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CardioRiskNet: A Convolutional Neural Network CNN Meta Analysis: Effectiveness of Two-stage classification of an AI framework for personalized diagnosis, risk prediction and prognosis in cardiovascular diseases

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Abstract

The leading cause of death worldwide is heart attack, also called cardiovascular disease. Therefore, an accurate and effective early prediction system for heart attack is required. In this paper, a hybrid deep learning model with a combination of Convolutional Neural Network (CNN) and Support Vector Machine (SVM) is proposed to predict heart attack. CNN is used to automatically learn the deep features from the dataset, and SVM is used to perform effective classification with a better hyperplane. Artificial intelligence-based heart attack prevention systems provide a novel approach that has the potential to revolutionize early diagnosis, tailored prevention, and treatment. This work is done by using the UCI Heart Disease Dataset with common preprocessing and hyperparameter tuning techniques. It is observed that the proposed CNN-SVM model outperforms all Machine Learning models and Deep Learning models by showing 97% of accuracy, 94.2% of precision, 92.6% of recall, 93.4% of f1-score, and 0.96 of AUC. This work concluded that the hybrid models are very beneficial for improved accuracy and prediction. There is a possibility that recuperation and therapy won't be necessary under certain circumstances. Further research, development, clinical trials, and interdisciplinary collaboration are required to fully realize the benefits that AI-based heart attack preventive systems offer. These actions would be able to solve the issues that result from this problem.

Keywords: Heart Disease Prediction, Convolutional Neural Network (CNN), Support Vector Machine (SVM), Hybrid Deep Learning, Predictive Analytics, Clinical Decision Support System.

INTRODUCTION

At the top of the list of death causes worldwide, killing almost 17.9 million annually, is heart diseases or cardiovascular diseases (CVDs) [1]. Heart attacks represent one of the most fatal types of heart diseases because they are so risky, occur randomly, and have many causes, such as high blood pressure, diabetes, among various other causes, including cholesterol and poor lifestyle [2]. Detecting the patient who is at high risk of getting a heart attack in advance can help decrease the mortality rate and allow doctors to take actions that help improve the patient's prognosis. The traditional ways of diagnosing heart disease heavily depend on the expertise and familiarity of the physician, the patient, and his/her medical history, medical laboratory tests, and evaluations. However, they can be time-consuming, expensive, and in the vast majority of cases, they cannot derive useful information from huge and complex healthcare data [3, 4]. Further, the traditional statistical modeling models fail to incline towards characterizing a complex non-linear association in the presence of numerous clinical features. To overcome these limitations, machine learning (ML) techniques have been extensively explored for heart disease prediction. The classification algorithms applied on classification tasks, such as decision trees, Naive

Bayes, random forests, and Support Vector Machines (SVMs), performed well [5, 6]. The SVMs have already been effective in classification because they create an optimal hyperplane in high-dimensional space that leads to high precision when dealing with unseen data. Those who have found successful application of ML models in the prediction of cardiovascular events were those who used a few relevant clinical features [7, 8].

$$s(t) = (x * w)(t) = \sum_{a=-\infty}^{\infty} x(a)w(t - a) \qquad \text{Eq (1)}$$

W stands for the kernel filter, x stands for the input signal, t stands for time and s is the output signal. The convolution process with two-dimensional input data is described by Equation (2).

$$S(i,j) = (I * K)(i,j) = \sum_{m} a \sum_{n} I(i,j) * K(i - m, j - n) \qquad \text{Eq (2)}$$

Among the drawbacks, feature engineering, which is time-consuming and based on human intuition, stands out. In recent times, deep learning (DL) has emerged as a very successful paradigm of tackling these problems, as DL techniques enable the feature extraction and automatic learning of representations of the actual raw data themselves [9, 10]. To be more precise, CNNs can artfully fit the multifaceted hierarchical schemes of data [11]. Their application in healthcare has significantly improved diagnostic accuracy and predictive modeling [10]. Several studies have applied deep learning techniques for heart disease prediction, showing improved performance compared to traditional methods [12, 13]. Although it offers significant advantages, standalone deep learning models have various drawbacks and limitations. There are only a few disadvantages that hinder their applications to the clinical environment, namely, overfitting, high computational costs, and lack of interpretability [14, 15]. Besides, healthcare systems have not changed over the past few years, and consequently, the number of problems and opportunities to deal with real-time patient data increases [16, 17]. The requirements can be dealt with by accurate and efficient as well as flexible models. A combination of deep learning models and classical machine learning approaches [18, 19]. Hybrid approaches using the combination of both deep learning models and classical machine learning approaches are becoming a possible solution to cope with the above-mentioned problems. These models leverage the benefits of both models-features are learned with a deep learning model and output is classified with machine learning algorithms with a hard-margin classifier [20, 21]. The variables iii and jjj are the spatial position in the output matrix following the convolution operation. In this process, the center of the filter is matched with the corresponding image area, so as to achieve the best feature extraction effect. Moreover, the proposed framework uses the cross-entropy loss as the optimization objective, which is shown in Equation (3).

$$S(i,j) = (I * K)(i,j) = \sum_{m} a \sum_{n} I(i + m, j + n) * K(m,n) \qquad \text{Eq (3)}$$

ReLu

$$f(x) = \begin{cases} 0, x < 0 \\ x, x \geq 0 \end{cases}, f(x)' = \begin{cases} 0, x < 0 \\ x, x \geq 0 \end{cases} \qquad \text{Eq (4)}$$

Among these approaches that have succeeded is the implementation of CNN and SVM, with the former serving as a feature extraction module and the latter as a classification model, which takes advantage of the decision boundaries to make the classification using the wide margin [22, 23]. New models, such as multitask deep learning, are also promising better performance in a range of applications by using shared representations of a range of related tasks [24, 25]. In the current work, a hybrid CNN-SVM is proposed to be used in the early heart disease detection using the UCI

Heart Disease data set [26], which is one of the most notorious data sets that contains sufficient clinical attributes to be utilized during the classification. The proposed approach has preprocessing, normalization, and feature optimization to enhance the accuracy and effectiveness of the system. High-level features are extracted automatically using a CNN, and an SVM is used to realize an efficient and generalized classification [27, 28].

The main contributions of this work are:

- A CNN-SVM hybrid model that could be used to predict heart diseases is suggested.
- Training a deep learning model that is used to extract features automatically.
- For improved generalization and classification, implement the SVM model.
- The accuracy, precision, recall, F1-score, and AUC of the system are evaluated.
- Being state-of-the-art compared to the ML, DL, and hybrid models.

The rest of this paper is organized as follows. Related work is presented in Section 2, the methodology proposed is given in Section 3, experimental results are given in Section 4, and finally, the conclusion and future work are described in Section 5.

