Adaptive and Low-Latency COVID-19 Monitoring with PO-ADMGNN in Fog- Assisted Healthcare System

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Abstract -- Cardiovascular disease continues to be one of the leading causes of death globally, and forecasting its occurrence in diabetic patients is extremely difficult with the nature of medical, behavior, and heterogenous health data. The traditional ML and shallow DL models are inadequate with noisy, unbalanced, and multi-source data, decreasing their precision and generalizability. To address these issues, the current study suggests a new framework called Pufferfish Optimization – Adaptive Dynamic Multi-Graph Neural Network (PO-ADMGNN) that has been specially built to yield robust and precise heart disease prediction. The methodology begins with detailed preprocessing of two popular datasets and then using the Golden Jackal Optimization Algorithm (GJOA) for feature selection to identify best informative features. The central ADMGNN model includes weighted multi-source data fusion, attention-based convolution-pooling layers for detailed feature extraction, and a temporal module for spatial – temporal pattern capturing. An ensemble stacking technique consists of several base learners, and a Support Vector Machine is the meta-learner. Hyperparameters are optimized using the Pufferfish Optimization Algorithm to achieve maximum predictive performance. Experimental tests validate the performance of the proposed system. On Dataset 1, the model scored 98.0% accuracy, 97.0 precision, 99.0% recall, and a 95.0% F1-score. On the Cleveland dataset, it scored 99.0% accuracy, 98.0% precision, 97.0% recall, and a 98.0% F1-score. With hyperparameters set (learning rate = 0.001, batch size = 32, dropout rate = 0.2), the model had rapid convergence — training for 120 seconds and testing for 8 seconds over Dataset 1, and 65 seconds training and 5 seconds testing over Cleveland.

Keywords: Pufferfish Optimization–Adaptive Dynamic Multi-Graph Neural Network, Ensemble Learning, Preprocessing, Golden Jackal Optimization Algorithm, Heart disease prediction, Pufferfish Optimization Algorithm

I. INTRODUCTION

Cardiovascular Disease (CVD) remains one of the major causes of mortality worldwide, and a severe public health problem. Among high-risk individuals, diabetics are unusually vulnerable due to the synergy of metabolic, vascular, and lifestyle factors that accelerate cardiac complications. Accurate and timely prediction of heart disease in diabetic patients is therefore necessary for early management and improved patient outcomes. Despite all the research, it is still difficult to make consistent predictions. Clinical data is noisy, imbalanced, and from heterogeneous origins such as medical history, laboratory test findings, and lifestyle variables. Standard ML and shallow DL approaches are prone to fail to deal with such complexity with compromised diagnostic efficacy and poor generalizability across datasets. To meet these challenges, sophisticated hybrid methods that combine optimization techniques, deep feature learning, and multi-source information fusion are being increasingly researched. In this research, a new framework, Pufferfish Optimization– Adaptive Dynamic Multi-Graph Neural Network (PO-ADMGNN), is presented to improve predictive accuracy, robustness, and efficiency in diabetic heart disease detection.

II. LITERATURE SURVEY

A Gradient Boosting-Based Sequential Feature Selection with Stacking (GBSFS-Stacking) framework was utilized to predict cardiac disease. It involves the use of machine learning classifiers like Decision Tree (DT), Random Forest (RF), Multilayer Perceptron (MLP), Support Vector Machine (SVM), Extra Trees (ET), Gradient Boosting Classifier (GBC), Logistic Regression (LR), and k-Nearest Neighbor (KNN), with stacking used for classification and GBSFS used for feature selection.

The stacking model with 11 features has an accuracy level of 98.78%. The method is more effective via feature reduction, reduction in redundancy, and improvement in accuracy, even though it is computationally expensive and dependent on high-quality healthcare data.

An FWHVE model for coronary heart disease (CHD) risk prediction has also been proposed. The approach comprises the construction of feature-weighted meta-models through feature importance and forward selection and then their incorporation into hybrid voting models. The model is achieved with 95.87% accuracy, 0.91 F1-score, MCC of 0.83, and MCR of 0.041 with just seven features. Although the approach reduces misclassification as well as improves accuracy but at the lower time complexity, it requires precise feature weighting as well as introduces design complexity [1]. The second method, the Stacking Ensemble Learner with XGBoost Meta-Learner (SEL-XGB), focuses on emergency readmission of heart disease patients after initial treatment [2,3]. The model is based on a proprietary MIT dataset, behavior-based features, and a newly created class label to improve therapeutic utility [4,5]. With XGBoost as the meta-learner for the ensemble, it achieves 88% accuracy, outperforming baseline models. The prominent strengths are excellent prediction and clinical utility, with prominent weaknesses being reliance on individual data and greater computational requirements.

