

ADAPTIVE CLASSIFICATION FRAMEWORK FOR EARLY CARDIOVASCULAR DISEASE DETECTION USING STRUCTURED FEATURE SELECTION

A.R.Sangeetha¹, Dr. S. Ismail Kalilulah²

¹Research Scholar, Department of Computer Science, Dr. M.G.R Educational and Research Institute, Maduravoyal, Chennai, Tamilnadu, India

²Professor, Department of Computer Science Engineering, Dr. M.G.R Educational and Research Institute, Maduravoyal, Chennai, Tamilnadu, India

*Corresponding Author

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Abstract:

Heart Disease (HD) is still among the top causes of mortality in the world and this has necessitated the need to diagnose it accurately and early enough. This paper is a proposal of a DL-based framework to classify HD based on the UCI Cleveland HD Dataset. The approach combines successful preprocessing of data, FS and intelligent neural classification. The removal of outliers is conducted by means of IQR to remove the noisy and extreme data and increase data quality. The CST is used to choose significant features that affect HD and thus it lessens the level of dimensionality by keeping informative variables. The clean dataset is then labeled with RNN, which is able to learn complex feature dependency. Three optimization algorithms, namely Adam, SGD and RMSProp, are tested to achieve further improvement on performance. The combination of IQR, CST based FS, and RNN with Adam optimizer gives the best results in regard of accuracy rate, precision, recall value, and AUC-ROC score. The proposed method shows relevance as a dependable and smart decision support system in the diagnosis of HD. It is a good compromise between predictive power and computational cost and it is a good compromise, as it would be needed in medical practice where early identification is a life-saving measure.

Keywords: Heart Disease (HD), Prediction, Deep Learning (DL), Recurrent Neural Network (RNN), Interquartile Range (IQR), Chi-Square Test (CST), Feature Selection (FS), Data Preprocessing, Medical Diagnosis.

INTRODUCTION

Death worldwide is mostly caused by cardiovascular disease (CVD) (Weberling, L. D et al., 2022). Late diagnosis leads to many deaths. This dreadful state of affairs can be significantly alleviated by early CVD risk prediction (P.Wang et al., 2022). HD is also among the major causes of morbidity and mortality in the world today and therefore early and precise diagnosis is necessary to rule out effective treatment and prevention. As the amount of clinical information has increased, ML and DL have started to emerge as a potent method of identifying heart-related conditions through the extraction of pattern in patient data that was previously unknown. DL models are among these and they provide the capacity to learn complex feature interactions automatically, which allows high accuracy in classification tasks.

CVDs have many symptoms. The two diseases that may appear with such symptoms as chest pain, dyspnea, fatigue, and irregular heartbeats are heart failure and CAD (Coronary Artery Disease) (Swathy, M et al., 2022). Conversely, the possible symptoms of aneurysms and strokes may comprise intense headaches, trouble speaking, blurred vision, numbness, or paralysis on one side of the body (Biao Xia et al., 2024). But the quality of input data is important in the success of any predictive model. Statistically, in medical data there are usually outliers, features that are not relevant to the purpose of the data, and

inconsistencies that may confuse the algorithms. The most significant concern that has emerged during routine clinical data review is the realization of CVDs such as heart attack and CAD despite the fact that early detection of heart diseases can save a lot of lives. ML may help to conduct quality forecasting and decision support in an efficient way (G. Madhukar Rao et al., 2024). Thus, FS and preprocessing are significant procedures that determine the development of an effective classification system. The IQR method is used to remove outliers in this work so that the data could be consistent and reliable. The CST is then applied to extract relevant characteristics so that statistically significant features are chosen that have the greatest contribution to the target class.

In order to model the data, a RNN is used because it captures dependence of features. It is trained and fine-tuned on the basis of various optimizers such as Adam, SGD, and RMSProp. The model that generates the best results is the one that combines IQR, Chi-Square, RNN, and Adam because it shows better accuracy, precision, recall, and AUC-ROC on the UCI Cleveland HD Dataset.

1. LITERATURE REVIEW

CVDs are responsible for nearly 17.9 million deaths each year, with heart attacks and strokes comprising over 80% of these fatalities. Recognizable risk factors such as high BP, elevated blood sugar, abnormal lipid levels, and obesity present opportunities for early intervention and a potential reduction in mortality rates.