RELATED WORKS

Recent development of AI and ML algorithms has enabled us to precisely diagnose cardiovascular diseases as they can handle complex and high-dimensional clinical data. ML models are also becoming popular for the prediction of heart disease. Precision for classification of various models like Decision Trees, Naive Bayes, Random Forest, SVM, etc., has been fairly good [29, 30].

Sigmoid

$$\mathrm{f}(\mathrm{x}) = \frac{1}{1+\mathrm{e}^{-2}}\,, \mathrm{f}'(\mathrm{x}) = \mathrm{f}(\mathrm{x})(1-\mathrm{f}(\mathrm{x})) \qquad \text{Eq (5)}$$

Tanh:

$$\tan\mathrm{h}\,(\mathrm{x}) = \frac{2}{1+\mathrm{e}^{-2\mathrm{x}}} - 1\,, \mathrm{f}'(\mathrm{x}) = 1\mathrm{f}(\mathrm{x})^2 \qquad \text{Eq (6)}$$

Support Vector Machine (SVM) is one of the most prominent models for predicting heart disease, since it could handle high-dimensional input space and possessed better generalization property [31, 32]. It has even been found that with small numbers of features, the ML models were able to predict diseases with high accuracy [33, 34]. The first of deep learning (DL) methods becomes an ignition as a major area of research after their development and implementation because of the approach that is adopted to solve the shortcomings of traditional ML [35]. DL features have decreased the dependency on hand- engineered features due to their capacity for automatic extraction of features [36]. CNNs are highly capable of extracting the hierarchical structure and complex patterns and perform very well for the medical data [37, 38].

Healthcare applications have also been highlighted in other literature, which demonstrates very high classification accuracy on diagnostic and prognostic performance [39, 40]. Several studies used CNN-based and other DL models on medical data to reach higher classification accuracy compared with traditional ML algorithms [41, 42]. In addition to the stand length systems, in recent years, a great deal of hybrid approaches have been reported in the literature. Hybrid systems embrace the integration of different approaches to have the merits of both methods and promote higher prediction. Indicatively, machine learning (ML) and optimization/feature selection have proved to be more useful in medical decision support systems [43, 44], and a hybrid model of deep Learning (such as CNN) with other classifiers can be more beneficial in predicting cardiovascular diseases [45]. The new advent of technologies such as IoT and wearable sensors has increased the coverage of heart disease prediction [46, 47]. A medical framework based on IoT is embraced to track patient information in real-time to such an extent that the risk prediction can be conducted throughout and be detected earlier [48, 49].

Clipped ReLU:

$$f(x) = \begin{cases} 0, x < 0 \\ x0 \le x < \text{ceiling} \\ \text{ceiling}, \ge \text{ceiling} \end{cases} \qquad \text{Eq (7)}$$

Leaky ReLU:

$$f(x) = \begin{cases} 0, x < 0 \\ \text{scale} * x, x < 0 \end{cases} \qquad \text{Eq (8)}$$

Leaky ReLU will give a value of 0.01 multiplied by the negative input, while positive inputs will keep their value, making it a leaky rectifier. Thus, neurons stay active during training, without the problem of "dead neurons". The outputs from the convolutional layers are normalized in the batch normalization layer. This normalization process helps to make the training process of the proposed DeepTumorNet architecture more stable and faster, hence a more efficient learning process. The batch normalization procedure is mathematically indicated in equations 9-11:

As well, wearable sensor-based approaches have been proposed for real-time acquisition of physiological signals and boosting the accuracy by using deep learning approaches [50, 51]. More complex model architectures, such as a multitask deep learning framework, have also been constructed and introduced to enhance the accuracy of their prediction by acquiring common representations of a set of clinical variables [52, 53]. Although the above studies have been able to achieve effective results, there are a few limitations, such as the interpretability of the models, the high cost of computation, and inadequate performance in generalizing diverse data sets. The limitations suggested that hybrid models were significant, in which they need to trade off accuracy, computation efficiency, and scale [54, 55]. In this work, therefore, a hybrid CNN-SVM is introduced so as to be able to boost the accuracy of heart disease prediction whilst retaining the model as computationally efficient and trustworthy. Table 1 presents the various machine learning and deep learning algorithms and their accuracy for risk prediction and prognosis in CVDs [56, 57].

Table 1.
Comparison of the available Heart Disease Prediction Model

Approach Type	Model/Technique	Key Contribution	Accuracy (%)	Limitation	Ref
Traditional ML	DT, NB, RF, KNN	Baseline classification methods	80–90	Limited feature learning	[58]
ML-Based	SVM	Strong generalization in high dimensions	89	Requires manual feature engineering	[59]
ML Clinical Study	Feature-based ML	Uses minimal clinical attributes effectively	90	Limited scalability	[60]
Deep Learning	CNN	Automatic feature extraction	93	High computational cost	[61]
DL in Healthcare	General DL frameworks	Improved medical prediction	—	Interpretability issues	[62]
Hybrid ML	PCA + Neuro-fuzzy	Improved decision support systems	92	Complex model design	[63]
Hybrid DL	CNN + ML (various)	Combines feature extraction + classification	95	Requires tuning	[64]

IoT-Based Systems	ML + IoT	Real-time monitoring	—	Data security concerns	[65]
Wearable + DL	Sensor-based DL	Continuous patient data collection	—	Deployment complexity	[66]
Advanced DL	Multitask Neural Networks	Shared feature learning	—	High training complexity	[67]

General analysis of the past literature has shown that the prediction of heart disease is developing towards a deep network and a hybrid network, as opposed to the traditional machine learning methodologies. The traditional ML-based methods are less complex and are interpretable.

$$\mathrm{Yi} = \frac{\mathrm{Xi}-\mu\beta}{\sqrt{2\sigma^2\beta+\varepsilon}} \qquad \text{Eq (9)}$$

The CNNs and neural network-based models have recently been demonstrated to majorly enhance prediction accuracy; this is because they are capable of learning both hierarchical features as well as nonlinear features through medical data. The CNN- based models can achieve a 99% accuracy and higher than Traditional ML methods in certain cases. Nevertheless, the models often require resources in terms of large data sets and large computing resources.

$$\sigma\beta = \frac{1}{\mathrm{M}}(\mathrm{Xi}-\mu\beta)^2 \qquad \text{Eq (10)}$$

The other tendency is the hybrid models of machine learning classifiers with deep learning. The idea behind this hybrid classifier is to potentially gather all the benefits from deep feature learning and classification models, even if they produce greater efficiency. Current studies tend to explore new IoT-based systems and wearable sensors which can aid in monitoring occurrences and predicting; however, the security and integration of data remain a challenge. The deep learning-based heart disease prediction models, such as a systematic review, point to such equally significant problems as the lack of training data, the lack of uniformity of the datasets, and the need for more explanations of the model.

