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PROGNOSTIC MODELING FOR HEPATIC DISORDERS: A PARADIGM OF EQUILIBRATED AND GENERALIZED MACHINE LEARNING METHODOLOGIES

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ABSTRACT

In human physiology, the liver is a vital organ responsible for performing critical functions such as bile production, bilirubin excretion, metabolism of proteins and carbohydrates, enzyme activation, glycogen storage, and plasma protein synthesis. However, it is highly susceptible to damage due to alcohol consumption, certain medications, and poor dietary habits. Traditional diagnostic methods for liver disorders, including blood tests and imaging, are time-consuming and costly, often delaying crucial treatment. This study introduces a machine learning-based prognostic framework to enhance the speed and accuracy of liver disease diagnosis. The proposed approach integrates advanced algorithms, including Random Forest, Gradient Boosting, XGBoost, and LightGBM, combined with an ensemble voting method to leverage their complementary strengths. Preprocessing techniques such as Principal Component Analysis (PCA) for dimensionality reduction and Synthetic Minority Oversampling Technique (SMOTE) to address class imbalance were employed to refine the dataset. Evaluation metrics like precision, recall, F1-score, accuracy, and ROC-AUC revealed the ensemble model's superior performance, achieving the highest accuracy of 98% and a ROC-AUC of 0.9963, significantly outperforming individual models. This study offers a scalable and cost-effective solution that reduces diagnostic time and improves predictive reliability. The framework provides significant advantages for medical applications, serving as a decision support tool to aid healthcare professionals in timely and accurate liver disorder diagnosis, particularly in resource-limited settings.

KEYWORDS

Ensemble Learning, Hepatic Disorders, Machine Learning, Healthcare Data Analytics, Random Forest Classifier, Gradient Boosting Methods, XGBoost Algorithm

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INTRODUCTION

Liver disorders affect an estimated 2 billion individuals globally, with conditions such as cirrhosis, hepatitis, and nonalcoholic fatty liver disease (NAFLD) contributing to over 2 million deaths annually (G. L. C. Collaborators, 2021; Dyson & Hudson, 2020). These conditions are among the leading causes of morbidity, imposing a significant burden on healthcare systems worldwide. Early diagnosis and timely intervention are crucial for mitigating severe complications, yet current diagnostic approaches, which rely heavily on blood tests and imaging, remain time-intensive, expensive, and often inaccessible in resource-limited healthcare settings (Asrani, Devarbhavi, Eaton, & Kamath 2021). Consequently, delayed interventions exacerbate the progression of liver-related conditions, further complicating treatment and patient outcomes (Patel & Singh, 2021). Existing diagnostic methods for liver disorders face critical challenges, including inefficiency, high costs, and limited accessibility in under-resourced settings. Computational diagnostic models, though promising, are often hindered by issues such as overfitting, inadequate generalizability, and poor handling of complex, imbalanced clinical datasets. These limitations restrict their applicability in real-world scenarios, necessitating the development of robust and scalable solutions (Patel & Singh, 2021); Chawla, Bowyer, Hall, & Kegelmeyer, 2021).The proposed research aims to develop an advanced machine learning-based prognostic framework for enhancing the diagnostic accuracy, robustness, and generalizability of liver disorder detection. This innovative approach addresses critical challenges in the field, including class imbalance, high-dimensional feature spaces, and overfitting, to provide healthcare professionals with an efficient and reliable decision support tool (Luo, Lu, Yuan, & Xie, 2022). The study introduces a hybrid machine learning framework that integrates ensemble learning algorithms, specifically Random Forest, Gradient Boosting, XGBoost, and LightGBM, with sophisticated data preprocessing techniques. This combination is designed to optimize data representation, enhance model performance, and ensure scalability for realworld clinical applications. The ensemble learning approach enhances predictive performance by combining outputs from multiple models.

The framework has demonstrated exceptional performance, potentially setting a new benchmark in computational hepatology. It significantly reduces the risk of misdiagnosis through high precision and reliability, while its adaptable design ensures applicability across diverse healthcare environments and datasets. Moreover, the proposed solution reduces dependency on costly diagnostic tests and imaging techniques, streamlining the diagnostic process through automation and enabling timely interventions. This research contributes to the field of hepatology by offering a scalable, efficient, and innovative solution for liver disorder diagnosis (Jones & Woolfenden, 2023). By addressing limitations of existing methods, it advances precision medicine in hepatology and provides a robust decision support tool to assist clinicians in making accurate and timely diagnoses.

RELATED WORKS

Advancements in machine learning (ML) and deep learning (DL) have significantly improved liver disease prediction, surpassing traditional diagnostic methods in accuracy and efficiency. However, challenges remain in managing high-dimensional datasets and optimizing model performance through hyperparameter tuning. Ghosh et al. (2024) and Hanif and Khan (2022) proposed a machine learning framework for liver cirrhosis prediction using Random Forest, Decision Tree, and Support Vector Machine (SVM) models. Leveraging the Liver Cirrhosis dataset, their approach achieved a highest accuracy of 97% with Random Forest, demonstrating robust predictive capabilities but lacking advanced hyperparameter tuning methods, such as GridSearchCV, which could further enhance model optimization and reliability.

Lin et al. (2009) proposed a machine-learning monitoring system to predict mortality and classify patients with noncancer end-stage liver disease (ESLD). Utilizing supervised models such as Random Forest and Adaptive Boosting on a retrospective dataset of 1214 patients for training and 689 patients for validation, the Random Forest model achieved the highest ROC-AUC of 0.852. Key predictors included blood urea nitrogen, bilirubin, and sodium, complemented by clustering techniques to differentiate acute death and palliative care groups. While the system demonstrated strong predictive performance, further validation and optimization could enhance its clinical applicability in ESLD management.

