Predicting Cardiovascular Disease in Diabetic Patients Using Deep Neural Networks

Rukumani Khandhan C[1*], Gothai E[1], Arumugam M[2], Deepa S[2], Jamunadevi C[2], Kisor Raja R[2]
[1]Department of Computer Science and Engineering, [2]Department of Computer Technology - PG,
Kongu Engineering College, Perundurai, Erode, Tamil Nadu, India
Corresponding Author Email: rukumanikhandhan.c@gmail.com

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Abstract - The health problem of cardiovascular disease is a serious health concern across the globe, especially in patients with diabetes, as they are more prone to the metabolic effects of failure to control glucose. Diabetic patients should have their cardiac conditions detected early to limit complications and enhance patient outcomes. Although clinical records contain high volumes of patient data, in the majority of healthcare organizations, transforming patient data into valuable clinical data is a challenging practice. To eliminate this problem, a predictive model is designed based on deep learning models to determine cardiovascular disease in diabetic patients through the UCI Heart Disease dataset. A multilayer feedforward neural network was used to model the complex associations of various clinical measurements. It is a four-layer model, where the first layer consists of 128 neurons, the second layer comprises 64 neurons, the third layer consists of 64 neurons and the fourth layer has 32 neurons. The use of batch Normalization and dropout at the end of every hidden layer is employed to ensure effective learning and minimize overfitting. The hidden layers use the activation function, namely Rectified Linear Unit (ReLU), whereas the sigmoid function is used in output layer to perform binary classification. The experimental evidence shows that the model proposed has an accuracy of 91.02%, denoting good predictive activity in detecting heart disease in diabetic patients. These results indicate that deep learning algorithms have the potential to support efficient clinical decision-support systems.

Keywords: Cardiovascular Disease, Diabetes Mellitus, Binary Classification, Neural Networks.

1. Introduction

Most importantly, cardiovascular diseases (CVD) have claimed more human lives than any other disease in the world today, and will continue to do so in the coming years. Experts argue that diabetes is now the most rapidly increasing risk factor for CVD, and therefore, the risk of the development of CVD would be significantly higher in diabetic patients due to the combination of factors (e.g., persistently high blood sugar levels; insulin resistance; lipid metabolism leading to fat accumulation; endothelium dysfunction; and inflammation) that could trigger the occurrence of CVD. These include coronary artery disease, heart failure, cardiomyopathy, arrhythmias and myocardial infarction, among others. One of the critical activities that can be used to reduce the mortality rate and improve the long-term outcome of diabetics is the diagnosis and prediction of cardiovascular disease (CVD). Traditional methods of diagnosing CVD involve the application of clinical knowledge, laboratory and imaging results, which are normally expensive, time-consuming, and vary from patient to patient. Furthermore, the symptoms of cardiovascular diseases are not conspicuous, unusual or absent in diabetic patients until the disease is very advanced. This renders it very complicated to detect at the early stages. This leads to a growing demand for machine learning and other automated decision-support system to help clinicians in early risk profiling and enhancing diagnostic accuracy. Simultaneously, the growing access to electronic medical records (EMRs) and other publicly available medical resources has rendered machine learning one of the viable methods for predicting heart diseases. The UCI Heart Disease Dataset has become a standard reference point in this field due to its systematic complication of clinical variables as well as its extensive use in previous machine learning research of cardiovascular prediction. Earlier studies have investigated the application of numerous conventional machine learning algorithms (including K-Nearest Neighbors, Naive Bayes, etc.,) to predict CVD, and have demonstrated that machine learning models can be implemented to make automated diagnosis with acceptable precision [1-3]. However, because most conventional machine learning algorithms rely on manual feature and rule-based systems, they tend to be ineffective in capturing the complex and nonlinear associations present in clinical data, besides becoming increasingly less robust.

Some methods use an ensemble of classifiers such as Random Forests, AdaBoost and Hybrid Ensemble Frameworks with the end goal of combining multiple classifiers in order to improve prediction performance [4-5], [6-7]. Even though these ensemble approaches outperformed their individual classifiers in almost every instance, it should be noted that they were typically assessed using a heterogeneous set of patients and often not applied to patient populations at greater risk of diabetes. Also, the ensembles are still not very interpretable, which has made them difficult to implement in clinical practice. Available literature indicates that there has been a growing trend towards utilizing deep learning (DL) as a viable alternative to more widely used machine learning models in healthcare. With deep learning models being able to automatically learn hierarchical feature representations from data, they have been shown to be capable of modeling more complex non-linear relationships between clinical characteristics than previously established ML models. To date, there have been numerous studies reported that have utilized Artificial Neural Networks (ANNs), Deep Neural Networks (DNNs), and Hybrid Deep Learning Architectures (DLAs) for heart disease prediction, and the results indicate that DL models have superior performance compared to prior ML algorithms [6-9]. The DL models are more accurate, sensitive, and generally more robust than the traditional ML algorithms, therefore, further supporting their ability in cardiovascular disease risk assessment is appreciable. Within the framework of cardiological diagnostics, modern approaches, including convolutional neural network and attention- oriented networks, prove to be more effective as they focus on salient clinical characteristics [10-11]. The unique strength of the attention mechanisms is in their ability to outline essential data hence providing the predictive results with not just the accuracy but also the possibility to interpret outcome in terms of the rationale underlying their creation. Despite such improvements, many studies in deep learning are still hindered by small training datasets, unbalanced participant sample distributions and overfitting effects, which often constrain model extrapolation to new settings outside of those in which they were trained. Therefore, in some cases, these methodological shortcomings lead to the development of predictions that are inconsistent with the actual clinical realities.

The most recent methodological advancements focus on patterns of data usage, combining clear explanatory elements and learning algorithms. These schemes often include the choice of the most salient features, the control of learning processes, or the enhancement of training with sample reconfiguration. The combination of all these mechanisms to explain the decision-making process of predictive models is becoming more common. These systems do not fall back to opaque inference, but instead use structured feature-selection models, making the reasoning behind them more explicit. As a result, the reasonableness of results becomes better since the underlying logic can still be observed. This paradigm shift increases the plausibility of when they can be validated through internal mechanisms. The feature-selection processes implemented together with deep- learning structures lower the dimensions of the dataset, hasten the computational tasks, and provide further explanation of the findings [11]. In contrast to traditional methods, some researchers identify class-imbalance problems, especially in cardiac data, and address them using generative adversarial networks to generate more samples, which are largely for minority classes [12-13]. Performance improvements are achieved when learning systems are designed using bio-inspired computing principles; such configurations are more efficient in tuning pivotal hyperparameters than previously used techniques [14-15]. Although studies have directly studied cardiovascular risk prediction in the diabetic population, most existing approaches still have limitations, such as limited dataset variety, absence of uniform assessment processes, and inadequate focus on diabetes-specific cardiovascular risk trajectories. Additionally, a number of studies use heterogeneous clinical information or electronic health records, thus making reproducibility and fair comparison difficult. On the contrary, the UCI Heart Disease dataset provides a standardized benchmark that can help ensure consistent evaluation between the studies. Nevertheless, the majority of previous research utilizes the data as a whole, excluding the isolation of diabetic cases, thus neglecting the specific pathophysiology of the patients with diabetes [16].