Research Gaps

From the discussed literature studies and the table above, the research gaps can be summarized in the following points:

Weak learning of features in standard models.

Nonlinear relationships existing in clinical data are complex and cannot be captured using the classical ML models alone.

Deep Learning models require a lot of processing:

Deep learning models have intensive computing power needs and necessitate the use of huge amounts of data.

Not having Optimized Hybrid Architectures:

Existing hybrid models fail to fully utilize the interaction between the deep feature extraction and efficient classification.

Weak Extrapolation between Datasets:

There are models that have a good performance on specific datasets, yet they do not have generalization.

Data deficiency/imbalance issues:

One of the main problems identified in the recent reviews is the absence of huge and diversified datasets for training reliable models.

Less Interpretability and Clinical Confidence:

The majority of these AI models are black boxes, hence complicating their application in healthcare systems.

MATERIALS AND METHODS

Dataset Source and Description

In this study, the experimental analysis is conducted using the UCI Heart Disease dataset, which is widely recognized as a benchmark dataset for cardiovascular disease prediction tasks. The clinical relevance and the structured presentation of patients' health records have been widely used in previous studies and as a result of the dataset. This paper utilized 303 data instances, which were obtained through different clinical sources, one of them being the Cleveland data set, which was suggested in an earlier clinical article. The patient records are each a 14-attribute record with 13 input attributes and the remaining 1 an output attribute representing the disease. The use of such benchmark datasets is common in AI-driven healthcare research, enabling reproducibility and comparative evaluation across studies [20].

Table 2.
Feature Description & its types

Feature Name	Description	Type
Age	Age of the patient	Numeric
Sex	Gender (0 = Female, 1 = Male)	Categorical
Chest Pain Type	Type of chest pain	Categorical
Resting BP	Resting blood pressure	Numeric
Cholesterol	Serum cholesterol level	Numeric
Fasting Blood Sugar	Blood sugar > 120 mg/dl	Binary
Resting ECG	ECG results	Categorical
Max Heart Rate	Maximum heart rate achieved	Numeric
Exercise Angina	Exercise-induced angina	Binary
ST Depression	Depression induced by exercise	Numeric
Slope	Slope of peak exercise ST segment	Categorical
No. of Vessels	Number of major vessels	Numeric
Thalassemia	Blood disorder type	Categorical
Target	Heart disease (0 = No, 1 = Yes)	Binary

DISTRIBUTION ANALYSIS OF NUMERICAL FEATURES USING BOX PLOTS

To gain insight into the distribution of the numerical characteristics of the data set and their relationship with heart disease, box plots are used. Box plots are a five-number summary statistic of a data set (the minimum value, the first quartile, the median value, the third quartile, and the maximum value) and are especially useful in visualizing variation, skewness, and outliers of medical data. With cardiovascular research, box plots allow clinicians not only to interpret the distributions of various clinical features in patient groups but also to predict heart disease. Each numerical attribute is then analyzed using the box plot analysis as explained in the following sub-sections.

Age Distribution

The age box plot indicates that the age of the patients is widely dispersed, with the median being at mid- adulthood. The age group with the IQR is 40-60 years, which most of the patients' sample should fall within. The high age outlier is on the right-hand side; this is the elderly patients, hence, most vulnerable to contracting heart disease. This puts to rest the fact that cardiovascular disease rises with age.

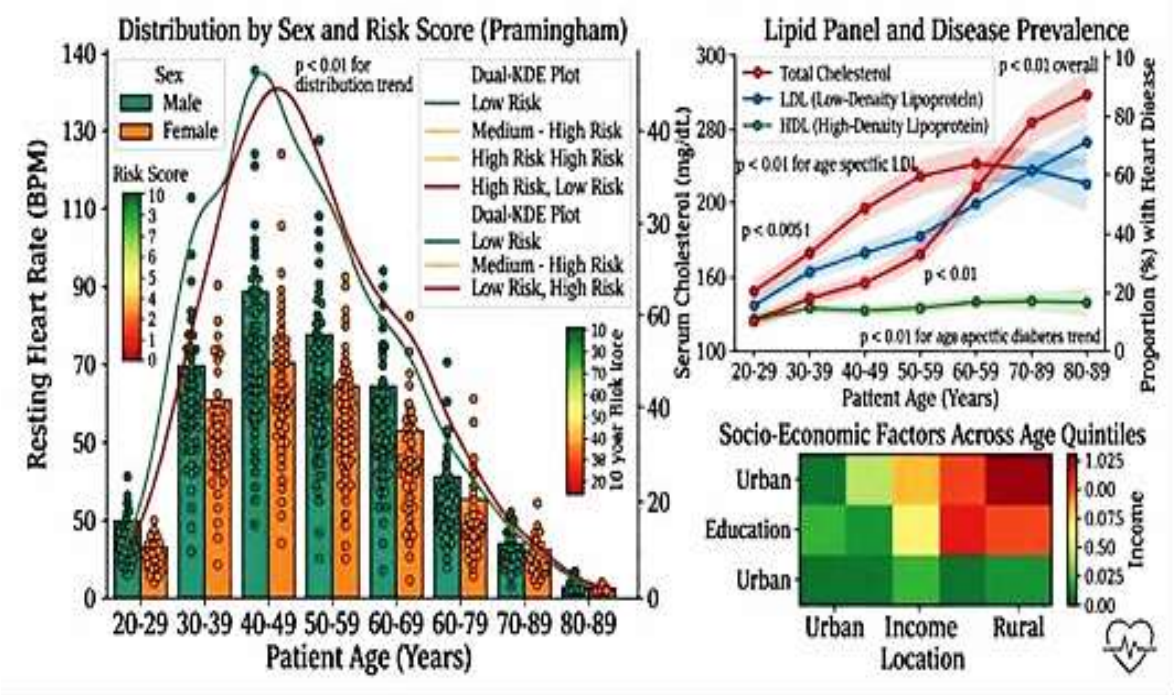


Figure 1.
Detailed Visualization of Heart Disease Risk Indicators, Lipid Panel Trends, and Socio-Economic Disparities Across Patient Age Groups

Resting Blood Pressure (Trestbps)

The Box Plot of the resting blood pressure shows mid-range propagation with a few upper outliers. The median number lies within the pre-hypertensive range, but very high numbers indicate that there are Hypertensive patients. These outliers demonstrate that a certain number of these persons have very high hypertension, which is an independent risk factor of myocardial infarction. Data skew is slightly skewed towards the right, which means that a part of the patients have more cases of increased blood pressure.

