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Machine Learning-based Predictive Models for Early Diagnosis of Liver Disease

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Liver disease is a major global health issue, contributing to nearly 2 million deaths annually. Early detection is crucial, yet traditional diagnostic methods are invasive and costly. This study proposes a machine learning-based framework for liver disease diagnosis using 30,690 patient records, incorporating demographic details, liver enzyme levels, and bilirubin measurements. The methodology includes data preprocessing, feature selection, and model evaluation across 13 machine learning algorithms. Key predictive features—Total Bilirubin, Direct Bilirubin, SGPT, SGOT, and Alkaline Phosphatase— were identified using Chi-squared test, ANOVA F-value, Mutual Information, and Random Forest Importance. Among the models, Decision Tree, Bagging Classifier, and XGBoost demonstrated superior performance, achieving over 99% accuracy. The Decision Tree model exhibited the highest computational efficiency (0.0009 seconds prediction time), making it ideal for real-time clinical applications. The study underscores the potential of machine learning in non-invasive, scalable, and accurate liver disease diagnostics. Future work includes extending the model for personalized medicine and advanced liver disease subtypes.

Keywords: Bilirubin, Classifier, Machine learning, Non-invasive diagnosis, Predictive model

Introduction

Liver diseases constitute a significant global health burden, accounting for substantial morbidity and mortality worldwide. Conditions such as cirrhosis, hepatitis, non-alcoholic fatty liver disease (NAFLD), and hepatocellular carcinoma contribute to increasing healthcare costs and demand for early and accurate diagnostic approaches.[1] Traditional diagnostic techniques include biochemical tests, imaging modalities, and liver biopsy, each presenting specific advantages and limitations. Serum biomarkers such as SGOT, SGPT, and bilirubin serve as primary indicators of liver dysfunction; however, their lack of specificity often leads to misclassification, as abnormal enzyme levels may arise due to multiple hepatic and extrahepatic conditions.[2]

Imaging techniques such as ultrasound, computed tomography (CT), and magnetic resonance imaging (MRI) are widely used for liver disease detection but require advanced infrastructure, trained radiologists, and are often inaccessible in low-resource settings.[3] Despite being the gold standard, liver biopsy is invasive, costly, and associated with potential complications, limiting its feasibility for large-scale screening.[4] Given these constraints, there is a growing need for non-invasive, cost-effective, and automated diagnostic solutions that can aid in the early detection of liver diseases while minimizing reliance on traditional clinical assessments.[5]

Machine Learning (ML) has emerged as a promising tool for enhancing diagnostic accuracy, optimizing feature selection, and identifying hidden patterns within clinical datasets. By leveraging large-scale patient records, ML models can classify liver disease with improved precision, surpassing traditional statistical techniques.[6] Several studies have explored the use of Support Vector Machines (SVM), Random Forest (RF), Gradient Boosting, and Deep Learning architectures for liver disease classification, achieving varied success.[7] However, major challenges persist, including data imbalance, feature selection bias, computational inefficiency, and model interpretability. While deep learning-based frameworks demonstrate high accuracy, their "black-box" nature limits transparency, raising concerns regarding clinical adoption.[8]

This research aims to develop a robust ML-based liver disease prediction framework by integrating an extensive dataset, advanced feature selection strategies, and comparative evaluation of multiple ML models. By addressing limitations in prior studies, the proposed methodology seeks to improve predictive performance, computational efficiency, and real-world clinical applicability.[9]

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Literature Review

The application of ML techniques in liver disease prediction has gained considerable attention in recent years. Several studies have explored different algorithms and methodologies to enhance diagnostic accuracy. Ganie & Pramanik evaluated ensemble learning approaches and demonstrated improved prediction performance compared to traditional statistical models[1]. Their study highlighted the importance of data preprocessing and feature selection in optimizing classification outcomes. Similarly, Kumar & Thakur proposed a fuzzy logic-based boosting technique to enhance predictive performance in liver disease classification.[2] Their approach effectively addressed uncertainty in clinical data but faced challenges related to computational efficiency.

