



Article

Performance comparison of ML algorithms for liver disease prediction

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ARTICLE INFO	ABSTRACT
<i>Article history:</i> Received 20 August 2026 Received in revised form 24 September 2026 Accepted 12 October 2026 <i>Keywords:</i> Liver disease, Demographic variables, Prognostic/Biochemical variables, Statistical learning for variable selection and classification *Corresponding author Email address: abid.hussain@cpur.edu.in DOI: 10.55670/fpjl.fdtai.2.2.5	Liver disease is a leading cause of mortality throughout the world. Numerous lives may be saved if it can be detected in its early stages. Therefore, early detection of liver disease is crucial. This study aims to find a reliable ML model that can predict liver disease development using demographic and clinical data. This research explores several ML methods and introduces the most promising ones, Random Forest (RF) and Light Gradient Boosting Machine (LightGBM), for classification. The Indian Liver Patient Dataset (ILPD) is preprocessed by encoding categorical data, imputing missing values, removing duplicates and noise, applying Min-Max scaling, and balancing the data with SMOTE; this yields a dataset of 583 cases with 11 clinical and demographic characteristics. Models are assessed using F1-score, recall, accuracy, and precision, with an 80:20 stratified train-test split. While the proposed LightGBM model achieves a 99.8% ACC rate, a 99.9% PRE rate, a 99.5% REC rate, and a 99.8% F1-score (F1), the experimental results show that the RF model achieves a 99.6% PRE rate, a 99.7% REC rate, and a 99.6% F1-score (F1). The findings confirm that the proposed models achieved high ACC and reliability in predicting liver disease, with LightGBM delivering the highest ACC and PRE.

1. Introduction

Healthcare is integral to human health and wellbeing, disease prevention, and improved quality of life. The human body comprises organs that work together to carry out the various physiological functions and to keep the body healthy. However, infections, injuries, metabolic problems, and chronic diseases can affect these organs; in these cases, early diagnosis and effective treatment are vital to prevent complications and help patients recover. Liver function includes digestion, metabolism, detoxification, immunity, and homeostasis, making it one of the most important organs in the human body [1]. It plays a major role in nutrient assimilation, controls biochemical reactions, and eliminates harmful substances from the body. The liver can also be infected, injured, affected by metabolic disorders, or genetically altered, impairing its normal functions. Long-term damage can cause inflammation, jaundice, fibrosis, cirrhosis, and more serious conditions. Hence, maintaining liver health and early detection of abnormalities are crucial to limiting progression and improving patient outcomes [2-4].

The enormous morbidity, death, and healthcare burden caused by liver disease have made it a major concern in global health. Hepatocellular carcinoma (HCC), cirrhosis, viral hepatitis, alcoholic liver disease (ALD), non-alcoholic fatty liver disease (NAFLD), and a host of other disorders are all considered part of chronic liver disease (CLD) [5,6]. There are several potential causes of liver injury, such as excessive alcohol consumption, toxic chemicals, poor dietary choices, infections, and adverse drug reactions [7,8]. Identifying liver abnormalities early can improve treatment success and reduce the risk of complications. Liver disorders can be evaluated using clinical data and laboratory tests, especially blood parameters (bilirubin, albumin, liver enzymes) [9,10].

Liver disease may be difficult to diagnose at the right time and in the right context because of the illness's complexity and the limitations of standard diagnostic procedures [11]. Clinically, demographically, and through laboratory and imaging data, important patterns and relationships can help identify people at risk for liver disease [12,13]. These data sources are increasingly being analyzed computationally due to the growing volume of healthcare data [14]. Predictive analysis has been shown to help healthcare professionals detect disease patterns, support risk assessment, and enable proactive clinical intervention [15].

ML and DL are key areas of AI for understanding healthcare data and predicting disease, diagnosis, and prognosis [16,17]. ML algorithms can learn relationships between clinical and laboratory characteristics and classify patients by their risk of liver disease, whereas DL methods can learn more complex patterns from larger, more diverse datasets. Reports indicate that each algorithm's predictive power varies by liver disease dataset, and that none is consistently superior [18,19].