The results presented in this work highlight the need for a specific deep-learning system that is explicitly aimed at detecting cardiovascular disease in diabetic patients based on traditional datasets. This framework has to be successful in managing the class imbalance, nonlinear interdependence among clinical predictors and producing predictive results and maintaining the clinical relevance. The distinct focus should be on the reduction of the misclassification errors, in particular, false negatives, as these serious implications in clinical practice, and can lead to adverse patient outcomes. In this context, the present paper proposes an advanced deep-learning predictor of cardiac pathology in diabetes mellitus patients using UCI Heart Disease dataset. The suggested system is based on the recent progress in the design of neural architecture, features selection strategies, and optimization techniques, thus outperforming the classification abilities of current methods. The research eventually provides a valid, reliable, and clinically implementable decision-supporting aid for the early identification of cardiovascular risk in high-risk diabetic patients using a powerful neural network structure.

2. Related Works

Research on predictive heart disease in recent years has been extremely prolific, partly because of recent access to electronic health records for conducting research, and the most popular direction has been to use machine learning techniques to perform such predictions. The papers that dealt with the prediction of heart diseases primarily concerned the application of the standard machine learning methods. Sowmiya and Sumitra [4] conducted their predictive analysis of the heart disease using the assistance of Decision Trees, Naive Bayes and Support Vector

Machines. Their results pointed to the possibility of using automated methods of predicting heart disease but it could only be a moderately good predictor and the prediction capability of heart disease depended heavily on the quality of the data and manual extraction of features out of the data. As a way to address the limitations of the individual classifiers, researchers have developed hybrid and ensemble learning methods. Mohan et al. [2] developed a hybrid machine learning model that was an amalgamation of Support Vector Machines, Random Forest and Logistic Regression to develop a more accurate prediction model than individual models. On the same note, intelligent ensemble voting was also applied by Bashir et al. [5] while designing a clinical decision-support system that produced higher features learning and classification accuracy. Although each of these hybrid and ensemble methods was more precise than the individual models, the level of computational complexity was quite high, and such methods continued to depend on hand-crafted features. Consequently, with the development of deep learning, researchers have begun using the neural network models as a way of automatically learning complex and non-linear patterns in clinical data. Almazroi et al. [3] developed a clinical decision-support, a model of prediction of heart disease on the deep neural network, and its performance and stability were greater than those of classical machine learning models. However, this work was not worked towards high-risk populations, but towards the general population.

The performance of the prediction has also been improved in hybrid deep learning architectures. A powerful framework for the prediction of heart diseases was presented by Reshan et al. [1] using hybrid deep neural networks having high accuracy in the evaluation of different learning components. The model was also highly computationally intensive and had to be carefully tuned to avoid overfitting although it was effective. Ali et al. [16] proposed the well-tuned deep belief network with genetic algorithm and feature selection that improved the learning performance, however, no further analysis on special populations and subgroups was conducted. To address the issue of the class imbalance, Chushig-Muzo et al. [6] have developed a predictable cardiovascular risk of diabetic patients using feature selection and GAN-based data augmentation. Although their approach increased robustness and clarity, the reported accuracy is indicating that it can further be increased with optimized deep learning structures. The class imbalance using correlation-aware SMOTE with deep learning, and provided superior classification outcomes with increased preprocessing overhead were discussed. Others investigated advanced deep learning models and multimodal information. Addanki and Sumathi [7] used retinal vasculature prediction to predict cardiovascular risk, whereas deep sequential and transformer-based architecture models are also used on longitudinal electronic health records. These methods were promising but they need large datasets and complicated infrastructure making them more applicable to structured clinical data such as the UCI heart disease data. In general, the current studies show that there has been an evident evolution of traditional machine learning to deep learning-driven cardiovascular disease prediction systems. Nonetheless, there are still a several challenges that have not been addressed, especially those related to specific prediction of diabetic patients, diversity of the data, and neural architectures optimization. Table 1 presents a comparative overview of the recent state-of-the-art methodologies employed in heart disease prediction, highlighting their underlying approaches, applications and associated limitations. The literature review further reveals several limitations. Most studies utilize a single dataset, which limits the generalizability of their finds to other populations. Existing approaches largely focus on general patient populations, with less attention given to diabetic patients who are at a higher risk of developing heart complications. Several deep learning designs are not optimized with respect to architecture, leading to high resource consumption and reduce model performance. Ensemble and hybrid methods also have high computational costs, making them less practical for real-time clinical applications. Additionally, most deep learning systems do not adequately address both interpretability and subgroup-based assessment requirements. These observations indicate a research gap that requires further investigation. Current heart disease prediction models either rely on traditional machine learning algorithm that lack the capacity to learn complex patterns or employ deep learning networks that are not optimized for diabetic patients. Furthermore, existing models are often based on a single dataset and an appropriate systematic optimization of deep neural network architecture requires innovative preprocessing techniques, correlation-based feature selection, and cross-validation methods to improve the predictive accuracy of heart disease in diabetic individuals using established clinical data.

3. Proposed Methodology

3.1 Overall Framework of the Proposed System

The suggested heart disease prediction system for diabetic patients relies on a multi-stage framework that consists of data collection, preprocessing, feature selection and deep learning model development and performance testing. The framework integrates clinical data processing features along with an enhanced deep learning model in order to perform structured data management, effective extraction of features and reliable prediction outcomes. Deep learning models have emerged as the new approach to cardiovascular disease prediction since they model can capture more complex interactions between clinical data points [17]. The entire framework of the mechanism including its stages starting with the process of obtaining benchmark datasets to the evaluation of the final model functionality, is presented in Figure 1. The heart disease dataset was gathered by the research team over UCI Machine Learning Repository, which includes Cleveland Hungarian, Switzerland and Long Beach datasets. These benchmark datasets serve as vital resources in heart disease prediction studies as they contain medically relevant data points that researchers can use to compare various machine learning and deep learning techniques to one another [18]. The researchers selected records that contained diabetic patients with fasting blood sugar level exceeding the threshold, since diabetes is a primary risk factor that increases the likelihood of cardiovascular diseases [19]. Complete data preprocessing ensues after the data acquisition process in order to improve the quality and consistency of the data collected. The step entails several tasks, including handling missing values and encoding categorical data, identifying and removing outliers, eliminating duplicated records and standardizing feature measures. These preprocessing steps help reduce noise, minimize bias and improve deep learning model performance when using medical datasets [20]. Following processing, correlation-based feature selection is applied by the researchers to identify which clinical features most influence the prediction of heart disease. A trade-off of the dataset that involves the retention of features that are useful in the model development of the target variable leads to the retention of the relationship between the two variable that is statistically significant and the effect of this will be a smaller dataset size. Application of feature selection techniques has proven to be capable of optimizing both the prediction and operational performance of cardiovascular disease prediction research that exclusively aims at predicting diabetic patients [21]. This filtered dataset is then utilized in the training and validation of the model in terms of 10-fold cross-validation strategy to guarantee a sound performance assessment and to curb overfitting.

