

Prediction of Liver Disease Using Deep Learning and Artificial Neural Networks

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Abstract:

Liver disease is a major cause of illness and death worldwide, and early diagnosis remains a challenge due to the limited availability of trained medical professionals for interpreting diagnostic tests. This paper presents a deep-learning-based approach for the prediction of liver disease using the Indian Liver Patient Dataset (ILPD), obtained from Kaggle and the UCI Machine Learning Repository, consisting of 583 patient records. Nine clinical attributes — age, sex, alanine aminotransferase (ALT), aspartate aminotransferase (AST), total bilirubin, albumin, total protein, albumin/globulin ratio, and alkaline phosphatase — were used to train and evaluate several classification models, namely Logistic Regression, Random Forest, and an Artificial Neural Network (ANN). The dataset was preprocessed to remove missing and duplicate values, encode categorical attributes, and normalize numerical features before being split into training (80%) and testing (20%) subsets. Feature-importance analysis identified ALT as the most influential predictor of liver disease and alkaline phosphatase as the least significant. The trained model was deployed through a Flask-based web application that allows users to input clinical parameters and receive an instant prediction. Experimental results demonstrate that the proposed system can effectively assist in the early screening of liver disease, offering a low-cost, accessible, and user-friendly diagnostic aid that bridges the gap between patients and healthcare providers.

Keywords: Liver Disease Prediction, Deep Learning, Artificial Neural Network, Indian Liver Patient Dataset, Random Forest, Logistic Regression, Flask, Healthcare Analytics

1. INTRODUCTION

Liver disease refers to a broad range of conditions that impair the liver's ability to filter blood and perform its essential metabolic functions. In India, non-communicable diseases account for a substantial share of annual deaths, and cardiovascular and hepatic conditions are among the leading contributors, particularly among adults aged 40–69. Early detection greatly improves treatment outcomes and survival rates; however, conventional diagnostic methods rely on imaging and laboratory tests that must be interpreted by trained specialists. In many regions, medical professionals cover large populations and are not consistently available, which delays diagnosis and treatment.

The objective of this work is to use publicly available clinical datasets to build and compare deep learning models capable of predicting liver disease, and to identify which algorithm — and which clinical attribute — contributes most to accurate prediction. The broader aim is to design a simple, cost-effective, and accessible prediction system that bridges the gap between patients and healthcare providers, reducing dependence on constant specialist availability while supporting faster, more informed clinical decisions.

2. RELATED WORK

Several existing disease-prediction systems rely on classical machine learning algorithms such as Decision Tree and Random Forest to predict disease presence from patient symptoms and test results, aiming to build a coordinated framework that improves patient satisfaction. However, most existing systems are designed to predict only a single disease at a time, requiring users to consult separate tools for different conditions, and they typically apply the same algorithm uniformly across all diseases regardless of whether it is the best fit for the data. This limits both flexibility and predictive accuracy. The system proposed in this paper addresses these limitations by combining several algorithms on a diverse, merged clinical dataset and selecting the best-performing model specifically for liver disease prediction.

3. PROPOSED METHODOLOGY

A. Dataset

The Indian Liver Patient Dataset (ILPD), sourced from Kaggle and the UCI Machine Learning Repository, was used for this study. It contains 583 patient records described by nine clinical attributes: age, sex, total bilirubin, direct bilirubin, alkaline phosphatase, alanine aminotransferase (ALT), aspartate aminotransferase (AST), total protein, albumin, and the albumin/globulin ratio. Of the 583 records, approximately 71.4% (416 patients) are labelled as liver disease cases, while the remaining patients are labelled as non-liver-disease cases, making this a moderately imbalanced binary classification problem.

B. Data Preprocessing

- Removal of missing or null values.
- Elimination of duplicate records.
- Encoding of the categorical "sex" attribute into numerical form.
- Normalization/scaling of numerical feature values.
- Exploratory visualization of feature relationships and class balance.

C. Train–Test Split

After preprocessing, the dataset was divided using an 80:20 train–test split. The training subset (80%) was used to fit each model, while the testing subset (20%) was held out to evaluate generalization performance on unseen patient records.

D. Classification Algorithms

Three supervised learning algorithms were trained and compared:

- Random Forest — an ensemble of decision trees that reduces overfitting through bagging.
- Logistic Regression — a linear classification algorithm that models the probability of liver disease using a logistic (sigmoid) function.
- Artificial Neural Network (ANN) — a fully-connected feed-forward network with an input layer sized to the nine clinical attributes, one or more hidden layers with ReLU activation, and a sigmoid output neuron for binary classification of liver disease presence.

Each model was implemented using Keras (with a TensorFlow backend) and standard deep-learning libraries, trained within a Jupyter Notebook environment, and the best-performing model was serialized as a Pickle (.pkl) file for deployment.

4. SYSTEM ARCHITECTURE

The system follows a five-stage pipeline: (1) data collection from the Kaggle/UCI source, (2) data preprocessing and cleaning, (3) train–test splitting, (4) model training and comparison across the three algorithms described above, and (5) deployment of the best-performing model through a Flask-based web application. The web interface accepts the nine clinical attributes as user input, validates them, passes them to the trained model, and returns a real-time liver disease prediction to the user.

5. EVALUATION METRICS

Model performance was evaluated on the held-out test set using four standard classification metrics: Accuracy, Precision, Recall, and F1-Score. These metrics together capture both the overall correctness of predictions and the model's ability to correctly identify positive (disease) cases while limiting false positives and false negatives.

6. RESULTS AND DISCUSSION

Feature-importance analysis across the trained models consistently identified alanine aminotransferase (ALT) as the most influential predictor of liver disease, which is consistent with its clinical role as a key liver-enzyme marker. Alkaline phosphatase was found to be the least significant contributor among the nine attributes considered. Table I summarizes the comparative performance of the three algorithms on the test dataset.

Table I summarizes the results for all three algorithms:

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Logistic Regression	65.5	64.8	98.6	78.2
Random Forest	62.9	65.3	87.6	74.8
ANN	63.7	67.8	80.8	73.7

Table I. Comparative performance of the three algorithms on the test dataset.

The trained model with the highest accuracy was integrated into the Flask web application, which presents users with a simple form for entering clinical parameters and instantly returns a prediction indicating the likelihood of liver disease. This confirms that a deep-learning-based screening tool can provide a fast, low-cost, and accessible complement to traditional diagnostic procedures.

7. CONCLUSION AND FUTURE WORK

This paper presented a deep-learning-based system for the early prediction of liver disease using the Indian Liver Patient Dataset. By comparing Logistic Regression, Random Forest, and an Artificial Neural Network, the study identified ALT as the most significant predictive attribute and demonstrated that the resulting model can be deployed through a simple, user-friendly Flask web interface. By automating the prediction process, the system reduces manual diagnostic effort, delivers faster results, and can assist healthcare professionals in making informed decisions.

Future work will focus on extending the system to support the prediction of multiple diseases within a single application, integrating real-time patient health data from wearable sensors or IoT devices, deploying the application on a cloud-based or mobile platform for wider accessibility, and providing personalized health recommendations based on prediction outcomes.

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