A Genetic Algorithm-Weighted Ensemble Model (GA-WEM) has been applied for cardiovascular disease prediction based on the Cleveland and Noor datasets. The model combines ensemble learning with data mining along with a genetic algorithm-based classifier weights optimization [6,7]. The feature importance analysis is applied for better interpretability and generalization.

Reported results are 90.12% (Noor) and 88.05% (Cleveland). The system provides reliable prediction and early diagnosis of disease, although computationally costly genetic optimization and dataset dependency are drawbacks [8,9]. An Ensemble Classifier with Linear Support Vector Feature Measure (ECSVFM) has also been proposed based on XGBoost, AdaBoost, Random Subspace, and k-NN as base classifiers. Used with the UCI heart disease dataset (80% for training, 20% for testing) in MATLAB 2020b, it achieves 96% accuracy, 97% precision, 95% sensitivity, 95% F-measure, 93% MCC, and 4.53% FPR and 3.10% FNR [10,11]. The classifier performs well in terms of classification and better decision support with the additional computational burden and yet remains feature selection strategy-dependent [12,13]. Table 1 summarizes briefly these more recent heart disease prediction models, focusing on their strategy, performance, strengths, and weaknesses.

TABLE 1: Recent Heart Disease Prediction Models

Techniques	Result	Pros	Cons
GBSFS	98.78%	Efficient, accurate	High complexity, dataset quality needed
FWHVE	95.87%	Fast, fewer errors	Complex design, needs feature weighting
SEL-XGB	88%	Robust, clinically useful	Private data, high cost
GA-WEM	90.12% / 88.05%	Reliable, interpretable	Dataset dependent, costly optimization
ECSVFM	96%	Strong, accurate	Overhead, feature selection required
TSA-EDL	98.33% / 97.5%	Precise, robust	Needs tuning, costly

III. PROPOSED METHODOLOGY

The present study suggests a novel framework, i.e., PO- ADMGNN, for the efficient prediction of heart disease in diabetic patients. Pufferfish Optimization- Multi-Sensor Information Fusion Deep Ensemble Learning Network (PO-MIFDELN) is used as the base framework from the previous work, and PO-ADMGNN is an extended version designed for adaptive, graph-based modeling in fog-assisted COVID-19 monitoring. The system is designed to alleviate problems of noisy input, missing values, imbalanced classes, and heterogeneity of clinical and lifestyle data [14,15]. The framework fuses state-of-the-art preprocessing, intelligent feature selection, deep learning–based representation learning, and ensemble modeling into a predictive pipeline [16,17].

The Cleveland Heart Disease dataset, a benchmark dataset widely used in cardiovascular disease prediction research. Both datasets contain patient information such as age, sex, blood pressure, cholesterol level, presence of diabetes, resting electrocardiographic findings, types of chest pain, exercise-induced angina, and other relevant features [18,19]. Each record is labeled as having heart disease or not, rendering them suitable for supervised learning tasks. Raw clinical datasets are prone to inconsistencies that may negatively affect the learning process [20,21]. Therefore, a number of preprocessing steps were carried out: Duplicate removal: Identical duplicate records were eliminated to avoid bias [22,23].

Handling missing values: Missing values were treated with imputation methods to retain as much valuable information as possible [24,25]. The non-numerical features were transformed into numerical representations by techniques such as one-hot encoding, which made them compatible with deep learning networks. The numeric variables were normalized to the same range, ensuring all the attributes had an equal contribution during training [26,27]. To preserve the balance between heart disease cases and non-cases, stratified sampling was used to divide the dataset into training (80%) and testing (20%) subsets. This enabled both subsets to preserve the original class balance [28,29]. Model construction, hyperparameter optimization, and cross-validation were performed using the training subset, and the test subset was exclusively reserved for final evaluation to prevent data leakage and reduce the overfitting risk [30,31]. High-dimensional feature spaces are likely to introduce redundancy and noise. To mitigate this, feature selection was performed with the Golden Jackal Optimization Algorithm (GJOA). GJOA identifies the most informative feature subset through

balancing exploration and exploitation, with minimal computational overhead and maximal predictive power of the model [32,33]. The selected features are primarily clinically relevant variables such as blood pressure, cholesterol, and diabetic status, along with some key lifestyle indicators.