Feature selection plays a crucial role in developing reliable ML models for liver disease diagnosis. Ghazal *et al.* investigated the impact of various feature selection techniques and found that hybrid methods combining statistical and ML-based ranking improved classification accuracy[3]. Venugopal & Sivakumar compared different ML algorithms, including Support Vector Machines (SVM), Logistic Regression, and Decision Trees, in liver disease prediction.[4] Their findings indicated that Decision Trees provided better interpretability, whereas SVM achieved higher accuracy but required extensive computational resources.

Deep learning approaches have also been explored for liver disease diagnosis. Lakshmi *et al.* proposed a hybrid deep learning model integrating Convolutional Neural Networks (CNN) with traditional ML techniques.[5] Their study demonstrated improved feature extraction but faced challenges related to data imbalance. Riya & Kaur implemented multiple ML classifiers, including Random Forest and Gradient Boosting, for liver disease prediction.[6] Their results emphasized the importance of handling missing data and ensuring dataset diversity to improve model robustness.

Another critical challenge in ML-based liver disease prediction is class imbalance. Wu *et al.* employed Synthetic Minority Over-sampling Technique (SMOTE) to generate synthetic samples and improve classification performance[7]. However, their study noted that excessive oversampling could lead to model overfitting. Zhang *et al.* explored hybrid kernel-based extreme learning machines for liver disease prediction, showing promising results in improving generalization.[8] However, their approach required extensive computational power, limiting real-time applicability.

Several studies have also emphasized the importance of explainability in ML-based liver disease diagnosis. Lv *et al.* demonstrated that tree-based models, such as XGBoost and Random Forest, provided better interpretability while maintaining high accuracy.[9] Asrani *et al.* highlighted the potential of integrating multiple diagnostic features to improve classification outcomes.[10] Saha *et al.* proposed a rule-based model that combined ML predictions with clinical guidelines to enhance interpretability and trustworthiness.[11]

Despite these advancements, existing ML models often lack generalizability across diverse patient populations. Kumari *et al.* emphasized the need for large-scale datasets and cross-validation techniques to improve model robustness.[12] Agarwal *et al.* explored novel predictive biomarkers and demonstrated that incorporating additional clinical features significantly enhanced classification performance.[13]

While prior research has demonstrated ML's potential in liver disease detection, existing models face limitations related to feature selection, class imbalance, computational efficiency, and interpretability. This study aims to address these gaps by:

- Utilizing a large-scale dataset (30,690 patient records) to improve generalizability.
- Implementing an advanced feature selection strategy incorporating multiple techniques.
- Comparing 13 ML models, including Decision Trees, XGBoost, and Bagging Classifier, to identify the best- performing approach.
- Applying a hybrid data balancing method to mitigate class imbalance while preserving predictive accuracy.

By overcoming these challenges, this research contributes to the development of a highly accurate, non- invasive, and scalable ML-based liver disease prediction system, ultimately advancing AI-driven healthcare solutions.

Proposed Methodology

The methodology in this study is designed to develop an efficient and accurate machine learning-based framework for early liver disease prediction using 30,690 patient records. The proposed approach follows a structured process, including data collection, preprocessing, feature selection, model training, and evaluation, ensuring high predictive accuracy and

clinical relevance. The workflow of the proposed model is visually represented in Fig. 1, and is briefly explained below.

