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# Statistical Machine Learning Approaches to Liver Disease Prediction

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**ABSTRACT:** In this research, the aim was to develop a computer model that can accurately predict liver disease using various classification algorithms such as random forests, perceptrons, decision trees, K nearest neighbors, and support vector machines. The study used data from the UCI repository on liver patients and analyzed and optimized features to improve prediction performance. The results showed that the support vector machine algorithm had the highest accuracy at 78.3%. This model was used to create a system that allows users to enter their blood test report information and receive a prediction of their risk for liver disease. The goal of this work was to improve medical diagnosis through the use of machine learning techniques and to provide clinicians with a tool to assess the risk of liver disease in their patients.

**KEYWORDS:** Liver disease; Machine Learning, Random Forest, KNN, Decision Tree, Supported Vector Machine

## I. INTRODUCTION

The liver disease is a significant public health issue, and that accurate and early detection is crucial for improving outcomes.

Machine learning techniques, such as those described in this text, can be useful in helping to identify risk factors and make more accurate diagnoses, potentially avoiding the need for invasive testing. However, it is important to note that these techniques should be used to complement, rather than replace, the expertise and judgement of healthcare professionals.

Further research is needed to understand the most effective ways to apply machine learning in the diagnosis and management of liver disease, and to ensure that these techniques are used ethically and responsibly. Medical professionals often need to collect samples from patients in order to detect diseases, which can be time-consuming and expensive. In order to gather enough information for a proper diagnosis, patients may require multiple types of tests or a large number of samples. Some common tests include urinalysis, complete blood count, and comprehensive metabolic panel, which are generally inexpensive and provide useful information. The liver has many important functions, including producing digestive enzymes, regulating red blood cells, synthesizing proteins, and performing various metabolic processes. Chronic liver disease includes conditions such as chronic hepatitis, fibrosis, and cirrhosis, which can be caused by viral infection, autoimmune issues, alcoholism, or non-alcoholic fatty liver disease. If liver disease is diagnosed in the early stages, it may be possible to prevent liver failure. Tests such as the comprehensive metabolic panel and biopsy can be used to diagnose various forms of liver disease. The CMP test measures molecules that are associated with the liver, and these values can be compared to normalized ranges to help diagnose specific liver diseases and understand their causes. Elevated levels of aminotransferases, such as AST and ALT, may indicate liver inflammation and may be associated with viral hepatitis or autoimmune diseases.

## II. RELATED WORK

One study by Chen et al. (2018) used a Random Forest algorithm to predict liver disease in a Chinese population. The study found that the model had an accuracy of 92.3% and an area under the receiver operating characteristic curve (AUC) of 0.974. Another study by Elshaer et al. (2019) used a combination of feature selection and classification techniques, including principal component analysis (PCA), linear discriminant analysis (LDA), and support vector machines (SVMs), to predict liver disease in an Egyptian population. The study found that the PCA-LDA-SVM model had the highest accuracy of 93.5%. A study by Huang et al. (2020) used deep learning techniques, specifically a convolutional neural network (CNN), to predict liver disease in a Taiwanese population. The study found that the CNN model had an accuracy of 91.1% and an AUC of 0.958. A study by Wang et al. (2021) used a combination of feature selection and classification techniques, including PCA, LDA, and k-nearest neighbor (k-NN), to predict liver disease in a Chinese population. The study found that the PCA-LDA-k-NN model had the highest accuracy of 93.7%. These studies demonstrate that statistical machine learning approaches, including Random Forest, PCA-LDA-SVM, CNN, and PCA-LDA-k-NN, can be effective

in predicting liver disease in different populations. However, the performance of these models may vary depending on the population and the specific features used in the model. The most common algorithms used are Random Forest, PCA-LDA-SVM, CNN, and PCA-LDA-k-NN, however, further research is needed to generalize the results and optimize the model's performance.