Ghazal et al. (2022) proposed an intelligent machine learning model for early prediction of liver disease, addressing the high costs and time-consuming nature of traditional diagnostic methods. The study evaluated multiple ML algorithms, developing a comprehensive predictive framework that

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achieved an accuracy of 88.4% and a miss-rate of 11.6%. While the model demonstrated reliable performance, further enhancements such as advanced feature engineering and hyperparameter optimization could improve its diagnostic precision and clinical utility.

Sorino et al. (2020) proposed a machine learning framework for diagnosing Non-Alcoholic Fatty Liver Disease (NAFLD) using a meta-learner approach to identify the best predictive algorithm. Utilizing a dataset of 2970 subjects and testing with eight ML algorithms, Support Vector Machine (SVM) emerged as the most effective model. Among three predictive models, the highest accuracy of 77% was achieved with Model 3, comprising BRI, GLUCOSE, GGT, SEX, and AGE as predictors. Despite robust performance, further optimization could enhance predictive accuracy and reduce variance, making the SVM model a promising yet improvable solution for NAFLD diagnosis and cost reduction. Afrin et al. (2021) proposed a machine learning-based framework for liver disease prediction utilizing algorithms such as Logistic Regression, Decision Tree, Random Forest, AdaBoost, KNN, Gradient Boosting, Linear Discriminant Analysis, and Support Vector Machine (SVM). Employing the LASSO feature selection technique, the study identified highly correlated attributes for liver disease. With 10-fold crossvalidation, the Decision Tree algorithm demonstrated the best performance, achieving an accuracy of 94.3%, along with precision, sensitivity, and F1-score values of 92%, 99%, and 96%, respectively. While the framework effectively integrates feature selection to improve predictive accuracy, further exploration of advanced ensemble techniques could enhance its robustness and applicability.

Tahmasebi et al. (2023) proposed an ultrasound-based machine learning model for detecting nonalcoholic fatty liver disease (NAFLD) as an alternative to invasive biopsies or MR-based fat quantification. Using ultrasound images collected from 120 subjects and validated against MRI-derived proton density fat fraction (PDFF) findings, the AutoML-based model achieved an accuracy of 83.4%, with a specificity of 94.6% and a sensitivity of 72.2%. The study demonstrated high positive predictive value (PPV) of 93.1% and an average agreement of 92% for individual subjects. While the model showed promising results as a cost-effective and noninvasive screening tool, further enhancements in sensitivity could improve its diagnostic utility for high-risk patients. Atsawarungruangkit et al. (2021) proposed machine learning models to predict nonalcoholic fatty liver disease (NAFLD) using the NHANES 1988–1994 dataset, which included 3235 participants and 30 NAFLD-related factors. Among the 24 algorithms applied, the ensemble of RUS-boosted trees achieved the highest F1 score (0.56) and an accuracy of 71.1% in the testing phase. A simpler interpretable model, coarse trees, attained a higher accuracy of 74.9% but with a lower F1 score (0.33). While the ensemble model offered better overall performance, the coarse trees model, leveraging only fasting C-peptide and waist circumference, demonstrated the value of simplicity in clinical applications despite trade-offs in predictive accuracy. Straw et al. (2022) studied the presence of sex bias in liver disease prediction models using the Indian Liver Patient Dataset (ILPD). They recreated machine learning models such as Random Forest, Support Vector Machine (SVM), Gaussian Na¨ıve Bayes, and Logistic Regression, testing them on both sex-balanced and unbalanced datasets, with and without feature selection. The models showed accuracies between 71.31% (Logistic Regression) and 79.40% (SVM). However, they found that females had a higher chance of being misdiagnosed due to higher false negative rates (FNR), with Random Forest and Logistic Regression showing the largest gaps. The study highlights the importance of identifying and addressing biases in AI models to ensure fair and accurate healthcare solutions for all patients. In comparison to the aforementioned studies,, our research integrates traditional models like Logistic Regression, Random Forest, and XGBoost with advanced techniques such as PCA, SMOTE, and GridSearchCV for optimization. Our framework offers a scalable, robust, and efficient solution for liver disease prediction in real-world healthcare settings.

METHODOLOGY

In this study, The "Liver Disease Patient Dataset" (Shrivastava, 2024), sourced from Kaggle, contains clinical data from 583 patients. It includes demographic information and critical laboratory markers such as age, gender, bilirubin levels, alkaline phosphatase, and albumin. The dataset supports binary classification for liver disease diagnosis. Its availability and comprehensive attributes make it well-suited for predictive modeling in hepatology. Figure 2 represents the distribution plot highlights key patterns in the selected features. Age shows a normal distribution centered between 30–60 years. Total Proteins peaks above 2.0 warranting further analysis. Figure 3 represents the pair plot illustrating relationships between Age, Total Proteins, Albumin, and A G Ratio, colored by the target variable.

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Age shows a clear unimodal distribution, while Total Proteins and Albumin exhibit positive correlations. Moreover, strong correlations are observed between Total Bilirubin and Direct Bilirubin (0.89) and between Total Proteins, Albumin, and A G Ratio (moderate correlations of 0.68–0.78). Age shows a normal distribution centered between 30–60 years. Total Proteins peaks around 7.0, while Albumin exhibits a bimodal pattern near 3.5 and 4.0. A G Ratio is skewed, clustering around 1.0, with sidos. A G Ratio is skewed with lower variance. No strong separability between classes is observed, suggesting potential challenges in direct classification.