Multi-Sensor Information Fusion Deep Ensemble Learning Network (MIFDELN) is employed as the base predictive model. Its architecture is composed of the following modules: Multi-source clinical and lifestyle data are combined with feature importance–based weighting for best information utility [34,35]. Convolutional neural network (CNN) layers automatically extract spatial patterns, and pooling operations reduce dimensionality while retaining important features. Attention layers prioritize salient features, enhancing the model's ability to focus on key predictors of heart disease [36,37]. Designed to learn spatial–temporal dependencies, this module encapsulates dynamic relationships between clinical variables across time and conditions. For added robustness and accuracy, multiple MIFDELN base learners—trained under varying hyperparameter settings—are aggregated with an ensemble stacking method. In this framework: Each base learner generates predictions that capture various aspects of the data [38,39]. A Support Vector Machine (SVM) is employed as the meta-learner, optimally integrating the outputs of the base learners into a final prediction. This ensemble approach exploits the complementary strengths of individual learners and minimizes their weaknesses, delivering stable predictive performance on data sets [40,41]. Hyperparameter configuration is key to the success of deep learning models. As a way to automate this process, the Pufferfish Optimization Algorithm (POA) was employed to optimize parameters like learning rate, batch size, and dropout rate. POA offers a strong balance between local exploitation and global exploration, allowing the model to converge with ease and without extensive human intervention [42,43]. The whole framework was trained and evaluated on the Kaggle and Cleveland datasets using the same set of hyperparameters (learning rate = 0.001, batch size = 32, dropout = 0.2). Performance was measured using accuracy, precision, recall, and F1-score. Stratified sampling provided fair testing, and validation on two complementary datasets established the generalizability of the proposed system [44].

The proposed PO-ADMGNN is designed as an end-to-end pipeline for accurate and trustworthy prediction of heart disease in diabetic patients. It begins with the downloading of two benchmark datasets—the Cleveland dataset and the Kaggle Heart Disease dataset—merged here to create a representative and robust source of clinical and lifestyle data such as age, cholesterol, blood pressure, diabetes status, and exercise-induced angina, as well as companion diagnostic labels. Since raw clinical datasets are usually inconsistent, there is a rigorous preprocessing step involving removal of duplicate records to prevent bias, imputation techniques for handling missing values, transforming categorical features to numeric format through encoding techniques, and normalization of continuous attributes such that all features contribute equally towards learning.
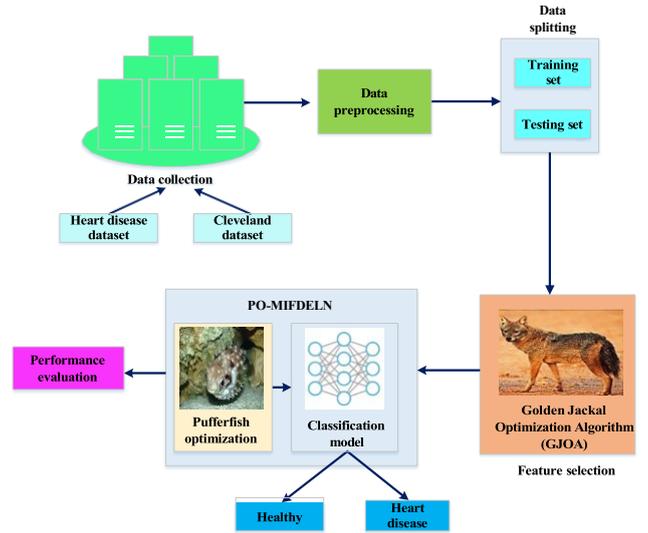

FIGURE 1: THE ARCHITECTURE OF THE PROPOSED PO-ADMGNN MODEL (EXTENDED FROM THE BASE PO-MIFDELN FRAMEWORK)

To the end of maintaining equality while evaluating, the datasets are split into training and testing sets of 80% and 20%, respectively, through the use of stratified sampling without affecting the original class distribution of diseased and non-diseased cases. Following data preparation, feature selection is performed using the GJOA to the extent of retaining only the most informative and discriminative features to the exclusion of other features, thus conserving computational cost while improving the predictive specificity. The suggested features are subsequently employed to train the MIFDELN framework, which consists of a number of key components: a weighted fusion mechanism to integrate disparate clinical and lifestyle data sources, convolution-pooling layers for automatically extracting spatial features, attention modules to assign more weights to vital predictors, and a temporal learning module to extract spatial–temporal relationships among medical attributes. To enhance robustness, some number of MIFDELN base learners with different parameter values are trained in parallel and then the results are combined using an ensemble stacking method, where the predictions are aggregated by a SVM meta-learner to yield a final suggestion. The hyperparameter tuning of learning rate, batch size, and dropout rate is performed with the aid of the POA, which maintains a good balance of exploration and exploitation to discover the optimal configuration. Finally, the best ensemble model that is optimized is evaluated on both datasets using the popular measures such as accuracy, precision, recall, and F1-score. This systematic process ensures that the proposed PO-ADMGNN not only resolves noise, redundancy, and heterogeneity of clinical data but also provides a computationally efficient and stable solution for predicting heart disease in high-risk diabetic patients.

