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A hybrid extreme machine learning model for predicting heart disease

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ABSTRACT

Heart disease (HD), the leading cause of death for adults over 65, can affect anyone at any time. Additionally, modern lifestyles, poor diets, and other factors have led to an increased risk of HD among teenagers. One significant challenge is managing and analysing vast amounts of data, often surpassing terabytes, which is crucial for researching, diagnosing, and predicting cardiovascular diseases quickly. To enhance primary health care, especially in early and rapid diagnosis of heart attacks and to assist less experienced doctors in understanding clinical HD data, we propose a hybrid method called the "hybrid extreme machine learning model (HEMLM)". This technique combines the strengths of multi-layer perceptron (MLP), random layers, and logistic regression (LR). The model offers various feature patterns and multiple classification techniques. Compared to support vector machine (SVM), LR, and Naive Bayes (NB), the HEMLM algorithm demonstrates superior performance and efficiency. Testing results show identification accuracies of 94.91%, 94.77%, 92.42%, and 87.14% for data splitting ratios of 85:15, 80:20, 70:30, and 60:40, respectively.

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1. INTRODUCTION

Heart disease (HD) remains one of the leading causes of mortality in today's competitive world. Accurate prognosis of HD is essential for analyzing clinical data, as heart-related issues are the primary contributors to illness and death. Identifying HD based on risk factors like diabetes, high blood pressure, high cholesterol, abnormal heart rate, and others can be challenging. The increasing number of individuals affected by these conditions, combined with unhealthy habits like smoking and excessive drinking, raises the risk of cardiovascular disease [1], [2]. Therefore, timely diagnosis is crucial for protecting affected patients. Additionally, lifestyle and dietary habits significantly impact individual health, making it vital to analyze patient history for early prediction and diagnosis of HD.

Learning algorithms offer valuable insights by making predictions from the vast amount of medical data available. Machine learning (ML) techniques have been increasingly used in conjunction with advancements in the internet of things (IoT). Many studies have utilized ML to provide concise predictions of HD. Techniques like data mining (DM) and neural networks (NN) have been widely applied to understand the significance of HD among individuals [3], [4]. Various methods, such as k-nearest neighbor (KNN), decision trees (DT), genetic algorithms (GA), and Naive Bayes (NB) have been employed to categorize the severity of HD. However, HD is a complex condition that must be managed carefully; failure to do so can lead to severe consequences, including death [5], [6]. Clinical science and DM concepts are utilized to identify different metabolic disorders, with artificial neural networks (ANN) showing the highest accuracy in clinical predictions.

Despite the success of these algorithms, their accuracy in HD detection and prevention is not always sufficient. This has led to the belief that hybrid models can enhance prediction accuracy. The key contributions of this research are as follows:

- We propose a hybrid approach, named the "hybrid extreme machine learning model (HEMLM)," to investigate and predict HD as early as possible.
- We use data visualization methods to provide insights into the feature values and their relationships used in the analysis.
- The proposed model combines multi-layer perceptron (MLP) with random layers and logistic regression (LR).
- After selecting the dataset features, the projection model is tested with various feature patterns and well-known classification methods.
- The HEMLM approach is compared with existing methods such as support vector machine (SVM), LR, and NB. Experimental results show an accuracy of 94.91%, significantly outperforming existing ML methods.

2. LITERATURE REVIEW

Classification procedures in DM assume a critical part in expectation and information investigation. Classification methods, for example, DT, have been utilized in anticipating the precision and occasions identified with coronary heart disease (CHD). Based Abdullah and Rajalaxmi [7], a DM model was created using random forest (RF) classifiers to develop the forecast precision further and explore different occasions identified with CHD. Also, in [8], the particle swarm optimization (PSO) approach, which is quite possibly the most remarkable evolutionary algorithm (EA), is utilized to create rules for HD. To begin with, the random standards are encoded, and afterward, they are improved depending on their precision using the PSO calculation. However, diagnosing HD is one of the significant issues, and numerous specialists explore ways to foster smart decision support systems (DSS) to work on the capacity of the doctors. NN is a widely used tool for predicting an HD diagnosis. For example, NN develops an HD prediction system in [9]. Also, in [6], [10], DM techniques, specifically NB, NN, and DT calculations, are applied to clinical datasets. The authors propose to foster an application that can foresee the weakness of an HD given fundamental side effects like age, sex, heart rate, and so on. The ML results of NN have been demonstrated to be the most reliable and solid, and consequently utilized in the proposed framework. To analyze various research works done on HDs prediction and classification using various ML and deep learning (DL) techniques, Rajamhoana *et al.* [11] review most of the recent approaches and conclude which techniques are more effective and accurate.