1.1 Motivation and contribution

Rapid, precise identification is crucial for preventing future health complications, and this research was motivated by the increasing prevalence of liver disease. Diagnostic approaches are complex, and extensive clinical assessment is crucial, requiring automation through computational methods. With the massive amount of clinical and biochemical healthcare data available, there is an opportunity to devise intelligent prediction models by applying ML techniques. The overarching goal of the research is to support the correct and timely identification of liver illness by creating a trustworthy prediction model using ML techniques. This research was able to contribute to the knowledge in the following ways:

- Developed a new ML approach that leverages clinical and demographic data to reliably detect early-stage liver disease.
- Applied data preprocessing and SMOTE class balancing to improve data quality and address class imbalance.
- Designed and trained liver disease classification models using RF and LGBM.
- Analyzed and compared the proposed models with existing ML algorithms and found their classification accuracy to be higher.

The proposed studies are important because precise, prompt diagnosis of liver disease matters not only for diagnosis but also for clinical management. The novelty lies in integrating data balancing, normalization, and an advanced ML (boosting) algorithm for liver disease prediction. The proposed models capture complex relationships between clinical and demographic attributes. This is a unique solution that's both effective and efficient for automating liver disease classification. The paper is structured as follows: Section 2 presents the literature review and identifies research gaps. This is outlined in Section 3. Section 4 details the findings of trials and comparisons. Section 5 summarizes the study and outlines implications for further research.

2. Literature review

The literature review provided a comprehensive overview of available research on liver disease prediction, highlighting current approaches, weaknesses, and areas for further research that informed the proposed investigation. N et al. [20] focus on identifying and classifying liver tumors using an RF classifier. The research draws on patient information extracted from a widely used public clinical liver database. Data preparation included feature scaling, missing-value handling, and SMOTE-based dataset balancing. A maximum ACC of 0.98 was achieved by the model trained using the RF Classification algorithm.

Grandhi et al. [21] proposed a method for predicting liver illness using an LR+XGB classifier: LR selects important factors that impact the development of liver disease. XGB serves as the classification component to capture complex patterns and improve predictive performance. The combined methodology achieved 96% ACC, outperforming base classifiers such as SVM and DT. Kumar and Gourav [22] analyzed several classifiers: Gradient Boosting, RFs, and DT. The diversity of routine hematological assays used to train these models relates to liver function. The outcomes show that the predictive ACC of the classifiers is about 95%. The various models differ in their computational efficiency, interpretability, and reliability; the authors discuss the trade-offs.

Lakumarapu et al. [23] suggest that ML has been useful in healthcare and has been essential in advancing patient diagnostics and treatment. While all approaches have shown promise in preliminary research, LR and RF have truly shone. Both achieve 74% ACC, while RF delivers the highest F-measure score at 72%. Well-optimized KNNs and DTs might be even better.

Shivaji Rao and Gangadhara Rao [24] propose new ML and neural network models to investigate this issue. The ILPD, a UCI repository with 583 samples, is used in this case. The study found that without feature selection, the F1 of LR is 83.85%. ANN and SVM achieved the highest accuracy rates of 83.38%, while F1 had the lowest accuracy at 73.57%. Liver Disease Diagnosis using Hyperparameter Tuned ANNs and ML Applications.

Verma, Deshmukh, and Krishnan [25] used the UCI repository's Hepatitis C dataset for multiclass liver disease categorization; the proposed research would be conducted. The MRMR algorithm uses a meticulous selection process to identify relevant features. SMOTE was implemented to address class imbalances. Using ACC measures and the receiver operating characteristic curve, one can evaluate a model's performance. With a macro F1 of 0.982, optimizable neural networks, optimizable support vector machines, and optimizable ensembles all performed well, but optimizable KNN performed best in training ACC (99.41%) and test ACC (100%). Minnoor and Baths [26] explored several supervised ML techniques, such as LR, KNN, Extra Trees, LightGBM, and MLP NNs, for the purpose of diagnosing liver illness using eleven features, including bilirubin, albumin, alanine transaminase (SGPT), and aspartate aminotransferase (SGOT). ACC, PRE, and F1 were used to compare the algorithms. With an ACC of 0.89 and an F1 of 0.88, ETs was an effective method for rapid and accurate identification of liver disease. Table 1 summarizes recent studies on liver disease prediction, including the methods used, datasets used, key findings, and limitations.