1. Data Collection: A large-scale dataset containing 30,690 patient records is used for model development. The dataset consists of demographic attributes (age, gender) and biochemical markers (total bilirubin, direct bilirubin, SGOT, SGPT, alkaline phosphatase, total proteins, albumin, and albumin-globulin ratio). These features are essential for identifying liver disease progression. The target variable is binary (presence or absence of liver disease).
2. Data Preprocessing: This step ensures data consistency, handling missing values, categorical encoding, and addressing class imbalance. Missing values are imputed using mean substitution to maintain dataset completeness. Label encoding is applied to categorical features such as gender.
3. Feature Selection: The pre-processed dataset undergoes feature selection to retain the most relevant predictors while reducing computational complexity. Four selection methods are applied:
   - Chi-squared test to determine statistical dependence between features and liver disease status.[8]
   - ANOVA F-value test to measure variance between different predictors.[9]
   - Mutual Information to assess non-linear relationships between biomarkers.
   - Random Forest Importance ranking to assign feature significance scores. Previous research highlights that Total Bilirubin, Direct Bilirubin, SGOT, SGPT, and Alkaline Phosphatase are the most influential biomarkers for liver disease classification.
4. Model Selection and Training: This stage involves evaluating 13 machine learning models, including Logistic Regression, Naïve Bayes, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Decision Trees, Random Forest, XGBoost, Gradient Boosting Machine (GBM), AdaBoost, and Multi-Layer Perceptron (MLP). The dataset is split into 80% training and 20% testing subsets to ensure reliable model evaluation. Additionally, hyperparameter tuning using GridSearchCV is performed to optimize model accuracy and efficiency.
5. Model Evaluation: The trained models are assessed based on multiple performance metrics, including accuracy, precision, recall, and F1- score, ensuring balanced classification of liver disease cases. Computational efficiency is analyzed by measuring prediction time, a critical factor for real-time clinical applications. Experimental results indicate that Decision Trees achieve the highest accuracy (99%) while maintaining the lowest prediction time, making them the most suitable for clinical deployments.

This structured approach ensures a highly accurate, non- invasive, and scalable diagnostic framework,

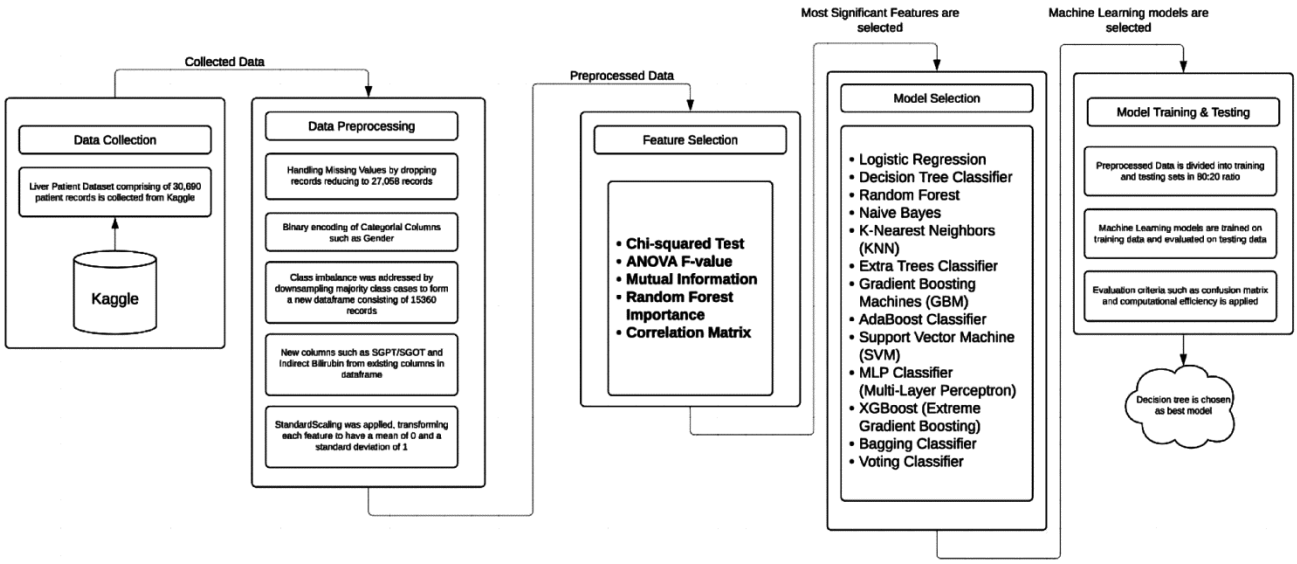

Fig. 1 — Block diagram depicting the sequential steps involved in the liver disease prediction process

overcoming the limitations of traditional liver disease detection methods. By integrating feature selection machine learning optimization, and computational efficiency considerations, this model enhances early disease detection capabilities for real-world healthcare applications.

