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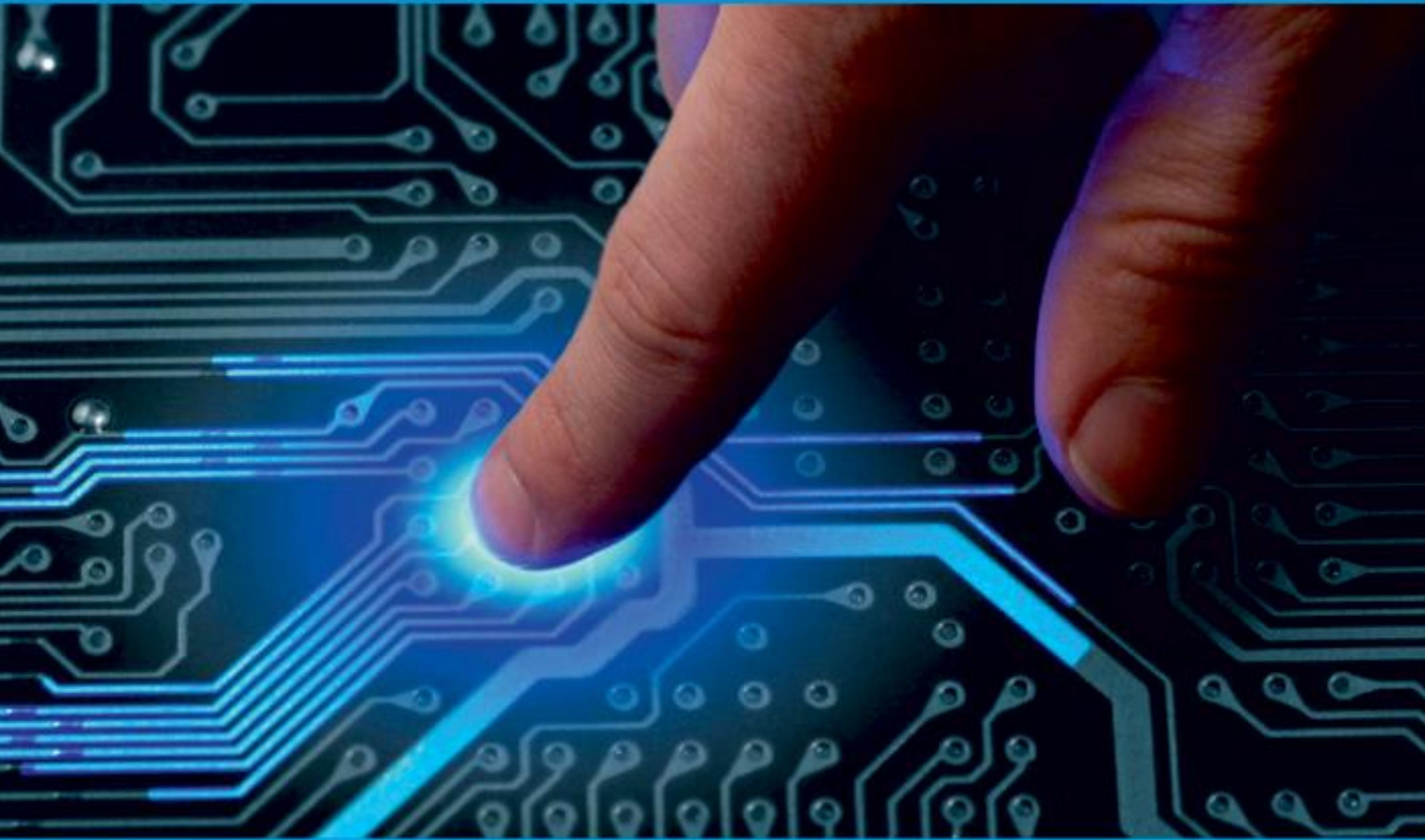

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Hepatitis Disease Prediction Using SVM

Mr. Manoj.M [1], **Mr. ADARSH MJ** [2]

PG Student, Dept. of Master of Computer Applications, Jawaharlal Nehru New College of Engineering, Shivamogga, India

Assistant Professor, Dept. of Master of Computer Applications, Jawaharlal Nehru New College of Engineering, Shivamogga, India

ABSTRACT: The aim of this effort is to determine the most effective method for hepatitis diagnosis, detection, and life expectancy estimation in patients. In this research, a comparison of several machine learning techniques and neural networks was conducted. The accuracy rate and mean square error serve as the foundation for the performance statistic. The Support Vector Machines (SVM), K Nearest Neighbour (KNN), and Artificial Neural Network (ANN) Machine Learning (ML) algorithms were taken into consideration as the classification and prediction methods for diagnosing Hepatitis disease. Based on the accuracy of the predicted disease diagnosis, a brief analysis of the aforementioned algorithms was conducted. MATLAB software was used to implement and validate each ML method.