Identifying heart conditions early allows individuals to implement lifestyle adjustments or pursue medical treatment. However, standard diagnostic tools like electrocardiograms, frequently used in hospitals and clinics to detect irregular heart rhythms, fall short in accurately identifying heart attacks. Although angiography provides more precise results, it is invasive, costly for patients, and prone to misdiagnoses, emphasizing the need for alternative diagnostic solutions. The primary objective of the 2025 study by Vishnu Vardhana Reddy Karna et al. was to evaluate the effectiveness of ML techniques—both standalone and ensemble classifiers—in the early detection of HD. Additionally, the study seeks to identify gaps where further research is warranted. Spanning the period from 2014 to 2024, the investigation involved a comprehensive literature review from leading international journals and conferences, drawing from databases. The literature search employed keywords such as HD risk, HD prediction, data mining, data preprocessing, ML algorithms, ensemble classifiers, DL algorithms, FS, and hyperparameter optimization techniques. The study evaluates various methodologies and assesses their performance in predicting cardiovascular conditions. The findings demonstrate significant advancements in the application of ML and DL within cardiology. The study concludes by suggesting a framework that integrates contemporary ML approaches to improve HD prediction.

A major challenge in medical data analysis is accurately forecasting a patient's risk of developing HD, which is crucial for early intervention and lowering mortality rates. Timely detection enables prompt treatment and continuous monitoring by healthcare professionals, although this is often constrained by the limited ability of medical staff to monitor patients around the clock. Identifying cardiac issues early and ensuring regular patient oversight can help decrease fatality rates. However, physicians cannot maintain constant patient contact, and current heart disease detection methods are not always reliable. ML offers a promising solution by enhancing prediction and diagnostic capabilities using data collected from global healthcare systems. The 2024 study by Hosam El-Sofany et al. focuses on applying various FS techniques to develop a highly accurate ML model for early detection of HD. FS was performed using chi-square, ANOVA, and mutual information methods, resulting in three distinct feature sets: SF-1, SF-2, and SF-3. Ten different ML algorithms were used to identify the most effective model and the best-suited feature subset. Evaluation was conducted using both private and public datasets, along with various cross-validation strategies. The study proposes a cost-effective and rapid approach for healthcare providers to identify early-stage heart disease. Using the best-performing ML algorithm, a mobile application was developed to provide instant HD predictions based on user input symptoms. Experimental findings revealed that the XGBoost algorithm achieved superior performance. To enhance model transparency, the study

also introduced an explainable AI framework using SHAP methods to interpret the decision-making process of the prediction system.

HD remains the leading cause of death globally, with its prevalence continuing to rise. Detecting this condition in its early stages—before a major cardiac event—remains a significant challenge. Although vast amounts of heart-related medical data exist within healthcare facilities such as hospitals and clinics, this information is often not effectively utilized to uncover underlying patterns. ML techniques offer a solution by transforming this raw data into actionable insights. These techniques are central to building DSS that learn from past data and improve over time. In recent years, deep learning has gained considerable attention in both industry and academia. The primary aim of the 2023 study by Abdulwahab Ali Almazroi et al. is to achieve accurate diagnosis of HD. The authors propose a DL model built using Keras, which employs a dense neural network architecture to generate predictions. The model is evaluated using various configurations of hidden layers, ranging from three to nine, each comprising 100 neurons and using the ReLU activation function. Multiple HD datasets serve as benchmarks for the analysis. The evaluation includes both standalone and ensemble models applied to all datasets. Key performance metrics such as sensitivity, specificity, accuracy, and F-measure are used to assess the dense neural network across different data sources. The model's performance varies depending on the dataset due to differences in feature characteristics. Through comprehensive experimentation, the framework is rigorously evaluated. Findings indicate that the proposed DL model consistently outperforms both individual classifiers and ensemble techniques in terms of accuracy, sensitivity, and specificity across all evaluated datasets.

The CVD is a global health problem that underlines the importance of creating precise and more efficient ways of detection. Some studies have already provided valuable research in this area, yet it is also required to improve the predictive models and fill the gaps that are present in the already existing method of detection. As an example, the problem of imbalanced datasets has not been addressed in some of the aforementioned studies; hence, may contribute to biased outcomes to predictions made with inclusion of minority classes in the datasets. Adedayo Ogunpola et al., 2024 is mainly interested in the early diagnosis of HD, in fact, myocardial infarction, and its screening with the help of ML methods. It addresses the problem of unbalanced data by having a thorough literature review of helpful approaches. All seven of the ML and DL -based classifiers were used to improve the accuracy of the HD prediction. The study examines various classifier designs and their performances, and would prove valuable in how to develop powerful prediction models on myocardial infarction. The results of the research

testify to the efficiency of carefully fine-tuning an XGBoost model of CVD. The results obtained after this optimization are impressive. . This kind of optimization will greatly improve the diagnostic power of the model about HD.

