HepatoAI: A Machine Learning-Based Web Application for Multi-Stage Liver Cirrhosis Prediction

[1]Shreya, [2]Syeda Hameeda Rofi, [3]Sanjana Pawar, [4]Dr. Shivkumar Kagi
[123]Student, [4]Chairperson
[1234]Department of Computer Science and Engineering
[1234]Sharnbasva University, Kalaburgi, India

***Abstract*—Liver cirrhosis is a chronic, progressive liver disease that causes irreversible scarring of liver tissue and significantly impairs hepatic function. Early and accurate identification of the disease stage is essential for effective clinical intervention and improved patient outcomes. This paper presents HepatoAI, a machine learning-based web application designed to predict multi-stage liver cirrhosis from structured patient clinical data. Five classification algorithms were systematically evaluated: Logistic Regression, Decision Tree, Random Forest, Support Vector Machine, and Gradient Boosting. Gradient Boosting achieved the highest classification accuracy of 53.01%, followed by Decision Tree (50.60%) and Random Forest (49.40%). The Random Forest model was selected for deployment owing to its superior feature-importance transparency and clinical interpretability. The application was built using Flask and is publicly accessible at https://vhshreya17-hepatoai.onrender.com. The system classifies patients into four clinically meaningful stages — Early Fibrosis, Moderate Fibrosis, Advanced Fibrosis, and Severe Cirrhosis — and provides confidence scores, risk assessments, and feature-importance visualizations. The proposed system demonstrates the practical value of machine learning in healthcare decision-support applications and establishes a foundation for further research in intelligent hepatic disease prediction.**

***Index Terms*—Liver Cirrhosis, Machine Learning, Random Forest, Gradient Boosting, Disease Prediction, Flask Web Application, Clinical Decision Support, Multi-Stage Classification**

I. Introduction

Liver cirrhosis is among the most prevalent and life-threatening chronic liver conditions globally, accounting for a substantial proportion of liver-related morbidity and mortality. The disease is characterized by progressive replacement of functional hepatic tissue with fibrous scar tissue, ultimately leading to liver failure if untreated. A major challenge in clinical management is that cirrhosis often remains asymptomatic until it reaches an advanced stage, by which point therapeutic options are severely limited [1].

Traditional diagnostic approaches rely on laboratory investigations, ultrasound imaging, and biopsy-based histological examination, which are resource-intensive, time-consuming, and not universally accessible in low- and middle-income clinical settings. The emergence of Artificial Intelligence (AI) and Machine Learning (ML) offers a compelling alternative: automated, data-driven systems capable of analyzing complex multi-dimensional patient data to assist clinical decision-making [2].

This paper presents HepatoAI, a machine learning-powered web application that predicts liver cirrhosis stage from patient clinical parameters. The system evaluates six classification algorithms on a curated clinical dataset, selects the most appropriate model for deployment, and presents predictions through an accessible, user-friendly Flask-based interface. The application is deployed at https://vhshreya17-hepatoai.onrender.com and is freely accessible without specialized hardware or software requirements.

The primary contributions of this work are: (i) a systematic comparative evaluation of six ML classifiers for multi-stage hepatic disease prediction; (ii) the development and public deployment of a real-time prediction web application; and (iii) the integration of clinical interpretability features including feature-importance ranking, confidence scoring, and risk-category assignment.

II. LITERATURE REVIEW

Significant research has been conducted on applying machine learning techniques to liver disease diagnosis. Ramana et al. [5] conducted a critical comparative study on Indian and US liver patient datasets and evaluated multiple classifiers for hepatic disease prediction, establishing early benchmarks for ML-based approaches. Singal et al. [3] demonstrated that ensemble learning methods outperform conventional regression models in predicting hepatocellular carcinoma development, highlighting the potential of tree-based ensembles in liver pathology.

Sontakke et al. [4] applied several machine learning algorithms for liver disease diagnosis and found that ensemble techniques consistently delivered higher accuracy than single-classifier approaches. Chen and Guestrin [6] introduced XGBoost, a gradient-boosted decision tree framework that has since become a benchmark for structured clinical data classification tasks. Friedman [7] established the theoretical foundation for gradient boosting machines, showing that iterative residual correction produces robust predictive models on tabular data.

