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Comparative Analysis of Liver Disease Prediction Using Machine Learning Models

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Abstract

Liver disorders represent a major global health challenge and are responsible for a significant number of hospitalizations and long-term complications. Early identification of liver abnormalities is essential for improving treatment outcomes and reducing mortality. However, conventional diagnosis methods rely heavily on laboratory tests and expert interpretation, which are time-consuming and costly.

This paper presents a comparative study of machine learning algorithms for predicting liver disease using routinely collected clinical and biochemical parameters. Several supervised learning models, including Logistic Regression, Decision Tree, Random Forest, Support Vector Machine, K-Nearest Neighbour, Gradient Boosting and Neural Network based models, are implemented and evaluated. The Indian Liver Patient Dataset is used as the benchmark dataset.

A complete data processing pipeline is developed, consisting of data cleaning, feature transformation, attribute ranking and model evaluation. The performance of the models is analysed using accuracy, precision, recall and F1-score. Experimental results demonstrate that ensemble and neural-based models provide superior predictive performance compared to traditional classifiers. The study confirms that machine learning can serve as a reliable decision-support tool for early liver disease screening.

Keywords: *Liver disease prediction, machine learning, clinical data mining, classification, healthcare analytics.*

1. Introduction

Liver diseases such as hepatitis, fatty liver disease, cirrhosis and liver failure constitute a rapidly growing public health concern. The liver plays a vital role in metabolism, detoxification and digestion. Even moderate functional degradation can result in severe physiological consequences.

In routine clinical practice, liver disorders are detected through a combination of laboratory investigations, imaging techniques and expert analysis. Although these approaches are clinically effective, they are often expensive, invasive and dependent on specialist availability. Furthermore, early-stage liver abnormalities may remain unnoticed until the disease progresses.

Recent developments in data-driven healthcare have shown that machine learning techniques are capable of discovering complex patterns in medical datasets. Predictive models trained on historical patient records can support physicians by providing fast and consistent risk estimation.

This work investigates the feasibility of predicting liver disease using widely adopted machine learning algorithms and compares their effectiveness on a standardized clinical dataset. The main objectives of this study are:

- to build predictive models using multiple machine learning techniques,
- to evaluate and compare their classification performance,
- to identify influential clinical attributes for liver disease prediction, and
- to demonstrate the applicability of data-driven screening tools in healthcare environments.

2. Related Work

Machine learning methods have been increasingly adopted in medical diagnostics to assist clinicians in disease prediction and decision-making. Previous studies have employed classifiers such as Support Vector Machines, Decision Trees, Naïve Bayes and Artificial Neural Networks for liver disease analysis.

Several works focus on feature extraction from biochemical indicators such as bilirubin levels, transaminase enzymes and protein measurements. Ensemble learning techniques have been reported to improve prediction reliability by reducing variance and overfitting. In addition, neural models have demonstrated promising performance in capturing nonlinear relationships among clinical variables.

Despite these advancements, most studies concentrate on a limited set of algorithms or lack systematic comparison under identical experimental settings. Therefore, a comprehensive evaluation of both classical and advanced learning models on the same dataset remains necessary.

3. Dataset Description and Pre-processing

The experimental analysis uses the publicly available Indian Liver Patient Dataset, which contains records of both liver-affected and non-affected individuals. The dataset includes demographic information and laboratory measurements such as bilirubin values, liver enzymes and protein levels.