To construct an information-based clinical DSS that physically utilizes information from clinical experts and pushes this data into PC approaches [12]. This process can be misleading, and trusting clinical experts' viewpoints that may be emotional, can lead to wrong decisions. Therefore, ML strategies have been created to acquire information naturally from models or crude data. At the same time, multi-criteria decision-making (MCDM) techniques are relied upon to look for the best option as indicated by certain criteria. Every standard has a worth comparative with every other option. There are just two sets: a set of criteria and a set of choices.

Baccour [3] combines MCDM strategies TOPSIS and VIKOR and adjusted them to be utilized for classification. The used sets are three: the classes, the items, and the traits (features) portraying the articles. Henceforth, ATOVIC, another classification calculation, is proposed. Also, in [13], the authors endeavor to build a model for assessing childhood apraxia of speech (CAS) visualization by ANN. The information of 317 patients from the Taiwan NHIRD is utilized to prepare and test the built ANN model. Another study is conducted in [14], where data on cardiovascular patients are gathered from the UCI and used for applying revelation design calculations, including DT, NN, rough set, SVM, and NB. The authors analyze these algorithms' precision and prediction, and they propose a half-breed calculation to expand the exactness of the used calculations. However, in MCDM, a few criteria having diverse significance are utilized to select the best option from many others. Subsequently, unique weight techniques exist to assess the significance of every measure.

For instance, TOPSIS [15], an MCDM strategy, is applied to utilize a new dataset with various methods of different weights, whereas the NN ensemble technique was the focal point of the proposed framework in [4]. Furthermore, the hybrid approaches can generate new models by joining the back probabilities or the anticipated qualities from multiple predecessor models. The results are compared with the existing works in the same domain. Similarly, M and V [5] try to forecast the existence of HD using the MLP of ANN. In addition, the authors in [16], [17] review various DM and NN classifications utilized to anticipate the danger of HDs depending on hazard factors. The danger level of an individual is characterized by utilizing methods such as KNN, DT, GA, NB, and so forth. The accuracy turns out to be high when utilizing hybrid approaches.

Since the heart is a critical part of living beings, analysis and prediction of heart-related illnesses require more accuracy and precision, where a small error may cost a life [18]. However, anticipating and controlling sicknesses is difficult in the clinical field. Thus, research is directed to help the medical teams in predicting HD. For instance, in [19], the authors propose an AI system to predict the chance of having HD utilizing different approaches. Mohan *et al.* [20] have examined the HD forecast utilizing KStar, J48, SMO, Bayes Net, and MLP through the Weka tool.

An extreme learning machine (ELM) approach is utilized in [21] to demonstrate these elements. Their proposed framework can supplant expensive clinical tests with a notification framework for patients of the plausible presence of HD with 80% accuracy, whereas our proposed HEMLM approach is able to get 94.91% accuracy in disease prediction at an early stage. Also, Bashir *et al.* [22] introduce the expectation of HD in the clinical field by utilizing data science. The researchers in [23]-[27] mainly focus on decision strategies and computations where different HD datasets are utilized for experimental investigation and to improve precision.

By utilizing the rapid digger as the device, DT, LR, SVM, NB, and RF calculations are utilized as highlight determination methods. Bharti *et al.* [28], DL and ML are used to analyze the results and findings of the UCI dataset. Mayourian *et al.* [29] developed a CNN model to assess left ventricular ejection fraction (LVEF) of 40% or less using paired ECG-echocardiograms in CHD. The model, showed high performance (AUROC 0.95 internal; AUROC 0.96 external). The work presented in [30] contrast four ML approaches, NB, RF, SVM, and DT, for HD prediction. Ahmed *et al.* [31], the automatic disease finding model is premeditated using the ML models. Rani *et al.* [32] have introduced a hybrid DSS that can aid in the early identification of HD, depending on the clinical boundaries of the patient.

El-Sofany *et al.* [33] aim to offer an improved method with feature selection and classification procedures to predict death in congestive HF patients. The utilized approaches in this paper are by varying the data split and NN. According to Casalino *et al.* [34], they suggest using neuro-fuzzy systems to help decision making in cardiovascular risk assessment by learning predictive models from data in the form of fuzzy rules. Several ML and DL techniques are used to the UCI ML HD dataset, and the results and analyses are compared and contrasted [35]. They present a technique that is based on density and does not involve supervision for identifying abnormalities in patients who have HDs [36].

