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Prediction of Chronic Liver Disease Patients Using Machine and Deep Learning Technique

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ABSTRACT: The human liver performs over 500 essential functions in the body, and any disruption to its function can lead to severe health complications, potentially resulting in fatal outcomes. Detecting and treating liver diseases promptly are critical for improving patient survival rates. Machine learning (ML) techniques offer valuable assistance to healthcare professionals in diagnosing hepatic conditions. A typical ML framework involves several key stages, including data preprocessing, feature extraction, and classification. By carefully preparing the data, relevant features are extracted, and sophisticated classification algorithms are utilized to identify patterns indicative of liver disease accurately. Integrating ML into the diagnostic process empowers healthcare practitioners to make better decisions, facilitating earlier detection and intervention, ultimately enhancing patient outcomes and prognosis. This study specifically focuses on classifying liver patients using machine learning techniques, particularly Support Vector Machines (SVM) and Neural Networks (NN). The dataset used encompasses various clinical features such as age, gender, and liver function tests. Initially, the dataset undergoes preprocessing to address missing values and categorical variables. Subsequently, SVM is applied with hyperparameter tuning via cross-validation to achieve optimal performance. Following that, a neural network model is deployed to further investigate the classification task. The accuracy and confusion matrix are assessed for both models to gauge their effectiveness in classifying liver patients.

KEYWORDS: Liver disease, Support Vector Machines, SVM, Neural Networks, Classification, Hyper parameter tuning, Preprocessing, Machine Learning.

I. INTRODUCTION

Computer-aided diagnosis systems are powerful applications that have emerged as a result of the application of machine learning techniques in the medical profession. These technologies' encouraging outcomes spur more biomedical machine learning applications. The development of software and hardware technologies contributed to the improvement of biomedical research and investigations. Improvements in data availability and storage capacity typically promote the gathering of superfluous elements that appear beneficial. Because of the advancements in hardware and software technologies, it is anticipated that the obtained medical data will be substantial in size and feature set. The continuous and real qualities that relate to the patients' studies are used to depict these data.

The volume of data generated by the growing number of computerized medical procedures places a heavy pressure on storage needs. Data pools are more affordable and larger because to storage technology. Data mining provides the doctor with excellent software technological support. The goal of the data mining process, a stage in the knowledge discovery process, is to extract meaningful insights from vast amounts of data. Many biological disciplines, such as the diagnosis and prognosis of cardiac disorders, the identification of liver patients, and other complex diseases, have successfully employed machine learning and data mining approaches.

One of the primary issues in biomedical data mining and analysis is detection accuracy since biological data is often large, noisy, and uneven. Specifically, noise can have a detrimental effect on the accuracy of classification, the time it takes to create the classifier, and the size of the classifier. Because of this, most learning algorithms in use today include a number of techniques to increase their ability to learn in noisy environments; yet, noise can still have negative consequences. Most inductive learning algorithms include a noise management mechanism, and machine learning research has focused a lot of emphasis on the topic of learning in noisy environments.

Decision trees have put in significant work to tackle sparse data and class noise in order to prevent overfitting during decision tree induction. Pruning aims to reduce the chances of trees overfitting to noise during training. Pruning might not significantly enhance system performance due to the lower accuracy of classifiers trained on noisy data, which is particularly evident in the presence of high noise levels. Data noise, which refers to inaccurate data within an example's variables, is possibly the most common problem affecting data quality.

Data noise comes in two forms: attribute noise and class noise. Erroneous values in a dataset's independent attributes are known as attribute noise, but inaccurate values in the dependent attribute are referred to as class noise. Class noise has a higher negative impact on classification performance than attribute noise, according to earlier studies comparing these two types of noise. Identifying and eliminating potentially noisy cases from the training dataset is known as noise filtering, and it is another technique for mitigating class noise. Noisy instances are once more found using a very similar technique called noise correction, but this time, rather than eliminating the instances completely, the class names are altered.

Diverse methods have been investigated to determine which examples to classify as noisy. In some procedures, the data points are analyzed based on the class labels to search for outliers (without explicitly applying a typical classification algorithm). Classification filtering, on the other hand, is a more common technique. It involves building and evaluating a classifier using training data, commonly using cross-validation, and classifying misclassified examples as noisy. Unlike the previous researchers, the main idea of this article is that we should use the noisy cases to build the classifier, rather than recognizing and avoiding them.

The naïve Bayesian logic procedure will be reversed once the model is built using noisy cases. This is also known as "complement based learning." It has strong classification accuracy and cuts down on the number of instances needed to form the model, which in turn shortens calculation time. In practice, there are a lot of problems that call for two class problem classification techniques, such as the Indian Liver Patient Dataset (ILPD) and the Single Photon Emission Computed Tomography (SPECT) Heart Datasets, where the class is either normal or abnormal. However, this approach is only applicable to two class problems.