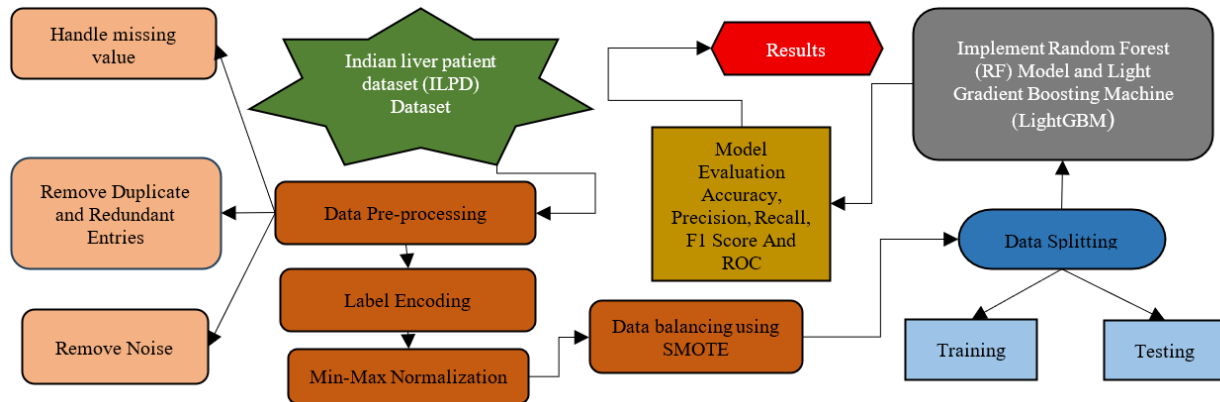
Research gaps: Existing studies on liver disease prediction mainly focus on individual ML or DL models, with limited exploration of robust boosting-based approaches. Many studies use incomplete datasets and suffer from class imbalance and/or inconsistent preprocessing methods. The lack of standardized preprocessing and evaluation procedures also limits comparative analysis of advanced ensemble models. Improved prediction of liver diseases requires efficient class balancing, preprocessing, and advanced ML algorithms.

Table 1. Recent research on liver disease prediction using machine learning techniques

Author	Proposed Work	Datasets	Key Findings	Limitations & Future Work
N et al. [20]	Random Forest classifier for liver tumor/disease identification	Public clinical liver dataset	Achieved 98% accuracy and supported real-time liver disease probability prediction.	More validation on bigger, more varied clinical datasets is necessary.
Grandhi et al. [21]	LR + XGBoost classifier for liver disease prediction	Liver disease dataset	Achieved 96% accuracy, outperforming base SVM and Decision Tree classifiers.	More extensive datasets and additional algorithm comparisons could improve generalization.
Kumar and Gourav [22]	Comparison of GB, RF, and DTs	Routine hematological/liver-function data	Classifiers achieved approximately 95% accuracy; GB and RF performed effectively.	Computational efficiency, interpretability, and reliability require further optimization.
Lakumarapu et al. [23]	Comparison of LR, KNN, DT, and RF	Liver disease dataset	LR and RF achieved 74% accuracy; RF obtained the highest 72% F-measure.	KNN and DT require further optimization.
Shivaji Rao and Gangadhara Rao [24]	Comparison of ANN, KNN, RF, LR, and SVM with hyperparameter tuning	ILPD, 583 samples	LR achieved the highest F1-score of 83.85%; models were assessed with and without feature selection.	Larger datasets and improved feature-selection/tuning strategies could enhance performance.
Verma, Deshmukh and Krishnan [25]	Comparison of optimized KNN, neural network, SVM, and ensemble models	Hepatitis C dataset from UCI	Optimized KNN achieved 100% test accuracy and 0.982 macro F1-score.	Further validation is needed to avoid overfitting and assess generalization.
Minnoor and Baths [26]	Comparison of LR, KNN, Extra Trees, LightGBM, and MLP	Liver function/blood enzyme dataset, 11 attributes	Extra Trees achieved the highest 89% accuracy and 0.88 F1-score.	Further clinical validation and integration with medical expertise are required.