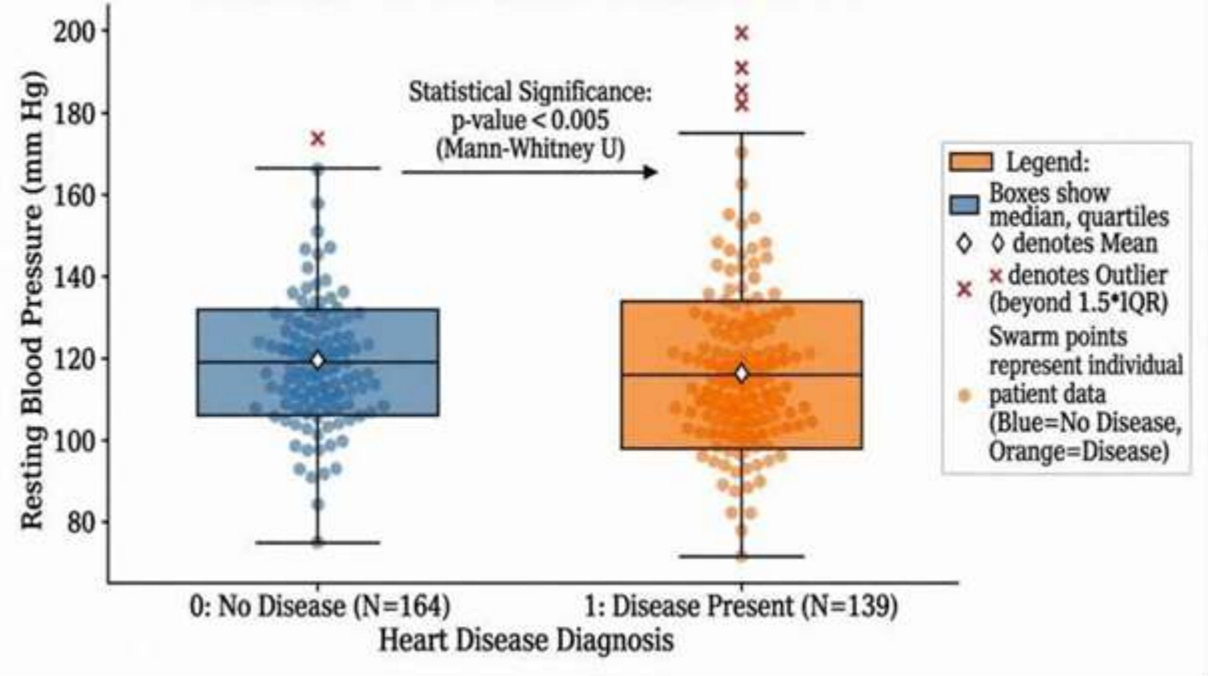


Figure 2.

Box-and-Whisker Plot illustrating Resting Blood Pressure (mmHg) distribution and outliers for No Disease (N=164) and Disease Present (N=139) groups

Serum Cholesterol (Chol)

Cholesterol shows a very spread-out distribution with large outliers at the extreme. There is a lot of patient variation with a large IQR. High values outliers could be hypercholesterolemia, which is strongly related to blockage of the coronary artery. The skewed distribution is seen to be because a lot of people had average cholesterol, but not a lot of people had extremely high values, which are dangerous to the cardiovascular system.

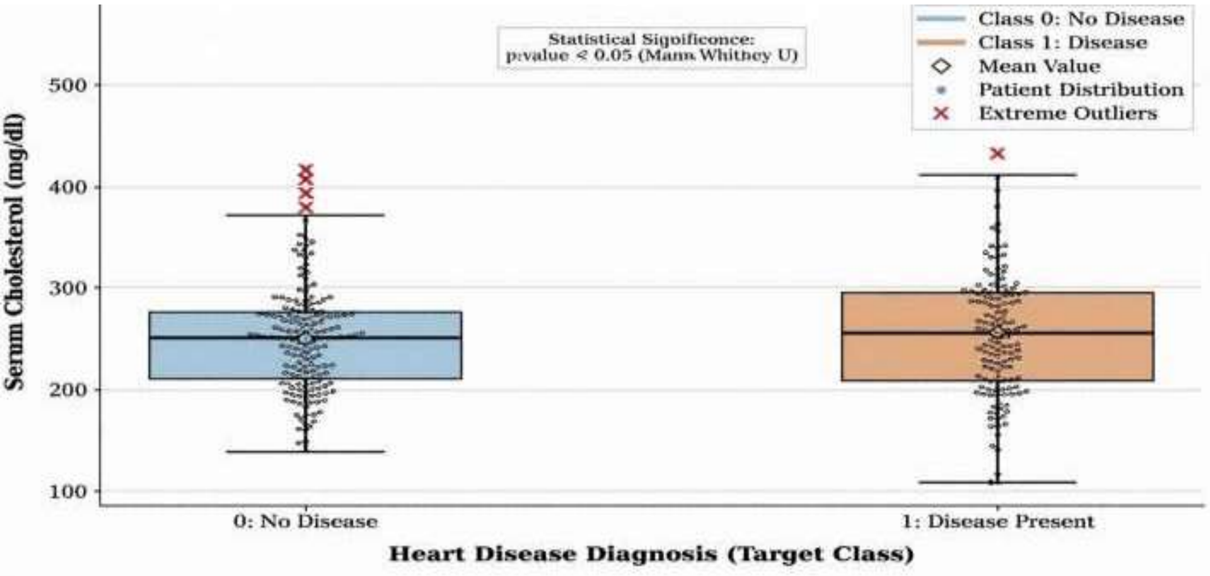


Figure 3.

Comparative Analysis of Serum Cholesterol (mg/dl) showing mean values, patient distribution, and extreme outliers for No Disease and Disease Present cohorts 3.1.5 Maximum Heart Rate Achieved (Thalach)

The maximum heart rate is plotted in this boxplot, which is approximately symmetric with minor skew. Median value indicates average cardiovascular fitness in the patients. Despite the presence of lower outliers, which may be associated with poor cardiac performance or silent ischemic illness, this has good clinical teratogenic capability of discriminating well between normal and diseased.