Over a million people worldwide receive a liver disease diagnosis each year. Common liver illnesses include liver cancer, hepatitis A, B, and C, and liver cirrhosis. Liver cirrhosis claimed the lives of 1.32 million more people worldwide in 2017 than it did in 1990, with 33.3% of the victims being women and 66.7% of men. Despite the fact that overall mortality is decreasing as a result of advances in cutting-edge medical care and leading healthy lives. However, 3.5% of all deaths this century were attributable to liver-related causes.

Obesity, diabetes, alcoholism, and drug abuse are the primary causes of liver damage. If these potentially fatal illnesses are identified early on, they are treatable. The healthcare industry makes extensive use of machine learning and deep learning techniques, especially for the diagnosis and categorization of specific diseases based on characteristic data. These technologies will enable more intelligent and accurate patient decision-making by clinicians.

A major worldwide health burden, chronic liver disease (CLD) is defined by gradual liver damage over time, which frequently results in liver failure and related consequences. It includes a range of diseases and disorders of the liver, such as cirrhosis, fatty liver disease, hepatitis, and liver cancer. In order to lessen the effects of CLD on patient health outcomes and healthcare systems, prompt diagnosis and efficient management are essential.

The majority of conventional methods for diagnosing CLD include invasive techniques like liver biopsies, which can be risky and uncomfortable for patients. Furthermore, these techniques could not always offer prompt insights on the course of the disease. In order to improve CLD diagnosis and prediction, there is an increasing interest in utilizing machine learning (ML) and deep learning (DL) approaches.

Large amounts of patient data, including clinical, imaging, and genetic data, can be analyzed using ML and DL to find patterns and associations that might not be seen using more traditional methods. These methods can help CLD patients with early detection, risk assessment, and individualized therapy planning by training models on a variety of datasets

II. RELATED WORK

Compared to previous decades, the prevalence of human diseases is rising today. The number of people affected by liver illnesses is constantly increasing when compared to other significant diseases [14]. However, in their early stages, most liver illnesses do not exhibit any noticeable symptoms. With today's sophisticated databases, extracting data and gaining insights to help treat any illness is a straightforward process [15]. The researcher uses a variety of techniques to try and get insights from the dataset. While some of these are employed in feature extraction or selection processes with ML classifiers, others are not. Data are generated and stored in an unremarkable way now a days. The researcher was able to solve any problem in domains including medical imaging, finance, genetics, transactions, encroachment, and more with the help of the readily available data. If the amount of required and extraneous data is high, it might have an impact on the machine learning process. The most correlated feature space can be chosen and extracted using a variety of techniques in order to anticipate any illness or object.

To anticipate cardiac conditions The heart disease datasets from Cleveland, Hungary, Switzerland, and Statlog were examined by Pasha and Mohamed et al. [16]. As part of their working technique, they used a novel feature reduction (NFR) model to predict heart disease. First, they processed the dataset, and then they used a range of statistical approaches, such as weighted least squares (WLS) and correlation matrices, to identify the attributes that made a substantial contribution. The AUC and accuracy are measured by the Data Mining (DM) and Machine Learning (ML) algorithms on the dwindling feature set, and then on each individual reduced feature. The boosted regression trees (BRT) in their suggested NFR model obtained the maximum accuracy of 93.53% by LR and the highest AUC of 96.68% on the Cleveland dataset. Using the Hungarian dataset, the LR obtained the greatest accuracy of 85.06% and AUC of 92.51% by BRT and SVM. In the Statlog dataset, BRT obtained the maximum accuracy of 87.65% using SVM and RF, as well as the highest AUC of 91.79%.

By comparing the NFR and non-NFR models, the author shows that the suggested NFR model has a higher Accuracy and AUC in heart disease prediction. The same author [17] used the same datasets and an advanced hybrid ensemble gain ratio (AHEGR) feature selection method to create heart disease risk prediction. In their suggested ensemble system, all four feature selection techniques—ensemble feature selection, gain ratio feature selection, backward feature removal, and area under the curve (AUC)—have been used.

Authors investigated the efficacy of various classification techniques in the diagnosis of liver disorders in this work [10]. Naive Bayes, Decision Trees, Multilayer Perceptrons, Random Forests, K-Nearest Neighbors, and Logistic Regression were some of these techniques. The authors employed criteria like precision, recall, sensitivity, and specificity to assess their performance. Out of all the algorithms tested, Naive Bayes produced the best results in terms of precision, according to the findings. Additionally, it was discovered that when recall was taken into account, the Random Forest and Logistic Regression algorithms produced good results. The WEKA tool was used in [11] to develop a model for analyzing liver disease. The Naive Bayes, Decision Tree (DT), and J48 algorithms were used to develop their proposed model.