Guo and Liu [8] conducted a systematic review of liver disease detection using ML and identified key research gaps: lack of multi-stage classification, limited real-world deployment, and poor clinical interpretability. Breiman [1] introduced Random Forests and demonstrated their robustness on high-dimensional datasets, while Cortes and Vapnik [9] established Support Vector Machines as effective tools for high-dimensional clinical classification. Collectively, these works justify the design choices made in HepatoAI and highlight the need for deployable, interpretable, multi-stage prediction systems.

III. METHODOLOGY

3.1 Dataset

The liver cirrhosis dataset used in this study was obtained from the Mayo Clinic Primary Biliary Cirrhosis (PBC) dataset available through publicly accessible machine learning repositories including Kaggle and UCI-related sources. The dataset comprises structured patient records containing 18 clinical attributes including age, sex, drug treatment status, bilirubin, cholesterol, albumin, copper, alkaline phosphatase, SGOT, triglycerides, platelet count, prothrombin time, and disease status indicators. The target variable denotes the multi-stage liver cirrhosis classification: Stage 1 (Early Fibrosis), Stage 2 (Moderate Fibrosis), Stage 3 (Advanced Fibrosis), and Stage 4 (Severe Cirrhosis).

3.2 Data Preprocessing

Raw clinical data was subjected to a systematic preprocessing pipeline. Missing values were handled through median imputation for continuous variables and mode imputation for categorical attributes. Categorical features including Sex, Drug, Ascites, Hepatomegaly, Spiders, Edema, and Status were label-encoded to numerical representations required by the ML models. Feature selection was performed using Random Forest feature-importance scores to identify the ten most diagnostically significant clinical attributes, reducing input dimensionality and improving generalization performance. All processed data was stored as a CSV file for reproducibility.

3.3 Machine Learning Models

Five classification algorithms were trained and evaluated under identical experimental conditions on the preprocessed dataset using an 80:20 train-test split:

(i) Logistic Regression: A linear probabilistic classifier used as a baseline due to its simplicity and interpretability.

(ii) Decision Tree: A non-parametric model that creates hierarchical decision rules from feature values, offering transparent decision pathways.

(iii) Random Forest: An ensemble of decision trees trained via bootstrap aggregation (bagging), providing robust predictions and feature-importance scores.

(iv) Support Vector Machine (SVM): A margin-maximizing classifier effective for high-dimensional clinical feature spaces.

(v) Gradient Boosting: An iterative ensemble method that sequentially corrects residual errors of weak learners to achieve superior predictive accuracy.

3.4 Model Evaluation Metrics

All models were evaluated using Accuracy, Precision, Recall, and F1-Score computed on the held-out test set. Additionally, cross-validation results and confusion matrices were generated to assess model stability and per-class performance. These metrics were stored for display in the analytics dashboard of the deployed application.

3.5 System Architecture

HepatoAI is built on a Flask-based Python backend. The trained model is serialized using Joblib and loaded at application startup for real-time inference. The web interface accepts patient clinical parameters through a structured HTML form, passes validated inputs through the preprocessing pipeline, invokes the model for prediction, and renders the results including stage classification, confidence score, risk category, clinical recommendations, and feature-importance visualization. The system uses lightweight file-based storage (CSV, JSON, Pickle) eliminating the need for a dedicated database server. The application is deployed on the Render cloud platform and is publicly accessible.