Figure 1: Workflow diagram across the whole procedure

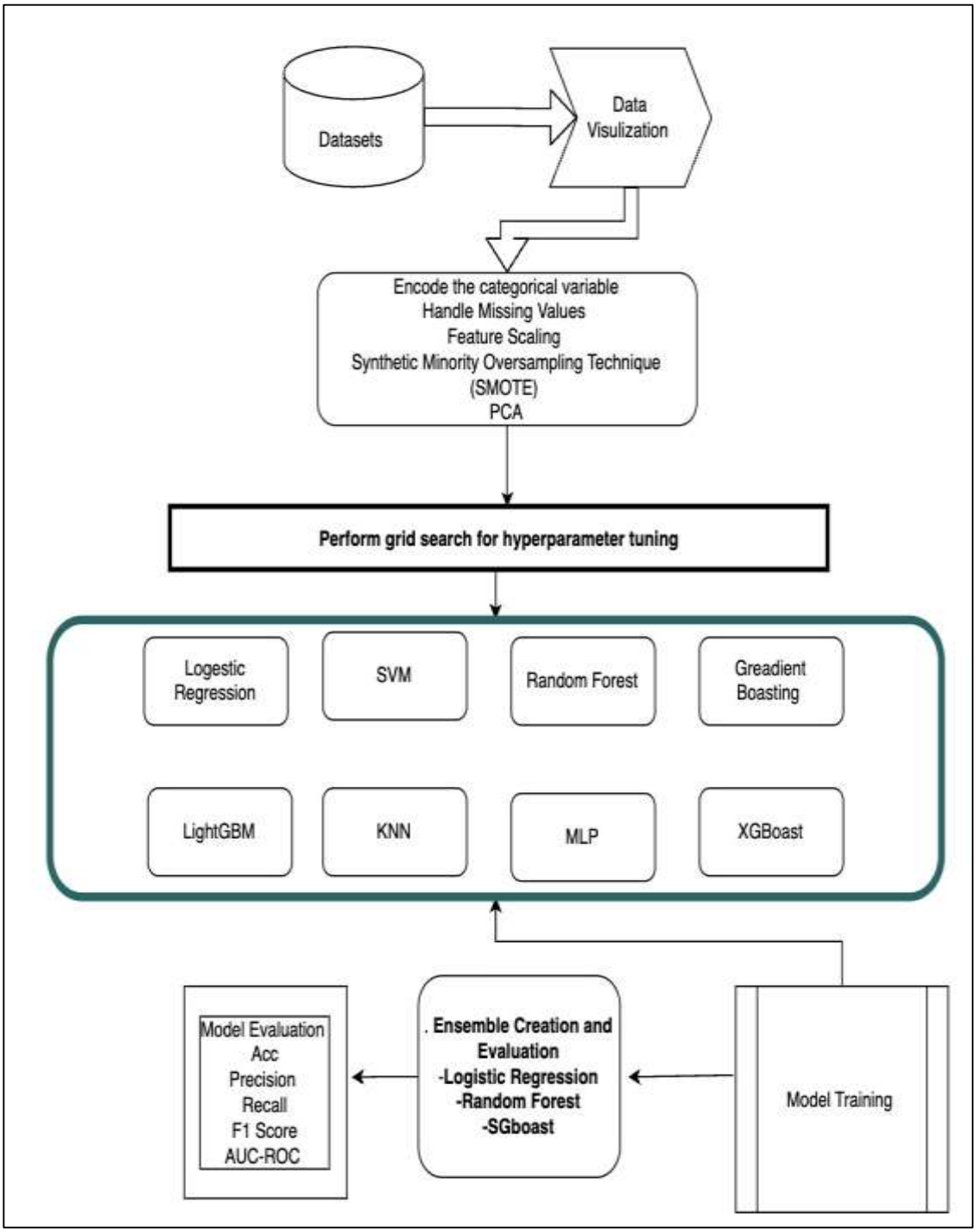

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Figure 2: Distribution of Target Variable