The accuracy and execution time of the algorithms were measured, and the outcomes were contrasted with those of the other possibilities. The results showed that the J48 and DT algorithms performed more accurately than the Naive Bayes method. Utilizing a dataset of liver patients from India, [12] applies a number of classification algorithms, such as LR, K-NN, and SVM. Confusion matrix was also employed to compare the algorithms with one another. The experimental examination of these algorithms was looked at and assessed based on how accurate they were. The results show that while LR has a more sensitivity, KNN approaches can also attain a significant level of accuracy. From this, it follows that LR is a suitable approach for illness prediction.

In [13], [14], and [15], a feature model incorporating the classification techniques of Random Forest, SVM, J48, Bayesian Net, and MLP. A research for the prediction of liver illness is examined and put into practice using three different processes. In the first step, the normalisation method min-max was analysed and evaluated on the dataset including records of liver disorders. The second stage selects the elements of the dataset required for liver disease prediction using the PSO feature selection technique. In the third step, the classification algorithms were put into practice and the approaches' performance was assessed based on accuracy.

Following testing of his suggested approach, the integrated TANBN employing a cost-sensitive method (AdaC-TANBN) produced an accuracy of 69.03%, surpassing the outcomes of the other methods. Abdar et al. [19] employ a variety of classification techniques, including the automatic chi-square interaction detector (CHAID) with boosting methodology, the classification and regression tree (CART), and the decision tree (C5.0).

III. PROPOSED METHODOLOGY

The project's suggested methodology takes a thorough approach to predicting chronic liver disease by combining deep learning strategies like neural networks with more conventional machine learning approaches like Support Vector Machine (SVM). The project starts with the collection of a dataset that includes several characteristics related to liver health, such as biochemical markers, blood test results, and demographic data. The basis for developing predictive models to identify people at risk of chronic liver disease is this dataset.

Preparing the dataset for modeling purposes is the main goal of the project's first phase. This involves coding categorical variables into a numerical representation and managing missing values. The initiative guarantees that subsequent modeling efforts are grounded in dependable and high-quality data by tackling data quality issues early on. Neural network modeling and SVM modeling with hyperparameter tuning are the two different modeling techniques used. Neural networks are excellent at identifying complex patterns and nonlinear relationships in the data, while support vector machines (SVM) offer interpretability and robustness. These two approaches complement one other well in predictive modeling.

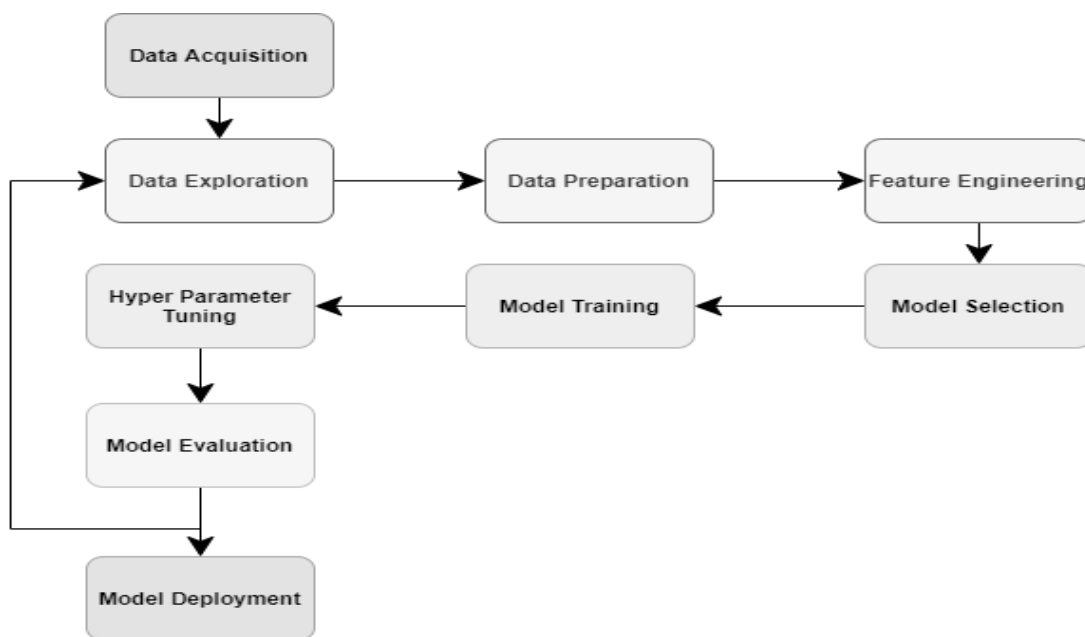


Fig1:Model Building Using Hyper Parameter Tuning

The dataset is split into features and labels in the SVM technique, and feature scaling is used to standardize the data. Next, using k-fold cross-validation, hyperparameter tweaking is used to optimize the SVM model's configuration, including the selection of the kernel function and regularization parameter. The most efficient set of hyperparameters to maximize the predictive performance of the model is found through this iterative procedure.