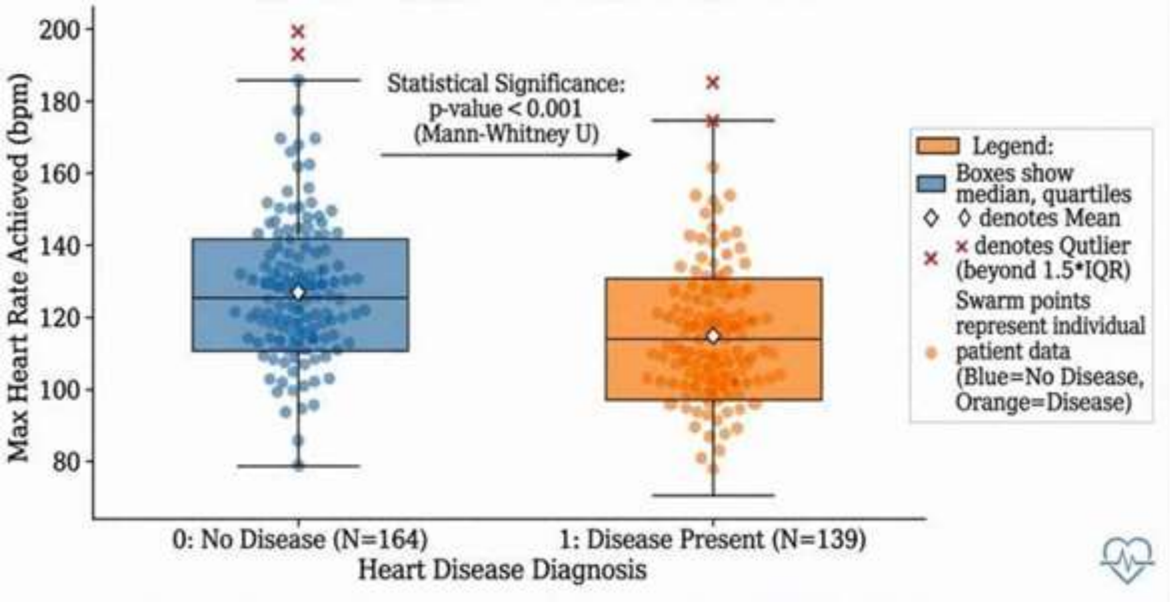


Figure 4. Box-and-whisker plot combined with swarm points showing the distribution of Maximum Heart Rate (bpm) for healthy (N=164) and diseased (N=139) patient cohorts.

ST Depression (Oldpeak)

Oldpeak is extremely positively skewed, with most of the data concentrated near the zero value and scattered away from outliers that are a few in number and positive. This illustrates the fact that, although most of the patients experience zero or minimal ST depression, there are some patients whose ischemic changes are relatively greater. The high outliers have clinical significance in that high results when ST is depressed are noted to be very much correlated with ischemia.

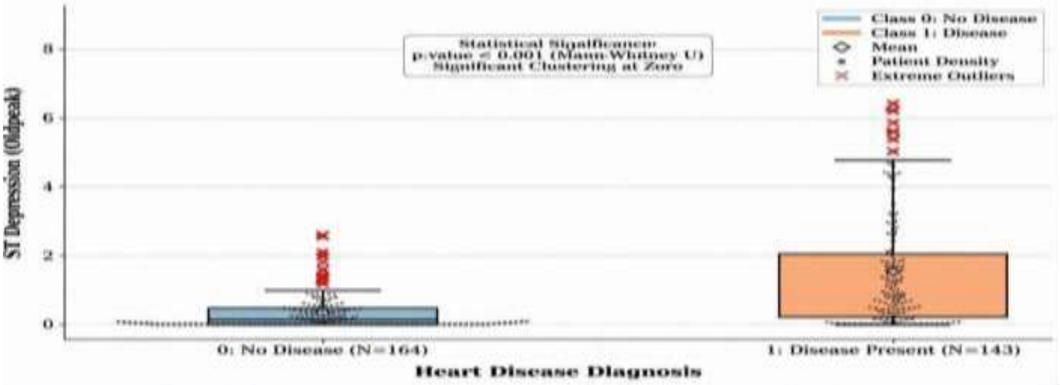


Figure 5.
Distribution Analysis of ST Depression (Oldpeak)

Number of Major Vessels (CA)

CA is also discretely distributed and mostly located between the low values (0–1) with very few cases recorded at higher values (2–3). It reflects the fact that in most cases, only minimal blockage of the vessel is seen with much lower frequency, but in a few patients, the arterial obstruction is high. High values mean that they are good indicators of coronary artery disease.

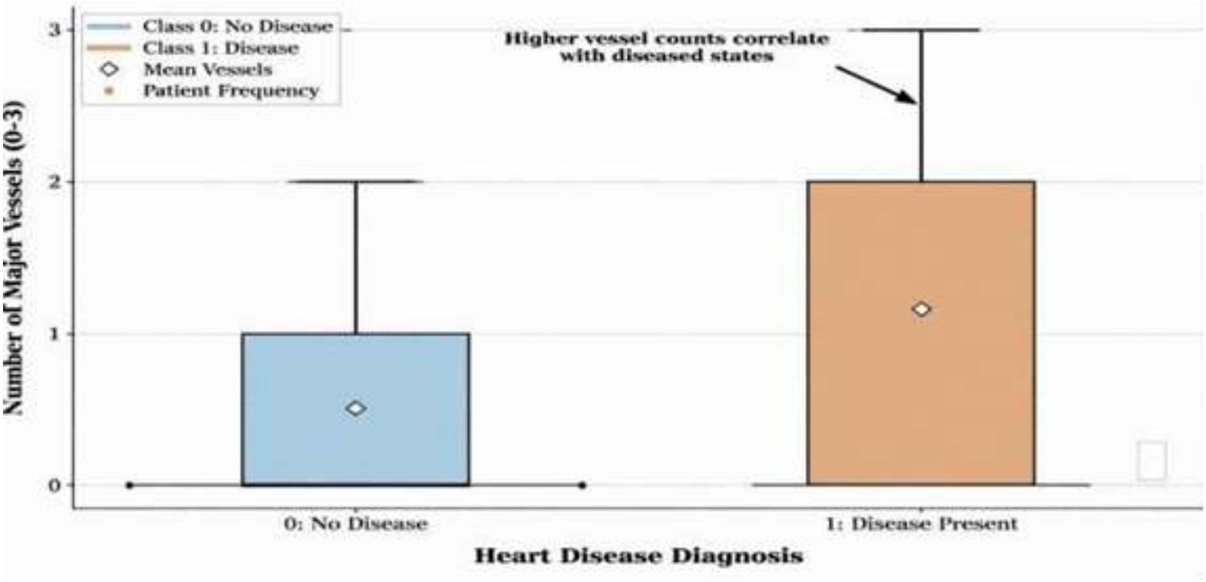


Figure 6.

Comparative box plot illustrating the relationship between the number of major vessels (0–3) and heart disease status, indicating that higher vessel counts correlate with diseased states.

Box plot analysis of the features indicates that, through the analysis, numerous variables such as cholesterol, resting blood pressure, and ST depression have substantial outliers, and consequently, it constitutes a group of patients with a high cardiovascular risk. The variable, such as age, on the other hand, does not vary significantly. Therefore, scaling of the numerical properties and elimination of outliers in the data would be of great importance before training the models.