3. HEMLM PROPOSED MODEL

This paper aims at evaluating the performance of various classification and prediction algorithms, including SVM, NB, and LR, for HD prediction. We believe that those approaches proved to be efficient in various areas, but they are not good enough for HD prediction. Figure 1 shows the architecture of the proposed system. As can be seen in Figure 1, the proposed architecture consists of five stages, which are: data pre-processing, feature selection, classification or prediction, performance evaluation, and the results. The data is structured for the next processing phase in the pre-processing module.

Also, the dataset is cleaned by eliminating records with missing data for accurate results. Next, the dataset is partitioned into two sections: training and testing. All classifiers can create the prepared model utilizing training information. For better accuracy, this paper proposes a hybrid technique named "HEMLM". HEMLM combines MLP with random layering and LR techniques. This hybrid approach has better HD prediction accuracy algorithms than the current SVM, NB, and LR algorithms.

The HEMLM module is an additional module that is used for augmentation purposes. This module depends on a high-level extreme ML calculation that can improve expectation accuracy compared with all other measures. Extreme ML is a smart strategy for pattern classification. It is a single feed-forward NN with a single layer of hidden nodes in which the loads between the inputs and the hidden nodes are randomly assigned and kept constant during the training and anticipation phases. Payloads linking hidden nodes to gains can be prepared exceptionally quickly, despite general expectations. The pseudo-code for the overall system is given in Algorithm 1.

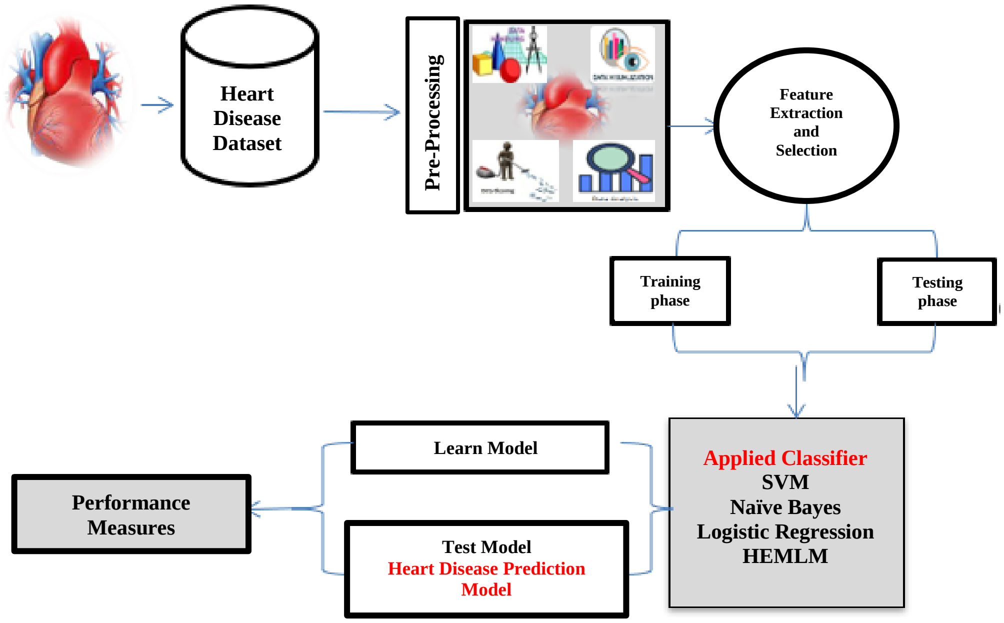

Figure 1. Structure of a hybrid extreme ML model

Algorithm 1. The pseudo code of the HEMLM

```
Input: training set and testing set
Output: classification/prediction accuracy
Start
 Data_Handeling and Cleaning ()
 Split (data)
    A_train, A_test,
    B_train, B_test.
    delete cleaning Processing
 Initialize LogisticRegression (LR) and HEMLM_acc
 Initialize MLP Layer
 I nitialize Gen HELM Classifier using log_rieg
 Fit (A-train, B-train)
 Performance Mesure _test model()
End
```

4. DATASET VISUALIZATION

To evaluate the proposed hybrid approach, we utilized the dataset referenced in [37], which comprises 76 attributes. After thorough analysis and trials, we determined that a subset of 14 attributes would be most effective for our study. The "goal" field within the dataset indicates the presence of HD in the patient, with values ranging from 0 (no disease) to 4 (severe HD). The specific attributes selected for analysis are: age, sex, chest pain (cp) type, resting blood pressure (trestbps), cholesterol level (chol), fasting blood sugar (fbs), resting electrocardiogram results (restecg), maximum heart rate achieved (thalach), exercise-induced angina (exang), ST depression induced by exercise relative to rest (oldpeak), slope of the peak exercise ST segment (slope), number of major vessels colored by fluoroscopy (ca), thalassemia (thal), and the diagnosis of HD (num).