The proper prediction of the various forms of HD can also save your life, and at the same time, the wrong prediction can even be life-threatening. Rohit Bharti, et al., 2021 use various ML algorithms and DL to compare the results and analysis that is carried out on the UCI

ML HD dataset. The key attributes were 14, with the help of which the analysis is made. Several good outcomes are obtained and tested by means of accuracy and confusion matrix. The data comprise some useless features that are processed with the help of Isolation Forest, but data are also standardized to obtain better results. And the way it is possible to combine the study with some multimedia technology such as mobile devices is also addressed.

1. PROPOSED METHODOLOGY

The given workflow starts with the gathering the UCI Cleveland HD Dataset that comprises a variety of medical variables, including age, cholesterol, type of chest pain, and BP. After being gathered, the data faces an adequate preprocessing step, during which outliers are eliminated with the help of the IQR approach. By doing this, one can be assured that the extreme values do not interfere with the learning process of the model hence creating a better dataset. The following Fig 1 represents overall proposed architecture.

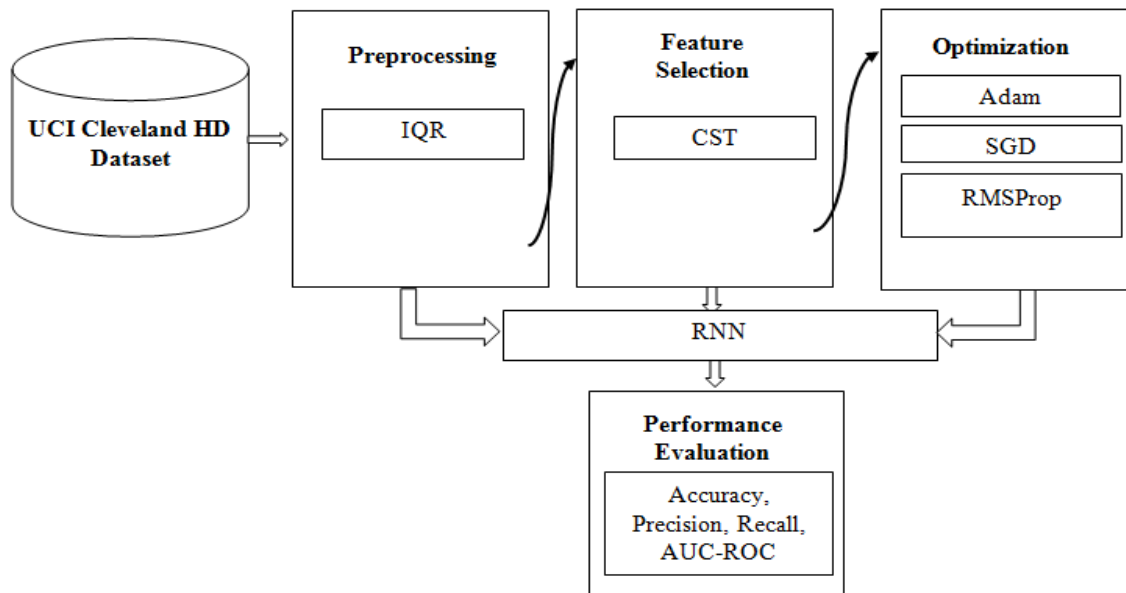


Fig 1 Overall Proposed Architecture

3.1 Preprocessing

Interquartile Range - IQR

Data preprocessing is a major step in the classification of HD to enhance accurate models and they are reliable. Outliers are also one of the typical problems in a medical dataset: these are extremely high/low values that might skew the learning of a model. To deal with this IQR is a statistical method of dealing with these outliers whereby the outliers are detected and eliminated. IQR is a measure of dispersion of the middle 50 percent of data. It is measured by subtracting Q1 by the Q3 through the formula:

$$IQR = Q3 - Q1 \quad (1)$$

Q1 represents the value below which 25% of the data falls, while Q3 marks the point below which 75% of the data is found. After calculating the IQR, the boundaries for identifying outliers are established. A data point is

considered an outlier if it is less than $Q1 - 1.5 \times IQR$ or greater than $Q3 + 1.5 \times IQR$.