The top-performing SVM model is then trained on the complete dataset, and cross-validation is used to gauge how well it can generalize results. The model's resilience and suitability for use with untested data are revealed by this methodical testing on several data subsets.

Simultaneously, the best features produced by the best SVM model are used to train a neural network model. By maximizing the use of the most illuminating characteristics found by the SVM model, this method improves the neural network's capacity to recognize pertinent patterns and correlations in the data.

Numerous parameters, including the number of hidden layers, neurons per layer, and activation functions, are configured in the neural network design. These parameters are selected in order to create a neural network architecture that is highly suitable for chronic liver disease prediction, taking into account domain knowledge, empirical evidence, and experimentation.

During neural network training, options for hold-out ratio, maximum epochs, transfer functions, and other pertinent parameters must be specified. The neural network's learning process is optimized by adjusting these parameters, which also increase the neural network's convergence speed and capacity for generalization. To ensure that the neural network generalizes well to new data and avoid overfitting, strategies like early termination may be used.

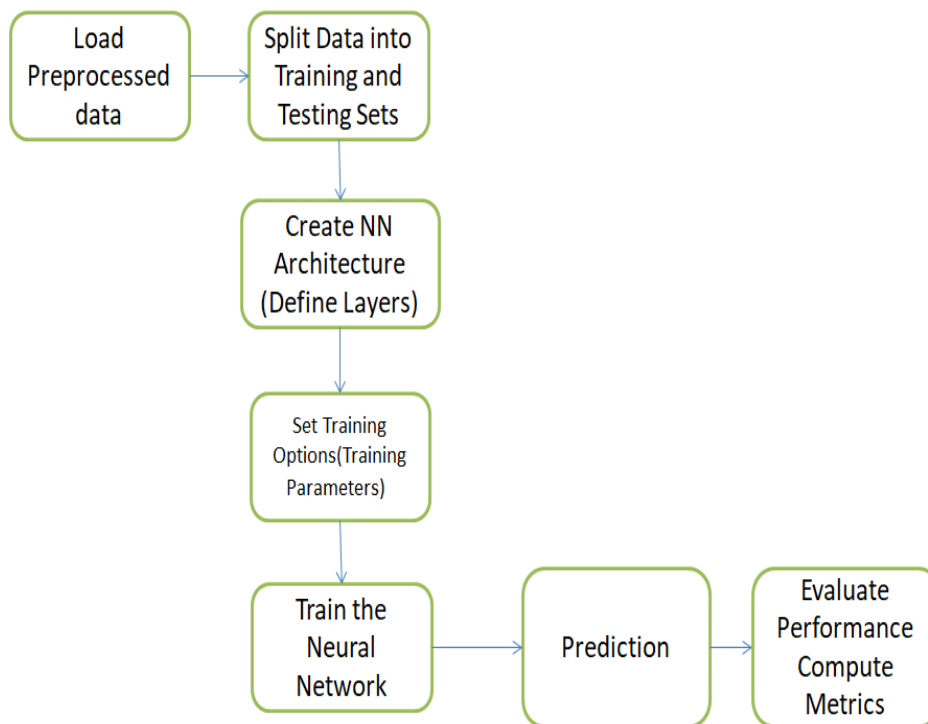


Fig2:Neural Network Block diagram

The neural network model's performance is assessed using suitable evaluation measures, such as accuracy, precision, recall, and F1-score, once it has been trained using the best features. To evaluate the model's accuracy in assigning people to various risk categories for chronic liver disease, a confusion matrix is created. Strict evaluation methods are used throughout the project to guarantee the efficacy and dependability of the created models, including confusion matrix analysis, cross-validation, and performance indicators. Strong and clinically useful predictive models for chronic liver disease can be made more easily thanks to this iterative process of model construction, optimization, and assessment.