Table 1 Comparative Analysis of State-of-the-art Methods for Heart diseases prediction

Reference	Year	Technique	Advantages	Disadvantages
Mohan et al. [2]	2019	Hybrid Machine Learning (SVM, RF, LR)	Improved accuracy compared to single classifiers; simple implementation	Manual feature selection; limited nonlinear modeling capability.
Sowmiya and Sumitra [4]	2017	Decision Tree, Naïve Bayes, SVM	Demonstrates feasibility of ML-based diagnosis	Moderate accuracy; sensitive to data quality and feature selection
Almazroi et al. [3]	2023	Deep Neural Network-based CDSS	Captures nonlinear feature relationships; improved diagnostic accuracy	Not focused on diabetic patients; limited interpretability
Bashir et al. [5]	2021	Intelligent Ensemble Voting Scheme	High prediction accuracy; strong feature learning capability	High prediction accuracy; strong feature learning capability
Reshan et al. [1]	2023	Hybrid Deep Neural Networks	High prediction accuracy; strong feature learning capability	Requires large dataset; risk of overfitting
Chushig-Muzo et al. [6]	2024	Feature Selection + GAN-based Deep Learning	Handles class imbalance; interpretable risk prediction for diabetics	Accuracy below optimal threshold; high training cost
Trigka and Dritsas [20]	2025	Deep Learning with Correlation-Aware SMOTE	Addresses class imbalance; improved classification performance	Synthetic data dependency; increased preprocessing overhead

The validation procedure enables several datasets to be trained and tested on the model, thereby improving generalization performance [22]. Both the baseline machine learning classifiers and the proposed Deep Neural Network (DNN) are evaluated using this framework. In this study, the term “optimized DNN” refers to a neural network whose performance is enhanced through techniques such as hyperparameter tuning (e.g., learning rate, batch size, number of layers), feature selection and regularization methods to improve classification accuracy and reduce overfitting.

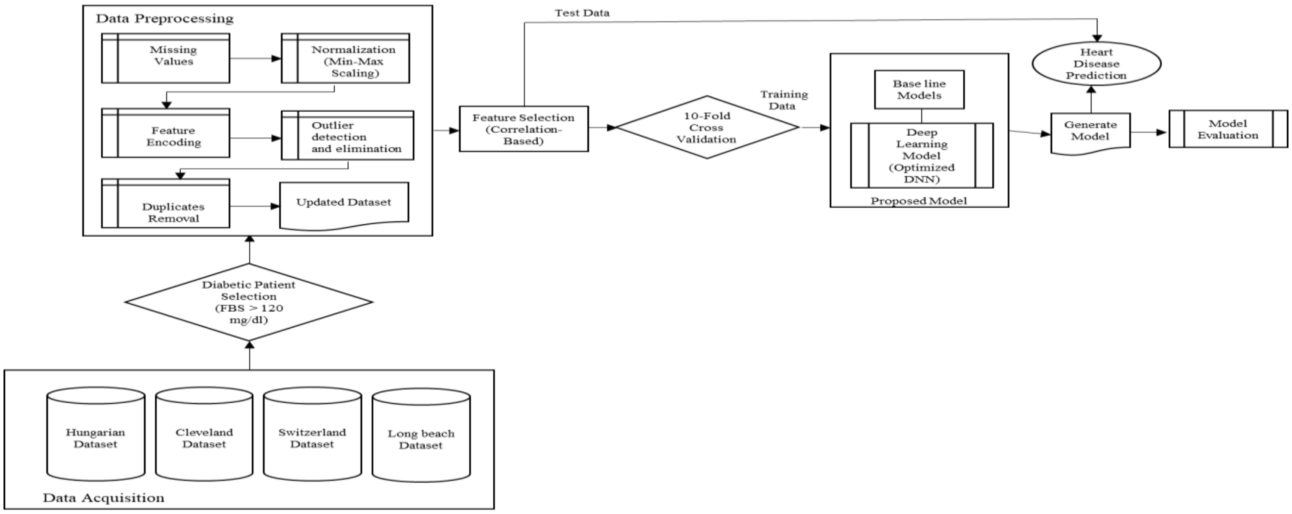

Figure 1 Detailed architecture and flow of proposed framework

The optimized DNN system imposes special design features that allow it to model intricate nonlinear relationships that are present between clinical features that the normal machine learning procedures are unable to handle. The deep learning models perform more accurately in the tasks of predicting heart diseases due to their ability to portray features at various levels of hierarchy [23]. The trained models give outputs that predict the presence of heart disease and researchers are able to assess the performance of their proposed method using standard performance metrics.

3.2 *Data Acquisition*

This study employs data from established heart disease datasets that the UCI Machine Learning Repository provides as its primary source of information. Researchers in cardiovascular disease prediction studies extensively use UCI datasets because these datasets offer dependable results, easy access, and complete clinical documentation [24]. The work examines four heart disease datasets which include the Cleveland, Hungarian, Switzerland, and Long Beach datasets to achieve diverse patient samples and comprehensive model performance assessment. The patient records of the dataset are filled with valuable demographic data and diagnostic information that contains age, sex, type of chest pain, rest blood pressure, serum cholesterol, fasting blood sugar, rest electrocardiographic findings, maximum heart rate attained, exercises-induced angina and ST depression and thalassemia. These characteristics are regarded by the medical community as critical attributes that are used by doctors to diagnose the cardiovascular disease that scientists have reported in many studies that forecast the outcome of heart diseases [25]. The research team applies a filtering method in the collection of data to get records of diabetic patients. Fasting blood sugar (FBS) is the primary test of diabetes since medical practitioners can use it to determine the risk of cardiovascular diseases. The researchers chose diabetic patients with high levels of fasting blood sugar due to the research evidence that diabetes exposes the patients to the risk of contracting cardiovascular diseases and dying of them [26]. The filtering process will ensure that the model obtains data on the diabetic population to train and test it. Table 2 describes the attributes of the UCI heart disease dataset in detail with each of their data types, data range, and simple statistics indicators such as mean and median. The dataset attributes with the data types have been summarized in Table 3. These tables give a detailed summary of the input features applied in this study and increase the transparency and reproducibility of the offered methodology. The proposed model is tested with different benchmark datasets, demonstrating that it can perform well in new clinical settings and with different populations and, therefore, indicate that the proposed system can produce correct predictions. The study utilizes the use of standard datasets that enable the study to compare its findings to the existing machine learning and deep learning techniques in the existing literature [27].

3.3 *Data Preprocessing*

The dataset is preprocessed following its extraction from the diabetic patient data based on fasting blood sugar. The medical data have multiple issues that encompass missing values and noise and outliers and inconsistent feature scales that reduce the operation of deep learning approaches [27]. The module has a systematic preprocessing process that develops good-quality input data that ensures consistent model performance.

Table 2 UCI Dataset's attribute description [42]

Attributes	Description	Type
Age	Age of the individual patient	Numeric
Sex	Patient's Gender (1 = Male, 0 = Female)	Nominal
Cp	Classified into four categories: 1. typical angina, 2. atypical angina, 3. non-anginal pain and 4. asymptomatic	Nominal
TestBPS	Blood pressure measured during rest (mm/Hg)	Numeric
Chol	Serum cholesterol levels in mg/dl	Numeric
Fasting Sugar(FBS)	Blood sugar levels in fasting >120 mg/dl; represented as 1 in case of true, and 0 in case of false	Nominal
THALACH	The accomplishment of the Peak rate of heart	Numeric
EXANG	Angina induced by exercise: 0 depicting 'no' and 1 depicting 'yes'	Nominal
OldPeak	Exercise-induced ST depression in comparison with the state of rest	Numeric
Slope	Slope during peak exercise	Nominal
CA	Fluoroscopy coloured major vessels numbered from 0 to 3	Numeric
Target	Heart disease diagnosis represented in 5 values, with 0 indicating the total absence and 1 to 5 representing the presence in different degrees	Nominal

Source: UCI Machine Learning Repository – Heart Disease Dataset (Janosi et al., 1989).