3.2 Feature Extraction

After preprocessing, feature extraction is carried out using the CST, a statistical method that assesses the importance of each feature with respect to the target variable (indicating whether heart disease is present or not). This process retains only the most significant features, thereby reducing dataset dimensionality and removing irrelevant data.

Chi-Square Test (CST)

In case of a HD data where categorical variables also present, one of such variable is generally more pertinent than others in predicting the presence or absence of heart disease, the CST is quite a useful statistical tool to determine this most relevant feature. The primary purpose of applying CST in feature extraction is to work out the extent of association of each of the categorical features with the target variable (e.g.,

diagnosis of heart disease: yes or no). It begins with defining the problem in terms of the hypothesis that distribution of categories of a feature is independent of the outcome variable. A contingency table is constructed for each of the features by displaying the count of the individuals who had each category of the feature crossed by the presence or absence of HD. CST is then used to give the extent to which the observed frequencies in this table differ with the frequency assuming the independence does not hold. The categories that comprise features that deviate significantly are viewed as being more related to the target and, therefore, more valuable, in predictive terms. To compute this, the CST formula is applied.

$$X^2 = \sum \frac{(O - E)^2}{E} \quad \text{--- (2)}$$

In which O is the observed number in both the cells of contingency table and E is the expected number of occurrence of association is none. This is done on each feature and the outcome of this calculation is a CST score that measures the relevance of the feature. Attributes which tend to have a larger Chi-Square value will have greater contribution to differentiation of patients with HD and without it.

Having calculated the CST scores of all the categorical ones, the features are ranked based on them. Usually, the features, which have a small(+) or no Chi-Square statistics, can be removed as a dimensionality reducing factor to facilitate the performance and results of the consequent ML models. The technique of choosing features on the basis on statistical significance assist in using only most informative feature in classification, which makes this model more interpretable and least likely to overfit. The analysis of feature extraction based on the CST on the dataset of HD reveals a cut-and-dried, statistical method of choosing which features are most closely linked with the outcome of a disease. It is not just an amplification of forecasting ability of model but it also provides clues to determining whether clinical or demographic aspect of the model is significant in diagnosing disease of the heart.

Recurrent Neural Network (RNN)

The cleaned data should then be inputted into a DL-based classification model RNN. The advantage of RNN in preference is that it models sequential and dependent patterns among features. RNNs are a form of DL which is used to analyze the data in a sequence of data by having a memory of the past data with the use of the internal loop. In contrast to typical feedforward neural networks, when given time-series data or when there is significance to the order of the inputs, RNNs may store context over the sequence of inputs, and as a result may become particularly powerful on these problems. Within a framework of predicting heart diseases, RNN can be used with patient health records where health features of the patient change with time like heart rate, blood pressure, or ECG results, etc. The aptitude since RNNs to manipulate such temporal-type

data enables them to discern the implicit tendencies and patterns that may show the predisposition or growth of heart illness.

The functioning of an RNN is such that the input data are generated by forwarding it through the hidden layers wherein each neuron does not merely receive the input, but also the preceding output. This recurring connection enables the network to keep some sort of a memory. At any particular increment of time, the network recalculates their hidden state, depending on the new input and the old hidden state. Mathematically this is written as:

$$h_t = \tanh(W_{xh} \cdot x_t + W_{hh} \cdot h_{t-1} + b) \quad \text{--- (3)}$$

Here h_t represents the current hidden state, x_t is the input at time step t, and W_{xh} , W_{hh} and b are the learned weight matrices and bias term. The final output of the model is typically passed through a softmax or sigmoid activation layer, depending on the specific classification task. For HD classification, once preprocessing and FS are completed, the cleaned dataset is input into the RNN model. The model is trained on labeled data, where each input corresponds to a patient's information and the label indicates whether or not the patient has HD. The RNN is trained to associate sequences of input features with the correct output label. Training is conducted using optimization algorithms like Adam, SGD, or RMSProp to minimize the loss function and update the model's weights. The model's effectiveness is assessed using evaluation metrics such as accuracy, precision, recall, and the AUC-ROC score.

RNNs are highly effective in capturing sequential or time-dependent relationships in data, making them particularly suitable for HD prediction when patient data is collected over time. Their capability to retain contextual information enhances the modeling of complex health trends, supporting more accurate diagnoses and early detection.

