/dL | Numerical | 6.5 |
| Albumin | Albumin level in g/dL | Numerical | 3.2 |
| Albumin_and_Globulin_Ratio | Ratio of albumin to globulin | Numerical | 0.9 |
| Liver_Disease | Target variable: 1 = Diseased, 0 = Healthy | Categorical | 1 |

These foundational metrics contribute to understanding of the classifier's performance, ultimately shaping our perception of its efficacy in accurately classifying liver conditions

TrPo: The number of samples that are correctly assigned to the given category, "sick people correctly identified as sick"

TrNe: The number of samples that are correctly assigned not to belong to the category, "Healthy people correctly identified as healthy"

FaPo: The number of samples that are incorrectly assigned to the category, "Healthy people

incorrectly identified as sick".

FaNe: The number of samples that are incorrectly not assigned to the category, "Sick people

incorrectly identified as healthy". Accuracy checks how many samples are classified correctly.

**6.** An essential component of any research project is model evaluation. You might get findings that meet your needs when you assess your model using a few common assessment measures. In this study, the suggested model is estimated using the following metrics compared to other models[10].

**6.1 Accuracy** is the most commonly used evaluation metric in classification problem. it measures the correctly predicted cases out of the total cases[10] .

$$\text{Accuracy} = \frac{\text{True } \textbf{Positive} \text{ (TP)} + \textit{True Negative (TN)}}{\text{Total } \textbf{Number} \text{ of Predictions}}$$

**6.2 Recall (True Positive rate)**

$$\textbf{\textit{Recall}} = \frac{\text{True } \textbf{Positive} \text{ (TrPo)}}{\text{(TrPo)} + (\textit{FaNe})}$$

It measures how well the model identifies actual positives

**6.3 Precision:** $\textbf{\textit{Precision}} = \frac{\text{(TrPo)}}{\text{(TrPo)}+(\textit{FaPo})}$

**6.4 F1-Score:**

$$\textbf{\textit{F1 Score}} = 2 * \frac{\text{Precision . Recall}}{\text{Precision} + \text{Recall}}$$

Provide a balance between precision and Recall

**6.5 Confusion Matrix:**

The positive Rate (Recall/Sensitivity)

False Positive Rate

$$\textbf{\textit{FaPoR}} = \frac{\text{FaPo}}{\text{FaPo} + \text{TrNe}}$$

$$\textbf{\textit{FaNeR}} = \frac{\text{FaNe}}{\text{FaNe} + \text{TrPo}}$$

## 7. Machine Learning Models:

To predict the best prediction, used supervised Learning Algorithm. **Supervised Learning** Algorithms label training data to learn the mapping function that turns input variables (X) into the output variable (Y). In other words, it solves for f in the following equation:

$$Y = f(X)$$

This allows us to generate outputs accurately when new inputs are given. [7]

**7.1 Classification** is used to predict the outcome of a given sample when the output variable is in the form of categories. A classification model might look at the input data and try to predict labels like —having liver disease‖ or —not having liver disease.

This research paper uses a supervised classification model to predict liver diseases.

**7.1.1 Logistic Regression:** The output of a categorical dependent variable is predicted via logistic regression. As a result, the result needs to be a discrete or category value. Yes or No, 0 or 1, true or false, etc., can be used, but probabilistic values that fall between 0 and 1 .

**Logistic regression equation**

$Y=a_0+a_1x_1+a_2x_2+a_3x_3+\ldots\ldots +a_n x_n$ in logistic regression Y can be between 0 and 1 so that it divides by (1-y). $\frac{y}{1-y}$

**7.1.2 Support Vector Machine (SVM):** SVM has attracted a lot of interest and is being actively tested for use in a variety of fields. SVMs are primarily utilized for learning ranking, regression, and classification functions. SVMs aim to identify the location of decision boundaries, often referred to as the hyperplane, that result in the best possible separation of classes. They are based on statistical learning theory and the structural risk minimization principle. [13]