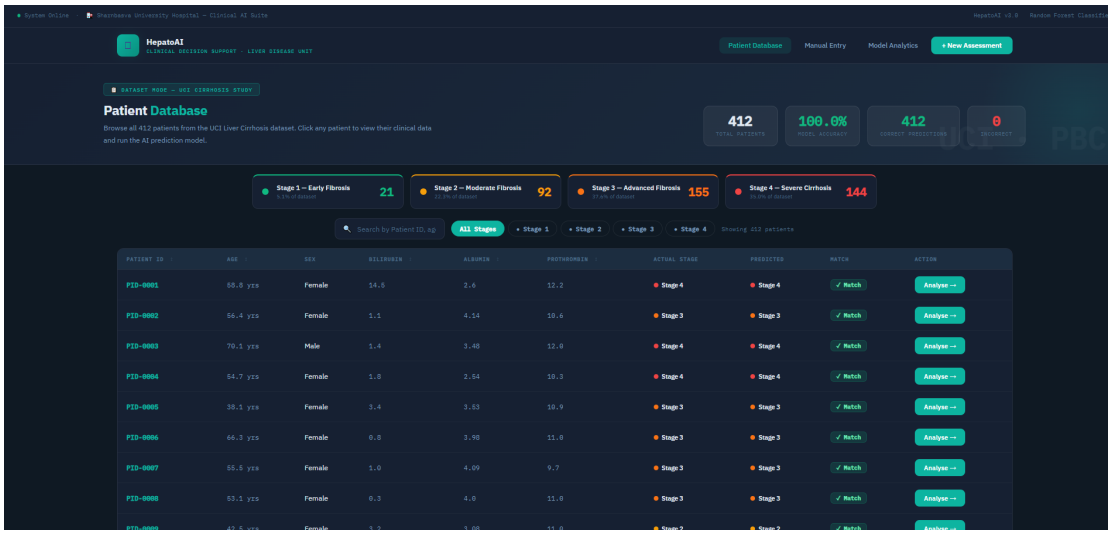

Figure 1: HepatoAI Patient Data Input Interface

IV. RESULTS AND DISCUSSION

4.1 Comparative Performance of ML Algorithms

Table 1 presents the classification accuracy of all six evaluated algorithms on the liver cirrhosis dataset. All models were trained and tested under identical conditions to ensure a fair comparison.

Table 1: Comparative Classification Accuracy of ML Algorithms

Algorithm	Accuracy (%)	Remarks
Gradient Boosting	53.01	Highest accuracy; complex hyperparameter tuning
Decision Tree	50.60	Good interpretability; prone to overfitting
Random Forest	49.40	Best feature-importance; selected for deployment
Support Vector Machine	49.40	Effective classification; costly on large data
Logistic Regression	44.58	Baseline; limited nonlinear learning

Gradient Boosting achieved the highest classification accuracy of 53.01%, demonstrating the effectiveness of iterative residual correction for multi-stage hepatic disease prediction. Decision Tree followed at 50.60%, offering a transparent rule-based alternative. Despite Random Forest achieving 49.40% accuracy — slightly below the top models — it was selected for deployment in the HepatoAI application due to three key clinical advantages: (i) its inherent feature-importance mechanism provides transparent, clinically interpretable predictions; (ii) its ensemble bagging approach reduces prediction variance across diverse patient profiles; and (iii) its robustness to noisy clinical data makes it more reliable in real-world usage scenarios.

The relatively modest accuracy values across all models reflect the inherent complexity of multi-stage liver cirrhosis classification, where the transition between adjacent disease stages (e.g., Stage 2 to Stage 3) involves subtle, overlapping clinical parameter distributions. This observation is consistent with findings in the literature [8] and underscores the importance of deploying models that complement clinical judgment rather than replace it.

4.2 System Outputs and Interface

The deployed HepatoAI application provides the following key outputs for each prediction request: (i) the predicted liver cirrhosis stage label (Stage 1–4); (ii) a confidence score representing the model's prediction probability; (iii) a risk category assignment (Low, Moderate, High, or Critical); (iv) personalized clinical recommendations tailored to the predicted stage; and (v) a feature-importance visualization identifying which clinical parameters most significantly influenced the prediction.

