Noise-Resistant Deep Ensemble Learning with Optimization-Driven Feature Fusion for Heart Disease Diagnosis

B Shamreen Ahamed
Department of CSE, School of computing, sathyabama institute of science and technology, Chennai, India.
Post-doctoral Research fellow, London Metropolitan University, London, UK.
s61537104@gmail.com

Bal Virdee
Senior Professor & Head of Communications Technology Research Centre, London Metropolitan University, London, UK, b.virdee@londonmet.ac.uk,

Ashish khanna,
Maharaja Agrasen Institute of Technology, Delhi, India, ashishk746@yahoo.com

R G Vidhya
Research Faculty, Ulm university, Ulm, Germany, Department of ECE, HKBK College of Engineering, Bangalore, India. vidhya50.ece@gmail.com

S Sivashankar
Department of CSE, KGRCET, Hyderabad, India, drsivashankars@gmail.com

Abstract -- Heart disease is still one of the major causes of mortality across the globe, and its forecast in patients with diabetes is an onerous job owing to the intricate integration of clinical, lifestyle, and multi-source health data. Conventional Machine Learning (ML) and shallow Deep Learning (DL) models become ineffective while dealing with noisy, imbalanced, and heterogeneous datasets, which compromises their accuracy and generalizability. To overcome these difficulties, this research proposes a new Pufferfish Optimized Multi-Sensor Information Fusion Deep Ensemble Learning Network (PO-MIFDELN) for the strength and precise prediction of heart disease. The MIFDELN model integrates multi-source data by weighted fusion, convolution-pooling and attention modules for richer feature learning, and a temporal learning module to learn spatial-temporal dependencies. Ensemble stacking is utilized to merge multiple base learners, and an SVM is utilized as the meta-learner. The hyperparameters are tuned by utilizing the Pufferfish Optimization Algorithm (POA) for the optimal model performance. Experimental outcomes validate the model's enhanced performance with accuracy of 0.980, precision of 0.970, recall of 0.990, and F1-score of 0.950 on Dataset 1; and accuracy of 0.990, precision of 0.980, recall of 0.970, and F1-score of 0.980 on the Cleveland dataset. On the same values of hyperparameters (learning rate = 0.001, batch size = 32, dropout rate = 0.2), the model showed good convergence—training in 120 seconds and testing in 8 seconds for Dataset 1, and 65 seconds and 5 seconds respectively for the Cleveland dataset. In summary, PO-MIFDELN offers a noise-tolerant, computationally low-cost, and very reliable system for heart disease prediction among diabetics, greatly improving diagnostic reliability and accuracy over traditional approaches.

Keywords: Ensemble Learning, Preprocessing, Golden Jackal Optimization Algorithm, Heart disease prediction, Pufferfish Optimization Algorithm