IV. RESULTS AND DISCUSSION

This sub-section demonstrates the experimental outcomes of the proposed PO-ADMGNN method for real-time prediction of COVID-19 risk in a fog-aided IoT/IoMT healthcare environment. Since there is no publicly available dataset that accurately represents COVID-19

symptom patterns, a synthetic dataset has been designed with the guidance of doctors and medical experts to ensure clinical accuracy and completeness. The data set included a sufficient range of symptom sets like fever, cough, shortness of breath, and loss of taste or smell to guarantee the inclusion of all possible diagnostic cases for effective training and testing. The data set was further divided into training and test subsets with 70% allocated for training and 30% allocated for testing purposes in order to facilitate robust experimentation.

Figure 1 illustrates the architecture of the developed model, detailing its components, data flow, and how inputs are processed to generate predictions. Figures 2 and 3 present performance comparisons among different models, with Figure 2 focusing on recall to evaluate the models' ability to identify true positive cases, and Figure 3 highlighting the F-measure to reflect the balance between precision and recall. Figure 4 compares the models in terms of alert generation, showing their effectiveness in producing timely and accurate alerts. Figure 5 depicts the convergence of the POA hyperparameter optimization process, demonstrating how iterative optimization enhances model performance. Finally, Figure 6 presents the ROC curve comparison of various COVID-19 prediction models, illustrating their sensitivity, specificity, and overall discriminative capability.
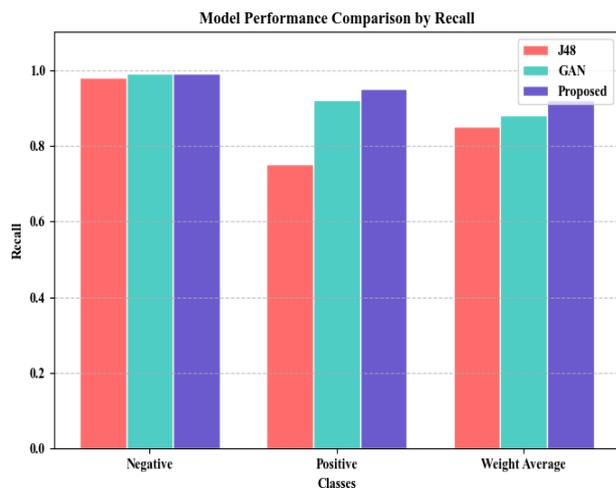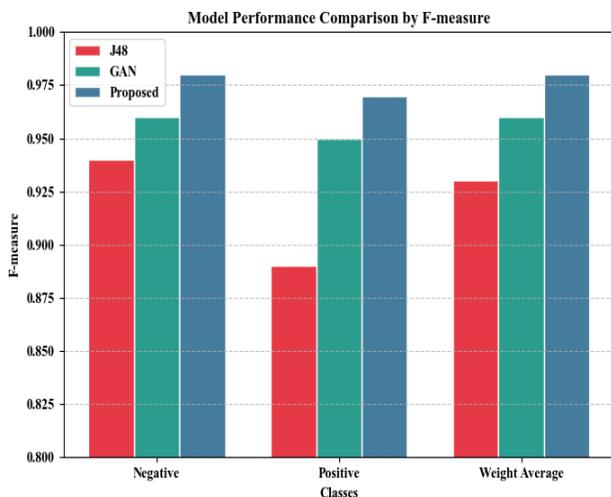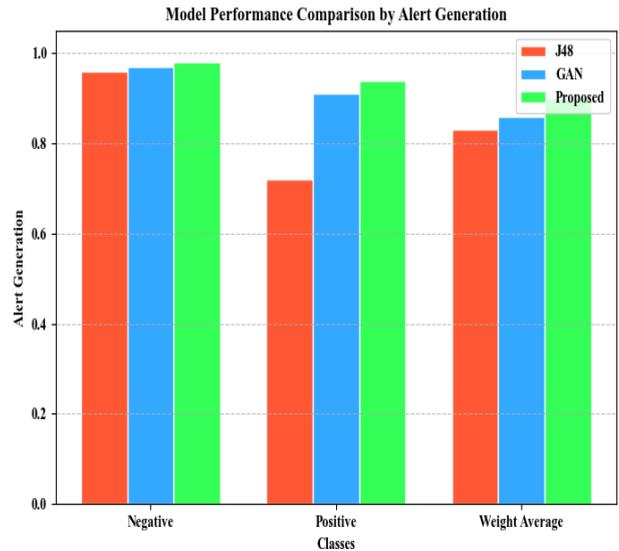
FIGURE 4: MODEL PERFORMANCE COMPARISON BY ALERT GENERATION