KEYWORDS: Hepatitis, Support Vector Machines (SVM),Artificial Neural Network(ANN),K Nearest Neighbour(KNN).

I. INTRODUCTION

A major public health concern that causes liver cancer and is 100 times more contagious than HIV/AIDS is the hepatitis B virus (HBV). One in three people worldwide have HBV infection, which affects almost two billion people. There are around 1.5 million new cases of chronic illness each year, affecting over 300 million individuals. Low vaccination rates among those aged 18 and up cause 820,000 deaths annually due to complications caused by HBV. Despite the availability of trustworthy preventative vaccines and diagnostic procedures, HBV continues to be a significant public health issue. Antivirals can totally cure HBV infection, but if you stop taking them, the virus can come back. Patients with HBV infection are classified according to biochemical and virological standards in conventional medical practices. However, due to multicollinearity concerns with highly dimensional medical data, traditional statistical methods may be skewed. Complex viral disease cases can benefit from the use of advanced analytics, such as machine learning (ML) methods. Medical data can be effectively analyzed using ML models to derive knowledge and generate accurate predictions for HBV diagnosis. Studies have used ML models to infer information about hepatitis B from clinical records, with SVM having the highest cross-validation accuracy.

II. RELATED WORK

Ghumbre S. U.; Ghalot A.A, “Hepatitis B Diagnosis using Logical Inference And Self Organizing Map”, 2008 ; Journal of Computer Science ISSN 1549-3636. Medical diagnosis remains an art form, with current computing equipment unable to replace human expertise. Artificial intelligence (AI) has gained popularity in various fields, including education, business, medicine, and industry. This study assessed the potential of AI methods in healthcare, specifically in diagnosing hepatitis B. The study used an AI system to determine if a patient was suffering from hepatitis B, and used Kohonen's self-organizing map network to forecast infection severity. The proposed model improved hepatitis B prediction accuracy and has the potential to become a standard tool for this purpose.[1]

M. A. Chinnaratha, G. P. Jeffrey, G. Macquillan, E. Rossi, B. W. D. Boer, D. J. Speers, and L. A. Adams, “Prediction of morbidity and mortality in patients with chronic hepatitis c by non-invasive liver fibrosis models,” Liver International, vol. 34, no. 5, pp. 720–727, 2014. We wanted to see if liver biopsies and non-invasive markers were equally successful at predicting patients' risk of death and hospitalization from CHC.[2]

Roslina, A. H., and A. Noraziah. "Prediction of hepatitis prognosis using Support Vector Machines and Wrapper Method." In 2010 Seventh International Conference on Fuzzy Systems and Knowledge Discovery, vol. 5, pp. 2209-2211. IEEE, 2010. To lower mortality rates, hepatitis patients must get ongoing specialized medical care. Machine learning and clinical testing can aid in the classification of patients and the estimation of life expectancy. Wrapper

Methods remove irrelevant data to allow for accurate categorisation. Using several feature selection procedures enhances prediction accuracy across datasets[3].

G. H. Haydon, R. Jalan, M. Alakorpela, Y. Hiltunen, J. Hanley, L. M. Jarvis, C. A. Ludlum, and P. C. Hayes, “Prediction of cirrhosis in patients with chronic hepatitis c infection by artificial neural network analysis of virus and clinical factors,” Journal of Viral Hepatitis, vol. 5, no. 4, pp. 255–264, 2010. A study used artificial neural networks (ANN) and traditional clinical host and viral parameters to predict cirrhosis in patients infected with hepatitis C virus (HCV). RT-PCR and 15 conventional clinical and virological indicators were used to examine the results of 112 HCV-positive individuals. Ward-type ANNs fared best in the leave-one-out test, with a sensitivity of 92% and a specificity of 98.9%. Further validation of the ANN analysis is expected to result in the creation of a non-invasive test for identifying cirrhosis in HCV patients[4].

Atif Khan, John A. Doucette, Robin Cohen, “Integrating Machine Learning into a Medical Decision Support System to Address the Problem of Missing Patient Data”, 2012 IEEE DOI 10.1109/ICMLA.2012.82. This work describes a methodology for producing clinical judgments in patient datasets using machine learning techniques. The approach employs automated reasoning and ontology to address information gaps, hence boosting health information system communication and collaboration. To make effective medical decisions, the technique incorporates patient data, drug-drug interactions, and drug prescription recommendations. The study shows that machine learning can be used to predict chronic hepatitis risk using single nucleotide polymorphism (SNP) data. The support vector machine (67.53%) and the decision tree (72.68%) have the highest accuracy (73.20%). Both decision tree and decision rule are promising strategies for predicting chronic hepatitis risk using SNP data[5].