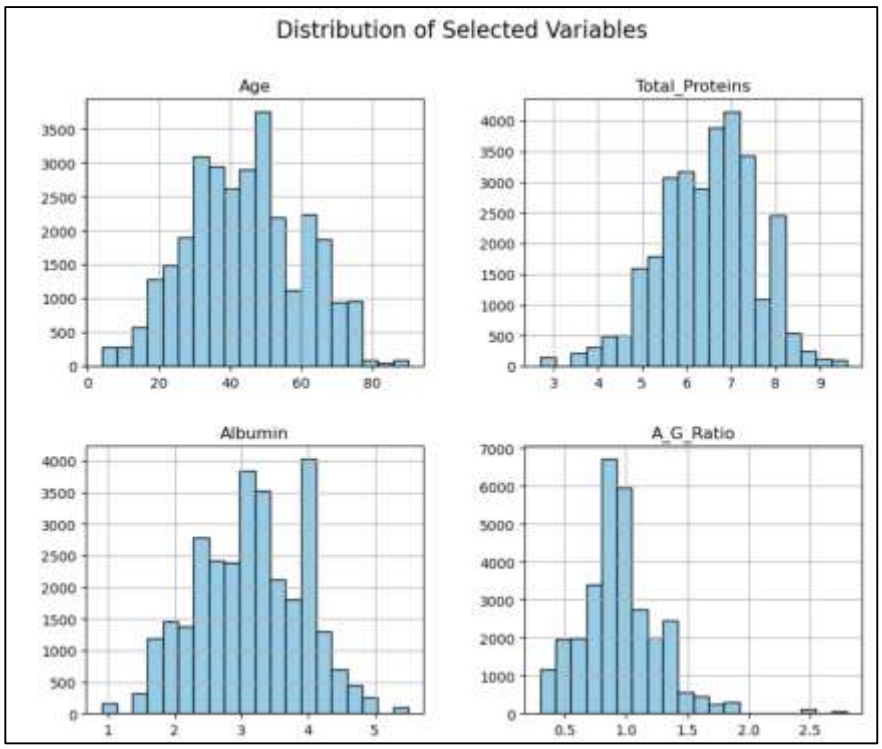

Figure 3: Pair Plot

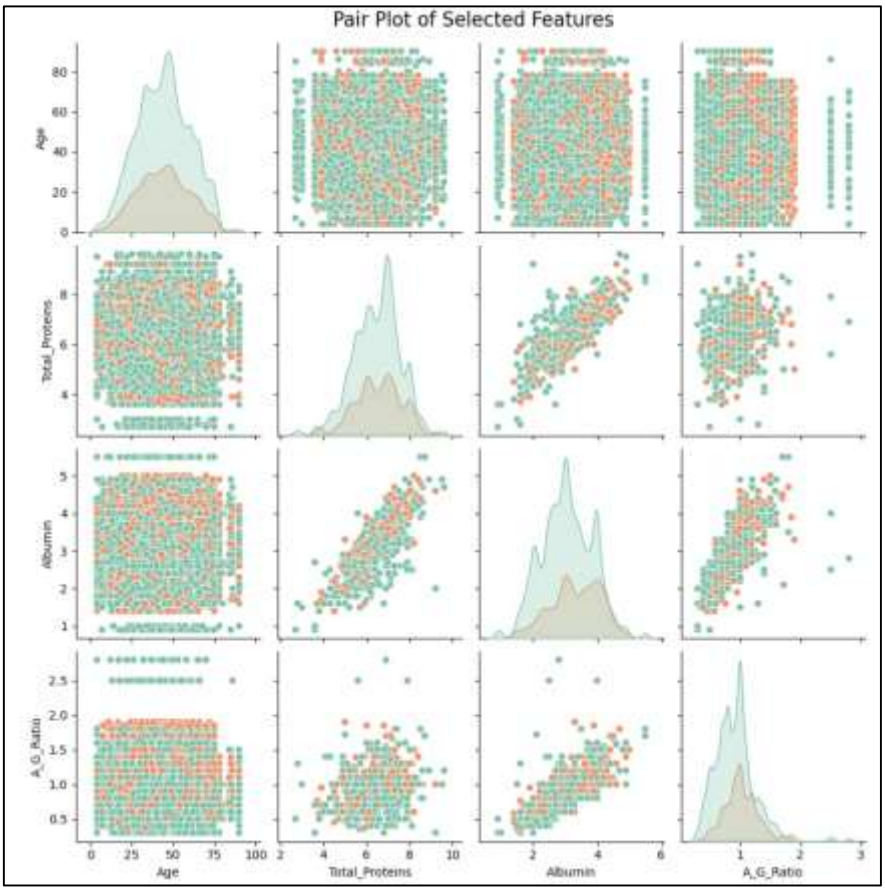

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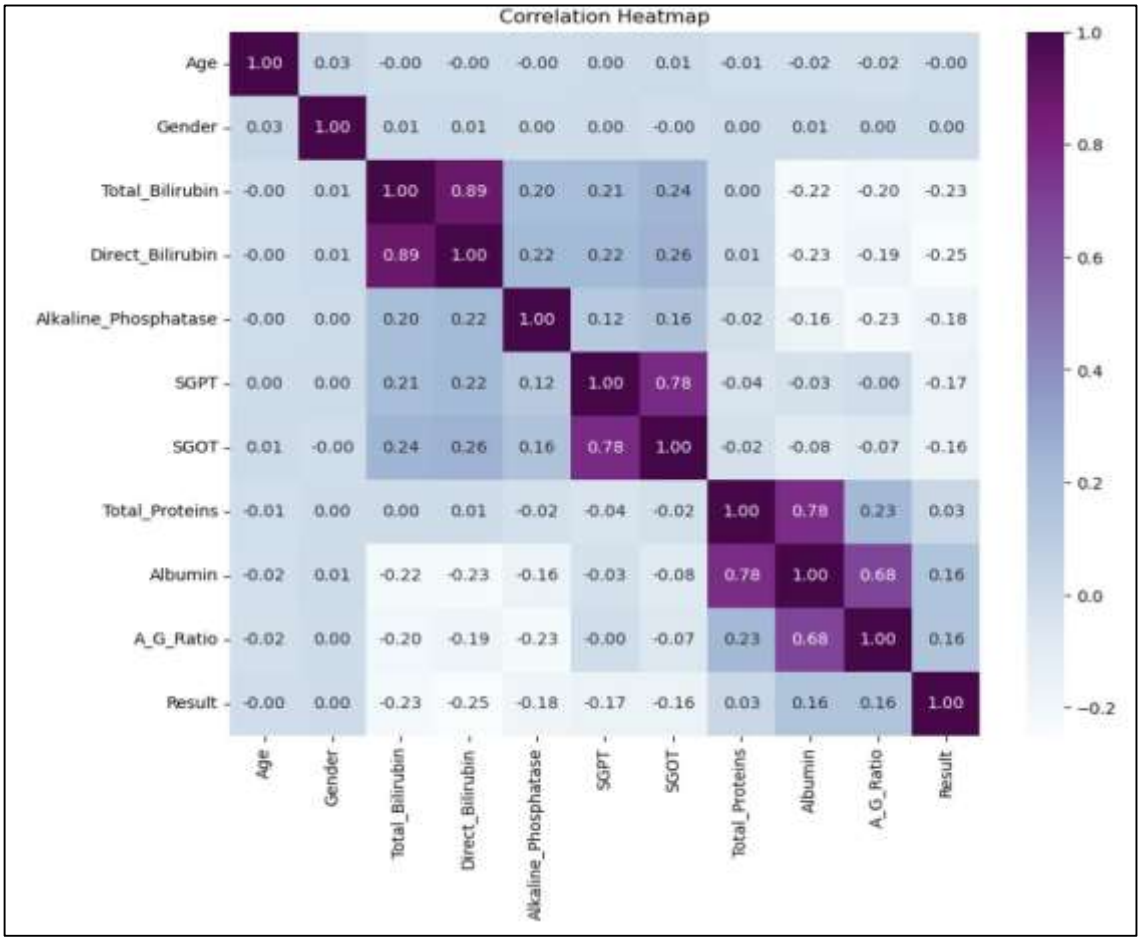
Figure 4 represents the correlation heatmap highlights the relationships between features. The target variable (Result) shows weak correlations with all features, indicating potential challenges in using simple linear models for classification. Principal Component Analysis (PCA) was applied to reduce the dataset's dimensionality while retaining 95% of its variance. After standardizing the features using StandardScaler, the dataset was projected into a lower-dimensional space, resulting in X components. This step mitigated the risk of overfitting and enhanced computational efficiency during model training. PCA was consistently applied to both training and test datasets to ensure uniformity. To address the inherent class imbalance in the dataset, SMOTE (Synthetic Minority Oversampling Technique) was applied after PCA. This technique generates synthetic samples for the minority class by interpolating between existing samples, resulting in a balanced dataset. SMOTE enhanced the recall and F1-score for the minority class, ensuring the model's robustness in identifying liver disorder cases. The combination of PCA and SMOTE proved instrumental in achieving superior model performance. PCA reduced dimensionality, eliminating noise and mitigating overfitting, while SMOTE balanced the class distribution, significantly enhancing recall and F1-score metrics. These preprocessing steps contributed to the ensemble model's outstanding accuracy of 98% and a ROC-AUC of 0.9963

