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Machine Learning–Based Noninvasive Assessment of Liver Fibrosis Severity in Chronic Hepatitis B Patients

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Abstract

Noninvasive assessment of liver fibrosis severity is essential for accurate histological evaluation and treatment decision-making in patients with chronic hepatitis B (HBV). This study develops a computer-assisted diagnostic system using machine learning classifiers to predict liver fibrosis severity based on physical examination data and serum biomarkers. A retrospective dataset of 920 patients was used to develop four machine learning models: Decision Tree Classifier (DTC), Random Forest Classifier[5] (RFC), Logistic Regression Classifier (LRC), and Support Vector Classifier (SVC). The dataset was partitioned equally for training and testing. The classifiers evaluated over 67 million indicator combinations from 24 clinical variables. Performance was compared with 19 existing diagnostic models using sensitivity, specificity, accuracy, and AUC-ROC. The RFC model, using nine selected indicators, achieved diagnostic accuracy above 0.83, outperforming all existing models. Machine learning demonstrates significant potential for improving noninvasive fibrosis assessment[1]. Further research with larger datasets integrating imaging and serum markers is recommended to enhance clinical applicability.

Keywords

Machine Learning; Liver Fibrosis; Chronic Hepatitis B; Random Forest Classifier; Noninvasive Diagnosis; Clinical Decision Support.

I. Introduction / Problem Definition

Chronic liver disease (CLD) is a major global health concern, with chronic hepatitis B (CHB) being a leading cause. Liver fibrosis staging plays a critical role in determining treatment strategies. Although liver biopsy is considered the gold standard, it is invasive, costly, and prone to sampling errors. Noninvasive diagnostic methods[1] using serological and imaging markers are increasingly preferred. Existing serological models, however, often fail to achieve consistently high diagnostic performance across key metrics such as AUC, sensitivity, and specificity. Machine learning offers a promising solution by capturing complex nonlinear relationships among clinical variables[2].

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II. Methods

A retrospective dataset of 920 chronic HBV cases collected from April 2007 to December 2018 at the Second Xiangya Hospital was used. Four machine learning classifiers—DTC, RFC, LRC, and SVC—were developed. The dataset was split evenly into training and testing subsets. From 24 clinical indicators, the models explored 67,108,760 possible feature combinations. Each classifier selected optimal indicator subsets to maximize performance. Model evaluation used accuracy, sensitivity, specificity, and AUC-ROC.

III. Results

The Random Forest Classifier[5] achieved the highest performance, with diagnostic accuracy exceeding 0.83[3]. It outperformed 19 existing serological fibrosis models across all metrics. Other classifiers—DTC, LRC, and SVC—achieved moderate performance, with accuracy ranging from 0.72 to 0.80. The RFC model demonstrated superior ability to identify optimal nonlinear relationships among clinical indicators[2].

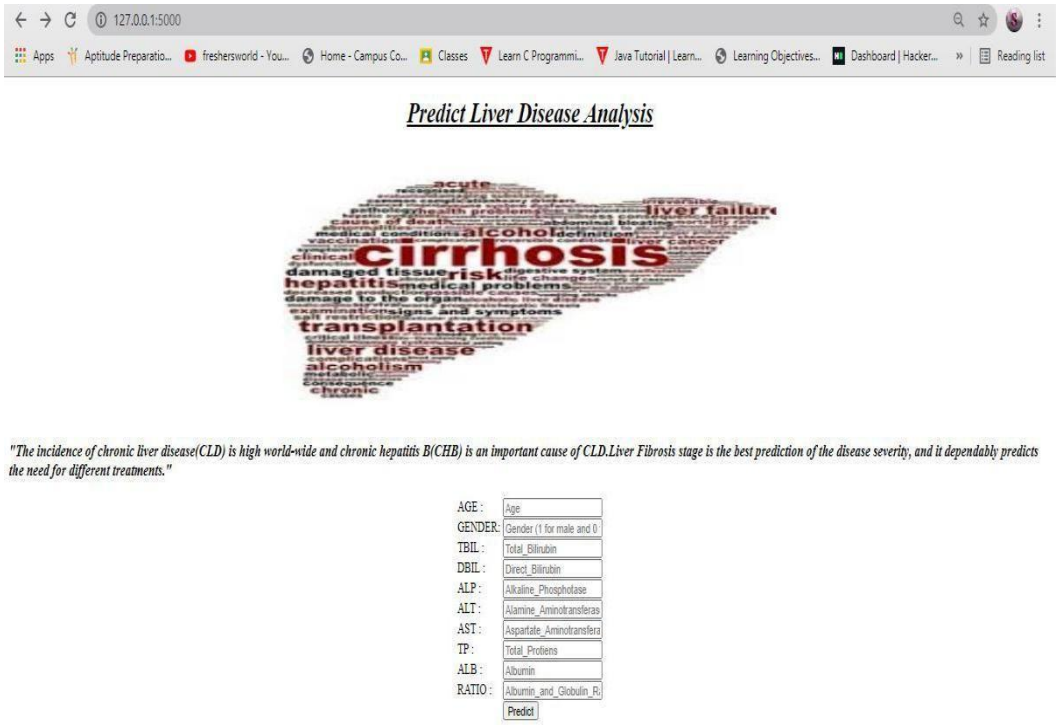

Fig: 3.1 Liver Disease analysis

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IV. Discussion

The study demonstrates that machine learning approaches, particularly ensemble methods like RFC, significantly enhance noninvasive liver fibrosis assessment. Traditional serological models rely on limited biomarkers, while machine learning captures complex interactions. Despite promising results, limitations include single-center data and absence of imaging features. Future work should include multi-center datasets and multimodal integration to further strengthen diagnostic reliability.

V. Conclusion

A machine learning-based system for noninvasive liver fibrosis assessment was developed and evaluated. The RFC model achieved superior diagnostic accuracy compared to 19 existing models. Machine learning presents strong potential to reduce reliance on liver biopsy and improve clinical decision-making[4] in CHB management[3]. Further research using diverse datasets and additional clinical features[4] will enhance clinical translation.

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