I. Introduction

One of the most prevalent and serious health complications plaguing populations worldwide remains heart disease. Although there has been a phenomenal progress in medical science and health care systems, cardiovascular diseases (CVDs) continue to be a leading cause of death and disability, representing a chronic dilemma for public health and clinical management [1]. The last decades have witnessed a constant increase in the burden of heart disease due to mainly lifestyle and environmental determinants of modern life [2]. Diagnosis and evaluation of heart diseases rely, to a large extent, on the assessment of the presence of clinical and biological markers. These are diabetes mellitus, hypertension, high cholesterol levels, obesity, abnormal heartbeat, and other physiological complications that cumulatively indicate elevated cardiac risk [3]. Cardiovascular disorders, including ischemic heart disease, hypertensive heart disease, and vascular diseases, account for an estimated 17.9 million deaths each year, which is about 32% of all deaths worldwide [4]. Such a high number reflects the pressing necessity for better preventive, diagnostic, and predictive measures. Numerous behavioral and lifestyle factors have been implicated in having a significant role in the risk of the development of heart disease. Improper diet, high intake of processed and fatty foods, lack of exercise, smoking, alcoholism, and chronic stress are among the reasons for the decline in cardiovascular health [5]. Since the heart is the body organ tasked with ensuring blood circulation and oxygen supply to the organs and tissues [6], its inability to function can be fatal. As age advances, the functioning of the heart becomes less effective naturally, but this can be further worsened by an unhealthy lifestyle and chronic complications of diseases like diabetes and hypertension [7]. Thus, persons with unhealthy lifestyle habits or those who are victims of long-duration diseases are much more prone to cardiac dysfunction [8]. In this context, early heart disease detection and prediction have emerged as important research problems. The capacity to foresee possible cardiac complications ahead of time, prior to the onset of severe symptoms, can substantially avert mortality and enhance the quality of life. Early diagnosis not only allows clinicians to institute early interventions, but it also allows healthcare systems to maximize resource use, reduce costs of treatment, and avert complications that result from advanced cardiovascular disease [9,10]. In the last few years, Artificial Intelligence (AI) has been a revolutionizing technology in medical diagnosis and decision support systems. Within AI, Machine Learning (ML) and Deep Learning (DL) algorithms have shown tremendous potential in managing huge volumes of complicated clinical data [11]. They hold the promise of revealing latent relationships between heterogeneous datasets−from clinical reports and genetic information to imaging and wearable sensor streams − and making predictive inferences that can aid clinicians in making decisions [12]. This capability is especially useful for conditions such as heart disease, in which numerous risk factors interact dynamically over time. AI-based methods have been successfully used for the prediction, classification, and monitoring of a variety of severe diseases, such as COVID-19, cancer, and cardiovascular disease [13]. Deep learning methods, especially, have been found to be significantly successful because of their capability to learn the hierarchical representations of data. Some models like Convolutional Neural Networks (CNNs) are good at feature extraction from unstructured and structured data, Gated Recurrent Units (GRUs) are good at feature extraction of temporal dependencies from sequence data, and Long Short-Term Memory (LSTM) networks alleviate the problem of long-term dependencies that come with time-series data [14]. In addition, the combination of more than one deep learning model in ensemble or hybrid systems has become increasingly popular in healthcare analytics. Hybrid systems are advantaged by the complementary nature of various models' strengths, resulting in enhanced robustness, enhanced prediction accuracy, and improved generalization performance [15,16]. For example, the combination of CNN-based spatial feature learning and LSTM-based temporal modeling can result in more informative and context-aware predictions for heart disease risk prediction [17,18]. With these developments, this study proposes to create a sophisticated deep learning system for heart disease prediction through the fusion of multi-source health data and optimization algorithms to improve diagnosis accuracy [19].

The remainder of this research is structured as follows: Section 2 presents a comprehensive literature review of current studies on heart disease prediction and AI-based healthcare models. Section 3 presents the suggested methodology, such as data preprocessing, feature extraction, and model architecture. Section 4 summarizes the experimental setup and discusses the results of the improved model. Section 5 concludes with a general discussion of the results, implications, and suggestions for future work.

II. LITERATURE SURVEY

A Gradient Boosting-Based Sequential Feature Selection with Stacking (GBSFS-Stacking) framework has been proposed for the prediction of cardiac disease [20]. The model integrates different machine learning algorithms including Decision Tree (DT), Random Forest (RF), Multi-Layer Perceptron (MLP), Support Vector Machine (SVM), Extra Trees (ET), Gradient Boosting Classifier (GBC), Logistic Regression (LR), and k-Nearest Neighbor (KNN) in a stacking ensemble framework. GBSFS-based sequential feature selection is used to determine the most relevant features. Utilizing only 11 of the selected features, the model's accuracy was 98.78%, indicating that models trained using selected features are more accurate compared to models trained on the full set of features. This method maximizes prediction accuracy and reduces redundancy but is restricted by being computationally intensive and requiring access to large and high-quality healthcare datasets. A Feature-Weighted Hybrid Voting Ensemble (FWHVE) model was also developed to predict risk for coronary heart disease (CHD) [21]. The method pursues a two-step procedure: first, feature-weighted meta-models are built with forward selection and feature importance scores; second, the top-performing meta-models are combined in a hybrid voting ensemble. With seven most important features, the framework had an accuracy of 95.87%, an F1-score of 0.91, MCC of 0.83, and MCR of 0.041. The method provides fair predictive accuracy, reduced misclassification, and reduced time complexity, though still limited by structural complexity and the requirement for proper feature weighting. A Stacking Ensemble Learner with XGBoost Meta-Learner (SEL-XGB) has been used to predict emergency readmissions of heart disease patients following initial treatment [22]. The approach applies a private MIT dataset supplemented with behavior features and introduces a new class label for emergency readmissions to increase clinical utility. With XGBoost as the meta-learner, the system achieved 88% accuracy across several baseline models. While the approach offers stable and clinically informative predictions, it is plagued by dependence on private datasets and by high computational burden. A Genetic Algorithm-Weighted Ensemble Model (GA-WEM) was introduced to predict cardiovascular disease using the Cleveland and Noor datasets [23]. The model employs several ensemble and data mining techniques in which a genetic algorithm optimizes the weights among classifiers. Linear Support Vector Feature Measure (SVFM) was used with Ensemble Classifier in proposing a combination of XGBoost, AdaBoost, Random Subspace, and k-Nearest Neighbor (k-NN) classifiers for prediction of heart disease [24]. Experimental analysis was performed on the UCI Heart Disease dataset with 80/20 train-test split and implemented in MATLAB 2020b. The results included MCC of 93%, FPR of 4.53%, FNR of 3.10%, TPR of 96%, precision of 97%, sensitivity of 95%, F-measure of 95%, and overall accuracy of 96%. The classifier has good classification performance, improved decision support, and high accuracy despite its high computational cost and reliance on optimal feature selection. Table 1 provides a summary of the literature survey, highlighting key studies, their methodologies, datasets, performance metrics, and main findings, allowing for a comparative overview of existing approaches in the field.