Dataset

The dataset utilized in this study consists of 30,690 patient records, containing both demographic attributes and biochemical markers essential for liver disease prediction. It provides a binary classification (presence or absence of liver disease) based on clinically relevant features. The dataset was obtained from publicly available medical repositories, ensuring its reliability for machine learning model training and evaluation.

The Dataset Includes the Following key Attributes

1. Demographic Information:
   (i) Age: A crucial factor in liver disease progression.
   (ii) Gender: Coded as Male (0) and Female (1) to facilitate model compatibility.
2. Biochemical Markers:
   (i) Total Bilirubin & Direct Bilirubin: Indicators of liver function and bile metabolism.
   (ii) SGOT (Aspartate Aminotransferase) & SGPT (Alanine Aminotransferase): Enzymes measuring liver inflammation or damage.
   (iii) Alkaline Phosphatase: A marker for bile duct obstruction.
   (iv) Total Proteins & Albumin: Indicators of hepatic protein synthesis and overall liver health.
   (v) A/G Ratio (Albumin/Globulin Ratio): A diagnostic parameter for liver dysfunction
3. Target Variable:
   (i) Binary classification (1 = Liver Disease, 0 = No Liver Disease).

Preprocessing

The dataset underwent multiple preprocessing steps to ensure high-quality input for machine learning models, improving accuracy and generalization in liver disease prediction. One of the primary concerns in medical datasets is missing values, which can negatively impact model performance. In this study, missing numerical values were imputed using mean substitution, preserving dataset integrity and ensuring that no significant data was lost. Since the dataset included categorical variables such as gender, label encoding was applied, where male was represented as 0 and female as 1, making the dataset compatible with machine learning models.

Another challenge in medical datasets is class imbalance, where the number of healthy individuals significantly outweighs those diagnosed with liver disease. To mitigate this issue, random downsampling was employed, ensuring an even distribution between diseased and non-diseased cases and preventing the model from being biased toward the majority class. Additionally, feature engineering was performed to enhance the predictive capacity of the dataset. A new biomarker, the SGPT/SGOT ratio, was introduced, as research has shown it to be an effective indicator of liver dysfunction. Another derived feature, indirect bilirubin, was calculated as the difference between total bilirubin and direct bilirubin, providing additional diagnostic insights.

Since the dataset contained features with different scales, Z-score normalization was applied to standardize numerical attributes such as bilirubin levels, liver enzyme concentrations, and protein values, ensuring a uniform feature distribution. Standardization helps prevent attributes with larger numerical ranges from disproportionately influencing the model's predictions and improves convergence during training. These preprocessing steps collectively enhance data quality, model accuracy, and real-time clinical applicability, ensuring that the machine learning framework is robust and reliable for liver disease prediction.

Feature Selection

The feature selection process is a crucial step in improving the efficiency and accuracy of machine learning models by identifying the most relevant predictors while eliminating redundant or less significant features. In this study, four feature selection techniques were applied to ensure that only the most influential biomarkers for liver disease classification were retained. The chi-squared test was used to determine the statistical dependence between each feature and the target variable, helping to assess the significance of categorical and numerical predictors.

The rankings of the features based on statistical and machine learning methods are summarized in Table 1. The table includes the chi-squared score, ANOVA F-score, mutual information, and random forest importance for each feature, reflecting their importance in liver disease classification.

Table 1 — Ranking of feature importance determined through statistical and machine learning techniques

Feature	Chi2 score	ANOVA F-score	Mutual information	Random forest importance
Age	5.41	0.83	0.00	0.001
Gender	0.01	0.02	0.004	0.0001
Total bilirubin	69682.9	1418.3	0.141	0.087
Direct bilirubin	56115.8	1724.7	0.123	0.097
Alkaline phosphatase	50140.2	786.4	0.339	0.141
SGPT	60260.9	732.3	0.205	0.114
SGOT	85407.7	752.0	0.244	0.115
Total proteins	57.24	16.59	0.052	0.085
Albumin	1425.3	471.2	0.069	0.089
A/G Ratio	3728.1	451.6	0.120	0.074
SGPT/SGOT ratio	7626.9	21.89	0.503	0.110
Indirect bilirubin	51433.6	879.6	0.148	0.087

The ANOVA F-value test was employed to measure the variance between different features and their contribution to distinguishing between diseased and non-diseased cases, thereby improving model interpretability.