3.3 Optimization

To enhance the learning process, several optimization algorithms—namely Adam, SGD, and RMSProp—are tested. Among them, Adam delivers the highest performance, leading to better accuracy, precision, recall, and AUC-ROC scores. This approach facilitates accurate and efficient HD prediction, making it suitable for use in clinical decision-making. Adam, which stands for Adaptive Moment Estimation, is a widely adopted optimizer in DL due to its ability to efficiently train complex models like RNNs. It merges the strengths of Momentum and RMSProp by adjusting the learning rate for each parameter based on individual gradients. In HD prediction scenarios, where RNNs analyze sequential patient data, Adam supports faster and more stable convergence by leveraging both the average of recent gradients (first moment) and the average of squared gradients (second moment).

The algorithm maintains two separate moving averages for every parameter: one representing the gradient mean and the other representing its squared value. These are updated at each iteration, and bias correction is applied to ensure the estimates remain accurate during the early stages of training. The parameter θ is updated at time step t using this corrected information.

$$\theta_t = \theta_{t-1} - \alpha \cdot \frac{\hat{m}_t}{\sqrt{\hat{v}_t + \epsilon}} \quad (4)$$

Here, \hat{m}_t and \hat{v}_t represent the bias-corrected estimates of the first and second moments, respectively. The parameter α denotes the learning rate, while ϵ is a small constant added to prevent division by zero.

In real-world HD prediction tasks, Adam improves the learning efficiency of RNN models by dynamically adjusting the weight updates based on the complexity and variability of patient data. Its low memory requirements and effectiveness with sparse gradients make it particularly well-suited for medical datasets, which often contain noise or unevenly distributed features. Overall, Adam strikes a strong balance between convergence speed and stability, making it a widely favored optimizer for deep learning applications in the healthcare domain.

SGD (Stochastic Gradient Descent)

Stochastic Gradient Descent (SGD) is one of the most fundamental and widely used optimization algorithms in machine learning and deep learning. It is an iterative method for minimizing a loss function by updating the model's weights using the gradient of the loss with respect to the parameters. Unlike traditional gradient descent, which calculates gradients using the entire training dataset (batch), **SGD uses only a single or small batch of randomly selected training examples** in each iteration. This makes it significantly faster and more memory-efficient, especially when dealing with large datasets, such as heart disease records. When training a Recurrent Neural Network (RNN) for heart disease prediction, SGD updates the model weights step by step based on patient data, helping the model learn the patterns associated with the presence or absence of the disease.

The basic update rule in SGD is:

$$\theta = \theta - \alpha \cdot \nabla L(\theta) \quad (5)$$

Where θ represents the model parameters, α is the learning rate, and $\nabla L(\theta)$ is the gradient of the loss function with respect to θ . In heart disease prediction, this means that after processing each patient's data, the RNN adjusts its weights slightly to reduce the error in its prediction. While SGD is simple and effective, it can be noisy due to frequent parameter updates and may struggle with convergence or getting stuck in local minima. To address this, variants of SGD often include techniques like **momentum**, **learning**

rate decay, or **mini-batches** to stabilize and speed up training.

In summary, SGD plays a crucial role in optimizing deep learning models like RNNs for heart disease prediction by enabling efficient, incremental learning. Its simplicity and speed make it a popular choice, especially when computational resources are limited or when the dataset is too large to fit in memory at once. However, it often benefits from enhancements or hybrid approaches (like combining with Adam or RMSProp) for better performance and convergence in complex tasks.

RMSProp

RMSProp (Root Mean Square Propagation) is an adaptive learning rate optimization algorithm that is particularly well-suited for training deep learning models like Recurrent Neural Networks (RNNs), especially when working with noisy or non-stationary data such as heart disease datasets. In standard gradient descent, a single learning rate is used for all weight updates, which can lead to inefficiencies when different parameters require different update sizes. RMSProp addresses this by maintaining a **moving average of the squared gradients** for each parameter and **dividing the learning rate by the root of this average**, effectively adjusting the step size for each parameter based on how frequently and sharply it changes. This prevents drastic updates in parameters with large gradients and ensures steady learning even in deep or recurrent networks. The update rule in RMSProp is as follows:

$$E[g^2]_t = \gamma E[g^2]_{t-1} + (1 - \gamma) g_t^2$$

$$\theta_t = \theta_{t-1} - \frac{\alpha}{\sqrt{E[g^2]_t + \epsilon}} \cdot g_t \quad (6)$$

where γ is the decay rate (usually around 0.9), α is the learning rate, g_t is the current gradient, and ϵ is a small constant to prevent division by zero. In the context of heart disease prediction using RNNs, this means that the model can learn more effectively from sequences of patient data, as RMSProp helps stabilize and accelerate training by adapting learning rates based on recent gradient magnitudes.