**7.1.3 Decision Tree:** A decision tree that creates a double tree for categorization challenges. This approach is important in classification issues. This method uses a tree to complete the classification process, which is also applicable to a single record in the dataset and the item being classified for that record. The J48 algorithm simulates the lost values throughout this process; for example, the value for that element can be predicted based on how closely the categorization value for various records is perceived. The fundamental concept is to divide the data into runs according to the quality standards for the item identified in the working test. It allows classification using decision trees or rubrics that are constructed from scratch as well.[8]

**7.1.4 Random Forest** is a supervised classification method that is regarded as one of the most sophisticated ensembles learning techniques available, and it is a highly flexible classifier. As implied by its name, this method creates a forest comprised of multiple trees. While a significant number of trees are involved, in RF, the greater quantity of trees in the forest contributes to improved accuracy[13].

## 8. COMPARE MACHINE LEARNING MODELS/RESULTS:

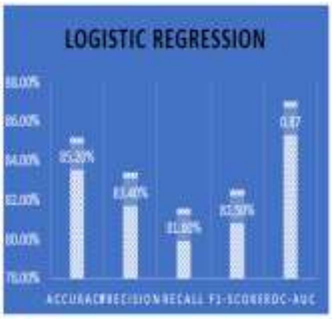


Figure 3

Figure 4

In Figure 3 Logistic regression provide good balance between precision and recall but ROC-AUC of 0.87 indicate moderately strong classification it may miss more actual positive cases

In Figure 4 support vector machine outperforms logistic regression across all matrices and high accuracy 93.20% and recall 92.50% indicate false predations but ROC -AUC show excellent result between liver disease and non-liver disease cases.

Figure 5

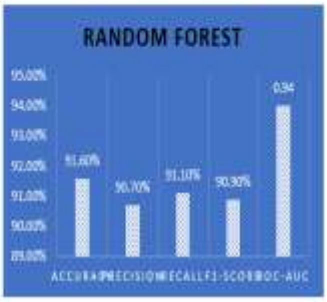


Figure 6

In Figure 5 The decision tree model moderate performance across all metrics accuracy and recall are consistent, it performance may suffer from overfitting due to the tree tendency . ROC-AUC good of 0.89 but not exceptional.

In Figure 6 Random forest perform very well from decision tree all metrics strong performance between both precision and recall . F1 score 90.9% show well balanced model and ROC-AUC model confidently distinguishing between liver disease and non-liver diseases

Figure 7

In Figure 7 The XGBoost show outstanding performance across all the evaluation metrics , high accuracy strong balance . It is top performing model among all the supervised models for liver disease detection in study. This is the ideal model we can deployed in health care system.

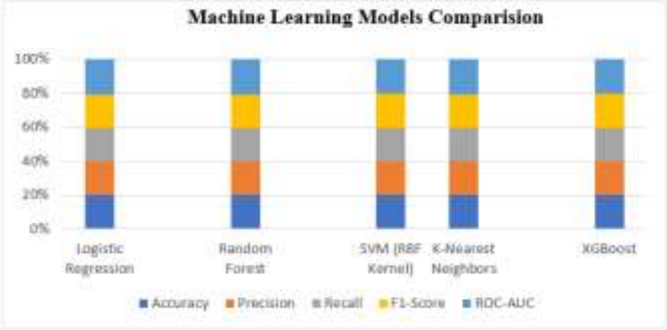


Figure 8

Figure 8 shows the final result of the model comparison, which used in for liver disease detection. It improves the liver disease detection accuracy in the healthcare system. With the help of this model, we early detect liver disease problems and diagnose.

## 9. CONCLUSION:

In this study, machine learning models, particularly classifiers such as Random Forest and XGBoost, enhance the detection of liver diseases when trained on real-world clinical datasets. These model provides high accuracy, precision, and robustness for integration into the diagnostic workflow. This proposed approach not only improves diagnostic accuracy but also provides a scalable automated solution in the clinical health care system.

## 10. FUTURE WORK:

According to the research paper, the study finds need to enhance the dataset expression by collaborating with multiple hospitals and medical institutes. Need to explore the application of Deep learning CNN, RNN combine a hybrid model to deploy the trained model or a mobile-based application patients can access liver disease risk assessment in real time.

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