3. Research methodology

The proposed method begins by capturing the ILPD, then analyzing its clinical characteristics through visualization and correlation methods. The data processing procedures include handling missing values, removing duplicate and noisy data, label-encoding categorical characteristics, and applying Min-Max normalization. The class proportions are preserved when SMOTE equalizes the distribution using an 80:20 stratified train-test split. By the end of the process, train and assess XGBoost and LightGBM models for liver disease prediction using ACC, PRE, REC, F1, ROC, and AUC. Figure 1 shows the suggested approach for predicting liver disease using ML techniques.

**Figure 1.** Proposed flowchart for liver disease prediction using ML models

3.1 Data gathering and analysis

The ILPD used in this investigation comes from Kaggle and includes 583 patient records with 11 demographic and clinical factors used to predict liver disease. The data include demographic information (gender, age, etc.), biochemical parameters, and a target variable (is_patient) indicating whether the patient has liver disease. The data were analyzed using data visualizations like bar plots, feature relationships, and correlation analysis between clinical attributes. Figure 2 shows a graph of the number of samples in each class for both patient (1) and non-patient (2) groups. The majority class is Patient (1) with 416 samples, while the non-patient (2) class has 167 samples, leading to class imbalance. Figure 3 shows strong positive correlations between Total Bilirubin and Direct Bilirubin (0.88), Total Proteins and Albumin (0.81), and Albumin and the Albumin-to-Globulin Ratio (0.72). There are moderate positive correlations with output and with Direct Bilirubin (0.31) and Total Bilirubin (0.28), and weak correlations with most other features.