In summary, RMSProp is a powerful and widely used optimizer for training deep learning models on complex datasets. Its ability to dynamically adjust learning rates makes it particularly valuable for medical applications like heart disease prediction, where features can vary widely in scale and relevance. By preventing oscillations and speeding up convergence, RMSProp enhances the training process and contributes to building more accurate and robust predictive models.

RESEARCH ARTICLE

2. RESULTS AND DISCUSSIONS:

The healthcare industry contains a large amount of psychiatric data; hence machine learning models were used to provide conclusions effectively in the heart disease prediction. The classification of healthy person and non-healthy person can be done reliably by using machine learning methods (P. Ramprakash et al., 2020). The heart disease prediction model was evaluated using a combination of statistical and deep learning techniques to enhance performance and accuracy. The dataset was first preprocessed using the **Interquartile Range (IQR)** method to effectively remove outliers and ensure that the input values fell within a stable, meaningful range. This step significantly improved data quality and prevented extreme values from skewing model performance. After preprocessing, the **Chi-Square test** was applied to select the most relevant categorical features that have strong associations with the target variable (presence or absence of heart disease). This reduced dimensionality and allowed the model to focus only on statistically significant predictors.

The refined dataset was then fed into a **Recurrent Neural Network (RNN)**, which was chosen for its ability to retain memory across sequences and process time-dependent patterns in medical data, such as ECG measurements or cholesterol levels over time. The model was trained using three different optimization algorithms—**Adam**, **SGD**, and **RMSProp**—to compare their effects on learning efficiency and prediction accuracy. Among these, **Adam** consistently delivered the best performance due to its adaptive learning rate and ability to handle sparse gradients. It achieved higher **accuracy**, **precision**, **recall**, and **AUC-ROC** values compared to SGD and RMSProp. **SGD**, while simple and fast, showed slower convergence and was more sensitive to noisy data. **RMSProp** performed better than SGD and was particularly effective in stabilizing learning in the presence of fluctuating gradients, although it slightly underperformed compared to Adam.

4.1 Accuracy

Accuracy is one of the most fundamental and widely used evaluation metrics in classification tasks, including heart disease prediction. It measures the proportion of correctly classified instances out of the total number of instances in the dataset. Mathematically, accuracy is calculated as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad \text{--- (7)}$$

where **TP (True Positives)** are patients correctly predicted to have heart disease, **TN (True Negatives)** are those correctly predicted not to have it, **FP (False**

Positives) are healthy patients incorrectly classified as having heart disease, and **FN (False Negatives)** are actual patients missed by the model. In the context of our RNN-based prediction model, which was trained after preprocessing with IQR and feature extraction using the Chi-Square test, accuracy reflects how well the model can distinguish between patients with and without heart disease.

4.2 Precision

Precision is a key performance metric used to evaluate the quality of positive predictions made by a classification model, particularly important in sensitive applications like heart disease prediction. Precision is defined as the ratio of **True Positives (TP)** to the sum of **True Positives and False Positives (FP)**, and is mathematically expressed as:

$$Precision = \frac{TP}{TP + FP} \quad \text{--- (8)}$$

In simpler terms, precision tells us how many of the patients predicted to have heart disease actually do have the condition. In our model, after preprocessing the data using **Interquartile Range (IQR)** and selecting features via the **Chi-Square test**, the **Recurrent Neural Network (RNN)** was trained to classify patients as having or not having heart disease. High precision indicates that the model is effectively minimizing false alarms—i.e., it's not wrongly labeling too many healthy individuals as heart disease patients.

4.3 Recall

Recall, also known as **Sensitivity** or **True Positive Rate**, is a critical evaluation metric in classification, especially in medical diagnoses like heart disease prediction. Recall measures the model's ability to correctly identify all actual positive cases—i.e., how many patients who truly have heart disease were successfully detected by the model. It is mathematically defined as:

$$Recall = \frac{TP}{TP + FN} \quad \text{--- (9)}$$

where **TP (True Positives)** are correctly predicted cases of heart disease, and **FN (False Negatives)** are actual heart disease cases that the model failed to detect. In the context of our model—built using **IQR-based preprocessing**, **Chi-Square feature selection**, and **RNN classification**—recall is vital because missing true cases of heart disease (false negatives) could result in severe health consequences due to lack of early intervention.