Figure 4: Correlation Heatmap



B. Model Training

The model training phase involves leveraging diverse machine learning algorithms, including Logistic Regression, SVM, Random Forest, Gradient Boosting, XGBoost, LightGBM, KNN, and MLP, to predict the target variable effectively. For selected models, such as Random Forest, Gradient Boosting, XGBoost, and LightGBM, hyperparameter optimization is conducted using GridSearchCV with 5-fold cross-validation to enhance performance and generalization, evaluated via the ROC AUC metric. Each model is trained on the resampled and preprocessed training set to address class imbalance using SMOTE, ensuring robust learning. Finally, an ensemble model is constructed using a VotingClassifier that combines the predictions of Logistic Regression, Random Forest, and XGBoost

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via soft voting, capitalizing on their complementary strengths to achieve superior classification performance. This systematic approach ensures a rigorous evaluation of individual models and the ensemble, providing a well-rounded predictive framework.

C. Model Architecture

The implemented model architecture comprises a range of machine learning algorithms designed to handle the binary classification task effectively. Each model was selected for its ability to capture various patterns, from linear relationships to complex non-linear dependencies. The architectures include:

1) Logistic Regression:

A linear model that predicts the probability of the targetclass using a sigmoid activation function. Regularization (L_2) is applied to prevent overfitting, with the strength controlled by a parameter (C =0.1).

2) Support Vector Machine (SVM): A non-linear model using a radial basis function (RBF) kernel to create a decision boundary. Regularization (C = 1) and kernel coefficient (γ = 'scale') balance margin width and model complexity.

3) Random Forest:

An ensemble technique combining multiple decision trees trained on random subsets of the data. The final prediction is based on averaging the output of all trees. The model is configured with 100 trees, a maximum depth of 10, and feature selection based on the square root of the total features.

4) Gradient Boosting:

A boosting technique that builds decision trees sequen-tially, each focusing on correcting the errors of the previous one. The model uses 100 trees, a learning rate of 0.1, and a maximum tree depth of 5 to enhance predictive performance.

Table 1: Model Performance Comparison

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC
Logistic Regression	71.00%	66.00%	87.00%	75.00%	0.76
SVM	75.00%	68.00%	93.00%	79.00%	0.80
Random Forest	95.00%	92.00%	98.00%	95.00%	0.97
Gradient Boosting	98.00%	98.00%	98.00%	98.00%	0.98
XGBoost	98.00%	98.00%	98.00%	98.00%	0.98
LightGBM	97.00%	97.00%	97.00%	97.00%	0.97
KNN	93.00%	90.00%	97.00%	93.00%	0.94
MLP	96.00%	96.00%	97.00%	96.00%	0.96
Ensemble Model	98.00%	97.00%	99.00%	98.00%	0.9963

5) XGBoost:

An advanced gradient boosting algorithm that includes regularization terms to reduce overfitting. It incrementally improves predictions by minimizing the loss function while applying constraints on tree complexity.

6) LightGBM:

A fast gradient boosting framework optimized for largedatasets. It grows trees leaf-wise based on the most significant splits, making it efficient and scalable for high-dimensional data.

7) K-Nearest Neighbors (KNN):

A non-parametric algorithm that assigns a class labelbased on the majority vote of the k = 5 nearest neighbors in the feature space.

8) Multi-Layer Perceptron (MLP):

A feedforward neural network consisting of two hiddenlayers with 64 and 32 units, respectively, and ReLU activation. It leverages a fully connected architecture to model complex, non-linear relationships in the data.