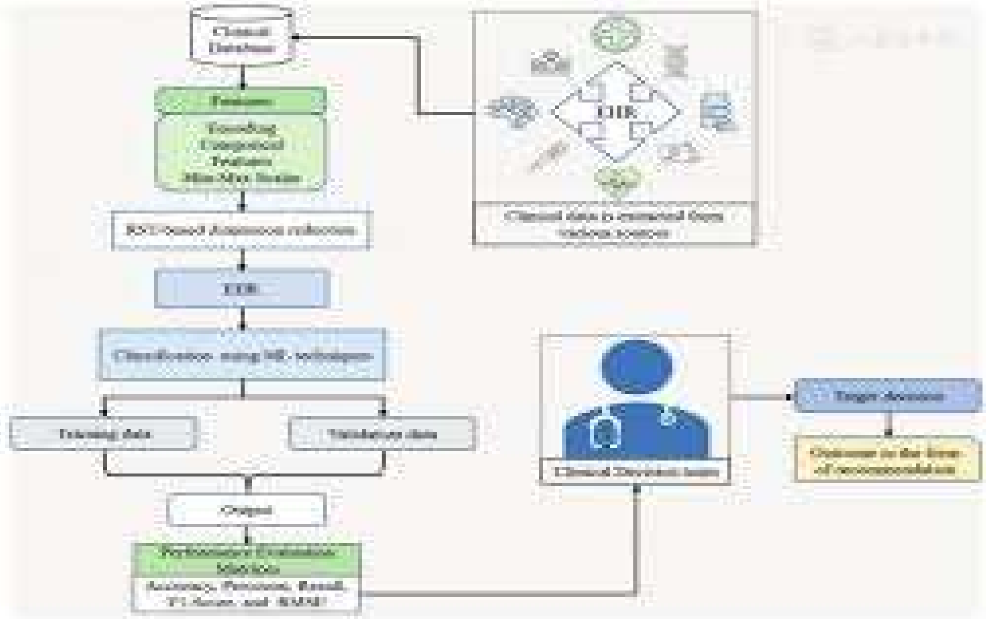
3.1 Data Preparation

The raw dataset contains missing values and categorical attributes. The following pre-processing operations are applied:

- removal of incomplete records,
- replacement of missing values using statistical imputation,
- conversion of categorical features into numerical representations,
- normalization of continuous attributes to improve learning stability.

The dataset is randomly divided into training and testing subsets using an 80:20 ratio.

4. Overall System Architecture

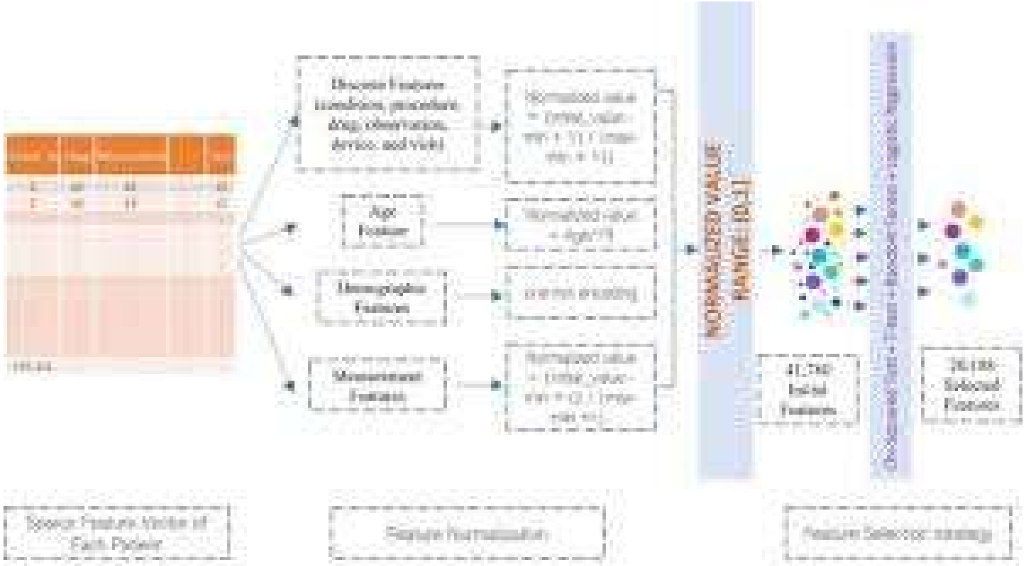


The proposed framework follows a modular architecture consisting of:

- data ingestion and cleaning module,
- feature processing and selection module,
- machine learning training and testing module,
- performance evaluation module, and
- user-oriented prediction interface.

This layered design allows independent modification of the learning models and simplifies deployment in real clinical environments.

5. Functional Workflow



The operational workflow of the system consists of the following stages:

1. acquisition of patient clinical data,
2. data cleaning and transformation,
3. feature selection and ranking,
4. training of classification models,
5. evaluation of model performance, and
6. generation of prediction results.

This pipeline ensures consistency and reproducibility across different classifiers

6. Feature Selection and Attribute Analysis

Clinical attributes such as total bilirubin, alkaline phosphatase, aspartate aminotransferase, alanine aminotransferase, albumin, total proteins and albumin-globulin ratio are considered in this study.

To reduce dimensionality and improve generalization, a statistical ranking approach is applied to identify the most influential features. Attributes with higher discriminatory power are prioritized during model training.

Feature selection improves training efficiency and helps mitigate the impact of redundant or weakly informative variables.