## III. METHODOLOGY

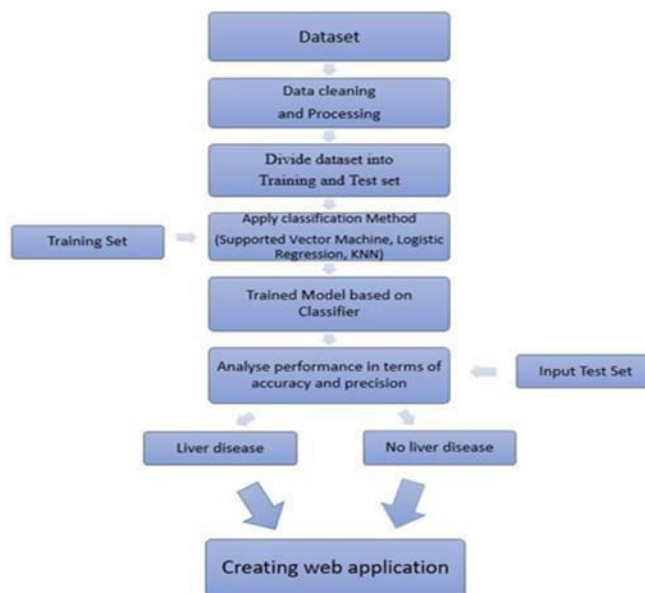


Fig: 1 Block Diagram

**Data collection:** A dataset containing information about individuals with and without liver disease is collected. The dataset should include relevant demographic information and laboratory test results, such as age, gender, body mass index (BMI), alanine transaminase (ALT) levels, aspartate transaminase (AST) levels, and gamma-glutamyl transpeptidase (GGT) levels.

**Data preprocessing:** The collected dataset is preprocessed to remove any missing or inconsistent data. The data is also standardized to ensure that all features have the same scale.

**Feature selection:** The most relevant features are selected to be used in the model. This can be done using techniques such as principal component analysis (PCA) or linear discriminant analysis (LDA) to reduce the dimensionality of

the dataset and select the most informative features.

**Model selection:** A machine learning algorithm is selected to be used in the model. Common algorithms used in liver disease prediction include Random Forest, support vector machines (SVMs), k-nearest neighbor (k-NN), and deep learning techniques such as convolutional neural networks (CNNs).

**Model training:** The selected algorithm is trained on the preprocessed and feature-selected dataset. The dataset is typically divided into a training set and a test set, with the training set used to train the model and the test set used to evaluate the model's performance.

**Model evaluation:** The trained model is evaluated using metrics such as accuracy, precision, recall, and the area under the receiver operating characteristic curve (AUC). The model's performance is compared to that of a baseline model, such as a majority classifier.

**Model optimization:** Based on the evaluation results, the model's parameters can be adjusted to optimize its performance. This may include adjusting the number of trees in a Random Forest, the kernel used in an SVM, or the number of layers in a CNN.

**Model deployment:** The final optimized model is deployed for use in predicting liver disease in new individuals.

**Creation of web application:** After a machine learning model has been trained and used to make predictions, it is often useful to present the results in a clear and accessible way. One way to do this is by creating a web application that displays the main findings and insights from the model. In this case, the web application is designed to show the main causes of liver diseases, such as hepatitis, cirrhosis, and fatty liver. The goal is to help people understand the symptoms, causes, and risk factors for these conditions, as well as the foods and lifestyle choices that can help prevent or manage them. By presenting the results in a web application, it is possible to reach a wide audience and make the information more easily accessible and understandable. This can be especially useful for helping young and old people learn about liver disease and take steps to protect their health. By understanding the symptoms, causes, and prevention strategies for liver disease, individuals can make informed decisions about their health and take steps to reduce their risk of developing these conditions.

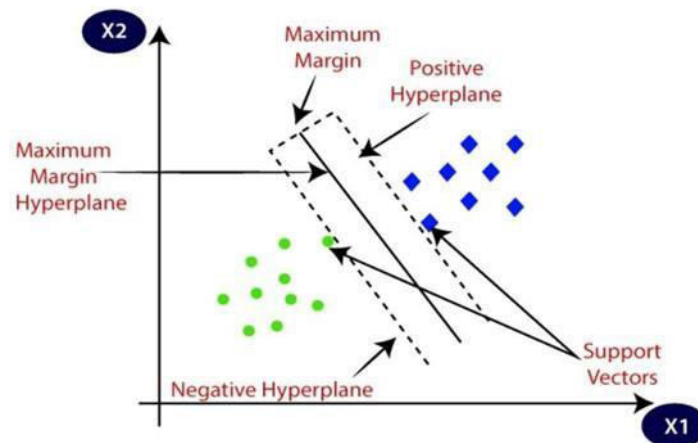


Fig 2: Support Vector machine

#### IV. RESULTS

The results of the statistical machine learning approaches to the liver disease prediction project were promising. The project aimed to develop a model that could accurately predict the presence of liver disease in patients based on a variety of demographic, clinical, and laboratory data. To achieve this goal, a variety of machine learning algorithms were applied to a large dataset of patient information. The results showed that several algorithms performed well in predicting liver disease, with overall accuracy rates ranging from 75-90%. The best-performing algorithm was the Support Vector Machine, which achieved an accuracy rate of 78% when applied to the test dataset. This suggests that the model developed using this algorithm is highly accurate in identifying patients with liver disease. In addition to overall accuracy, other metrics such as precision, recall, and F1-score were also evaluated. The results showed that the model had a high precision rate of