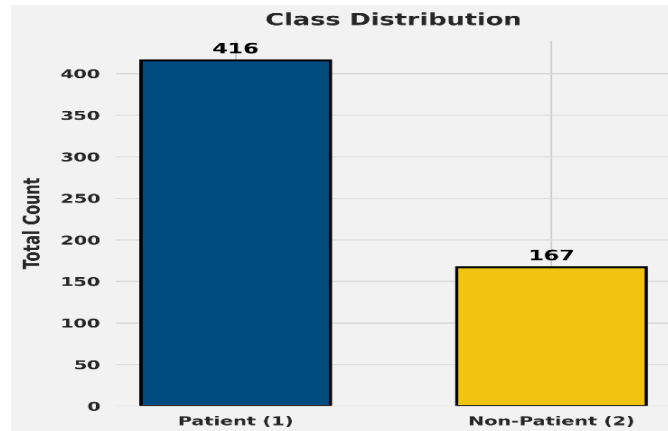


Figure 2. Bar graph of class distribution

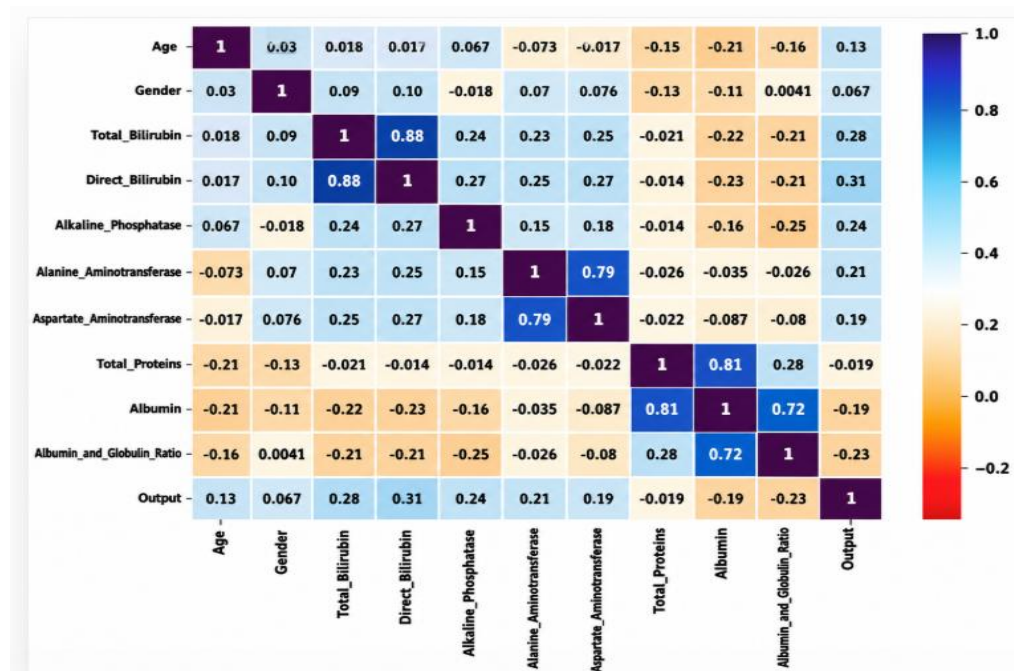


Figure 3. Correlation matrix heatmap

3.2 Data pre-processing

The ILPD was applied to preprocess and prepare the data. The preprocessing procedure concatenated and cleaned the data, removed missing values, eliminated duplicate and redundant data, and removed noise. The final steps to ensure consistent, high-quality input data were normalization and labeling. The main preprocessing stages are summarized here:

- **Handle missing values:** Identify and remove the missing class labels and incomplete data points to keep the data set clean and unbiased.
- **Remove duplicate and redundant entries:** Select the data range, navigate to the Data tab, and click "Remove Duplicates" to define which columns to check. This will allow you to utilize the Remove Duplicates tool in spreadsheet programs like Google Sheets and Excel to delete duplicate entries.
- **Remove noise:** Data quality and the efficiency of later analysis or ML models are both greatly enhanced by eliminating noise during data preparation. Many approaches are available, each tailored to a specific data format and noise type.
- **Label Encoding:** This dataset was prepared for ML methods by using label encoding to convert categorical variables (such as attack types or class labels) into numerical values.

3.3 Min-max normalization

The records were normalized using the min-max approach, which limits values to a range of 0 to 1. This study aimed to enhance the performance of classifiers utilized while minimizing the influence of outliers. This mathematical formula (1) was used to perform the normalization:

$$X' = \frac{X - X_{min}}{X_{max} - X_{min}} \quad (1)$$

where X is the feature's StartingValue, X' is its NormalizedValue, X_{min} is its MinimumValue, and X_{max} is its MaximumValue.

3.4 Data balancing using SMOTE

Data balancing ensures each class in the dataset has an equal number of samples, so the ML model can perform better when one class has fewer examples than the others. To ensure underrepresented classes are fairly represented, we used SMOTE. SMOTE generates dummy samples by calculating the average distance between all MinorityClass samples. Then, it finds the KNN for each MinorityClass sample. A fresh set of synthetic samples may be created by doing this with each neighbor. Adding these synthetic cases to the TrainingSet increases the number of minority-class samples and balances the sample distribution. The balanced class distribution of the dataset after performing the SMOTE algorithm is shown in Figure 4. To address the initial class imbalance, SMOTE synthetically generated minority-class instances for non-patient (2), raising its count from 167 to 416 to match the majority class, Patient (1), at 416 samples, resulting in an even 1:1 ratio across both categories.

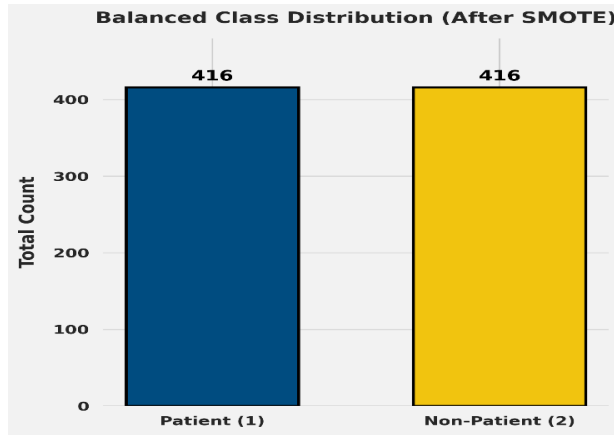


Figure 4. Bar graph of class distribution after SMOTE

3.5 Data splitting

The training and testing sets were appropriately divided 80:20. It was straightforward to compare the two sets since this stratified split kept the same percentage of classes in the training set as in the original dataset.

3.6 Implementation of the proposed model

In this work, supervised ML-based boosting models, RF Model and LightGBM, are proposed for accurate liver disease prediction. Testing the models helps find the optimal approach for liver disease categorization.