The selection of these 14 attributes was based on their significant statistical relevance and direct connection to the diagnosis and progression of HD. These attributes were chosen because they represent the most critical factors known to influence cardiovascular health. Demographic factors such as age and sex are well-established predictors of HD risk. Clinical measurements like cholesterol level, resting blood pressure, and maximum heart rate are key indicators of cardiovascular function. Additionally, attributes like cp type and fbs provide essential insights into the patient's condition, contributing to a more comprehensive risk assessment. By focusing on these 14 attributes, the model achieves a balance between accuracy and computational efficiency, ensuring robust and timely predictions.

To provide a clearer understanding of the dataset, Figures 2 through 9 visually represent its key characteristics:

- Figure 2 shows that the dataset contains more records of patients with HD than without.

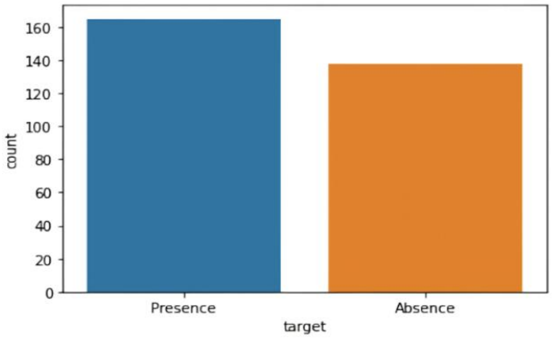

Figure 2. HD presence vs absence

- Figure 3 indicates that individuals aged between 40 and 60 have a higher likelihood of developing HD compared to other age groups, while Figure 4 compares the incidence of HD between males and females, revealing that while more females in the dataset have the disease, the overall count of males is higher.

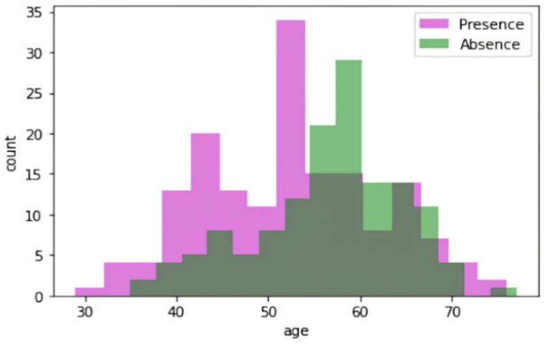

Figure 3. Age vs disease

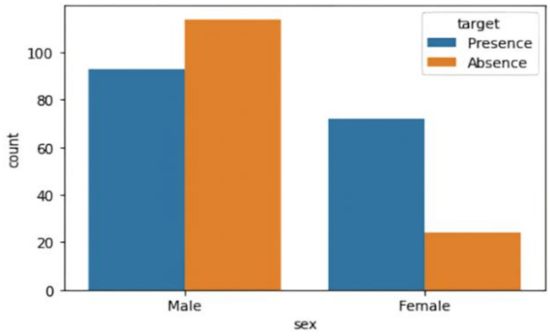

Figure 4. Chance of HD in male's vs females

- Figure 5 demonstrates that resting blood pressure levels are similar regardless of the presence or absence of disease, while Figure 6 highlights that serum cholesterol levels between 200 and 380 mg/dL are associated with a higher risk of HD.