Uhmn, Saangyong, Dong-Hoi Kim, Young-Woong Ko, Sungwon Cho, Jaeyoun Cheong, and Jin Kim. "A study on application of single nucleotide polymorphism and machine learning techniques to diagnosis of chronic hepatitis." Expert Systems 26, no. 1 (2009): 60- 69. The Hepatitis C virus is a highly dangerous human virus that affects 2-4% of the world's population. Interferon alpha and ribavirin can be used alone or in conjunction with new direct-acting antivirals. To uncover genetic drivers of therapeutic outcomes, current research use feature selection approaches and bioinformatics tools[6].

III. METHODOLOGY

Dataset exploration, data mutilation, feature selection, and dimensionality reduction are all part of the proposed strategy for constructing a disease prediction model. In Python, data exploration entails studying the dataset and its attributes, whereas data mutilation estimates missing values in factors. Feature selection entails avoiding multicollinearity, removing superfluous features, and improving efficiency. Backward selection eliminates unwanted features, and statistical tests determine data significance. The data is subjected to five classification algorithms: Logistic Regression, Decision Trees, Random Forest, Support Vector Machine (SVM), and Adaptive Boosting.The Train/Test split methodology is used to assess prediction accuracy. The sample size is set to 0.1, and 90% of the dataset is used for training and 10% for testing.

Existing system: Society susceptible to diseases due to environment & lifestyle. Early diagnosis vital. Predicting sickness is tough. Data mining key for disease prediction & uncovering hidden info. Helps assess medical history & current health status.

Proposed system:Complex hepatitis diagnosis. Benefits of automated systems & clinic tests. Challenges in extensive testing. Aim to identify dataset connections for a patient-friendly web app, reducing wasteful spending.

IV. DESIGN AND IMPLEMENTATION

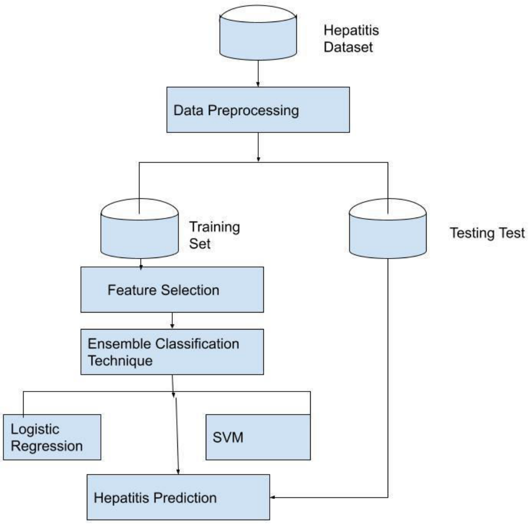

Figure 1: ARCHITECTUR EDIAGRAM

V. RESULTS AND DISCUSSION

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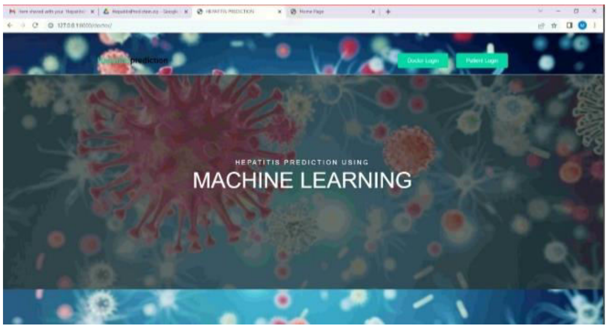

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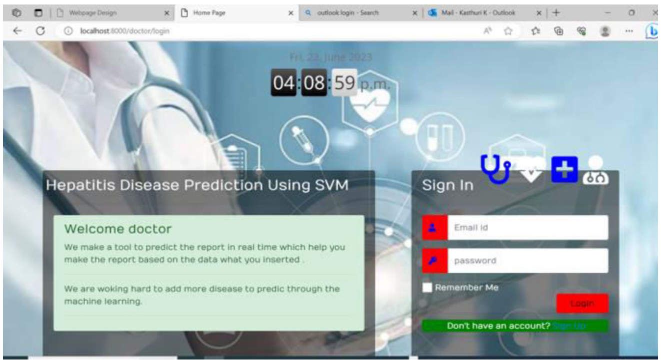

Hepatitis Disease Prediction Using SVM

Welcome doctor

We make a tool to predict the report in real time which help you make the report based on the data what you inserted .

We are woking hard to add more disease to predic through the machine learning.

VI. CONCLUSION

In this study, various machine learning methods and neural networks were applied to make a hepatitis diagnosis. We examined different approaches on the same data set to determine which ML + SVM algorithm was best accurate for detecting hepatitis disease. We used Support Vector Machine (SVM) techniques to produce an accurate diagnosis and prognosis. The results of this investigation reveal that has the best combination of prediction accuracy (96%) and mean square error (MSE) of all the models tested. Future research will employ similar concepts, such as using CNN to anticipate the onset of various diseases.

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