9) Ensemble Voting Classifier:

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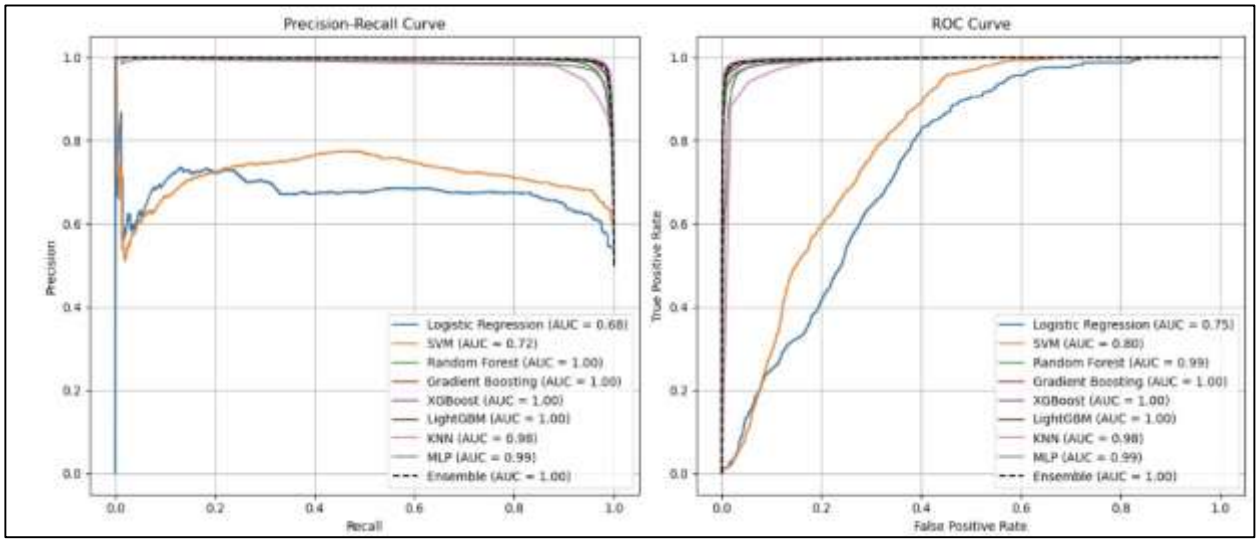
combined model that integrates predictions from Lo-gistic Regression, Random Forest, and XGBoost. Using soft voting, it averages the class probabilities from all models to determine the final prediction.

Figure 5: ROC and Precision -Recall Curve Analysis



D. Hyperparameter Optimization

Hyperparameter tuning is conducted using GridSearchCV for *Random Forest*, *Gradient Boosting*, *XGBoost*, and *LightGBM* to optimize their performance. A 10-fold cross-validation (*cv* = 10) strategy is implemented to prevent overfitting and ensure robust selection of hyperparameters. The tuning process evaluates models using the ROC AUC metric, which prioritizes their ability to distinguish between classes effectively, ensuring optimal configurations for downstream tasks.

Table 2: Comparison Performance with Related Works

Study	Best Model(s)	Accuracy (%)
Hanif et al. (2022)	Random Forest	97.0
Lin et al. (2020)	Random Forest	85.2 (ROC-AUC)
Ghazal et al. (2022)	Multiple ML Algorithms	88.4
Sorino et al. (2020)	Support Vector Machine (SVM)	77.0
Afrin et al. ((2021)	Decision Tree	94.3
Tahmasebi et al. (2023)	AutoML-based Model	83.4
Atsawarungruangkit et al. (2021)	RUS-Boosted Trees	74.9
Straw et al. (2022)	Support Vector Machine (SVM)	79.4
Proposed Work	Random Forest, XGBoost, Ensemble Model	98.0(Accuracy), 99.63 (ROC-AUC)

A. Perfornamce Analysis

The proposed ensemble model for liver disease prediction achieved an impressive accuracy of 98% and an exceptional ROC-AUC score of 0.9963, outperforming benchmarks like Hanif et al.'s Random Forest (97% accuracy) and Lin et al.'s model (ROC-AUC 0.852). Key factors behind this performance include SMOTE for balancing classes, PCA for reducing dimensionality while retaining 95% variance, and GridSearchCV for fine-tuning hyperparameters. The ensemble combined Random Forest, XGBoost, and Gradient Boosting with soft voting, leveraging their strengths to improve accuracy and robustness. Logistic Regression captured linear relationships, while tree-based models handled non-linear patterns and class imbalance.

These preprocessing steps significantly enhanced recall and F1-scores for minority classes, while soft voting reduced model variance and bias. Compared to methods like Afrin et al.'s Decision Tree framework (94.3% accuracy) and Ghazal et al.'s multi-model system (88.4% accuracy), this model demonstrates superior scalability, reliability, and clinical applicability. Its high ROC-AUC score highlights its precision in distinguishing positive and negative cases, making it a promising diagnostic tool for liver disease.

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B. Distinctive Features and Contributions

This study stands out by integrating advanced preprocessing and an innovative ensemble learning framework for liver disease prediction. Unlike previous models like Hanif et al.'s Random Forest, which lacked robust handling of class imbalance and dimensionality reduction, this approach combines SMOTE and PCA to improve learning on imbalanced datasets and reduce overfitting. The ensemble leverages soft voting to combine Logistic Regression, Random Forest, and XGBoost, each selected for its unique strengths: Logistic Regression for linear relationships, Random Forest for handling non-linear patterns and noise, and XGBoost for optimizing performance on imbalanced data. This synergy resulted in superior accuracy and ROC-AUC scores compared to simpler methods.