Algorithms used in Neural Network Training:

For Training:

trainsg: Scaled conjugate gradient backpropagation

train: This refers to the training process of a neural network, which involves adjusting the weights of the network based on input data and desired output to minimize the error or loss function.

sg: This stands for "scaled conjugate gradient." Conjugate gradient methods are a class of optimization algorithms used for finding the minimum of a function. In the context of neural networks, this function is typically the error or loss function that measures the difference between the actual output of the network and the desired output. "Scaled" refers to the fact that this particular variant incorporates scaling factors to adaptively adjust the step sizes in different directions, which can help improve convergence speed.



The "trainscg" algorithm is one of several optimization algorithms available for training neural networks in MATLAB's Neural Network Toolbox. It's often used when training feedforward neural networks, especially for problems where the training data is noisy or the error surface is complex and contains many local minima.

Syntax: net.trainFcn = 'trainscg' [trainedNet,tr] = train(net,...)

For Performance:

Cross Entropy:

Cross entropy, often referred to as "cross-entropy loss" or "log loss," is a measure used in classification tasks to quantify the difference between two probability distributions. It's commonly used as a loss function in training machine learning models, particularly in scenarios involving classification problems and neural networks.

Syntax:

perf = crossentropy(net, targets, outputs, perfWeights) perf =crossentropy(__,Name, Value)

The goal of the research is to create a comprehensive and precise predictive model that can help physicians with early diagnosis and treatment planning for chronic liver disease by integrating the advantages of SVM and neural network models and abiding by best practices in predictive modeling.

IV. RESULTS AND ANALYSIS

The project's outcomes demonstrate how well two different machine learning algorithms—Support Vector Machines, or SVM, and Neural Networks, or NN—perform in predicting liver disease using clinical and biochemical characteristics. The neural network demonstrated noticeably superior accuracy, reaching 93.33%, than the top SVM model, which only managed to attain 71.36%.

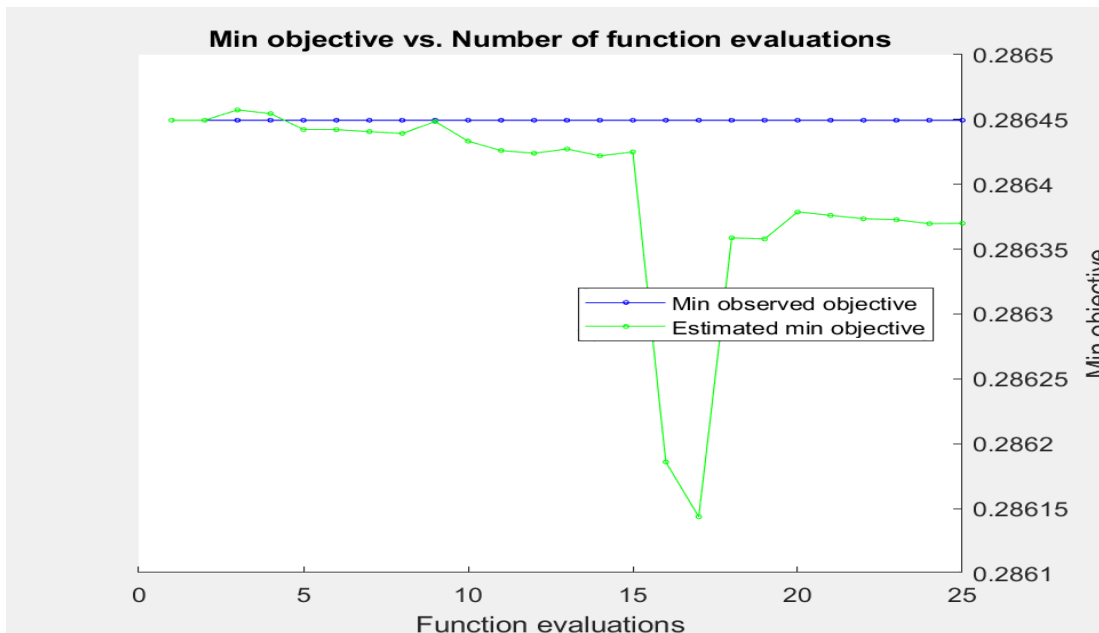


Fig3:Minimum Objective vs. Number of Function Evaluations

Minimum Objective vs. Number of Function Evaluations: This graph shows the correlation between the number of function evaluations the hyperparameter optimization algorithm performs and the minimum objective function value attained. The model's optimal performance during the hyperparameter tuning procedure is shown by the minimal objective function value.

The number of function evaluations is a measure of how much computing power the optimization method uses to explore various configurations of the hyperparameters. Usually, the graph displays how the minimum objective function value changes when more function evaluations are performed during the optimization process.