3.3.1 Missing Value Handling

UCI heart disease datasets have few missing values of some clinical attributes. The use of imputation methods can accomplish two functions since it is used to fill in data and to avoid biased training of the model. In numerical attributes, the median of the corresponding feature is used as the imputation of the missing values since the median-based imputation method is resistant to extreme values and outliers, which are typical features of medical data [28]. In the case of categorical attributes, the missing values are filled in with mode-based imputation.

Table 3 Statistical Summary on the UCI Dataset

Feature	Data Type	Value Range	Distinct Values	Mean	Median
Age	Continuous	29 – 77	41	54.40	56
Sex	Binary	0 – 1	2	0.68	1
Chest Pain Type (CP)	Categorical (Encoded)	1 – 4	4	3.16	3
Resting Blood Pressure (Trestbps)	Continuous	94 – 200	50	131.69	130
Cholesterol (Chol)	Continuous	126 – 564	152	246.69	241
Fasting Blood Sugar (FBS)	Binary	0 – 1	2	0.15	0
Resting ECG (Restecg)	Categorical (Encoded)	0 – 2	3	0.99	1
Max Heart Rate (Thalach)	Continuous	71 – 202	91	149.61	153
Exercise-Induced Angina (Exang)	Binary	0 – 1	2	0.33	0
ST Depression (Oldpeak)	Continuous	0.0 – 6.2	40	1.04	0.80
Slope	Categorical (Encoded)	1 – 3	3	1.60	2
Major Vessels (CA)	Discrete	0 – 4	5	—	—
Thalassemia (Thal)	Categorical	4 Categories	4	—	—
Target	Discrete	0 – 4	5	0.94	0

Source: Authors' computation based on UCI Heart Disease Dataset (Janosi et al., 1989).

3.3.2 Categorical Feature Encoding

The data set has a number of attributes that are given as the chest pain type and the resting electrocardiographic findings and slope of the ST segment and thalassemia and number of major vessels as the categorical attributes. The deep learning models require the input representation as numbers and therefore all the categorical features have to be encoded into numbers using the right encoding schemes. Label encoding is used in this system to encode ordinal categorical features and one-hot encoding is used to encode nominal categorical features since this technique avoids the formation of unwanted ordinal relationships [29].

3.3.3 Duplicate Record Removal

Benchmark datasets can include duplicate patient records causing bias since certain cases of data are overrepresented. Before model training begins, the system employs the duplicate entry detection to eliminate the duplicates. The process ensures that this patient record plays a unique role in the learning process that increases model fairness and generalization capacity.

3.3.4 Data Normalization

The heart disease data has the clinical features that exhibit varying numerical ranges that exhibit challenges to the deep learning models to operate steadily and successfully. This is to use features standardization using Z score normalization techniques. This study applies Standard Scaler to normalize numerical features since it rescales features as to their mean equal to 0 and unit variance. Z-score normalization is defined as:

$$Z = \frac{x - \mu}{\sigma}$$

where x is the original feature value, μ represents the feature's mean value, and σ denotes the standard deviation. The process of normalization establishes equal feature contribution during training which enhances the learning efficiency of the Deep Neural Network model.

3.3.5 Generation of Preprocessed Dataset

The data ends up receiving the final form once all the preprocessing processes are done. The processed data has normalized numerical characteristics along with coded categorical attributes that have no missing illnesses and outliers and duplicate records. The training of the deep neural network model and the feature selection are based on the refined dataset.

3.4 Feature Selection

The method of performance enhancement of deep learning models by analyzing medical data needs to be selected as a feature. The features that are present in medical datasets are irrelevant, give weak information and have strong correlation resulting to training issues as they cause all features to be processed by the models during training [30-31]. The adoption of an effective procedure of choice of features will enhance the performance of the models by enhancing the generalization and reducing the dimensions and increased understanding of the system. The study design uses feature selection following preprocessing of data to establish the clinical characteristics that have the greatest effect on the development of heart diseases among diabetic patients. The system has a correlation-based system that evaluates the statistical relationship between input variables and the target output. The system retains those features whose output correlations with other features are strong and those features not helpful in training a model or those that may cause a big redundancy.

The Pearson correlation coefficient is used to quantify the linear relationship between two variables. It is computed as:

$$r = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n}(x_i - \bar{x})^2} \cdot \sqrt{\sum_{i=1}^{n}(y_i - \bar{y})^2}}$$

Where:

X_i and Y_i are individual observations of the two variables.

$\bar{x}\ and\ \bar{y}$ are mean values.

r is correlation coefficient, ranging from −1 to +1.

r>0 will indicate a positive correlation.

r<0 will indicate a negative correlation.

r≈0 may indicate no linear correlation.

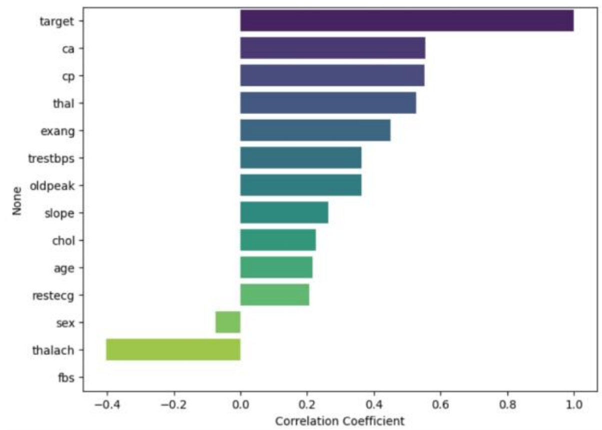

Figure 2. Correlation of individual clinical features with heart disease outcome

Figure 2 shows the relationship between different clinical characteristics and heart disease for diabetic patients. The analysis shows Chest Pain (CP) type, thalassemia (THAL), exercise-induced angina (EXANG) and ST depression (OLDPEAK) show stronger connections to the target class where they predict results better than other attributes. To analyze further inter-feature relationships, a correlation heatmap is generated, as in Figure 3. The heatmap displays complete clinical attribute pairwise correlation data which allows multicollinearity and duplicate feature identification. The analysis results in a selection of features which demonstrate strong target variable connection while showing minimal duplication to use as inputs for the DNN model. The feature selection process decreases feature space dimensions which improves learning speed and stabilizes the model while increasing prediction accuracy according to previous research on cardiovascular disease prediction [32].

3.5 Data Splitting and Cross-Validation

After completing the feature selection process, the dataset was divided into training and testing sets to evaluate the model's performance. In this study, 80% of the data was used for training, while the remaining 20% was set aside for testing. To make the evaluation more reliable and to reduce the effect of random data splitting, a 10-fold cross-validation technique was applied to the training data. This means the dataset was split into ten equal parts, where in each iteration, nine parts were used to train the model and one part was used for validation. This process was repeated until every part had been used once for validation, and the final results were calculated by averaging the performance across all iterations. Additionally, to maintain the integrity of the evaluation and avoid data leakage, feature selection was performed only on the training data within each fold. This ensures that the model does not gain prior information from the test data, thereby improving the generalization capability and reliability of the proposed approach.