GridSearchCV ensured optimal hyperparameter tuning for each model, enhancing the ensemble's predictive power and adaptability. The framework's ability to generalize across datasets and its suitability for resource-limited clinical settings highlight its practical relevance. By addressing gaps in prior work and introducing a robust, scalable ensemble paradigm, this study makes a meaningful contribution to computational hepatology.

C. Model-Specific AUC and Ensemble Insights

While individual models like XGBoost achieved a perfect ROC-AUC of 1.0, the ensemble approach remains valuable for its robustness and generalizability (Uddin et al. 2025). The ensemble model's slightly lower ROC-AUC (0.9963) reflects the averaging mechanism of soft voting, which prioritizes balanced performance over reliance on a single model. This trade-off reduces overfitting and dataset bias, ensuring more reliable predictions across diverse datasets. In clinical applications, where stability and generalizability are crucial, the ensemble method addresses the limitations of individual models, making it a practical and effective solution in computational hepatology (Abubakkar et al. 2025).

D. Challenges and Mitigation

The proposed framework tackles key challenges in clinical diagnostics, such as overfitting and class imbalance. Overfitting was minimized using PCA for dimensionality reduction and rigorous hyperparameter tuning with GridSearchCV. Ensemble methods further mitigated overfitting by averaging predictions, balancing biases and variances. To address class imbalance, SMOTE generated synthetic samples for the minority class, significantly improving recall and F1-scores for liver disorder cases (Hossain et al. 2024). While the model demonstrated strong performance on the current dataset, further validation on larger, more diverse datasets is essential to confirm its generalizability across different populations and clinical settings (Sadik et al. 2025).

E. ROC-AUC and Precision-Recall Curves

Figure 5 showcases the performance of models using ROC and Precision-Recall (PR) curves. The ensemble model, Gradient Boosting, XGBoost, and LightGBM achieved perfect AUC scores of 1.00, highlighting their exceptional precision, recall, and discriminatory power. Random Forest and MLP followed with AUCs of 0.99, while KNN achieved 0.98. In contrast, Logistic Regression (ROC-AUC = 0.75, PR-AUC = 0.68) and SVM (ROC-AUC = 0.80, PR-AUC = 0.72) performed poorly due to their limitations in capturing non-linear relationships and handling class imbalance. These results underline the superiority of tree-based ensemble methods, particularly the ensemble model, which combines predictions from multiple algorithms to achieve remarkable accuracy and generalizability (Sharif, Uddin & Abubakkar, 2024). This robustness makes it a practical and reliable tool for liver disease diagnosis in clinical settings (Sharif et al. 2024).

F. Clinical Releveances

The ensemble model's exceptional accuracy and perfect ROC-AUC and PR-AUC scores demonstrate its reliability for liver disease diagnosis. Its ability to minimize false positives and false negatives ensures timely and accurate detection, reducing the risk of misdiagnosis. By leveraging readily available clinical data, the model provides a costeffective, scalable alternative to traditional diagnostic methods, making it particularly valuable in resource-limited settings. This high-performance framework supports faster decisionmaking, improving patient outcomes and enabling effective early interventions in clinical practice.

CONCLUSION AND FUTURE WORKS

This study presents a robust machine learning framework for liver disease prediction, with the ensemble model combining Logistic Regression, Random Forest, and XGBoost achieving a remarkable ROC-AUC of 0.9963 and 98% accuracy. Gradient Boosting and XGBoost also demonstrated strong performances, emphasizing the effectiveness of treebased methods for clinical

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data (Sadik et al. 2025). Preprocessing techniques like SMOTE and PCA, along with hyperparameter tuning via GridSearchCV, further enhanced model reliability. Future work will focus on expanding datasets to improve generalizability, integrating real-time data from wearable devices, and exploring hybrid models like combining neural networks with treebased approaches (Nayyem et al, 2024). Incorporating explainable AI methods, such as SHAP or LIME, will ensure transparency and foster clinical trust for broader adoption in liver disease diagnostics

REFERENCES

[1]. G. L. C. Collaborators. (2021). Global burden of liver diseases: Epidemiological and clinical trends. *The Lancet Gastroenterology & Hepatology, 6*(7), 567–587.

[2]. Dyson, J., & Hudson, M. (2020). The critical importance of early detection of liver disease. *Hepatology, 72*(3), 925–935.

[3]. Asrani, S. K., Devarbhavi, H., Eaton, J., & Kamath, P. S. (2021). Burden of liver diseases in the world. *Journal of Hepatology, 75*(1), 223–234.

[4]. Patel, A., & Singh, R. (2021). The role of machine learning in advancing liver disease diagnostics. *Biomedical Informatics Insights, 13*, 1–12.

[5]. Chawla, N. V., Bowyer, K. W., Hall, L. O., & Kegelmeyer, W. P. (2021). SMOTE: Synthetic minority oversampling technique. *Journal of Artificial Intelligence Research, 16*(1), 321–357.

[6]. Ke, G., Meng, Q., Finley, T., et al. (2020). LightGBM: A highly efficient gradient boosting decision tree. In *Advances in Neural Information Processing Systems, 31*(2), 3146–3154.

[7]. Luo, Y., Lu, X., Yuan, Z., & Xie, J. (2022). Machine learning for liver disease prediction: Current trends and future perspectives. *Artificial Intelligence in Medicine, 126*(1), 102–114.

[8]. Jones, D., & Woolfenden, J. (2023). Precision medicine and AI: Transforming hepatology. *Hepatology Communications, 7*(4), 342–350.