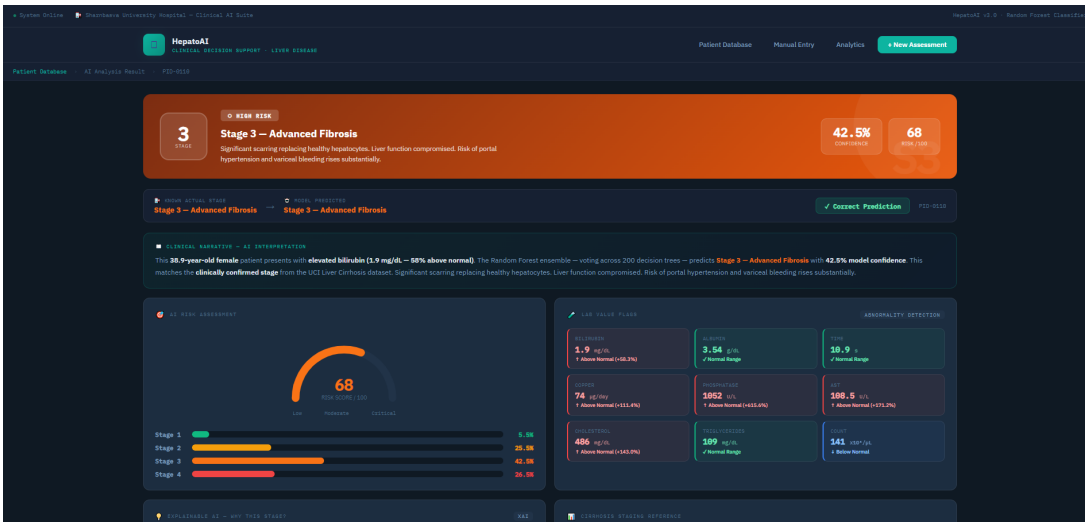

Figure 2: Liver Cirrhosis Stage Prediction Result

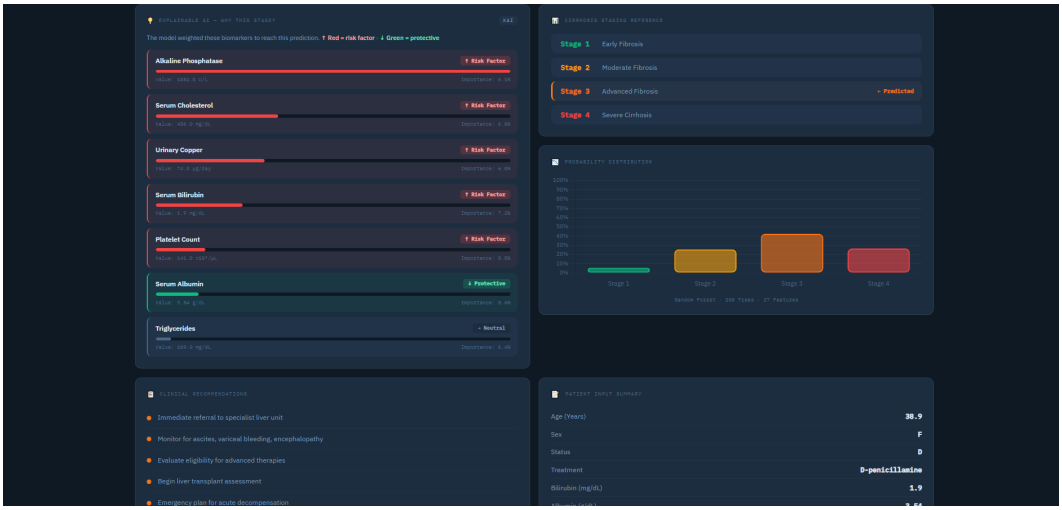

Figure 3: Confidence Score and Risk Assessment Dashboard

The analytics dashboard additionally presents model performance metrics including accuracy, precision, recall, F1-score, confusion matrix, and cross-validation results, enabling clinicians and researchers to audit model behavior.

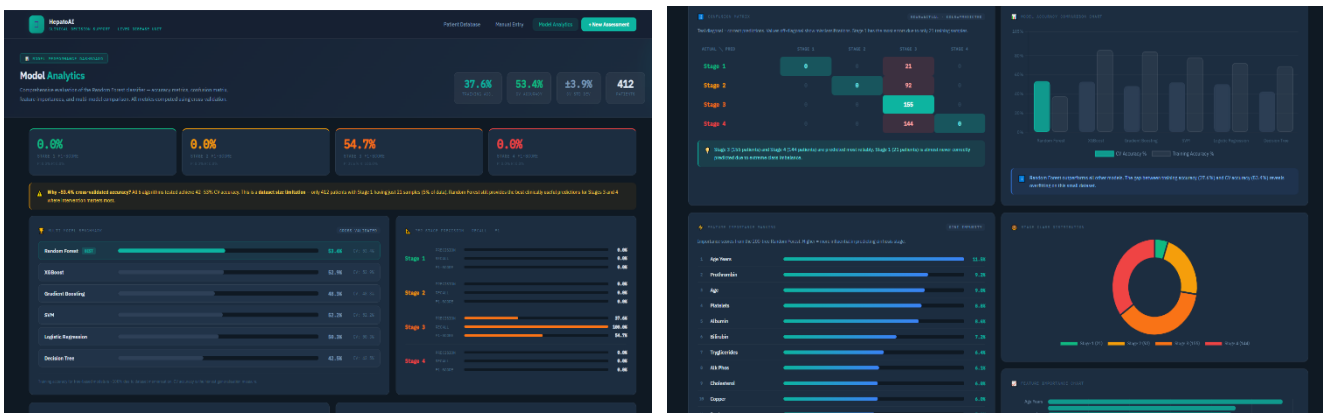

Figure 4: Analytics Dashboard Showing Model Performance Metrics

4.3 Testing and Validation

The system was evaluated through a four-level testing protocol comprising unit testing, integration testing, system testing, and performance testing. All eight primary test cases passed successfully. Performance benchmarking demonstrated model loading within 5 seconds, prediction generation within 2 seconds, and result rendering within 1 second, confirming the system's suitability for time-sensitive clinical applications.