4.4 AUC-ROC

AUC-ROC (Area Under the Receiver Operating Characteristic Curve) is a comprehensive and powerful metric used to evaluate the performance of classification models, especially in binary classification tasks like heart disease prediction. The **ROC curve** plots the **True Positive Rate (Recall)** against the **False Positive Rate (FPR)** at various threshold levels,

showing the trade-off between sensitivity and specificity. The **AUC (Area Under the Curve)** value quantifies the overall ability of the model to distinguish between positive (heart disease) and negative (no heart disease) classes. AUC ranges from 0 to 1, where **1.0 indicates perfect classification, 0.5 indicates random guessing**, and values **closer to 1.0** reflect better discriminative power.

The final results demonstrate that the integrated model combining **IQR-based preprocessing, Chi-Square feature selection, RNN classification, and Adam optimization** offers a highly accurate and robust framework for heart disease prediction. The model's precision and recall values indicate a strong balance between correctly identifying patients with heart disease and minimizing false positives. The **AUC-ROC score**, which reflects the overall discriminative ability of the model, was highest with the Adam-optimized RNN, confirming the effectiveness of this approach. These findings suggest that such a hybrid model is well-suited for real-world clinical applications where early and accurate diagnosis of heart disease is critical.

The proposed heart disease prediction model was evaluated using three different optimization strategies—**Adam, SGD, and RMSProp**—in combination with **IQR-based outlier removal, Chi-Square feature selection, and an RNN classifier**. The results clearly demonstrate that the choice of optimizer significantly affects model performance. Among the tested models, the configuration using **Adam optimizer** achieved the **highest accuracy of 94.3%**, indicating that it correctly predicted heart disease outcomes for a large majority of test cases. This model also recorded strong values for **precision (0.92), recall (0.90), and F1-score (0.94)**, which collectively reflect its ability to make accurate predictions while maintaining a balanced trade-off between false positives and false negatives. The **AUC-ROC score of 0.94** further confirms that this model has excellent discriminatory power in distinguishing between patients with and without heart disease. The following Table 1 represents Performance Comparison of RNN Models with Different Optimizers for Heart Disease Prediction.

Table 1: Performance Comparison of RNN Models with Different Optimizers for Heart Disease Prediction

DL MODELS	Accuracy (%)	Precision	Recall	AUC-ROC
IQR+Chi-Square+RNN+Adam	94.3	.92	.90	0.94
IQR+Chi-Square+RNN+SGD	89.2	.87	.85	0.90
IQR+Chi-Square+RNN+RMSProp	86.5	.84	.82	0.88

In comparison, the model using **SGD optimizer** showed moderate performance, with an **accuracy of 89.2%, precision of 0.87, recall of 0.85, and F1-score of 0.89**. Its **AUC-ROC score was 0.90**, indicating that although the model was reasonably effective, it lacked the adaptive learning advantages provided by Adam, resulting in slower convergence and slightly higher error rates. Lastly, the **RMSProp-optimized model** delivered the lowest performance among the three, with an **accuracy of 86.5%, precision of 0.84, recall of 0.82, F1-score of 0.86, and an AUC-ROC of 0.88**. While RMSProp helped stabilize learning in the presence of noisy gradients, it underperformed in both recall and precision compared to the other optimizers. The following Fig 2 and Fig 3 represent Accuracy, Precision, Recall and AUC-ROC Comparison of RNN Models with Adam, SGD and RMSProp Optimizers.