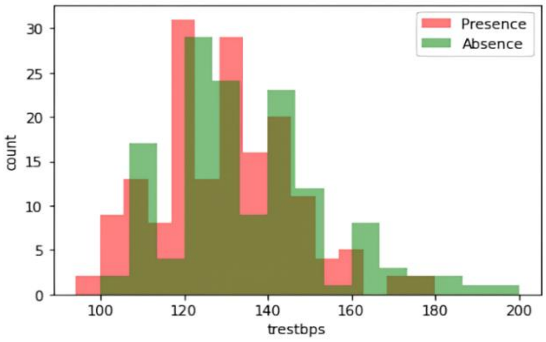

Figure 5. Resting blood pressure

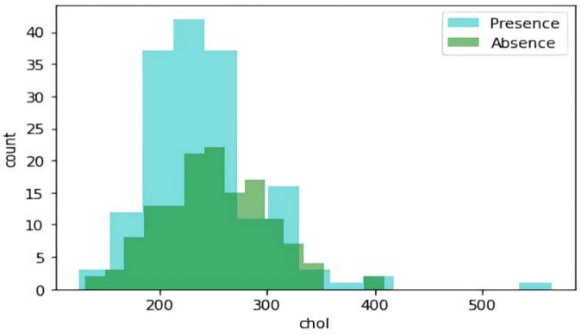

Figure 6. Serum cholesterol levels between 200 to 380 mg/dl

- Figure 7 shows that a maximum heart rate of 150 to 180 is linked to an increased risk of HD.
- Figure 8 presents the major vessels as visualized by fluoroscopy, indicating potential risk areas.

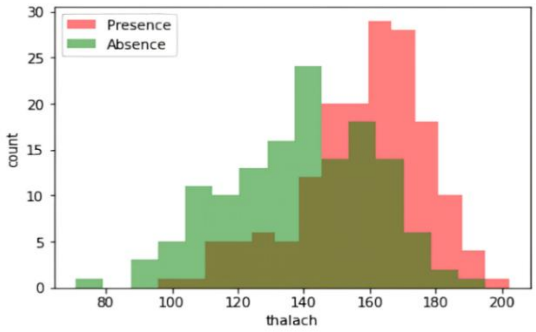

Figure 7. Maximum heart rate range between 150 to 180

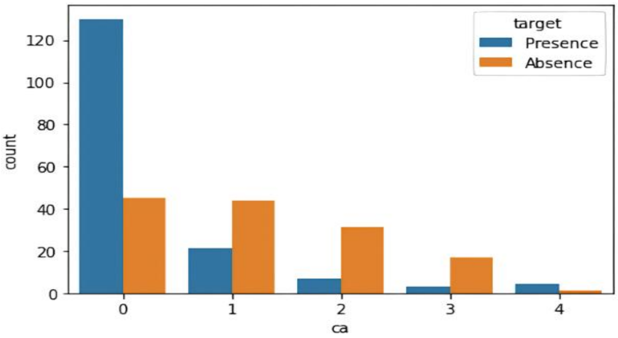

Figure 8. Less number of major vessels colored by fluoroscopy

- Finally, Figure 9 maps the relationships between multiple variables, allowing for a comprehensive analysis of how these factors interact. Each variable in the dataset is assigned its own axis, facilitating clear visualization even when units of measurement differ. By reordering the axes, deeper insights can be gained, particularly regarding attributes like sex, slope, ca, and thal, which exhibit less variability. This approach reduces clutter and enhances the clarity of the data, especially when mapping the presence or absence of HD.