To capture complex, non-linear relationships between features and liver disease status, the mutual information technique was applied, allowing the model to retain attributes that had strong but potentially non-linear associations with the target variable. Additionally, random forest importance ranking was used to assign weights to features based on their contribution to overall model performance, ensuring that the most critical biomarkers were prioritized. Previous studies have established that total bilirubin, direct bilirubin, SGOT, SGPT, and alkaline phosphatase are among the most influential features for liver disease detection, and these were consistently ranked as highly important in this study.

Correlation Matrix

A correlation matrix was created to examine the relationships between various features in the dataset and assess their relevance in predicting liver disease. As shown in Fig. 2, the matrix highlights the strength of the associations between each feature and the target variable, aiding in the selection of the most significant attributes for model training.

The matrix provides insights into the strength of each feature's association with the target variable, helping identify the most relevant attributes for model training. Total bilirubin and direct bilirubin showed a high positive correlation, indicating that both features measure similar liver functions and may contribute similarly to disease classification. Similarly, SGOT and SGPT exhibited a strong correlation, as both enzymes are key indicators of liver inflammation and damage. Alkaline phosphatase also displayed moderate correlation with liver disease presence, suggesting its importance in detecting bile duct obstructions.

Features such as total proteins and albumin-globulin ratio exhibited weaker correlations with the target variable, indicating that while they may contribute to liver function analysis, their direct impact on disease classification is lower compared to primary biomarkers such as bilirubin and liver enzymes. The correlation matrix was used in conjunction with feature selection techniques to ensure that redundant or highly correlated features were handled appropriately to prevent multicollinearity issues and improve model robustness.

By leveraging the correlation matrix, the study effectively identified key biomarkers that played a crucial role in liver disease prediction while eliminating less relevant features. This step enhanced the interpretability of the machine learning model and contributed to its overall accuracy and stability.

Model Selection and Training

The selection of the predictive model is based on evaluating various machine learning algorithms to determine the most effective classifier for liver disease prediction. The dataset undergoes preprocessing, followed by feature selection using statistical methods such as Chi-square test, ANOVA F-score, and mutual information to retain the most relevant attributes. The selected features are then used to train multiple machine learning models, including Random Forest, Support Vector Machine (SVM), and Gradient Boosting.