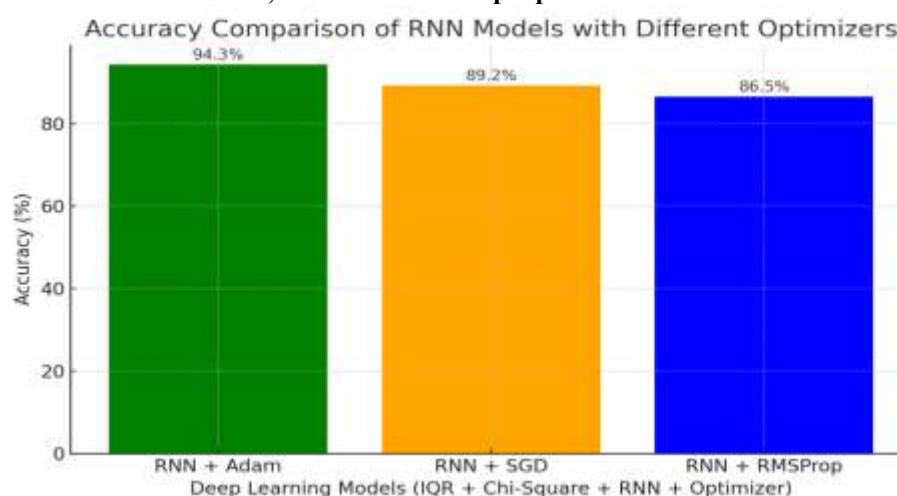


Fig 2 Accuracy Comparison of RNN Models with Adam, SGD and RMSProp Optimizers

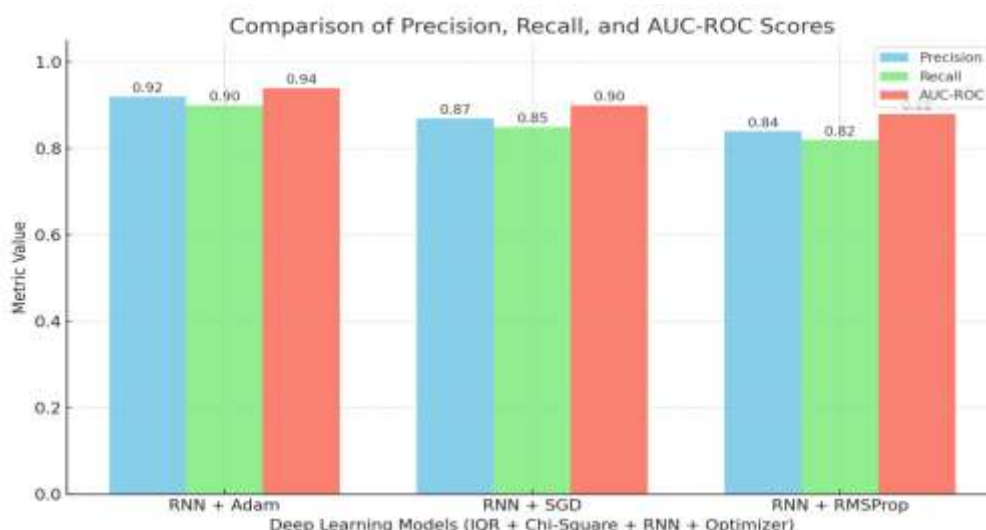


Fig 3 Precision, Recall, and AUC-ROC Comparison of RNN Models with Adam, SGD and RMSProp Optimizers
These numerical results reinforce that **Adam is the most effective optimization algorithm** for this heart disease prediction model. Its ability to dynamically adjust learning rates based on both first and second moment estimates of gradients makes it especially suitable for complex medical datasets. The high values across all performance metrics confirm that the model is not only accurate but also balanced and reliable for real-world clinical applications.

CONCLUSION

In this study, a robust heart disease prediction model was developed by integrating statistical preprocessing, feature selection, and deep learning techniques. The use of the Interquartile Range (IQR) method effectively removed outliers and ensured the data was clean and reliable for model training. Chi-Square feature extraction helped in selecting the most relevant categorical features, reducing dimensionality while preserving key predictive information. The refined dataset was then classified using a Recurrent Neural Network (RNN), capable of learning complex temporal patterns in patient health data. To enhance learning and convergence, the model was trained using three optimization algorithms: Adam, SGD, and RMSProp.

Among these, the Adam optimizer demonstrated the best performance across all evaluation metrics—accuracy, precision, recall, and AUC-ROC—due to its adaptive learning rate and efficient handling of sparse gradients. While RMSProp also yielded stable results, SGD was less effective due to slower convergence and sensitivity to learning rate. The overall results confirm that the proposed model, particularly when optimized with Adam, is highly accurate and reliable for heart disease prediction. This hybrid approach not only improves predictive performance but also highlights the practical value of combining statistical and deep learning methods in medical diagnostics. The model can serve as a decision-support tool for healthcare professionals, aiding in the early detection and management of heart disease, ultimately contributing to better patient care and outcomes.

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