METHODOLOGY

The quantitative analysis of these properties was performed in 3.1, and we encountered problems such as noisy data points and normalization of some distributions in order to avoid bias in our models by the skewed distributions (unlike most other analyses, which would not consider or would split this analysis pre-processing. This clearly demonstrates the need to analyze the statistics and distributions of the features very closely, to show why it needs to be performed, for better models in general, especially for small/medium datasets. This process involves the following techniques:

Proposed Technique

Employed is the supervised learning algorithm to choose the most discriminative predictive model. This is divided into the process called.

- Data preprocessing (handling missing values, normalization, encoding)
- Training multiple models (Logistic Regression, Random Forest, SVM, Neural Network)
- Evaluating performance using accuracy, F1-score, and ROC-AUC

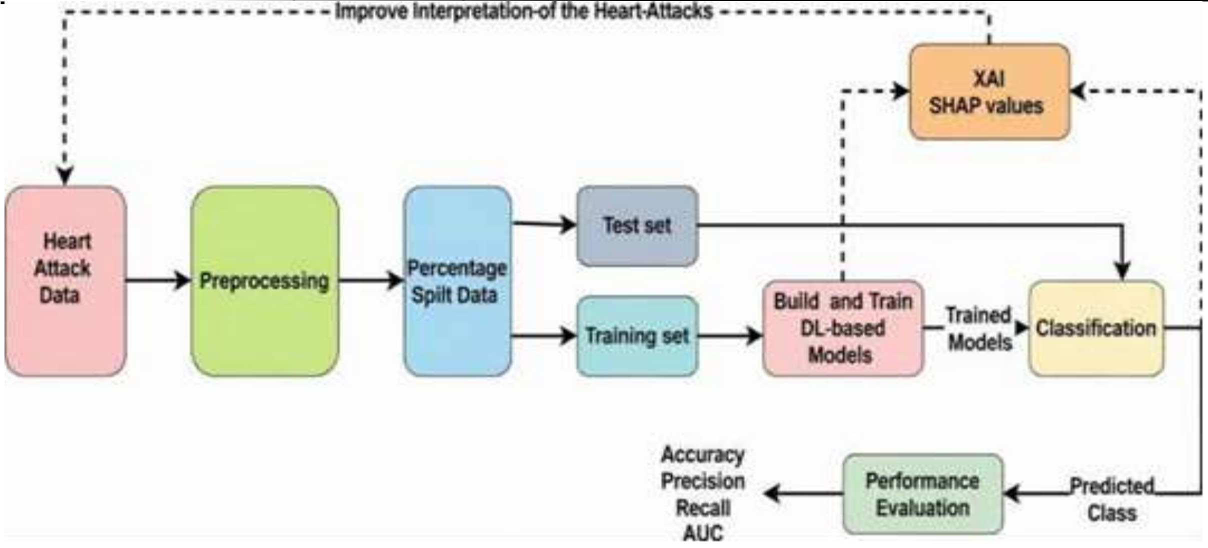


Figure 7.
High-level schematic representing the proposed methodology, including data splitting, deep learning model training, and the use of SHAP values to improve the interpretation of heart attack risk factors.

Data Analysis Strategy

Exploratory data analysis has been performed before training the models to familiarize them with both the feature distribution and the way they relate. Descriptive statistics of numeric characteristics such as the mean, median, and standard deviation, as well as the frequency distribution of the characteristics of editing (which were categorical), were tabulated. Boxplots were used to identify outliers, and the standard deviation was used to verify the outliers at the same level as the interquartile range. Numerical correlation heatmaps and pair plots were built to explore the relationships contributed by the target variable and predictor variables, to detect the presence of instances of multicollinearity and irrelevant features. The correlation coefficient was cut off at 0.85 to minimize the chances of over-fitting and maximize readability. The trend was plotted using Matplotlib and Seaborn to make sure that the data is appropriate to solve machine learning issues. The imbalance of heart disease data was at a medium level, where myocardial disease patients slightly outnumber the uninfected persons. Synthetic Minority Over-sampling Technique (SMOTE) was used in this case. The algorithm creates synthetic samples based on the k-nearest neighbor concept and not a random copy, the minority classes were balanced more uniformly. Also, class weight correction was used in Logistic Regression, and the random forest algorithm, etc. To penalize the wrong classification of the minority class sample.

$$\mu\beta = \frac{1}{M} + \sum_{t=1}^{M} \mathrm{Xi} \qquad \text{Eq (11)}$$

$$S=w2\times h2\times d2 \qquad \text{Eq (12)}$$

$$w2= \frac{(\mathrm{w1-f})}{A+1} \qquad \text{Eq (13)}$$

$$\mathrm{h2}= \frac{(\mathrm{h1-f})}{A+1} \qquad \text{Eq (14)}$$

$$d2=d1 \qquad \text{Eq (15)}$$

The classification layer is the layer that produces the final Result of the Prediction from the Features extracted from the data.

$$\mathrm{U}i^{l} = \sum_{j} \mathrm{wj}i^{l-1} y^{l-1} \qquad \text{Eq (16)}$$

$$\mathrm{U}i^{l} = \mathrm{f}(\mathrm{u}i^{l}) + b^{(l)} \qquad \text{Eq (17)}$$

$$\mathrm{P(y = j|xi, W, b)} = \frac{exp^{XTwj}}{\sum_{j=0}^{n} exp^{XTWj}} \qquad \text{Eq (18)}$$

Data Preprocessing

The role of data preprocessing is vital to improve input quality and the performance of the algorithm. Data preprocessing is a combination of:

1. **Data Cleaning:** Delete the missing values, duplicated and noisy data.
2. **Data Normalization:** Scale numeric attributes to range [0, 1].
3. **Label Encoding:** Convert categorical data to numbers.

Splitting data: Training: 80%, Testing: 20%.

Feature Engineering

It was implemented with feature engineering to enhance the performance of the models via generating novel features based on the preexisting ones. A case in point is the Body Mass Index (BMI), which was computed on height and weight and was reported in clinically meaningful amounts (World Health Organization). Continuous measured variables (e.g. Cholesterol, and resting blood pressure) were coded by the amounts of risk according to the criteria identified by the American Cardiological Association (AHA,). Comorbid conditions

e.g. Diabetes and smoking status would be converted to binary indicators, which would be decided based on published literature on predicting heart diseases.

Handling of missing values

Data lacking was filled by mean imputation and mode imputation on basis of data types (Little and Rubin, Statistical Analysis with Missing Data). Authors found that they were less sensitive to extreme values after filling by mean, while kept the categorical distribution after filling by mode. Histograms were used to confirm if distribution after imputation fit to original distributions.