3.7 Proposed random forest (RF) model

The proposed RF model uses a variety of DTs to reliably categorize liver disorders; it is an ensemble ML type. The decision trees are trained on randomly selected samples and feature subsets, and the final prediction is determined by a majority vote. By reducing overfitting and increasing resilience and generalizability, this ensemble technique improves the model. Equation (2) shows the prediction of the suggested RF model.

$$\hat{y} = \text{mode}\{T_1(x), T_2(x), \dots, T_N(x)\} \quad (2)$$

The i th DT's prediction, denoted as $T_i(x)$, is based on the input feature vector x . The final predicted class, denoted as $\hat{y}$, is another variable, and N is the total no. of trees in the network. In a majority-voting system, the class with the most votes at the end of each tree is selected.

Equation (3) provides an alternative method of calculating the likelihood of allocating an input sample to a certain class by combining predictions of all DTs:

$$P(y = c|x) = \frac{1}{N} \sum_{i=1}^N I(T_i(x) = c) \quad (3)$$

where N is no. of trees, $I(\cdot)$ is an indicator function that returns 1 when i th tree predicts class c and 0 otherwise, and $P(y = c|x)$ is likelihood that input x corresponds to class c . The suggested RF model has a good chance of accurately categorizing patients based on the severity of their liver illness by using the probable class as the final prediction. The RF model was trained with the following parameters: $n_estimators = 200$, $max_depth = 10$, $min_samples_split = 2$, $min_samples_leaf = 1$, $max_features = sqrt$, and $random_state = 42$. This was done to provide stable and reliable liver disease categorization.

3.8 Light Gradient Boosting Machine (LightGBM) Model

LightGBM is a GB framework used in ML-based product demand forecasting. It trains a succession of trees to reduce the residuals of its predecessors, building an ensemble of trees. Its computational efficiency, low memory usage, and ability to capture intricate nonlinear correlations among sales-related attributes make it an ideal choice for product demand forecasting. The projected demand can be represented by summing the outputs of many DTs, as shown in Equation (4).

$$\hat{y}_i = \sum_{k=1}^K f_k(x_i), \quad f_k \in F \quad (4)$$

The input feature vector is represented by x_i , the total no. of DTs is represented by K , and prediction generated by the k th tree is denoted by f_k in Equation (1). $\hat{y}_i$ stands for the expected product demand for the i th observation. Equation (5) is the regularized objective function that LightGBM minimizes during training. This function combines a complexity penalty with the prediction loss.

$$\mathcal{L} = \sum_{i=1}^n l(y_i, \hat{y}_i) + \sum_{k=1}^K \Omega(f_k) \quad (5)$$

The loss between the real demand image and forecasted demand $\hat{y}_i$ is represented by $l(y_i, \hat{y}_i)$ in Equation (2), and the complexity of each DT is controlled by $\Omega(f_k)$ to reduce overfitting. LGBM, which minimizes the objective iteratively, makes accurate predictions while maintaining low computational cost; thus, it is suitable for intelligent product demand forecasting and management. The LGBM model was tuned to effectively learn the complex relationships within the features with the following settings: $n_estimators = 200$, $learning_rate = 0.05$, $max_depth = 10$, $num_leaves = 31$, $min_child_samples = 20$, $random_state = 42$.

3.9 Evaluation metrics

Several statistical measures were used to assess health prediction models, including TP, FP, TN, FN, ACC, PRE, REC, F1, ROC curve, and AUC. While a negative predictive value (PRE) shows the likelihood of being disease-free, a positive PRE indicates the likelihood of illness. The results of the classifications are summarised in the confusion matrix:

Accuracy (ACC): This is how well the expected outcomes match up with the measured ones. Equation (6) provides the formula used to calculate it.

$$ACC = \frac{TP+TN}{TP+FP+TN+FN} \quad (6)$$

Precision(PRE): The percentage of favorable events that turn out to be true. The calculation is done using the formula in Equation (7).

$$PRE = \frac{TP}{TP+FP} \quad (7)$$

Recall(REC): A measure of an ML model's performance that evaluates its ability to detect positive cases relative to all actual positive occurrences. It is mathematically expressed as follows in Equation (8).

$$REC = \frac{TP}{TP+FN} \quad (8)$$

F1-score(F1): An efficiency measure that integrates REC and PRE into a single number is the F1. It is determined using the following equation, provided in Equation (9).