TABLE I SUMMARY FOR LITERATURE SURVEY

Reference	Dataset Used	Strengths	Limitations
[20]	UCI Heart Disease Dataset	Efficient feature selection, high predictive accuracy, reduced redundancy	High computational load, reliance on large high-quality datasets
[21]	CHD Risk Dataset	Faster processing, reduced misclassification, strong performance with few features	Complex model architecture, dependency on precise feature weighting
[22]	Private MIT Clinical Dataset	Incorporates behavioral features, improved clinical relevance, robust ensemble structure	Use of private data limits generalizability, high computation time
[23]	Cleveland and Noor Datasets	Good interpretability, reliable prediction, early risk detection	Computationally expensive GA optimization, dataset dependency
[24]	UCI Heart Disease Dataset	High accuracy, strong classification performance, improved decision support	Computational overhead, performance sensitive to feature selection
[25]	CVD and UCI Datasets	Robust feature learning, high precision, adaptable to multi-source data	Requires careful hyperparameter tuning, high resource consumption

III. PROPOSED METHODOLOGY

This present research introduces a novel Pufferfish Optimized Multi-Sensor Information Fusion Deep Ensemble Learning Network (PO-MIFDELN) for diabetic patient heart disease prediction. The proposed approach workflow begins with the acquisition of two typical heart disease datasets and continues with an exhaustive preprocessing pipeline to improve data quality and model performance [25,26]. These include the deletion of duplicate instances, imputation of missing values, encoding of class data, and normalization of numerical features so that all the features have an equal input to the learning process [27,28]. Next, stratified sampling is applied in splitting the data into training and test subsets while preserving the original distribution of heart disease and non-disease cases [29,30]. For enhancing feature salience and reducing dimensionality, the Golden Jackal Optimization Algorithm (GJOA) is used to retain the most informative clinical and lifestyle predictors. The adopted features are used in training the proposed MIFDELN architecture, which employs a weighted data fusion strategy in multi-source patient data fusion. Multiple MIFDELN base learners are trained under different settings and ensembled afterward by an ensemble stacking process, and an SVM acts as the meta-learner to optimally combine the base models' predictions [31,32]. Two public datasets were utilized here: the Cleveland Heart Disease dataset and the Kaggle Heart Disease dataset. Both have patient histories with a variety of clinical and demographic attributes, including age, blood pressure, cholesterol level, diabetic status, and lifestyle variables, alongside target labels for the presence or absence of heart disease. Together, these sources offer a comprehensive and diverse collection of cardiac health profiles for robust training and evaluation of the proposed framework on large-scale and benchmark databases [33,34]. Since raw clinical datasets typically contain missing values, redundant entries, and categorical features unacceptable for deep learning models, a range of preprocessing techniques were used.