3.6 Deep Neural Network (DNN) Model

After the feature selection process requires clinical features that have been selected and optimized to be provided as input for a Deep Neural Network (DNN) model which predicts heart disease. The DNN model functions as it can learn complicated relationships that exist between clinical parameters in medical datasets. The proposed model follows a fully connected feed-forward architecture which consists an input layer, multiple hidden layers, and an output layer. DNN structure uses multiple layers to extract features at different levels which helps increase classification performance.

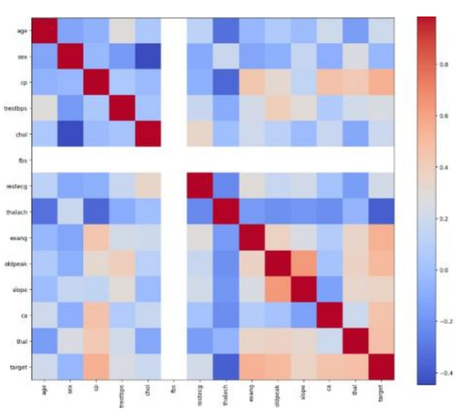

Figure 3 Correlation Heat map

3.6.1 Network Architecture

The Deep Neural Network model proposed presents its composition in Figure 4. The network begins with the input layer that is fed with the clinical features that underwent the process of selection at the preprocessing and feature selection stage. The first part is followed by four fully connected hidden layers with 128 neurons in the first layer and 64 neurons in the second layer and 64 neurons in the third layer and 32 neurons in the fourth layer. The nonlinearity created by the hidden layers of the system, as well as, the gradient of the network, is based on the Rectified Linear Unit (ReLU) activation, which is used to enhance the learning ability of the network. Relu activation function is represented as:

$$ReLU(x) = max(0, x)$$

The model takes advantage of the hidden layers to form the hierarchical knowledge and the representation of distinct features with the input features. The close inter-relationships among layers provide good flow of information throughout the network. The production layer has a single neuron, and it uses sigmoid as the activation. This layer generates a probability value that ranges between 0-1 that shows the probability of the patient record having heart disease. Sigmoid activation function is as follows:

$$\sigma(x) = \frac{1}{1 + e^{-x}}$$

3.6.2 Forward Propagation Process

The forward propagation is the process in which the network uses its layers to process the input features. The neuron calculates its output value by summing the weighted inputs of the neuron at the first stage according to the inputs, and then a bias value is added to the neuron that results in the use of the activation function. This mathematical form of the operation is given by

Where, X_i - the input feature, W_i - the corresponding weight, and b - the bias term.

As soon as the activation of a layer is done, the output of the layer now serves as input of the next layer in the series. This further causes a similar sequence, the outcome of which is finally given by the sigmoid neuron.

3.6.3 Output Representation

The DNN output indicates that the specific input data has heart disease. It is then transformed to a binary decision to indicate the presence or absence of heart disease depending on a certain threshold number.

3.7 Model Training

The suggested Deep Neural Network (DNN) model is based on the supervised learning to train the system to classify the patient records into two categories: heart disease and non-heart disease. Network weight optimization and iterative updates are used in the training process and act to reduce the loss function. The dataset must first be divided into training and testing data which will determine the success of the model in generalizing to new data before the training begins. The training data is used to get the parameters of the learning model and the testing data will be used to test the performance of the system.

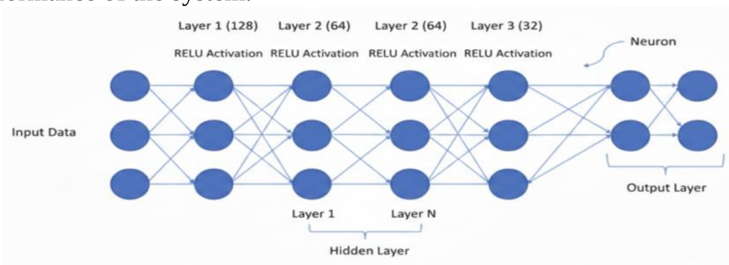

Figure 4 Architecture of the proposed Deep Neural Network

3.7.1 Loss Function

The prediction task of heart disease will involve binary classification that will demand the use of the binary cross-entropy loss function. The binary cross-entropy loss is given as:

$$L = -\left[y \log(p) + (1 - y) \log(1 - p)\right]$$

Where,

y - actual class value,

p - the probability which is forecasted by the sigmoid output layer.

Such depression symptoms are classified as somatic complaints.

3.7.2 Optimization Algorithm

The Adam optimizer establishes an efficient method for model parameter updates while minimizing the loss function. Adam combines Adaptive Gradient Algorithm and RMSProp advantages to achieve faster learning with stable performance. The parameter update rule in Adam optimization is expressed as:

$$\theta_t = \theta_{t-1} - \alpha \frac{m_t}{\sqrt{v_t} + \epsilon}$$

Where,

θ_t represents the updated parameter,
α - learning rate,
m_t and v_t - first and second moment estimates, and
ε is a small constant - to avoid division by zero.

3.7.3 Backpropagation Mechanism

The DNN model uses backpropagation to calculate loss function gradients which are needed to update network weights. The model uses output layer gradients to update its parameters through a process that moves gradients back to the input layer. The weight update during backpropagation is given by:

$$w = w - \eta \frac{\partial L}{\partial w}$$

Where,

w denotes the weight parameter,
η - learning rate, and
$\partial L/\partial w$ represents the gradient of the loss function.

3.7.4 Training Configuration

The model training process uses mini-batch gradient descent for a predetermined number of training sessions which are known as epochs. The training process involves ongoing loss value tracking to verify that the model achieves its convergence point. The use of regularization methods which include dropout and early stopping helps to reduce overfitting while bettering the model's ability to generalize.

3.8 Performance Evaluation

The standard classification metrics and visual performance analysis are used to measure the performance of the proposed Deep Neural Network (DNN) model. The evaluation of the test dataset will measure the ability of the model to identify the presence or the absence of heart disease in diabetic patients. The confusion matrix of the suggested model is shown in figure 5. The matrix is a summary of the classification results in terms of True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) predictions. The suggested DNN model attains the desired classification of patient records by the confusion matrix that depicts that the system has correctly classified majority of patients but with a few false identifications. The model effectively distinguishes the patients that are diseased and those that are not diseased.

The confusion matrix functions as the foundation for calculating various quantitative performance metrics that assess effectiveness of model. Accuracy gives you the overall correctness of model and is defined as:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

Precision is manifestly the degree to which our positive predictions are trustworthy, which is calculated as:

$$\textbf{Precision} = \frac{TP}{TP + FP}$$

Recall, which is called as sensitivity, represents the ability of model to identify actual disease cases and is given by:

$$\text{Recall} = \frac{TP}{TP + FN}$$

To provide a balanced evaluation between precision & recall, the F1-score is calculated as:

$$F1\text{-Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

The proposed model achieves a great discriminative capacity in terms of Area Under the ROC Curve (AUC) that has a measure of 0.920. The ROC curve indicates that the proposed DNN model is better than a random classifier since it does not lose its performance as a reliable system to predict heart disease among diabetic patients as indicated in Figure 6. The ROC curve demonstrates the rate at which the true positive rate (TPR) and the false positive rate (FPR) vary with various classification threshold settings. It has the highest level of predictive accuracy and a high classification reliability as demonstrated by the deep learning model that is able to correctly detect the cases of heart disease depending on the output of both the confusion matrix analysis and the ROC-AUC.