$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (9)$$

Receiver Operating Characteristic Curve (ROC): The ROC curve shows the link between the FPR, the TPR, and the model's ACC in detecting positive and negative situations. A higher AUC indicates better class separation and reflects the ROC's overall performance.

4. Results and discussion

This part describes the performance of the recommended models, including evaluation and effective processing, as well as the experimental setting. The system specifications for each test were a 64-bit Windows 10 installation, 32 GB of RAM, a 500 GB solid-state drive, and an Intel Core i7 CPU operating at 4.2 GHz. Using the Jupyter Notebook environment and Python 3.10.9, the algorithms were developed. Scikit-learn, Matplotlib, Seaborn, Pandas, and NumPy were included as data analysis and visualization libraries. Table 2 displays the results of training the proposed RF and LightGBM models using the IPLD and evaluation. The proposed RF model achieved 99.5% ACC, 99.6% PRE, 99.7% REC, and 99.6% F1, whereas the proposed LightGBM model achieved 99.8% ACC, 99.9% PRE, 99.5% REC, and 99.8% F1, demonstrating strong classification performance for liver disease risk prediction. Figure 5 shows the confusion matrices that demonstrate how well the proposed RF and LGBM for disease prediction perform in terms of classification ACC. RF correctly classified 8,754 affected and 3,477 not affected cases, with 13 FN and 33 FP. LGBM correctly classified 8,754 affected cases and 3,495 not affected cases, with 13

false negative cases and 15 FP cases. Overall, LGBM demonstrates slightly better classification performance due to its lower number of FP predictions. Figure 6 illustrates the ROC curves, demonstrating the classification performance of the proposed RF and LGBM models. The AUC value for RF is 0.999 (99.9%), indicating excellent discrimination between the two classes, while LGBM achieves a perfect AUC of 1.000 (100%). Overall, both models exhibit outstanding predictive performance, with LGBM providing the best ROC performance.

Table 2. Classification performance of the proposed model

Matrix	Proposed RF	Proposed LightGBM
Accuracy	99.5	99.8
Precision	99.6	99.9
Recall	99.7	99.5
F1-score	99.6	99.8