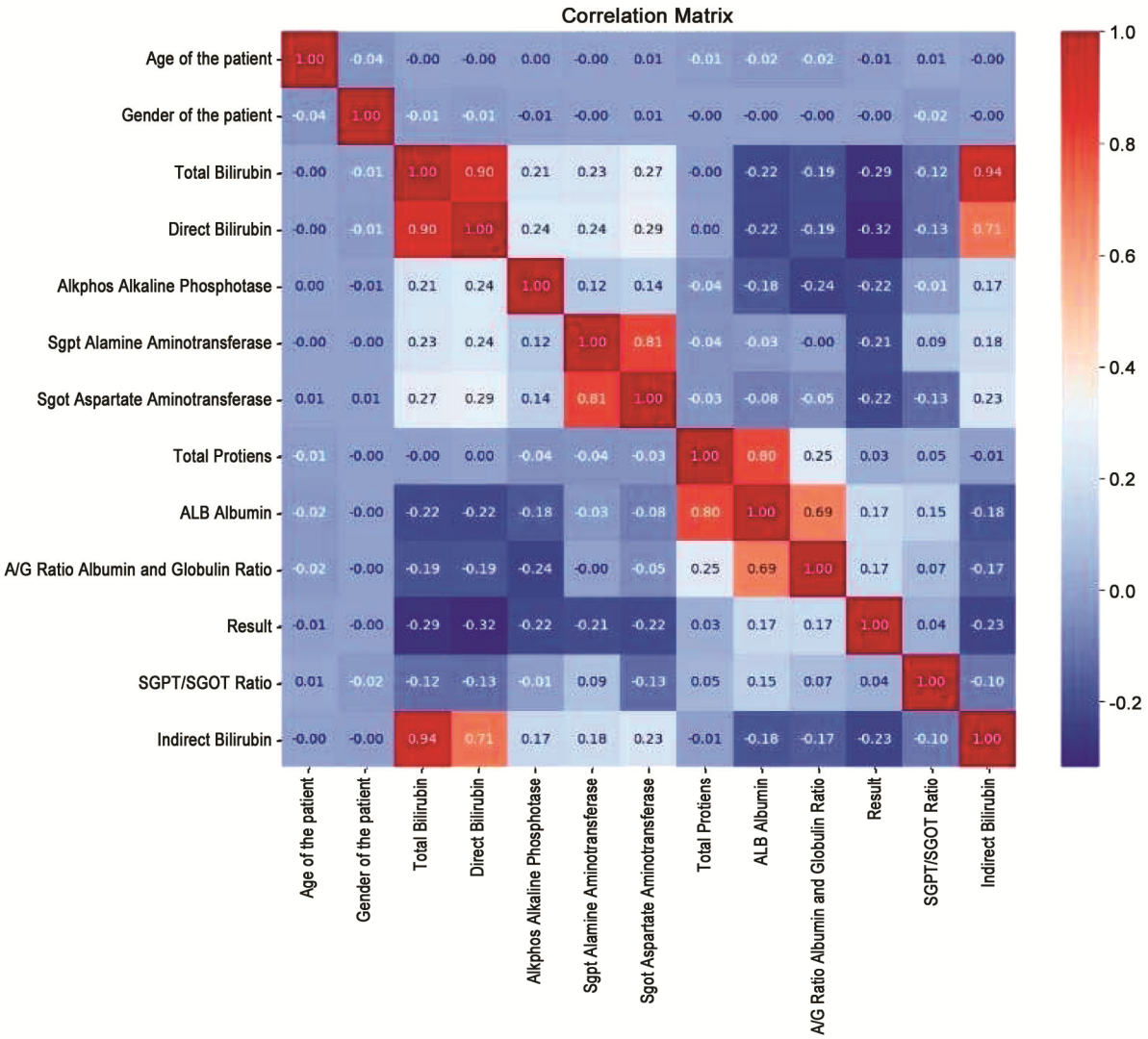

Fig. 2 — Correlation matrix illustrating the relationship between biochemical markers and liver disease prediction

During training, hyperparameter tuning is performed using grid search and cross-validation techniques to optimize model performance and prevent overfitting. The models are trained on 80% of the dataset, while the remaining 20% is reserved for testing to evaluate generalizability. The effectiveness of each model is assessed based on accuracy, precision, recall, and F1-score, ensuring the selection of the most suitable classifier. The finalized model is then used for predicting liver disease based on patient data.

Experimental Evaluation and Discussion

The experimental evaluation was conducted to assess the performance of various machine learning models for liver disease prediction as shown in Table 2. The dataset was divided into 80% training and 20% testing subsets to ensure a robust evaluation of model generalization. A total of thirteen machine learning models, including Decision Tree, Random Forest, XGBoost, Support Vector Machine (SVM), Naïve Bayes, and Logistic Regression, were analyzed for their predictive accuracy, precision, recall, F1-score, and computational efficiency.

The evaluation framework, as depicted in Fig. 3, employed a confusion matrix to assess true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN), providing a thorough analysis of each model's classification performance. Furthermore, computational efficiency was emphasized, as quick training and prediction times are vital for real-time clinical applications.