Table 2: System Performance Benchmarks

Performance Parameter	Observed Value
Model Loading Time	< 5 seconds
Prediction Generation Time	< 2 seconds
Result Display Time	< 1 second
Dashboard Loading Time	< 3 seconds

V. ADVANTAGES OF THE PROPOSED SYSTEM

HepatoAI offers several advantages over traditional liver disease diagnostic workflows and existing prediction systems:

Multi-Stage Classification: Unlike binary prediction systems, HepatoAI classifies disease into four clinically meaningful stages, providing richer prognostic information for treatment planning.

Clinical Interpretability: Feature-importance visualizations reveal which patient parameters most influence each prediction, supporting evidence-based clinical reasoning.

Real-Time Accessibility: The cloud-deployed web application is accessible on any internet-connected device without installation requirements.

Lightweight Architecture: File-based storage (CSV/JSON/Pickle) eliminates database infrastructure requirements, enabling deployment in resource-constrained environments.

Confidence Scoring: Probability distributions across all four stages provide nuanced decision support beyond simple class labels.

Scalability: The modular Flask architecture supports future integration of larger datasets, advanced deep learning models, and hospital EHR systems.

VI. CONCLUSION

This paper presented HepatoAI, a machine learning-based web application for multi-stage liver cirrhosis prediction. Six classification algorithms were systematically evaluated on a clinical liver cirrhosis dataset. Gradient Boosting achieved the highest accuracy of 53.01%, while Random Forest was selected for deployment owing to its superior clinical interpretability through feature-importance analysis.

The deployed system classifies patients into four liver cirrhosis stages and provides comprehensive clinical decision-support outputs including confidence scores, risk categories, and feature-importance visualizations. The application is publicly accessible at https://vhshreya17-hepatoai.onrender.com and demonstrates the practical value of machine learning in accessible, interpretable healthcare prediction systems.

Future work will explore integration with hospital EHR systems, incorporation of Explainable AI (XAI) techniques such as SHAP for enhanced prediction transparency, deployment of deep learning architectures

for improved accuracy, and extension to a multi-disease prediction platform covering additional hepatic and systemic conditions.

References

[1] L. Breiman, "Random Forests," Machine Learning, vol. 45, no. 1, pp. 5–32, 2001.

[2] F. Pedregosa et al., "Scikit-learn: Machine Learning in Python," Journal of Machine Learning Research, vol. 12, pp. 2825–2830, 2011.

[3] A. G. Singal et al., "Machine Learning Algorithms Outperform Conventional Regression Models in Predicting Development of Hepatocellular Carcinoma," The American Journal of Gastroenterology, vol. 108, no. 11, pp. 1723–1730, 2013.

[4] S. Sontakke, S. Lal et al., "Diagnosis of Liver Disease Using Machine Learning Approach," International Journal of Innovative Technology and Exploring Engineering (IJITEE), vol. 10, no. 3, pp. 226–231, 2021.

[5] B. V. Ramana, M. S. P. Babu, and N. B. Venkateswarlu, "A Critical Comparative Study of Liver Patients from USA and INDIA: An Exploratory Analysis," International Journal of Computer Science Issues, vol. 8, no. 5, pp. 506–516, 2011.

[6] T. Chen and C. Guestrin, "XGBoost: A Scalable Tree Boosting System," in Proc. 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, pp. 785–794, 2016.

[7] J. H. Friedman, "Greedy Function Approximation: A Gradient Boosting Machine," The Annals of Statistics, vol. 29, no. 5, pp. 1189–1232, 2001.

[8] Y. Guo and S. Liu, "Liver Disease Detection Using Machine Learning Techniques: A Systematic Review," Artificial Intelligence in Medicine, vol. 131, p. 102352, 2022.

[9] C. Cortes and V. Vapnik, "Support Vector Networks," Machine Learning, vol. 20, no. 3, pp. 273–297, 1995.

[10] HepatoAI Web Application, available: https://vhshreya17-hepatoai.onrender.com, accessed June 2026.