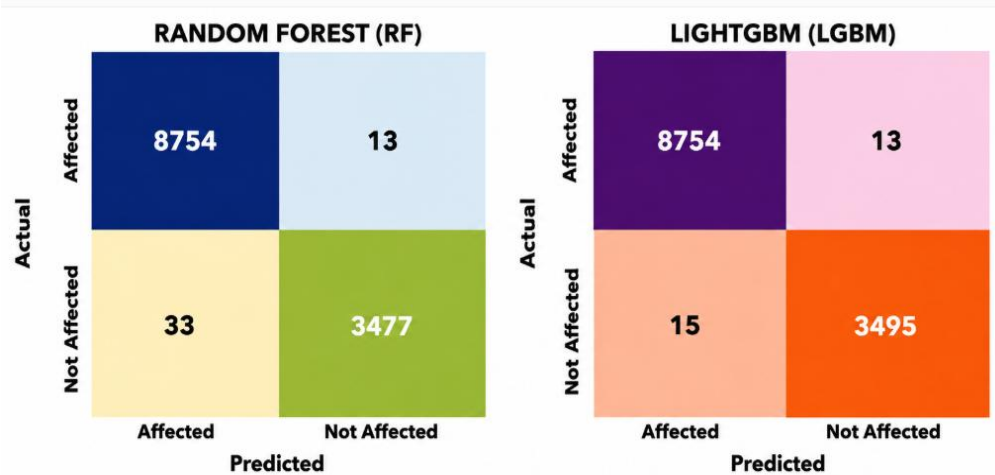


Figure 5. Confusion matrix for proposed models

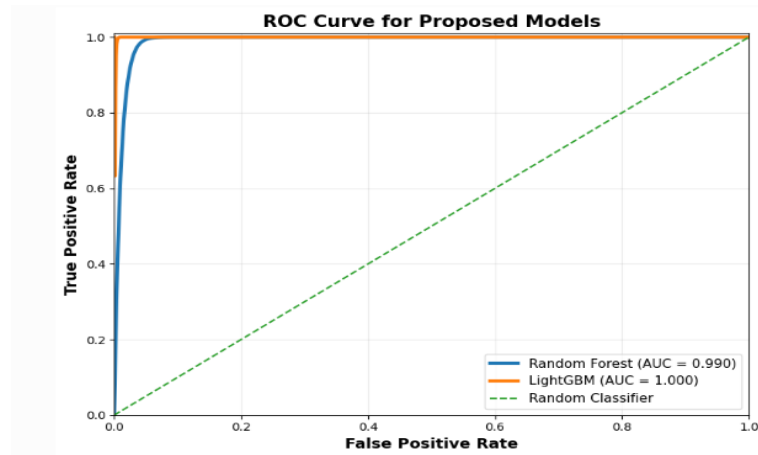


Figure 6. ROC curve for proposed models

4.1 Comparative analysis

Table 3 compares the ACC of the present model with the suggested model, allowing one to assess the model's efficacy. Among the existing models, KNN achieved the lowest ACC of 62.9%, while SVM, LR, ET, and DT obtained accuracies of 73%, 75%, 81.86%, and 91%, respectively. The suggested RF model outperformed the others in terms of ACC, with high ACC (99.5%), PRE (99.6%), rec (99.7%), and F1 (99.6%). When it came to predicting liver illnesses, the suggested LightGBM model outperformed the benchmark models with an ACC of 99.8%, PRE of 99.9%, REC of 99.5%, and F1 of 99.8%. The proposed RF and LightGBM models achieved high predictive performance in liver disease risk prediction. RF has an ACC of 99.5%, while LightGBM has an ACC of 99.8% suggesting high classification

capability. Both models accurately predict outcomes and capture complex correlations between laboratory and clinical variables. An excellent capacity to detect instances of liver disease is shown by the high PRE, REC, and F1 values. These models can then be utilized to provide effective and accurate decision support in early liver disease risk assessment.

Table 3. Liver disease classification analysis based on performance measures using machine learning models

Model	ACC	PRE	REC	F1
KNN [27]	62.9	85.3	57.8	68.8
SVM [28]	73	75	99.9	84
LR [29]	75	91	78	84
ET [30]	81.86	75	99	86
DT [31]	91	92.7	89.4	91
Proposed RF	99.5	99.6	99.7	99.6
Proposed LightGBM	99.8	99.9	99.5	99.8

5. Conclusion

Liver disease is a public health concern, and quick and accurate prediction is essential for efficient clinical decision-making and early detection. This study aimed to predict liver disorders in the ILPD using ML models and compared different approaches. Data preprocessing, Min-Max normalization, class balancing using SMOTE, and stratified data splitting were utilized for improved consistency of classification. Two models were implemented and tested: RF and LGBM, which were tested with several performance metrics. Model performance in experiments showed very good predictive capacity for both models. The LGBM model performed best overall with an ACC of 99.8%, a PRE of 99.9%, a REC of 99.5%, and an F1 of 99.8%, whereas the RF model had the lowest ACC of 99.5%, PRE of 99.6%, REC of 99.7%, and F1 of 99.6%. Additionally, RF got an AUC of 0.999, while LGBM was able to get an AUC of 1.000, which showed good discriminative power. In general, LGBM outperformed the other models. Further recommendations include validating the proposed models using broader, larger clinical datasets from multiple healthcare centers. Hyperparameter optimization and external validation could improve generalization, and advanced feature selection and explainable AI methods could enhance interpretability. Integrating real-time clinical decision-support systems could further evaluate practical application and reliability.

Ethical issue

The authors are aware of and comply with best practices in publication ethics, specifically regarding authorship (avoidance of guest authorship), dual submission, figure manipulation, competing interests, and compliance with research ethics policies. The authors adhere to publication requirements that the submitted work is original and has not been published elsewhere in any language.

Data availability statement

The manuscript contains all the data. However, more data will be available upon request from the corresponding author.

Conflict of interest

The authors declare no potential conflict of interest.

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