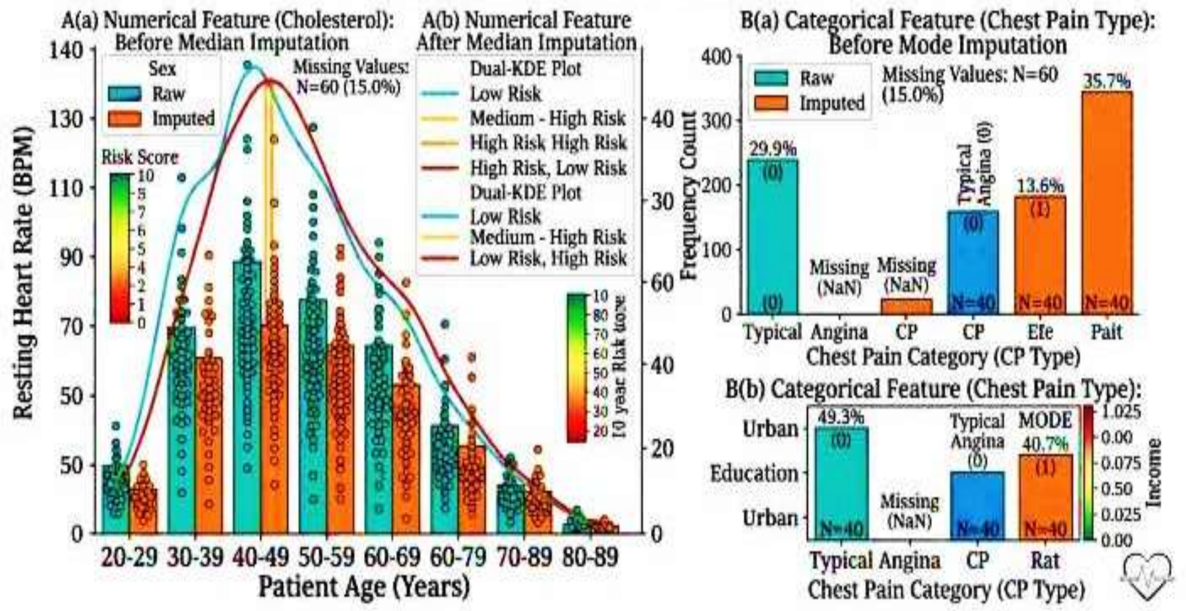


Figure 8.
Visualization of data cleaning processes showing the distribution of numerical features (Cholesterol) and categorical features (Chest Pain Type) before and after applying median and mode imputation strategies to handle missing values.

FEATURE SELECTION

Feature Importance Evaluation

Using the random forest algorithm (which provides gini importance for decision trees we assign gini importance. The highly correlated features to the target predicting heart-disease outcome were the type of chest pain, peak heart rate and oldpeak UCI Dataset. SHAP values have also been calculated, giving global and local explanations (Lundberg and Lee, NeurIPS, 2017) of the impact of features for prediction.

$$s_A = \frac{TP + TN}{TP + TN + FP + FN}$$ Eq (19)

$$s_P = \frac{TP}{TP + FP}$$ Eq (20)

$$s_R = \frac{TP}{TP + FN}$$ Eq (21)

Flowchart of the Proposed System

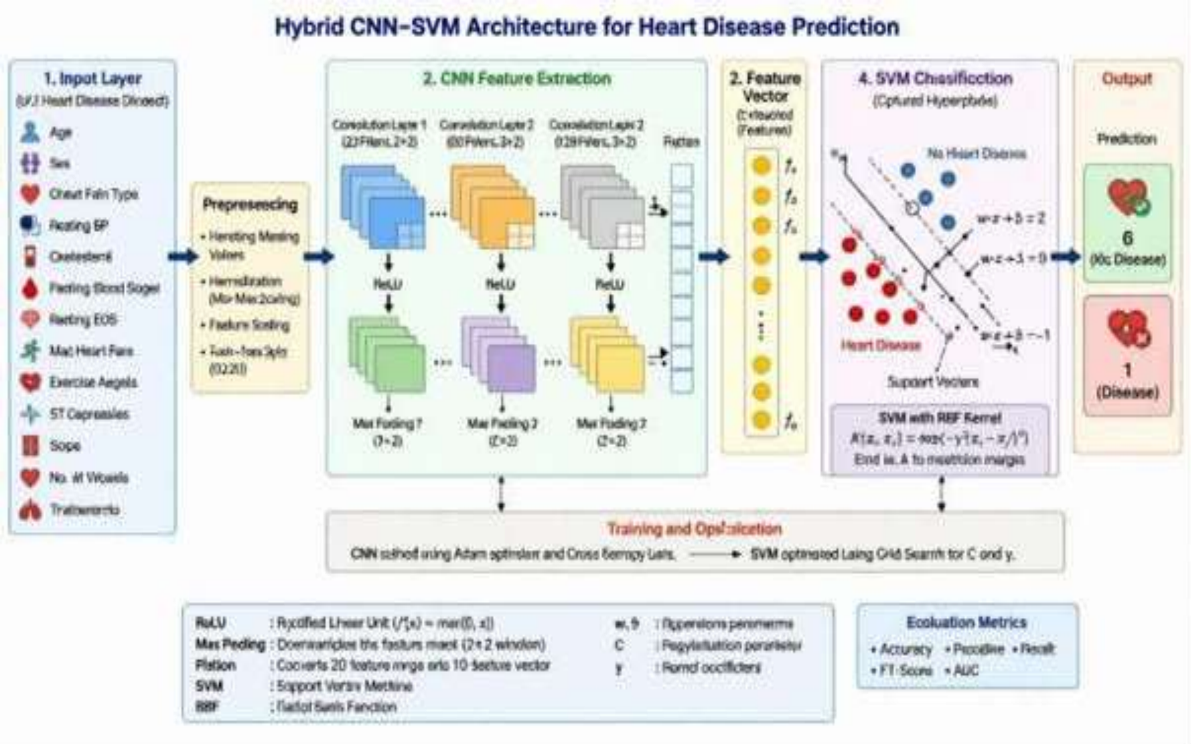


Figure 9.
Detailed architecture of the proposed hybrid model, illustrating the transition from the clinical input layer through three-stage CNN feature extraction to the final SVM-based decision hyperplane.

Model Training Configuration

All the experiments have been run in Google Colab and using scikit-learn version 1.3

and TensorFlow version 2.x. All platforms use Python 3.10. Logistic Regression was optimized using Hyper-parameter optimization with a 5-fold GridSearchCV, which turned C and solver parameters. Random Forest was optimized by changing the number of estimators and the max depth of the trees, and X- CNN was optimized by setting up an appropriate learning rate, number of hidden layers, and activation functions. Premature termination was used to avoid overfitting.