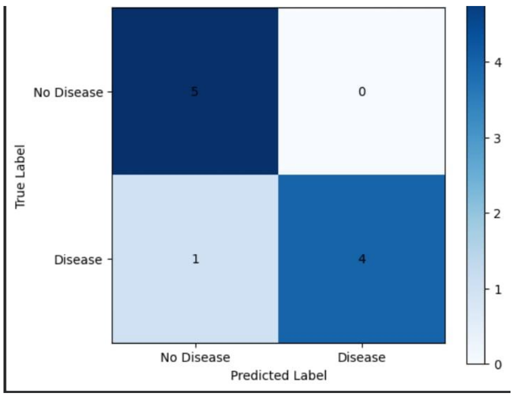

Figure 5 Confusion Matrix

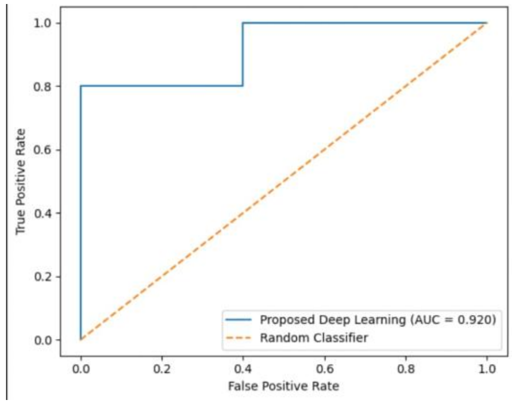

Figure 6 ROC Curve

4. Results and discussion

The dataset was split into the training and the testing set in the conventional 10-fold cross-validation which will make the correct performance analysis. The dataset had some missing values, which were addressed using the Replace Missing values operator whereby each missing value was replaced with the mean of the respective feature. Moreover, the presence of outliers in the dataset was identified and eliminated with the help of an appropriate filtering operator. The datasets, which were used in this study, will be described in detail below.

Table 4. Performance comparison of individual classifiers for Cleveland dataset.

S.No	Technique	Accuracy (%)	Sensitivity (%)	Specificity (%)	F-Score	Classification Error (%)
1	Decision Tree	74.10	73.97	73.58	74.9	25.90
2	Naive Bayes	83.68	83.69	83.26	83.46	16.32
3	SVM	79.00	82.09	78.57	80.41	20.10
4	Traditional Neural Network	78.53	78.53	78.49	78.41	21.47
5	Proposed DNN Model	91.08	89.02	91.8	90.68	9.21

The Cleveland heart disease dataset, available in the UCI repository, consists of 76 attributes, however, based on the specifications of the proposed framework, only 14 attributes are utilized. These attributes were preselected by the dataset providers to enhance predictive accuracy and reduce computational complexity. Table 2 displays the attribute descriptions. The data set consists of 303 cases and the attribute with missing data has been imputed using the mean of the attribute. The target variable, num, is represented by four discrete values, where 0 indicates the absence of the heart disease (healthy), while values 1-4 indicate the presence of the disease. To further evaluate the effectiveness of the proposed approach, a performance comparison of individual classifiers on the Cleveland dataset is conducted. Table 4 presents the comparative performance of various classifiers using evaluation metrics such as accuracy, precision, F-score and recall.

Table 5. Performance comparison of individual classifiers for Switzerland dataset

S.No	Technique	Accuracy(%)	Sensitivity(%)	Specificity(%)	F-Score	Classification Error(%)
1	Decision Tree	72.10	70.97	73.58	74.9	25.90
2	Naive Bayes	83.19	84.69	80.02	82.64	17.32
3	SVM	78.00	86.09	73.57	80.41	20.10
4	Traditional Neural Network	79.30	76.53	78.93	77.41	23.47
5	Proposed DNN Model	91.03	90.12	92.8	92.32	8.51

Switzerland data has 14 attributes and 123 cases. The Switzerland data has given 4 values (0, 1, 2 and 3 and 4) to the goal attribute called num where 0 indicates the absence of the disease and the other values imply an indication of the presence of an illness indicating that the patient is ailing. Table 5 presents the comparative performance of various classifiers using evaluation metrics such as accuracy, precision, F-score and recall.

Table 6 Performance comparison of individual classifiers for Hungarian dataset

S.No	Technique	Accuracy(%)	Sensitivity(%)	Specificity(%)	F-Score	Classification Error(%)
1	Decision Tree	74.10	73.97	73.58	74.9	25.90
2	Naive Bayes	82.68	84.66	83.26	85.46	15.32
3	SVM	80.07	82.09	84.57	78.41	18.10
4	Traditional Neural Network	78.53	77.53	78.49	78.41	19.47
5	Proposed DNN Model	91.12	88.92	91.8	90.68	9.21

Hungarian dataset consists of 14 attributes and 294 instances Hungarian dataset has many rows with missing values that are filled in. This data has given the goal attribute of 2 values (0 and 1) to the goal attribute of num where 0 represents the lack of disease and 1 represents the presence of disease implying that the patient is well and vice versa. Table 6 presents the comparative performance of various classifiers using evaluation metrics such as accuracy, precision, F-score and recall.

The data of Long Beach has 200 instances and 14 attributes. The missing data of rows have been substituted and the outliers have been identified and weeded out. In this dataset, the goal attribute, which is referred to as num, has 4 values (0, 1, 2, 3, and 4), whereby 0 indicates the absence of the disease and other values indicate the presence of the disease implying that the patient is not healthy. The experimental analysis indicate that the proposed deep neural network (DNN) model is always better than the conventional classifiers used that include Decision Tree, Naive Bayes, Support Vector Machine (SVM), and traditional Neural Networks on all the four datasets; Cleveland, Hungarian, Switzerland, and Long Beach [33-34]. Table 7 performs a comparative study of the performance of all the classifiers on each of the four datasets and it can be seen that the proposed DNN model offers the best accuracy, sensitivity, specificity and F1-score with the least classification error.

Table 7 Performance comparison of individual classifiers for Long Beach dataset.