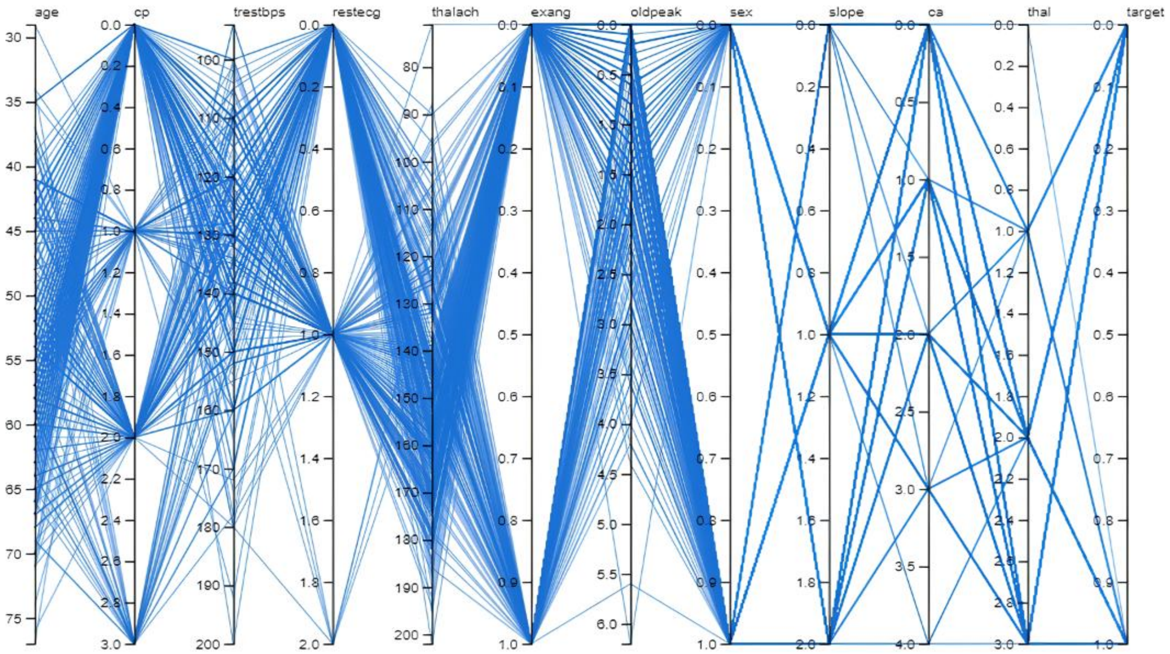

Figure 9. Parallel coordinates plot for dataset

5. PERFORMANCE EVALUATION AND DISCUSSIONS

5.1. Performance evaluation criteria

In the present work, for performance evaluation, we have considered the following criteria [30]-[33]:

Accuracy: it is how close an action's esteem is to genuine worth as in (1):

$$Accuracy = \frac{Number\_of\_correct\_predictions}{Total\_number\_of\_predictions} \quad (1)$$

Precision: it is how close measure esteems to one another as in (2):

$$Precision = \frac{True\_Positives}{True\_Positives+False\_Positives} \tag{2}$$

where, true positive is an outcome where the model correctly predicts the positive class and false positive is an outcome where the model incorrectly predicts the positive class.
Recall: it is a metric that evaluates the number of positive forecasts made from all positive expectations as in (3):

$$Recall = \frac{True\_Positive}{True\_Positive+False\_Negative} \tag{3}$$

False negative: it is an outcome where the model incorrectly predicts the negative class. F1-score: it is the weighted average of precision and recall as in (4):

$$F1 - score = 2 * \frac{Precision * Recall}{Precision + Recall} \tag{4}$$

Support: it is the number of true class events in the predetermined dataset.

5.2. Experimental results

We have explained in detail the experimental results acquired. Our focus is on the accuracy of the disease prediction by the various existing approaches and the proposed HEMLM method. Table 1 presents the gained results with the data spit ratio as 85:15. The training set size is chosen to be 257, and 46 is chosen as the testing set size. It is important to look first at the accuracy of the used algorithms. As can be seen in Table 1, the accuracy in the cases of SVM, NB, LR, and HEMLM are 71.73, 78.26, 76.08, and 94.91, respectively. These results are clarified in Figure 10, where the accuracy of all algorithms is depicted for clarity. This indicates that the proposed model overcomes the reset of the algorithms in terms of accuracy. At the same time, looking at other measurements, it seems that HEMLM is stable and within the range of other algorithms.

Table 1. Results with an 85:15 data split

Model	Target	Precision	Recall	F1-score	Support	Accuracy
SVM	0	0.86	0.52	0.65	23	71.73
	1	0.66	0.91	0.76	23	
NB	0	0.81	0.74	0.77	23	78.26
	1	0.76	0.83	0.79	23	
LR	0	0.8	0.7	0.74	23	76.08
	1	0.73	0.83	0.78	23	
Proposed HEMLM	0	0.74	0.74	0.74	23	94.91
	1	0.74	0.74	0.74	23	

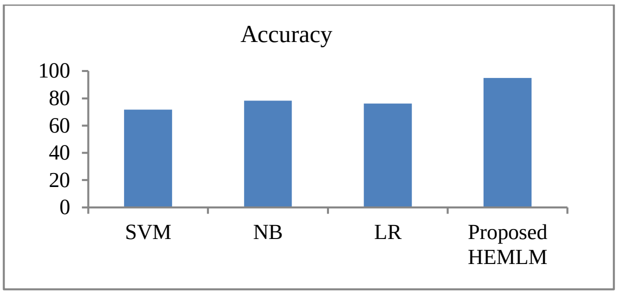

Figure 10. Accuracy plot for 85:15 data split

Another set of experiments is conducted by utilizing the data spitting ratio of 80:20 with a training set size of 242 and a testing set size of 61. The overall accuracy for both targets 0 and 1 is given in Table 2 and plotted in Figure 11. The figure shows that the accuracy seems to increase with the algorithms in the following sequence: SVM, NB, LR, and HEMLM. It turns out to be 70.49, 77.05, 72.13, and 94.77 for SVM, NB, LR, and HEMLM, respectively. Once more, the accuracy of HEMLM reached 94.77%, which is the largest among the other algorithms. Other parameters, such as precision, are much better in target 1 using HEMLM; however, other parameters seem close to the other algorithms' results with some variations.