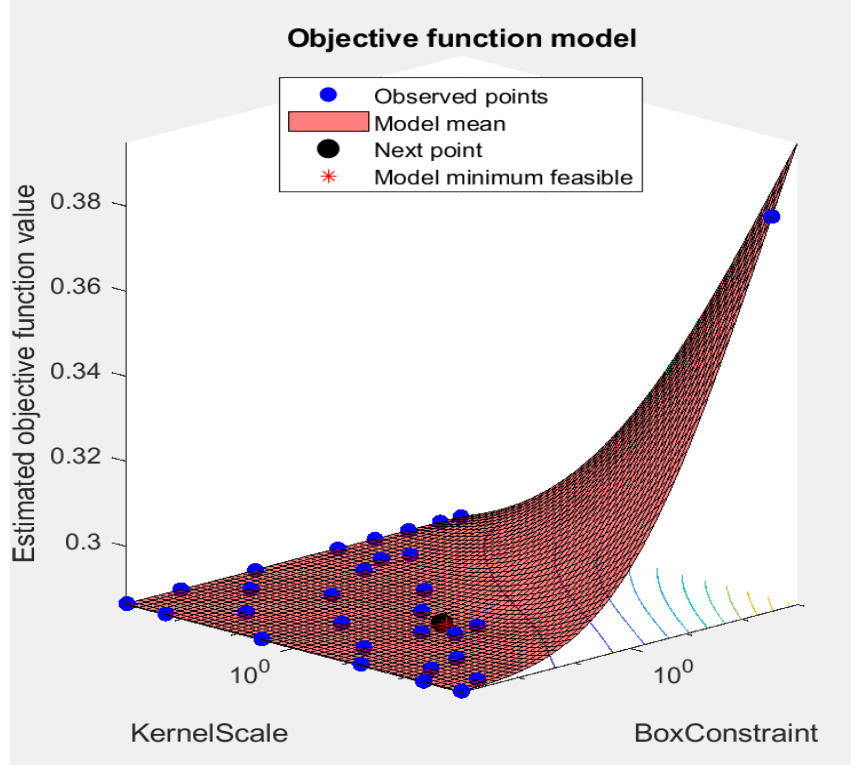


Fig 4: Objective Function Model

Objective Function Model: As the hyperparameter optimization method runs through several iterations, this graph shows how the objective function behaves. The quantity being optimized in the hyperparameter tuning process, such as the model's error rate or a particular metric like accuracy, is represented by the objective function. The neural network architecture appears to have been more appropriate for capturing the underlying patterns in the dataset, based on the discrepancy in accuracy between the SVM and neural network models.

Given their reputation for handling intricate data linkages and adapting to non-linear patterns, neural networks may have performed better in this test than support vector machines (SVMs). Furthermore, the neural network model's increased accuracy suggests that it may have been more successful at extrapolating from the training data to instances that weren't encountered.