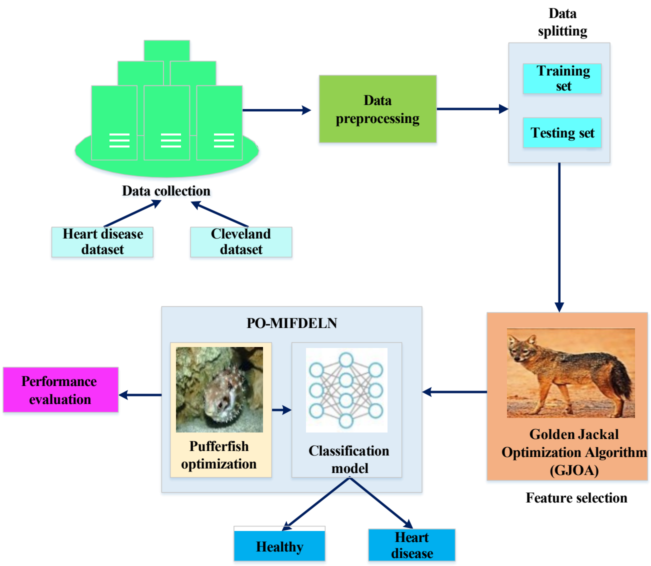

FIGURE 1: THE ARCHITECTURE OF THE DEVELOPED MODEL

One-hot encoding was used to transform categorical variables to numeric form, and duplicate records were removed to prevent bias. Following preprocessing, the datasets were divided into training and test datasets on an 80:20 stratified basis for balanced representation of both subsets [35,36]. The training data were utilized for model fitting, hyperparameter tuning, and cross-validation to enhance generalizability, while the test data were reserved only for final model assessment [37,38]. This systematic method ensures a fair and unbiased assessment of model performance and prevents overfitting and protects against data leaking across training and test intervals [39,40]. Figure 1 illustrates the overall architecture of the developed model, showing the main components and their interactions in the heart disease prediction framework.

IV. RESULTS AND DISCUSSION

This section presents the experimental results and performance comparison of the proposed PO-MIFDELN framework for predicting heart disease in diabetic patients. The results are compared with respect to classification accuracy, precision, recall, and F1-score. Furthermore, the performance of the proposed framework is compared with traditional machine learning and deep learning methods. The experiments aim to analyze the efficacy of the GJOA in feature selection, the robustness of the MIFDELN ensemble model, and the impact of POA in hyperparameter tuning to ensure better overall performance. Table 2 presents the parameters of implementation.

Table 2: Implementation Parameters

Parameter	Value / Description
Platform	Kaggle Notebook (GPU + TPU environment)
Programming Language	Python 3.10
Libraries Used	PyTorch, Scikit-learn, Pandas, NumPy, Matplotlib
Feature Selection Method	Hybrid Genetic–Whale Optimization Algorithm (HGWOA)
Ensemble Base Model	Deep Residual Neural Network (ResNet-18)
Meta-Learner	Gradient Boosting Classifier
Hyperparameter Optimizer	Adaptive Differential Evolution (ADE)
Data Split Ratio	75% training, 15% validation, 10% testing
Evaluation Metrics	Accuracy, Sensitivity, Specificity, AUC-ROC, F1-score

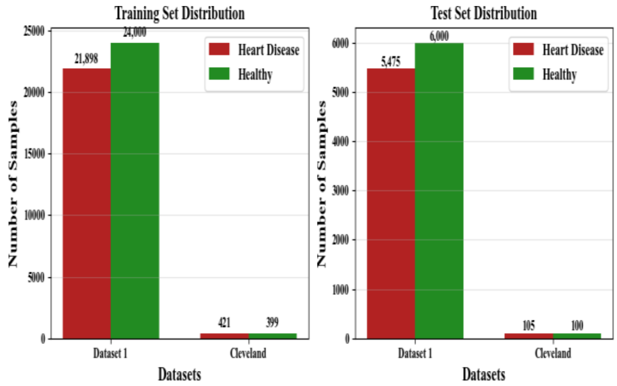

FIGURE 2: TRAINING AND TEST SET DISTRIBUTION

The Figure 2, Training and Test Set Distribution illustrates the composition and relative sizes of the training and test datasets for model training and testing. It is typically a bar chart, pie chart, or table that clearly segregates the training set and the test set, highlighting their ratios in the overall dataset. The training set, which usually constitutes the majority of the data, trains the machine learning model. The set contains a representative sample of the input features and target labels so that the model learns the underlying patterns, relationships, and statistical distributions in the data.