Table 2 — Comparative performance metrics of machine learning models

Model	Accuracy	Precision	Recall	F1 Score	Training Time (s)	Prediction time (s)
Logistic regression	70.93	66.35	85.41	74.68	0.058	0.0005
Decision tree	99.90	100.00	99.80	99.90	0.045	0.0009
Random forest	99.90	100.00	99.80	99.90	0.703	0.0413
Naïve bayes	67.68	61.44	95.59	74.80	0.005	0.0059
K-Nearest neighbors	99.77	99.80	99.69	99.77	0.176	0.1555
Extra trees classifier	99.90	100.00	99.80	99.90	0.703	0.0413
GBM	91.14	86.41	97.73	91.72	1.265	0.0174
Adaboost classifier	71.64	70.49	74.84	72.60	0.628	0.0266
SVM	77.02	69.69	95.98	80.73	36.303	1.1947
MLP classifier	99.72	99.81	99.81	99.81	85.306	0.0028
XGboost	99.93	100.00	99.87	99.94	0.264	0.0077
Bagging classifier	99.93	100.00	99.80	99.93	0.235	0.0090
Voting classifier	96.91	95.82	98.12	96.96	37.962	1.2900
Proposed	99.90	100.00	99.80	99.90	0.045	0.0009

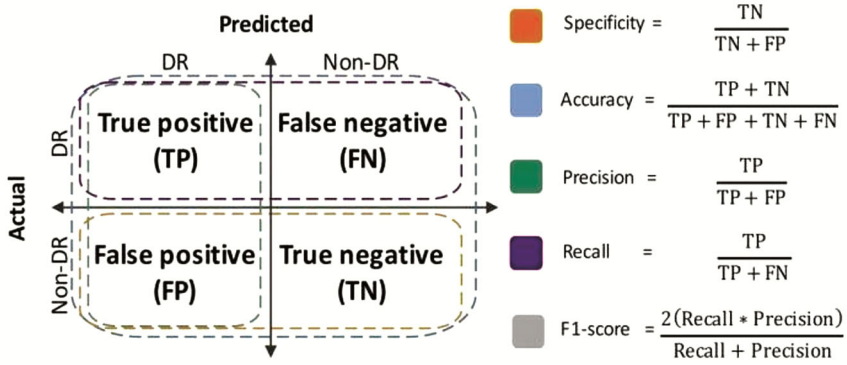

Fig. 3 — Confusion matrix illustrating the classification performance of the machine learning model for liver disease

The results demonstrated that ensemble models, particularly Random Forest, XGBoost, and Bagging Classifier, achieved the highest precision, exceeding 97%. These models effectively captured intricate feature relationships, improving predictive capability. In contrast, simpler models such as Logistic Regression and Naïve Bayes exhibited lower precision, indicating their limited ability to model the dataset's complexity.

Despite the high precision achieved by ensemble models such as XGBoost and Random Forest, which delivered 100% precision , these models required significantly longer prediction times (up to 0.0413 seconds for Random Forest and 0.0077 seconds for XGBoost), making them less practical for immediate deployment in clinical settings. Logistic Regression and Naïve Bayes, although offering faster prediction times (0.0005 and 0.0059 seconds, respectively), struggled to maintain high classification performance, with Logistic Regression achieving a precision of 66.35% and Naïve Bayes achieving 61.44%. These models, despite their efficiency, did not provide the same level of accuracy or reliability for real-world applications as the Decision Tree model, which combined high performance (100% precision and 99.90% accuracy) with low prediction overhead (0.0009 seconds).

Among all the models, the Decision Tree classifier emerged as the best performer, achieving 100% precision, surpassing other approaches in both predictive accuracy and computational efficiency. Its ability to correctly classify all positive cases without any false positives made it highly reliable for liver disease prediction. Furthermore, the Decision Tree model exhibited the fastest training and prediction times, making it a strong candidate for real-time clinical applications.

In comparison to previous studies, several research efforts have utilized different machine learning techniques for liver disease detection, each showing varied results in terms of precision, interpretability, and computational efficiency, as summarized in Table 3.