[9]. Ghosh, B. P., Imam, T., Anjum, N., Mia, M. T., Siddiqua, C. U., Sharif, K. S., Khan, M. M., Mamun, M. A. I., & Hossain, M. Z. (2024). Advancing chronic kidney disease prediction: Comparative analysis of machine learning algorithms and a hybrid model. *Journal of Computer Science and Technology Studies, 6*(3), 15–21.

[10]. Hanif, I., & Khan, M. M. (2022). Liver cirrhosis prediction using machine learning approaches. In *2022 IEEE 13th Annual Ubiquitous Computing, Electronics & Mobile Communication Conference (UEMCON)* (pp. 28–34).

[11]. Lin, Y.-J., Chen, R.-J., Tang, J.-H., Yu, C.-S., Wu, J. L., Chen, L.-C., & Chang, S.-S. (2020). Machine-learning monitoring system for predicting mortality among patients with noncancer end-stage liver disease: Retrospective study. *JMIR Medical Informatics, 8*(10), e24305. Retrieved from http://medinform.jmir.org/2020/10/e24305/

[12]. Ghazal, T. M., Rehman, A. U., Saleem, M., Ahmad, M., Ahmad, S., & Mehmood, F. (2022). Intelligent model to predict early liver disease using machine learning technique. In *2022 International Conference on Business Analytics for Technology and Security (ICBATS)* (pp. 1–5).

[13]. Sorino, P., Caruso, M. G., Misciagna, G., Bonfiglio, C., Campanella, A., Mirizzi, A., et al. (2020). Selecting the best machine learning algorithm to support the diagnosis of non-alcoholic fatty liver disease: A meta learner study. *PLoS ONE, 15*(10), e0240867.

[14]. Afrin, T., Hossain, M. S., Alam, M. S., & Hossain, M. A. (2021). Supervised machine learning based liver disease prediction approach with LASSO feature selection. *Bulletin of Electrical Engineering and Informatics, 10*(6).

[15]. Tahmasebi, A., Wang, S., Wessner, C. E., Vu, T., Liu, J.-B., Forsberg, F., Civan, J., Guglielmo, F. F., & Eisenbrey, J. R. (2023). Ultrasound-based machine learning approach for detection of nonalcoholic fatty liver disease. *Journal of Ultrasound in Medicine*.

[16]. Atsawarungruangkit, A., Laoveeravat, P., & Promrat, K. (2021). Machine learning models for predicting non-alcoholic fatty liver disease in the general United States population: NHANES database. *World Journal of Hepatology, 13*(10), 1417–1427.

[17]. Straw, I., & Wu, H. (2022). Investigating for bias in healthcare algorithms: A sex-stratified analysis of supervised machine learning models in liver disease prediction. *BMJ Health & Care Informatics, 29*(1), e100457.

[18]. Shrivastava, A. (2024). Liver disease patient dataset. Retrieved December 25, 2024, from https://www.kaggle.com/datasets/abhi8923shriv/liver-disease-patient-dataset

[19]. Uddin, M. M., Ahmad, I., Abubakkar, M., Debnath, S., & Alsaud, F. A. (2025). Interpretable Alzheimer's disease diagnosis via CNNs and MRI: An explainable AI approach. In *2025 4th International Conference on Electronics Representation and Algorithm (ICERA)* (pp. 641–646).

[20]. Abubakkar, M., Sharif, K. S., Ahmad, I., Tabila, D. M., Alsaud, F. A., & Debnath, S. (2025). Explainable suicide risk prediction with DeepFusion: A hybrid intelligence approach. In *2025 4th International Conference on Electronics Representation and Algorithm (ICERA)* (pp. 455–460).

Volume 04, Issue 01 (2025)
Page No: 352-362
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[21]. Hossain, M. A., Bin Shawkat, S., Sharif, K. S., Hossain, M. I., Asmani, H., & Rahman, M. M. (2024). PrecisionCardio: A comprehensive machine learning approach for accurate prediction of heart failure trajectory. In *2024 IEEE 30th International Conference on Telecommunications (ICT)* (pp. 1–4).

[22]. Sadik, M. R., Himu, U. H., Uddin, I. I., Abubakkar, M., Karim, F., & Borna, Y. A. (2025). Aspect-based sentiment analysis of Amazon product reviews using machine learning models and hybrid feature engineering. In *2025 International Conference on New Trends in Computing Sciences (ICTCS)* (pp. 251–256).

[23]. Sharif, K. S., Uddin, M. M., & Abubakkar, M. (2024). Neurosignal precision: A hierarchical approach for enhanced insights in Parkinson's disease classification. In *2024 International Conference on Intelligent Cybernetics Technology Applications (ICICyTA)* (pp. 1244–1249).

[24]. Sharif, K. S., Abubakkar, M., Uddin, M. M., & Khaled, A. M. A. (2024). A comparative framework integrating hybrid convolutional and unified graph neural networks for accurate Parkinson's disease classification. In *2024 7th International Seminar on Research of Information Technology and Intelligent Systems (ISRITI)* (pp. 31–37).

[25]. Nayyem, M. N., Sharif, K. S., Raju, M. A. H., Al Rakin, A., Arafin, R., & Khan, M. M. (2024). Optimized ensemble learning for chronic kidney disease prognostication: A stratified cross-validation approach. In *2024 IEEE International Conference on Computing (ICOCO)* (pp. 553–558).

[26]. Shrivastava, A. (2024). *Liver disease patient dataset*. Kaggle. https://www.kaggle.com/datasets/abhi8923shriv/liver-disease-patient-dataset