Table 2. Results with an 80:20 data split

Model	Target	Precision	Recall	F1-score	Support	Accuracy
SVM	0	0.74	0.52	0.61	27	70.49
	1	0.69	0.85	0.76	34	
NB	0	0.76	0.7	0.73	27	77.05
	1	0.78	0.82	0.8	34	
LR	0	0.71	0.63	0.67	27	72.13
	1	0.73	0.79	0.76	34	
Proposed HEMLM	0	0.68	0.78	0.72	27	94.77
	1	0.8	0.71	0.75	34	

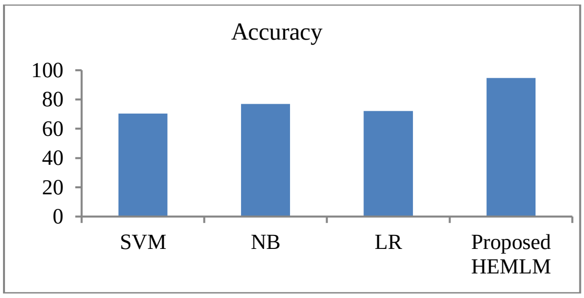

Figure 11. Accuracy plot for 80:20 data split

Another set of experiments is conducted with different dataset partitions for more performance examination. Here, the data spitting ratio of 70:30 is used in this set of experiments, with a training set size of 212 and a testing set size of 91. Again, as accuracy is considered the main performance measure, it has been plotted in Figure 12 and listed in Table 3. As can be seen, HEMLM gives the best accuracy measure with an average of 92.42. On the other hand, other parameters vary with the algorithms; however, the support seems to be the same for all algorithms.

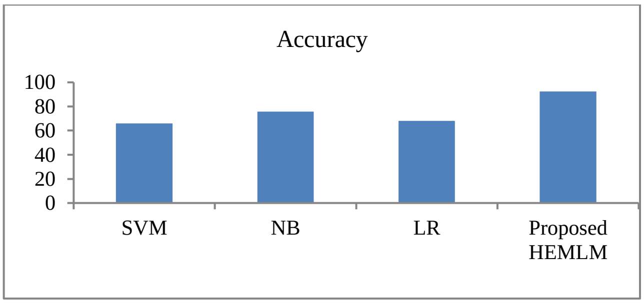

Figure 12. Accuracy plot for 70:30 data split

Table 3. Results with a 70:30 data split

Model	Target	Precision	Recall	F1-score	Support	Accuracy
SVM	0	0.74	0.45	0.56	44	65.93
	1	0.62	0.85	0.72	47	
NB	0	0.82	0.64	0.72	44	75.82
	1	0.72	0.87	0.79	47	
LR	0	0.74	0.52	0.61	44	68.13
	1	0.65	0.83	0.73	47	
Proposed HEMLM	0	0.69	0.75	0.72	44	92.42
	1	0.74	0.68	0.71	47	

Another set of experiments is conducted with different dataset partitions for more performance examination. Here, the data spitting ratio of 60:40 is used in this set of experiments, with a training set size of 181 and a testing set size of 122. Again, as accuracy is considered the main performance measure, it has been plotted in Figure 13 and listed in Table 4. As can be seen, HEMLM gives the best accuracy measure with an average of 87.14. On the other hand, other parameters vary with the algorithms; however, the support seems to be the same for all algorithms.

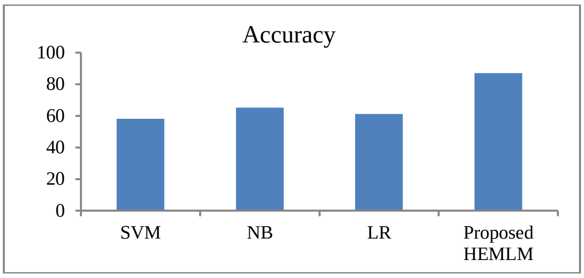

Figure 13. Accuracy plot for 60:40 data split

Table 4. Results with a 60:40 data split

Model	Target	Precision	Recall	F1-score	Support	Accuracy
SVM	0	0.61	0.34	0.44	58	58.19
	1	0.57	0.8	0.67	64	
NB	0	0.65	0.57	0.61	58	65.28
	1	0.65	0.72	0.68	64	
LR	0	0.68	0.6	0.62	58	61.16
	1	0.63	0.72	0.69	64	
Proposed HEMLM	0	0.62	0.71	0.68	58	87.14
	1	0.7	0.65	0.67	64	