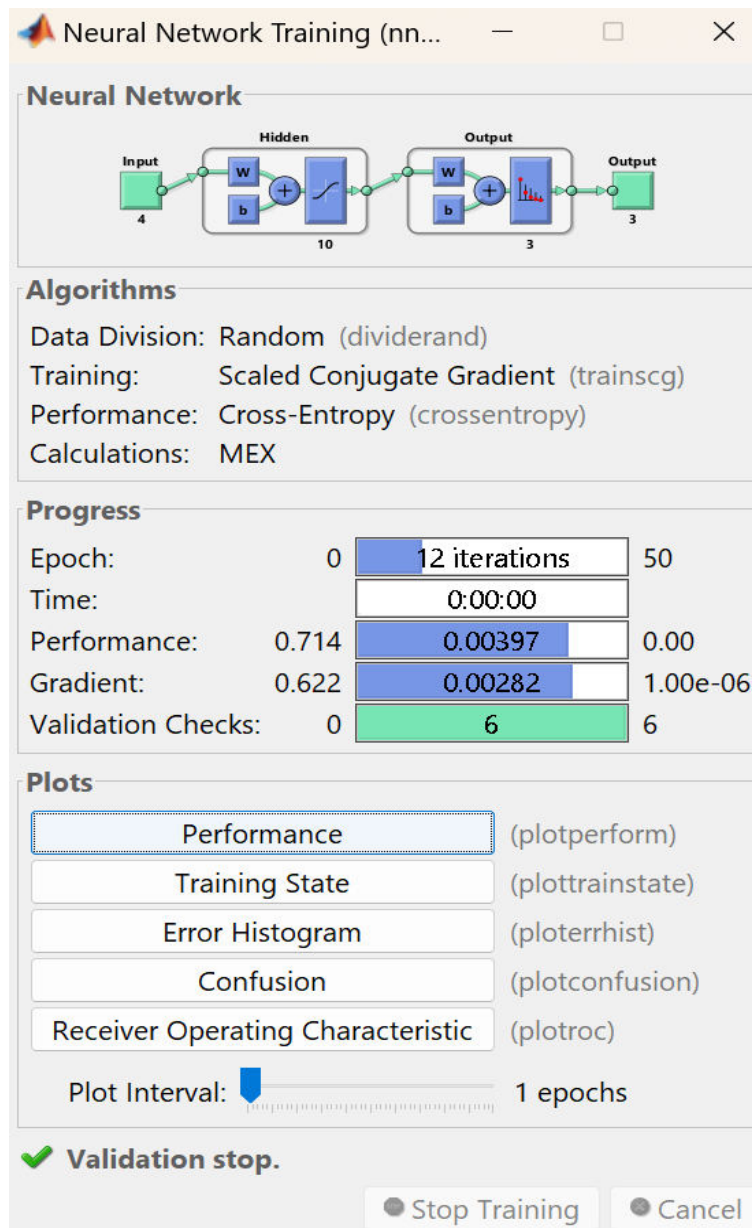


Fig 5:Neural Network Training

To fully comprehend the advantages and disadvantages of each model, more analysis must be done. Even if the neural network produced results with more accuracy, robustness, interpretability, and computational complexity must all be taken into account. SVMs are renowned for their ease of use, interpretability, and effectiveness when handling high-dimensional data.

Moreover, the quality and number of characteristics employed in each model may also be responsible for the discrepancy in accuracy. Model performance is heavily influenced by feature engineering and selection, and it's probable that the neural network would have performed better with a larger collection of features or more efficient feature extraction methods.



```

Optimization completed.
MaxObjectiveEvaluations of 30 reached.
Total function evaluations: 30
Total elapsed time: 116.4133 seconds
Total objective function evaluation time: 94.4884

Best observed feasible point:
      BoxConstraint      KernelScale
      _____      _____
           676.01           0.76989

Observed objective function value = 0.28645
Estimated objective function value = 0.28646
Function evaluation time = 2.8928

Best estimated feasible point (according to models):
      BoxConstraint      KernelScale
      _____      _____
           28.772           0.65743

Estimated objective function value = 0.28643
Estimated function evaluation time = 0.19905

Accuracy of the best model with cross-validation: 71.36%

Classification Accuracy using Neural Network (NN-HO) : 93.3333 %
Processing Time (s) : 0.337708
    
```

Fig6:Results of the Proposed Model

In conclusion, even though the neural network outperformed the SVM model in predicting liver disease, a thorough analysis taking into account variables like interpretability, computational complexity, and feature quality is required to identify the best model for actual use in a clinical setting. Furthermore, the performance of both models might be improved by more testing with other architectures, hyperparameters, and feature engineering strategies.

V. CONCLUSION

To sum up, the project's goal was to create and evaluate machine learning models that use biochemical and clinical characteristics to predict liver disease. The outcomes showed how useful neural networks (NN) and support vector machines (SVM) were for this task; the neural network model outperformed SVM in terms of accuracy. The discrepancy in accuracy emphasizes how crucial it is to choose the right machine learning algorithm depending on the type of data and the particular needs of the application. Even if the neural network performed better, factors like interpretability, computational complexity, and feature quality must be taken into account before deciding which final model to use.

The experiment also highlighted how important feature engineering and selection are to enhancing model performance. Experimentation with additional feature sets, topologies, and hyperparameters may improve the models' accuracy and resilience. All things considered, the study adds to the expanding corpus of literature on machine learning-based diagnostics in healthcare and emphasizes the significance of using cutting-edge computational methods to support illness prediction and diagnosis. Subsequent research endeavors may concentrate on enhancing the models'

functionality, integrating supplementary data sources, and carrying out meticulous validation tests to evaluate their practical applicability and influence in medical environments.