7. Machine Learning Models

The following supervised learning models are implemented:

- Logistic Regression
- Decision Tree Classifier
- Random Forest Classifier
- Support Vector Machine
- K-Nearest Neighbour
- Gradient Boosting Classifier
- Neural Network based model

Each model is trained under identical data partitions and evaluated using the same metrics to ensure fair comparison.

8. Model Training and Evaluation Strategy

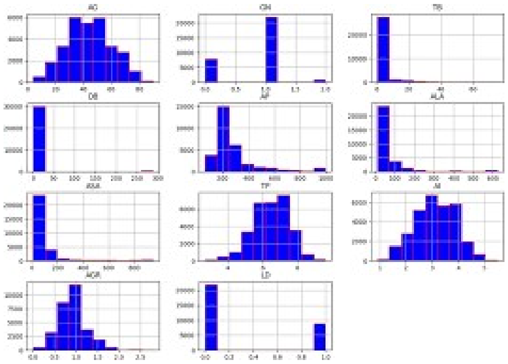
All models are trained on the training subset and validated on the unseen testing subset. Hyperparameters are tuned using cross-validation to avoid overfitting.

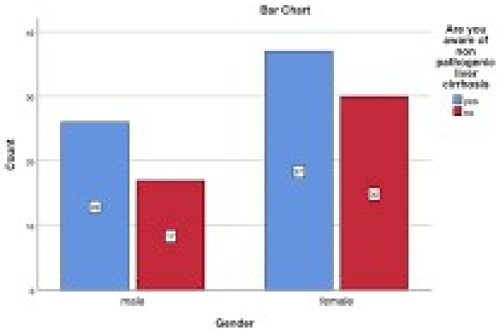
The performance metrics considered in this study include:

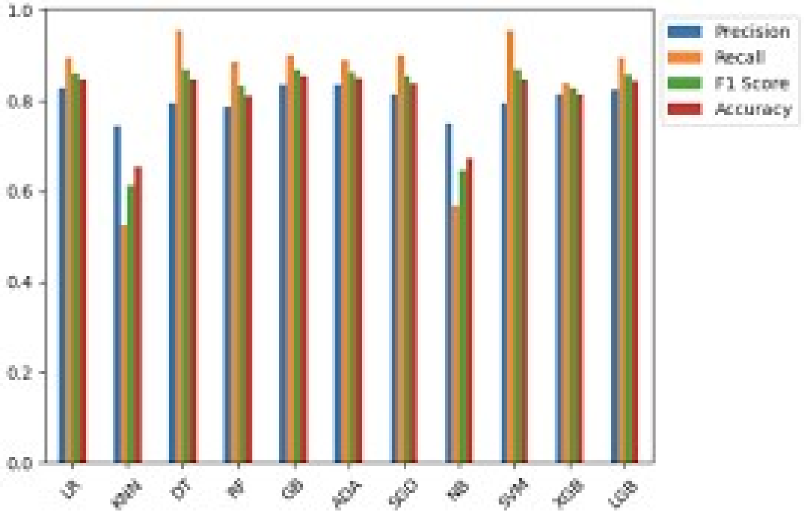
- accuracy,
- precision,
- recall, and
- F1-score.

These metrics provide balanced evaluation of both classification correctness and error behaviour.