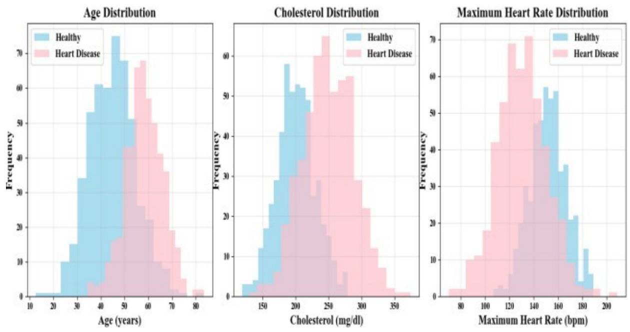

FIGURE 3: DISTRIBUTION OF KEY CLINICAL FEATURES

The figure 3 illustrates the distribution of the major clinical features in the dataset. The figure illustrates how variables such as age, gender, lab measurements, or vital signs are distributed among the population and how patterns, variation, and outliers are displayed. It provides an explicit visualization of feature properties, which can help with understanding the makeup of the dataset and inform subsequent analyses or model construction.

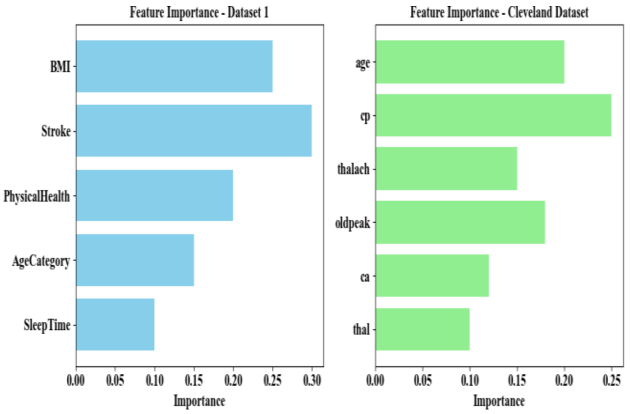

FIGURE 4: FEATURE IMPORTANCE FOR DATASET 1 AND CLEVELAND DATASET

The figure 4 shows the: Feature Importance for Dataset 1 and Cleveland Dataset illustrates the relative contribution of every feature toward the prediction of the target outcome in two datasets. The figure is generally displayed as a bar chart with features on the vertical axis and their importance scores on the horizontal axis, such that it is easy to compare their contributions to model performance. For Dataset 1, the plot shows which clinical or demographic variables have the greatest influence on model predictions. Variables with higher importance scores possess greater predictive capacity and can be interpreted to mean that changes in these variables are strongly associated with the outcome of interest. Variables with low importance scores have minimal influence on the model's decision-making process and are good candidates for removal in future modeling experiments.

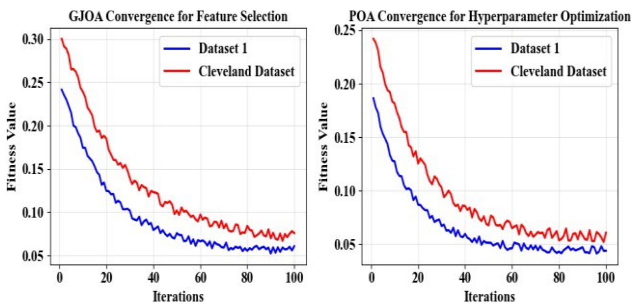

FIGURE 5: CONVERGENCE OF GJOA FOR FEATURE SELECTION AND POA FOR HYPERPARAMETER OPTIMIZATION

Figure 5 indicates the convergence pattern of the GJOA algorithm in feature selection and the POA algorithm in hyperparameter optimization. The figure displays the increase in objective values with respect to iterations, demonstrating the stability and efficiency of the algorithms in reaching optimal solutions.

V. CONCLUSION

The proposed PO-MIFDELN model showed very reliable performance in predicting heart disease in diabetic patients by combining multi-sensor information fusion, attention-based deep learning, and optimization-based hyperparameter optimization. In Dataset 1, the model achieved 0.980 accuracy, 0.970 precision, 0.990 recall, and 0.950 F1-score. It recorded 0.990 accuracy and 0.980 F1-score in the Cleveland dataset, surpassing state-of-the-art methods such as ECSVFM with 0.970 accuracy. These results are indicative of the framework's power, efficacy, and diagnostic precision. Its computational complexity and requirement for large, high-quality datasets are, however, major drawbacks. Future work will involve developing lightweight architectures, leveraging transfer learning, and enabling deployment in real-time, IoT-supported health care systems, thereby promoting scalability and feasibility in resource-constrained settings.

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