For more verifications, different model is implemented and compared in terms of accuracy to the proposed model, HEMLM. Algorithms such as HRLFM [18], HDPS [27], ELM-based NN [38], genetic NN based DM [23] and ELM [21] were proposed for the same purpose. Therefore, they are selected to be compared with SSML. The accuracy results are depicted in Table 5 and Figure 14, with the dataset division as 85:15. As shown in the table, HEMLM outperforms these approaches by an average of 6%. For instance, genetic NN-based DM accuracy is 89%, while HEMLM accuracy is 94.91%. Other algorithms are less accurate than the genetic NN-based DM algorithm.

Table 5. Comparative analysis

Reference	Model	Accuracy (%)
Reddy *et al.* [18]	HRLFM	88.70
Ismaeel *et al.* [21]	ELM	80
Amin *et al.* [23]	Genetic NN based DM	89
Chen *et al.* [27]	HDPS	80
Fathurachman *et al.* [38]	ELM based NN	88
Proposed HEMLM		94.91

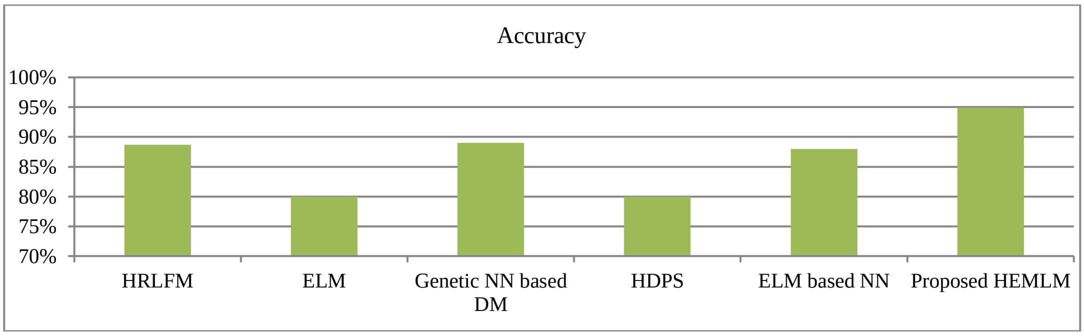

Figure 14. Comparison of accuracy level (%) for existing models vs proposed model

The proposed algorithm has high accuracy compared to other algorithms, but in terms of F1-score, it performs poorly. This factor can be explained. In this paper, the accuracy paradox and problems related to class imbalance are recognized as when classification accuracy alone cannot be trusted to determine whether a model or performance is good or not due to the small size of the data set. Through the experiments in this paper, we are introduced to the confusion matrix as a method for describing breakdown errors in predictions for an unseen dataset. Learn measures summarize the precision (exactness) and recall (completeness) of a model and a description of the balance between them in the F1-score.

6. CONCLUSION

The acceptance and management of HD in a medical environment are both challenging and essential. Understanding the clinical aspects of HD is crucial for early detection and intervention, which can significantly impact patient outcomes. ML techniques have provided valuable insights into HD by analyzing complex datasets and identifying key risk factors. However, the true potential of these techniques can only be realized when applied in real-world settings, such as hospitals and clinics.

To make this research applicable, it is important to outline how the HEMLM can be integrated into clinical workflows. The high accuracy demonstrated by the HEMLM method, which combines MLP with random layer and LR, suggests that it could be a powerful tool for early HD detection and prevention. For successful implementation, healthcare teams would need to incorporate specific tools and technologies, such as data integration platforms, patient monitoring systems, and decision support software, to seamlessly integrate this model into routine medical practice.

Additionally, expanding this research to include real-world datasets would provide more robust validation and help tailor the model to diverse patient populations. Future work could focus on refining the model by incorporating bio-inspired approaches for feature selection and exploring more advanced ML techniques to further enhance prediction accuracy. By bridging the gap between theoretical research and practical application, the HEMLM model could play a pivotal role in reducing the mortality rate associated with HD.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

No conflict of interest.

INFORMED CONSENT

We have obtained informed consent from all individuals included in this study.

DATA AVAILABILITY

The datasets used and/or analyzed during the current study are available from the corresponding author Abdelmoty M. Ahmed, (email: abd2005moty@yahoo.com) on reasonable request.

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