9. Experimental Results and Analysis





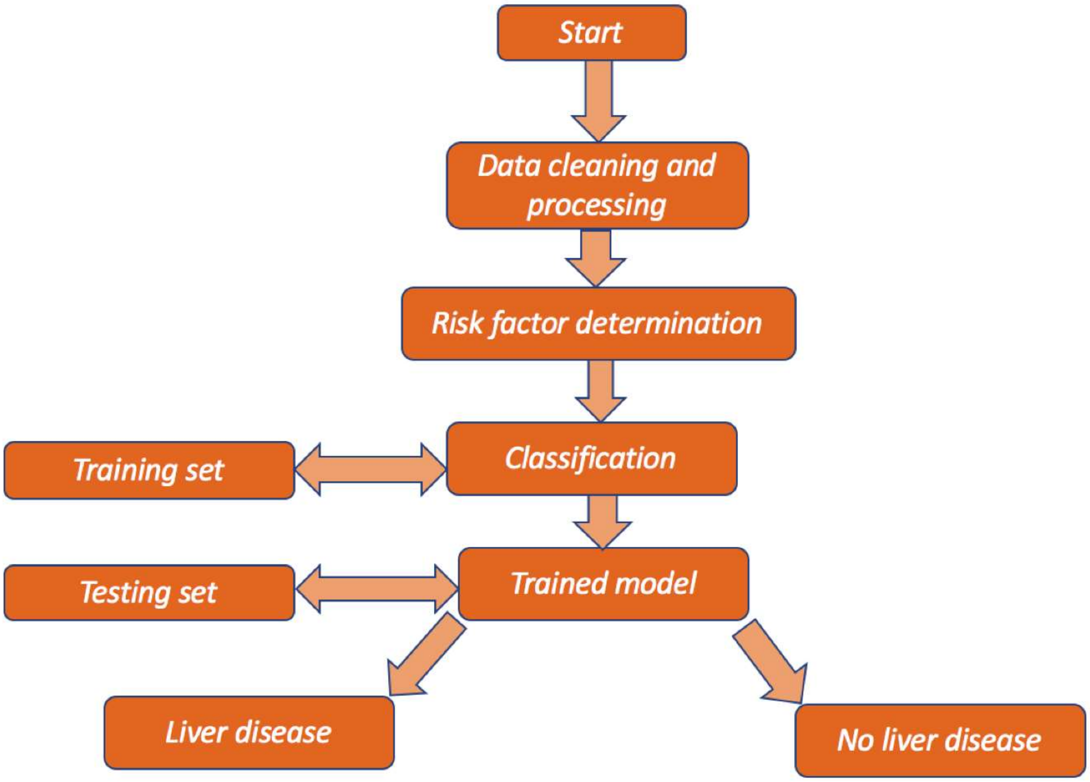


The comparative evaluation indicates that ensemble and neural-based classifiers consistently outperform simpler models. K-Nearest Neighbour and Random Forest classifiers achieve high predictive accuracy, while the neural model demonstrates strong robustness against data variability.

The experimental results show that advanced classifiers effectively capture nonlinear interactions among biochemical indicators. Decision Tree and Logistic Regression models offer interpretability advantages but exhibit lower predictive accuracy compared to ensemble approaches.

The evaluation confirms that combining multiple features derived from routine laboratory tests can produce reliable predictions suitable for early screening applications.

10. User Interface and Prototype Implementation



A lightweight web-based prototype is developed using a Python backend and a graphical interface. Users can enter patient attributes such as age, gender and laboratory measurements. The trained model then predicts the likelihood of liver disease in real time.

The prototype demonstrates the feasibility of deploying the developed classifiers as practical decision-support tools.

11. Discussion

The comparative study clearly shows that model performance varies significantly depending on algorithmic design and learning strategy. Ensemble models improve generalization by aggregating multiple weak learners, thereby reducing variance. Neural models capture complex interactions among attributes that cannot be easily represented by linear classifiers.

However, high predictive accuracy alone does not guarantee clinical reliability. Interpretability, data quality, bias and ethical considerations must be addressed before real-world deployment. The proposed system is designed as a supportive tool and not as a replacement for medical professionals.

12. Limitations

The present study relies on a single publicly available dataset. The dataset size is moderate and may not reflect the diversity of real clinical populations. In addition, the dataset does not include imaging data or longitudinal patient records, which could further improve prediction reliability.

13. Conclusion

This paper presented a systematic comparative analysis of machine learning models for liver disease prediction using routine clinical data. A complete processing pipeline covering data cleaning, feature selection, model training and performance evaluation was developed.

Experimental results demonstrate that ensemble and neural-based classifiers significantly outperform traditional models such as Decision Trees and Logistic Regression. The findings confirm that machine learning techniques can support early detection of liver disorders and can assist clinicians in preliminary risk assessment.

The proposed framework provides a scalable and efficient foundation for data-driven healthcare analytics.

14. Future Work

Future research directions include:

- validation using multi-hospital and multi-regional datasets,
- incorporation of imaging and longitudinal clinical records,
- development of explainable AI modules for clinical interpretability, and
- deployment of the system in real clinical workflows for pilot evaluation.

References

1. Reddy, D. S., Bharath, R., and Rajalakshmi, P., Deep learning approaches for liver disease classification.
2. Thirunavukkarasu, K., Singh, A. S., and Chowdhury, A., Liver disease prediction using classification algorithms.
3. Shaheamlung, G., Kaur, H., and Kaur, M., Survey of machine learning methods for liver disease detection.
4. Poonguzharselvi, B., et al., Feature-based prediction of liver disorders using machine learning.
5. Ayeldeen, H., et al., Decision-tree-based prediction of liver fibrosis.