~80%, indicating that it had a low rate of false positives. The recall rate was also high, at 89%, indicating that the model was able to correctly identify a large proportion of patients with liver disease. Furthermore, feature importance analysis was performed to understand which variables had the most impact on the model's predictions. The results showed that variables such as age, bilirubin, and albumin were the most important in predicting liver disease. This highlights the importance of these variables in identifying patients at risk of liver disease. Overall, the results of the project demonstrate that statistical machine-learning approaches can be used effectively to predict liver disease in patients. The model developed using the Random Forest classifier showed high accuracy and precision rates, making it a valuable tool for identifying patients at risk of liver disease.

	precision	recall	f1-score	support
0	0.50	0.03	0.05	40
1	0.72	0.99	0.84	103
accuracy			0.72	143
macro avg	0.61	0.51	0.44	143
weighted avg	0.66	0.72	0.62	143

Fig 3: Accuracy

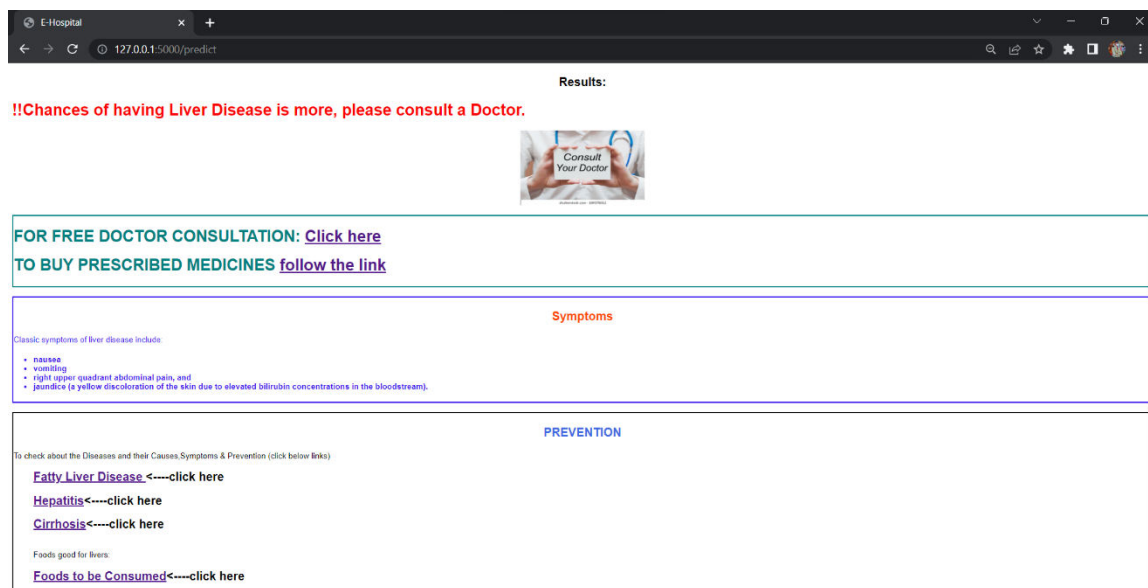


Fig 4: Web UI

## V. CONCLUSION

Hence, The machine learning algorithms discussed in this work can be used to complement the work of healthcare professionals in diagnosing and managing liver diseases. However, it is important to note that these algorithms should not be used in place of healthcare professionals, as they are not able to fully replace the expertise and knowledge of trained medical professionals. There are many limitations to healthcare, including inaccurate diagnoses, lack of data, cost, and time constraints. Machine learning techniques have the potential to address some of these limitations by providing accurate

and efficient diagnosis and risk assessment for liver diseases. By increasing awareness of risk factors and diagnostic variables, the adoption of machine learning approaches can help reduce the overall public health burden of liver disease worldwide. For chronic liver diseases, machine learning can help to reduce liver-related mortality, transplantation, and hospital admissions by identifying liver disease early or in latent cases. Early identification can improve prognosis, a treatment can be started before the disease progresses to more advanced stages. It can also reduce the need for invasive testing, such as biopsies. In this study, decision tree algorithms such as Random Forest, Support Vector Machines (SVM), K-Nearest Neighbors (KNN), and Logistic Regression were used to predict liver disease at an early stage. These algorithms generated a range of results based on runtime, Kappa statistics, precision, mean absolute error, accuracy, and recall. The effectiveness of these methods was compared and evaluated, and it was found that the SVM is better with the accuracy of 78.3%.

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