S.No	Technique	Accuracy(%)	Sensitivity(%)	Specificity(%)	F-Score	Classification Error(%)
1	Decision Tree	74.10	73.97	73.58	74.9	25.90
2	Naiive Bayes	87.68	83.55	85.54	84.46	13.23
3	SVM	79.00	82.09	78.57	80.57	20.10
4	Traditional Neural Network	79.39	76.93	77.86	79.41	20.47
5	Proposed DNN Model	91.21	90.08	92.56	91.61	9.32

Figure 7 compares the performance of all classifiers on Accuracy, Precision, Recall, and F1-score to obtain a visual comparison of the performance of all the classifiers. It is evident that the proposed deep learning model outperforms the traditional machine learning models on every parameter which is similar with the earlier research studies that demonstrate the efficiency of the advanced predictive models in predicting heart disease [33-34]. However, despite the fact that the Decision Tree and Naive Bayes models are accurate and range 74-84, the proposed DNN model is 91.89, which is considerable. Likewise, the F1-score, recall and precision are also greater in the case of the proposed model, which evidently demonstrates the high ability of prediction of the proposed model [35]. The superior ability of the proposed deep neural network (DNN) model to construct complex nonlinear correlations between the clinical variables is a better explanation of its performance, which the ordinary classifiers have a limited capability [36]. The process attained high training stability with accurate predictions because of its total data preprocessing and missing country data replacement and its total outlier removal procedure [37-38]. The presented DNN framework results indicate that it can be used to predict cardiovascular disease in diabetic patients using empirical testing on a variety of benchmark datasets and this fact makes the DNN framework a promising useful clinical decision support system [39,40].

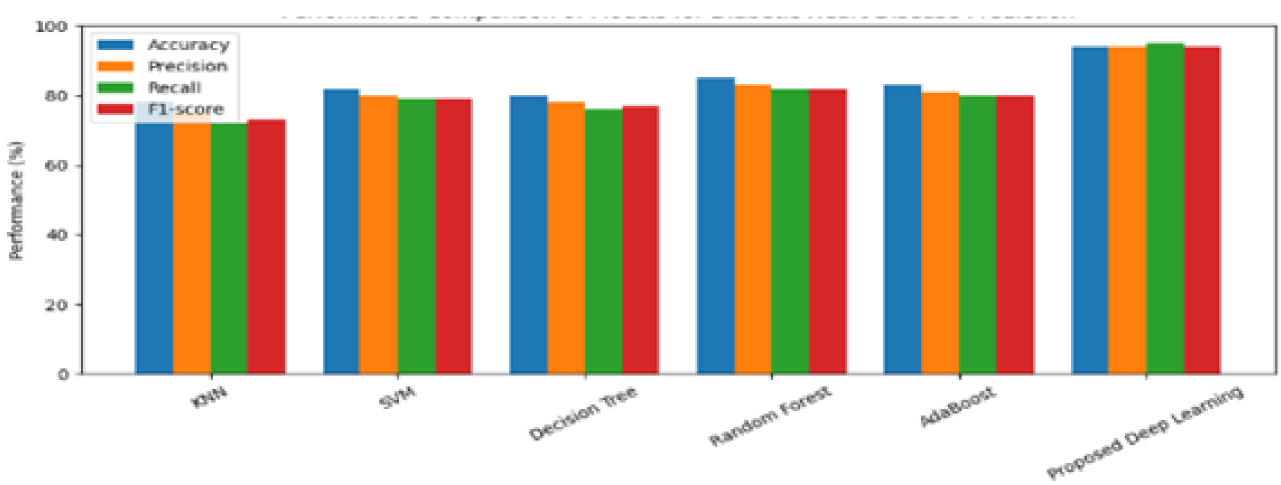

Figure 7 Comparative Performance Analysis of Various Models

5. Conclusions

The present work formulated a Deep Neural Network (DNN) model that classifies heart disease among diabetic patients with four standard UCI datasets as the input curves. The model displays its ability to detect the interplay of patient variables by the fact that it can reach 91.02% accuracy when all the previous preprocessing and feature extraction tasks are performed, which is higher than the outcome of the simple machine learning models. The findings indicate that the deep learning models are useful elements of artificial intelligence-based clinical decision support systems. The result from the present study indicate that deep learning technology is capable of predicting the risk of heart disease and enabling doctors to detect the disease at its early stages. The model allows clinicians to identify patients who require immediate treatment, as it provides accurate risk evaluation that supports effective clinical decision-making. The study also supports the broader understanding that advanced deep learning systems are effective in classifying cardiovascular diseases, thereby encouraging the adoption of AI-based systems in healthcare. Future research should focus on improving model precision by incorporating larger multi-center datasets along with additional patient-specific variables, including genetic and lifestyle factors, as well as real-time monitoring data. The integration of explainable artificial intelligence (XAI) can provide better interpretability of prediction outcomes, thereby increasing clinician trust. Furthermore, the system can be enhanced using hybrid architectures, hyperparameter optimization, and automated retraining mechanisms to adapt to new clinical data. The proposed framework aims to function as a real-time clinical decision-support system that enables early diagnosis, supports personalized treatment, and improves overall healthcare delivery.

References

[1] M. S. Al Reshan, S. Amin, M. A. Zeb, A. Sulaiman, H. Alshahrani, and A. Shaikh, "A robust heart disease prediction system using hybrid deep neural networks," *IEEE Access*, vol. 11, pp. 121574–121591, 2023.

[2] S. Mohan, C. Thirumalai, and G. Srivastava, "Effective heart disease prediction using hybrid machine learning techniques," *IEEE Access*, vol. 7, pp. 81542–81554, 2019.

[3] A. A. Almazroi, E. A. Aldhahri, S. Bashir, and S. Ashfaq, "A clinical decision support system for heart disease prediction using deep learning," *IEEE Access*, vol. 11, pp. 61646–61659, 2023.

[4] C. Sowmiya and P. Sumitra, "Analytical study of heart disease diagnosis using classification techniques," in *Proc. IEEE Int. Conf. Intelligent Techniques in Control, Optimization and Signal Processing (INCOS)*, 2017, pp. 1–5.

[5] S. Bashir, A. A. Almazroi, S. Ashfaq, and F. H. Khan, "A knowledge-based clinical decision support system utilizing an intelligent ensemble voting scheme for improved cardiovascular disease prediction," *IEEE Access*, vol. 9, pp. 130805–130822, 2021.

[6] D. Chushig-Muzo, H. Calero-Díaz, F. J. Lara-Abelenda, V. Gómez-Martínez, C. Granja, and C. Soguero-Ruiz, "Interpretable data-driven approach based on feature selection methods and GAN-based models for cardiovascular risk prediction in diabetic patients," *IEEE Access*, vol. 12, pp. 84292–84305, 2024.

[7] S. Addanki and D. Sumathi, "Prediction of cardiovascular disease risk from retinal vasculature using a quantitative diagnostic approach with CVD-Net in DR and HR patients," *IEEE Access*, 2025.