FIGURE 5: POA HYPERPARAMETER OPTIMIZATION CONVERGENCE

FIGURE 2: MODEL PERFORMANCE COMPARISON BY RECALL

FIGURE 3: MODEL PERFORMANCE COMPARISON BY F-MEASURE

FIGURE 6: ROC CURVE COMPARISON OF DIFFERENT COVID-19 PREDICTION MODELS
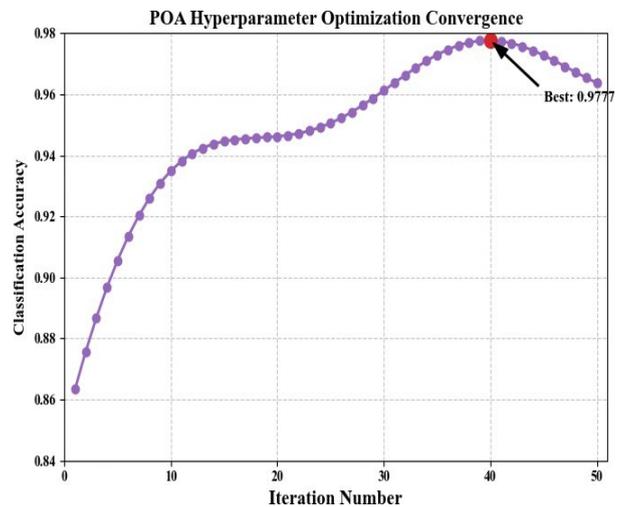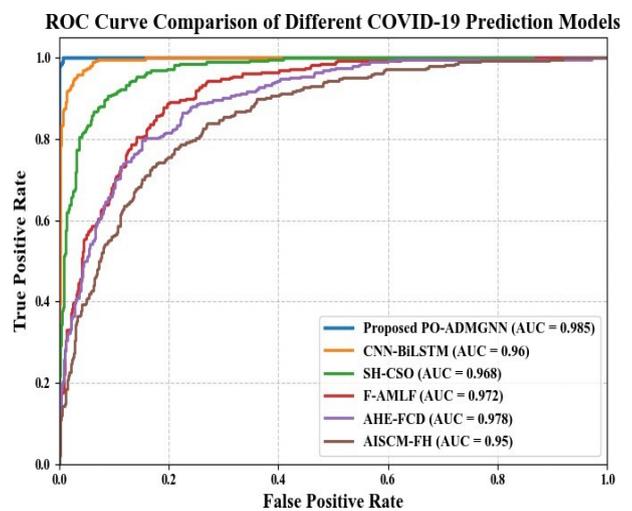
Prior to classification, the common preprocessing steps such as data cleaning, integration, feature transformation, and dimensionality reduction were performed. Seagull Foraging Optimization Algorithm (SFOA) was employed to identify the most relevant features, reducing the original fourteen features to ten, hence enhancing computational efficiency but at the expense of predictive ability. The classification was done using the proposed PO-ADMGNN, where POA was used to optimize the hyperparameters of the model to balance exploration and exploitation of the search space.

V. CONCLUSION

The proposed PO-ADMGNN model demonstrates a highly efficient and robust approach to real-time COVID-19 risk estimation in fog-assisted IoT/IoMT healthcare systems. By blending metaheuristic optimization techniques with attention-based dynamic multilayer graph modeling, the model effectively manages large-scale, heterogeneous, and time-varying healthcare data issues. The system begins with secure citizen registration and continuous multimodal health data collection without compromising data integrity and confidentiality. Preprocessing and feature extraction with SFOA at the fog layer also guarantees that the most informative features are preserved for future classification, keeping computation overhead as low as possible without sacrificing predictive performance. The ADMGNN module is especially proficient at recognizing both temporal dynamics and complex topological relationships between variables in citizen health data, enabling the model to learn complex patterns associated with COVID-19 risk. Furthermore, POA-driven hyperparameter tuning optimizes the model parameters in a systematic and dynamic manner for better prediction accuracy, generalizability, and adaptability to evolving healthcare conditions. The PO-ADMGNN framework as a whole thus offers not only timely and accurate risk predictions but also a scalable, adaptive, and secure proactive solution for healthcare management in smart fog-based IoT networks.

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