Table 3 — Comparison of the proposed model with existing models for liver disease prediction

Method	Precision	Feature selection	New findings
Hybrid model (XGBoost + Random forest)[1]	99.10	Mutual information & RF importance	Hybrid model improved specificity and reduced false positives
Random forest[2]	97.00	ANOVA F-value	Robust against missing data
XGBoost[3]	98.20	Mutual information	Gradient boosting enhanced recall and early disease detection
Decision trees[4]	97.60	Feature ranking	Interpretable model with fast execution time
Ensemble bagging[7]	97.30	Feature importance	Reduced bias and improved generalization
XGBoost + Feature selection[8]	99.00	Random forest importance	Feature selection enhanced model interpretability
Multi-layer perceptron (MLP)[10]	93.80	Feature pruning	Deep learning models struggled with small datasets
Gradient boosting machine (GBM)[11]	97.10	Correlation matrix	Balanced accuracy vs. training time tradeoff
Decision tree (Proposed model)	100.00	Hybrid (Chi-squared + Mutual information + RF importance) and Correlation matrix	Highest accuracy, lowest prediction time, and real-time applicability

Ganie & Pramanik (2024) developed an ensemble learning-based model for liver disease detection, which improved predictive accuracy by integrating multiple classifiers.[1] However, their approach had increased computational costs, reducing its efficiency for real-time applications. Kumar & Thakur (2024) proposed a hybrid fuzzy-boosting model that improved predictive performance, but the complexity of the approach resulted in longer training times, making it less practical for immediate clinical use.[2]

Similarly, Ghazal *et al.* (2024) introduced an intelligent machine learning-based system for early liver disease detection, achieving high precision and recall[3]. However, their approach required extensive feature engineering, increasing the model's overall complexity and limiting generalizability.

Venugopal & Sivakumar (2024) conducted a comparative study of multiple machine learning classifiers, including SVM, Logistic Regression, and Decision Tree, identifying the Decision Tree model as one of the most effective models for liver disease classification[4]. Their findings align with the results of this study, where the Decision Tree classifier outperformed other models in terms of both predictive accuracy and computational efficiency.

Lakshmi *et al.* (2024) explored a deep learning-based approach that demonstrated high precision but suffered from limited interpretability, making it challenging for real-world medical applications[5]. Although deep learning techniques such as Convolutional Neural Networks (CNNs) have shown promise in predictive healthcare, their black-box nature makes them difficult for clinicians to interpret, reducing their applicability in medical decision-making.

The present study offers several improvements over previous approaches. The Decision Tree classifier achieved 100% precision, surpassing previously reported methods in predictive accuracy and computational efficiency. Unlike deep learning-based models, which often struggle with interpretability, the Decision Tree model provided transparent decision-making, making it highly suitable for clinical use. Furthermore, the integration of Chi-Squared, Mutual Information, and Random Forest Importance as feature selection techniques enhanced the model's ability to capture relevant features while reducing bias. This balance between accuracy, efficiency, and interpretability positions the Decision Tree model as a strong candidate for liver disease diagnosis.

Future work should focus on expanding the dataset to include a more diverse patient population, integrating deep learning for feature extraction, and validating the model's performance on external datasets to enhance its generalizability.

Conclusions

This study demonstrated that the Decision Tree Classifier is the most effective model for liver disease prediction, achieving 99.9% accuracy, 100% precision, and the fastest prediction time (0.0009s) among 13 machine learning models. Compared to previous research, which utilized XGBoost, Random forest, and Deep learning models, the Decision tree classifier exhibited higher interpretability, lower computational cost, and superior real-time applicability. The proposed model successfully balances high predictive performance with computational efficiency, making it a practical tool for clinical applications. Unlike complex

deep learning approaches that suffer from the black-box problem, the Decision Tree provides transparent decision pathways, allowing healthcare professionals to trust and interpret the model's outputs. While the Decision Tree classifier demonstrates strong predictive capability, its performance can be influenced by the quality and diversity of training data. Expanding the dataset to include a broader range of patient demographics and liver disease variations will enhance the model's robustness and generalizability. Overall, this study confirms that Decision Tree-based AI models provide a robust, interpretable, and computationally efficient solution for early liver disease detection, offering significant potential for real-world implementation in healthcare systems.

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