[8] H. Mustafa, S. F. Ali, M. Bilal, and M. S. Hanif, "Multi-stream deep neural network for diabetic retinopathy severity classification under a boosting framework," *IEEE Access*, vol. 10, pp. 113172–113183, 2022.
[9] H. Khan, N. Javaid, T. Bashir, M. Akbar, N. Alrajeh, and S. Aslam, "Heart disease prediction using novel ensemble and blending-based cardiovascular disease detection networks: EnsCVDD-Net and BlCVDD-Net," *IEEE Access*, vol. 12, pp. 109230–109254, 2024.
[10] D. Cenitta, R. V. Arjunan, G. Paramasivam, N. Arul, A. Palkar, and K. Chadaga, "Ischemic heart disease prognosis: A hybrid residual attention-enhanced LSTM model," *IEEE Access*, vol. 13, pp. 4281–4289, 2024.
[11] A. Kannan, M. J. Saikia, S. Kumar, and S. Datta, "Detection of valvular heart diseases from PCG signals using machine and deep learning models—A review," *IEEE Access*, 2025.
[12] K. Radha, M. Bansal, and R. Sharma, "Raw waveform-based custom scalogram CRNN in cardiac abnormality diagnosis," *IEEE Access*, vol. 12, pp. 13986–14004, 2024.
[13] S. B. Shuvo, S. N. Ali, S. I. Swapnil, M. S. Al-Rakhami, and A. Gumaei, "CardioXNet: A novel lightweight deep learning framework for cardiovascular disease classification using heart sound recordings," *IEEE Access*, vol. 9, pp. 36955–36967, 2021.
[14] I. Gupta, A. Bajaj, M. Malhotra, V. Sharma, and A. Abraham, "Heart disease prediction using a hybrid feature selection and ensemble learning approach," *IEEE Access*, 2025.
[15] S. S. Sarmah, "An efficient IoT-based patient monitoring and heart disease prediction system using deep learning modified neural network," *IEEE Access*, vol. 8, pp. 135784–135797, 2020.
[16] S. A. Ali, B. Raza, A. K. Malik, A. R. Shahid, M. Faheem, H. Alquhayz, and Y. J. Kumar, "An optimally configured and improved deep belief network approach for heart disease prediction," *IEEE Access*, vol. 8, pp. 65947–65958, 2020.
[17] L. Ali, A. Rahman, A. Khan, M. Zhou, A. Javeed, and J. A. Khan, "An automated diagnostic system for heart disease prediction based on chi-square statistical model and optimally configured deep neural network," *IEEE Access*, vol. 7, pp. 34938–34945, 2019.
[18] F. Yazdi and S. Asadi, "Enhancing cardiovascular disease diagnosis: The power of optimized ensemble learning," *IEEE Access*, vol. 13, pp. 46747–46762, 2025.
[19] M. Obayya, J. M. Alsamri, M. A. Al-Hagery, A. Mohammed, and M. A. Hamza, "Automated cardiovascular disease diagnosis using honey badger optimization with modified deep learning model," *IEEE Access*, vol. 11, pp. 64272–64281, 2023.
[20] M. Trigka and E. Dritsas, "Improving cardiovascular disease prediction with deep learning and correlation-aware SMOTE," *IEEE Access*, 2025.
[21] B. Jin, C. Che, Z. Liu, S. Zhang, X. Yin, and X. Wei, "Predicting the risk of heart failure with EHR sequential data modeling," *IEEE Access*, vol. 6, pp. 9256–9261, 2018.
[22] M. Blanchard, M. Feuilloy, A. Sabil, C. Gerves-Pinquie, F. Gagnadoux, and J. M. Girault, "A deep survival learning approach for cardiovascular risk estimation in patients with sleep apnea," *IEEE Access*, vol. 10, pp. 133468–133478, 2022.
[23] Y. Li, M. Mamouei, G. Salimi-Khorshidi, S. Rao, A. Hassaine, D. Canoy, T. Lukasiewicz, and K. Rahimi, "Hi-BEHRT: Hierarchical transformer-based model for accurate prediction of clinical events using multimodal longitudinal electronic health records," *IEEE Journal of Biomedical and Health Informatics*, vol. 27, no. 2, pp. 1106–1117, 2022.
[24] M. A. Ahmad, C. Eckert, and A. Teredesai, "Interpretable machine learning in healthcare," in *Proc. ACM Int. Conf. Bioinformatics, Computational Biology, and Health Informatics*, 2018, pp. 559–560.
[25] W. Saeed and C. Omlin, "Explainable AI (XAI): A systematic meta-survey of current challenges and future opportunities," *Knowledge-Based Systems*, vol. 263, p. 110273, 2023.
[26] J. Wu, S. Luo, S. Wang, and H. Wang, "NLES: A novel lifetime extension scheme for safety-critical cyber-physical systems using SDN and NFV," *IEEE Internet of Things Journal*, vol. 6, no. 2, pp. 2463–2475, 2018.
[27] F. Ali, S. El-Sappagh, S. R. Islam, D. Kwak, A. Ali, M. Imran, and K. S. Kwak, "A smart healthcare monitoring system for heart disease prediction based on ensemble deep learning and feature fusion," *Information Fusion*, vol. 63, pp. 208–222, 2020.
[28] S. Mishra, A. Dash, P. Ranjan, and A. K. Jena, "Enhancing heart disorders prediction with attribute optimization," in *Proc. Int. Conf. Emerging Trends and Advances in Electrical Engineering and Renewable Energy*, 2020, pp. 139–145.
[29] X. H. Xu, B. Sun, S. Zhong, D. D. Wei, Z. Hong, and A. Q. Dong, "Diabetic retinopathy predicts cardiovascular mortality in diabetes: A meta-analysis," *BMC Cardiovascular Disorders*, vol. 20, no. 1, p. 478, 2020.
[30] P. Rani, R. Kumar, N. M. S. Ahmed, and A. Jain, "A decision support system for heart disease prediction based upon machine learning," *Journal of Reliable Intelligent Environments*, vol. 7, no. 3, pp. 263–275, 2021.

[31] B. A. Tama, S. Im, and S. Lee, "Improving an intelligent detection system for coronary heart disease using a two-tier classifier ensemble," *BioMed Research International*, vol. 2020, p. 9816142, 2020.
[32] J. Maiga and G. G. Hungilo, "Comparison of machine learning models in prediction of cardiovascular disease using health record data," in *Proc. Int. Conf. Informatics, Multimedia, Cyber and Information System (ICIMCIS)*, 2019, pp. 45–48.
[33] G. Tian, C. Lian, Z. Zeng, B. Xu, Y. Su, J. Zang, Z. Zhang, and C. Xue, "Imbalanced heart sound signal classification based on two-stage trained DSANet," *Cognitive Computation*, vol. 14, no. 4, pp. 1378–1391, 2022.
[34] E. Ghaderpour, S. D. Pagiatakis, and Q. K. Hassan, "A survey on change detection and time series analysis with applications," *Applied Sciences*, vol. 11, no. 13, p. 6141, 2021.
[35] S. Ismail and B. Ismail, "PCG signal classification using a hybrid multi-round transfer learning classifier," *Biocybernetics and Biomedical Engineering*, vol. 43, no. 1, pp. 313–334, 2023.
[36] A. Tiwari, A. Chugh, and A. Sharma, "Ensemble framework for cardiovascular disease prediction," *Computers in Biology and Medicine*, vol. 146, p. 105624, 2022.
[37] V. Chang, V. R. Bhavani, A. Q. Xu, and M. A. Hossain, "An artificial intelligence model for heart disease detection using machine learning algorithms," *Healthcare Analytics*, vol. 2, p. 100016, 2022.
[38] M. N. R. Chowdhury, E. Ahmed, M. A. D. Siddik, and A. U. Zaman, "Heart disease prognosis using machine learning classification techniques," in *Proc. Int. Conf. for Convergence in Technology (I2CT)*, 2021, pp. 1–6.
[39] M. A. Khan and F. Algarni, "A healthcare monitoring system for the diagnosis of heart disease in the IoMT cloud environment using MSSO-ANFIS," *IEEE Access*, vol. 8, pp. 122259–122269, 2020.
[40] A. Janosi, W. Steinbrunn, M. Pfisterer, and R. Detrano, "Heart disease dataset," *UCI Machine Learning Repository*, 1989