REFERENCES

- [1]. Lin RH. An intelligent model for liver disease diagnosis. *Artif Intell Med* 2009;47 (1):53–62. <https://doi.org/10.1016/j.artmed.2009.05.005>.
- [2]. Collaborators C. Articles the global, regional, and national burden of cirrhosis by cause in 195 countries and territories, 1990 – 2017 : a systematic analysis for the Global Burden of Disease Study 2017. 2017. p. 245–66. [https://doi.org/10.1016/S2468-1253\(19\)30349-8](https://doi.org/10.1016/S2468-1253(19)30349-8).
- [3]. Harshpreet Kaur GS. The diagnosis of chronic liver disease using machine learning techniques. *Inf. Technol. Ind.* 2021;9(2):554–64. <https://doi.org/10.17762/itii.v9i2.382>.
- [4]. Tapper EB, Parikh ND. Mortality due to cirrhosis and liver cancer in the United States, 1999-2016: observational study. *BMJ Jul.* 2018;362:2817. <https://doi.org/10.1136/BMJ.K2817>.
- [5]. Joloudari JH, Saadatfar H, Dehzangi A, Shamshirband S. Computer-aided decisionmaking for predicting liver disease using PSO-based optimized SVM with feature selection. *Inform Med Unlocked* 2019;17(August). <https://doi.org/10.1016/j.imu.2019.100255>.
- [6]. Jacob J, Mathew JC, Mathew J, Issac E. Diagnosis of liver disease using machine learning techniques. 2018.
- [7]. Ullah S, Awan MD, Sikander Hayat Khiyal M. Big data in cloud computing: a resource management perspective. *Sci Program* 2018. <https://doi.org/10.1155/2018/5418679>.
- [8]. Stone JV. Principal component analysis and factor analysis. *Indep. Compon. Anal.* 2018;2–3. <https://doi.org/10.7551/mitpress/3717.003.0017>.
- [9]. Singh J, Bagga S, Kaur R. Software-based prediction of liver disease with feature selection and classification techniques. *Procedia Comput Sci* 2020;167(2019): 1970–80. <https://doi.org/10.1016/j.procs.2020.03.226>.
- [10]. Sreejith S, Khanna Nehemiah H, Kannan A. Clinical data classification using an enhanced SMOTE and chaotic evolutionary feature selection. *Comput Biol Med* 2020;126(February):103991. <https://doi.org/10.1016/j.combiomed.2020.103991>.
- [11]. Kuzhippallil MA, Joseph C, Kannan A. Comparative analysis of machine learning techniques for Indian liver disease patients. In: 2020 6th Int. Conf. Adv. Comput. Commun. Syst. ICACCS 2020; 2020. p. 778–82. <https://doi.org/10.1109/ICACCS48705.2020.9074368>.
- [12]. Ali M, Shiaeles S, Bendiab G, Ghita B. Malgra: machine learning and N-GRAM malware feature extraction and detection system. *Electronics (Switzerland)* 2020;9 (11):1–20. <https://doi.org/10.3390/electronics9111777>.
- [13]. Johnson JM, Khoshgoftar TM. Survey on deep learning with class imbalance. *J. Big Data* 2019;6(1). <https://doi.org/10.1186/s40537-019-0192-5>.
- [14]. Pasyar P, Mahmoudi T, Kouzehkanan SM. Informatics in Medicine Unlocked Hybrid classification of diffuse liver diseases in ultrasound images using deep convolutional neural networks. *Inform Med Unlocked* 2021;22(December 2020): 100496. <https://doi.org/10.1016/j.imu.2020.100496>.
- [15]. Hassannataj J, Saadatfar H, Dehzangi A, Shamshirband S. Informatics in Medicine Unlocked Computer-aided decision-making for predicting liver disease using PSObased optimized SVM with feature selection. *Inform Med Unlocked* 2019;17 (August):100255. <https://doi.org/10.1016/j.imu.2019.100255>.
- [16]. Pasha SJ, Mohamed ES. Novel Feature Reduction (NFR) model with machine learning and data mining algorithms for effective disease risk prediction. *IEEE Access* 2020;8:184087–108. <https://doi.org/10.1109/ACCESS.2020.3028714>.
- [17]. Pasha SJ, Mohamed ES. Advanced hybrid ensemble gain ratio feature selection model using machine learning for enhanced disease risk prediction. *Inform Med Unlocked* 2022;32(June):101064. <https://doi.org/10.1016/j.imu.2022.101064>.
- [18]. Gan D, Shen J, An B, Xu M, Liu N. Integrating TANBN with cost-sensitive classification algorithm for imbalanced data in medical diagnosis. *Comput Ind Eng* 2020;140(January):106266. <https://doi.org/10.1016/j.cie.2019.106266>.
- [19]. Abdar M, Yen NY, Hung JCS. Improving the diagnosis of liver disease using multilayer perceptron neural network and boosted decision trees. *J Med Biol Eng* 2018;38(6):953–65. <https://doi.org/10.1007/s40846-017-0360-z>.
- [20]. Anagaw A, Chang YL. A new complement naïve Bayesian approach for biomedical data classification. *J Ambient Intell Hum Comput* 2019;10(10):3889–97. <https://doi.org/10.1007/s12652-018-1160-1>.
- [21]. Babu MSP, Ramjee M, Katta S, Swapna K. Implementation of partitional clustering on ILPD dataset to predict liver disorders. *Proc. IEEE Int. Conf. Softw. Eng. Serv. Sci. ICSESS* 2016:1094–7. <https://doi.org/10.1109/ICSESS.2016.7883256>.



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