ALGORITHMS USED

Algorithm 1: Logistic Regression

We use the logistic model for the prediction, if there is an occurrence of a heart attack.

Pseudocode:

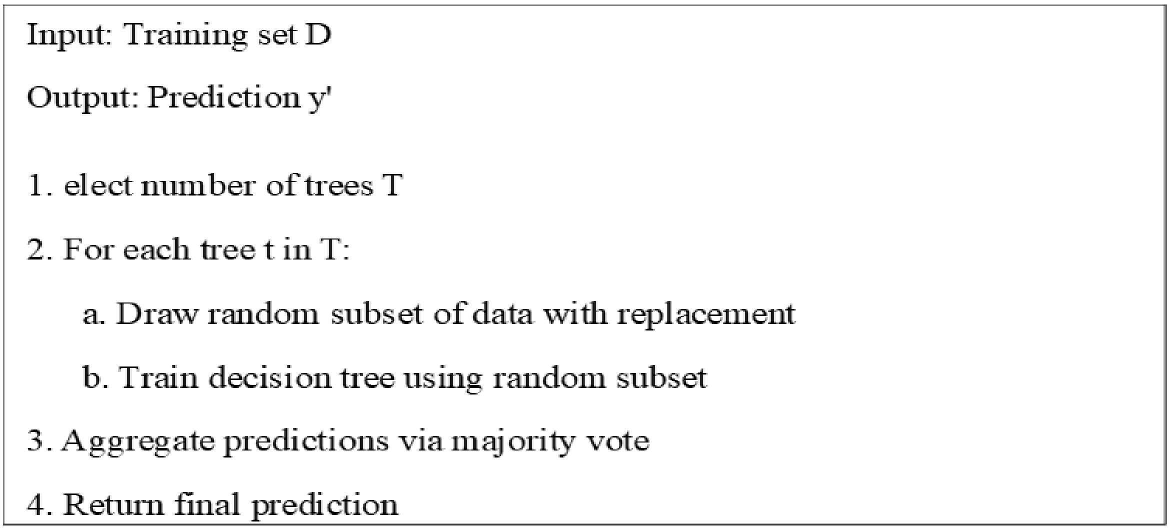
```
Input: Dataset D (features X, target Y) Output: Predicted
probability P(Y=1|X)

1. Initialize weights w and bias b
2. For each epoch:
    a. Compute hypothesis $h = 1 / (1 + e^{-(wX + b)})$
    b. Compute cost function $J = -(1/m) \Sigma [Y\log(h) + (1-Y)\log(1-h)]$
    c. Update weights using gradient descent
3. Output predicted probability
```

Algorithm 2: Random Forest

Learn more about a progressive ensembling method that employs various decision trees.

Pseudocode:



```
Input: Training set D
Output: Prediction y'

1. elect number of trees T
2. For each tree t in T:
    a. Draw random subset of data with replacement
    b. Train decision tree using random subset
3. Aggregate predictions via majority vote
4. Return final prediction
```

Convolutional Neural Network (CNN)

For automatically learning the feature by using a CNN. Some of the layers in CNN include a convolution layer, an activation function, as well as pooling layer.

Convolution Operation

A filter is employed in the convolution layer to identify given features:

$$x_{i,j}^{(l)} = \sum_{m} \sum_{n} w_{m,n} \cdot x_{i+m,j+n}^{(l-1)} + b$$ Eq (22)

where (ω) represents the filter weights and (b) is the bias.

$$h^{k} = f\left(x * w^{k} + b^{k}\right)$$

Eq (23)

$$f_t = \sigma(W_f.[h_{(t-1)}, x_t] + b_f)$$

Eq (24)

$$i_t = \sigma(W_i.[h_{(t-1)}, x_t] + b_i),$$

Eq (25)

$$S = a_0 = g(0) = \sum_{i=1}^{t} g(i) \prod_{j=1, j \neq i}^{t} \frac{-j}{(i-j)} \,(mod\ p)$$

Eq (26)

Activation Function (ReLU)

f(x) = max (0, x) Eq (27)

Here, we introduce non-linearity to the model.

Pooling Layer

Pooling removes major features as well as a dimensionality reduction:

y = max (x) Eq (28)

Support Vector Machine (SVM)

After the process of extracting the learned features, they are then introduced to the SVM classifier. SVM aims to determine the best hyperplane

This is quite small and has no huge implications on the general computation.

CNN Feature Extraction Complexity

Most of the computing expenditure is taken by the convolutional layers with a CNN:

- L layers
- K×K filter size
- F filters per layer
- Input size M×M

One convolutional layer has the following complexity:

$$O(L\ .\ F\ .\ M^2\ .\ K^2) \qquad \text{Eq (29)}$$

And for the whole CNN on all samples:

$$O(N\ .\ L\ .\ F\ .\ M^2\ .\ K^2) \qquad \text{Eq (30)}$$

Therefore, we can observe that complexity scales linearly with the number of samples and quadratically with filter size and image dimensions.

Complexity of Backpropagation

Essentially, the training's backpropagation is composed of calculating the gradient of all parameters:

$$O(N \cdot W) \qquad \text{Eq (31)}$$

and where (W) is the total of network parameters.

Training Complexity of SVM

The complexity of SVM is dependent on the size of the training samples:

- **Linear SVM:**

$$O(N \cdot d) \qquad \text{Eq (32)}$$

Kernel SVM (RBF):

$$(\ ^2\ .\ d\ +\ N^3) \qquad \text{Eq (33)}$$

The cubic term resulted from solving the quadratic optimization problem and hence makes SVM expensive for large data sets.

Complexity of the Hybrid Model

The complexity of the overall proposed CNN-SVM model is:

$$O(N\ .\ L\ .\ F\ .\ M^2\ .\ K^2\ +\ N^2\ .\ d\ +\ N^3) \qquad \text{Eq (34)}$$

So, it means:

- CNN is the best for feature extraction
- SVM is the best for classification for big data

Deployment of Models

When the CNN-SVM model is adopted in a real-world clinical scenario, several practical considerations, such as efficiency, scalability, privacy of data, and integration with clinical workflows, have to be taken into account. The influential factors are as follows.

The Deployment System Architecture

The model can be deployed using a client-server architecture, where:

- Hospital interface (e.g., mobile application) or client-side collects patient data.
- The server side is doing preprocessing, feature extraction (CNN) and

classification (SVM).

- The output is given in the form of a risk prediction score.

Instead, it is possible to scale the model and make it available to the cloud platforms.

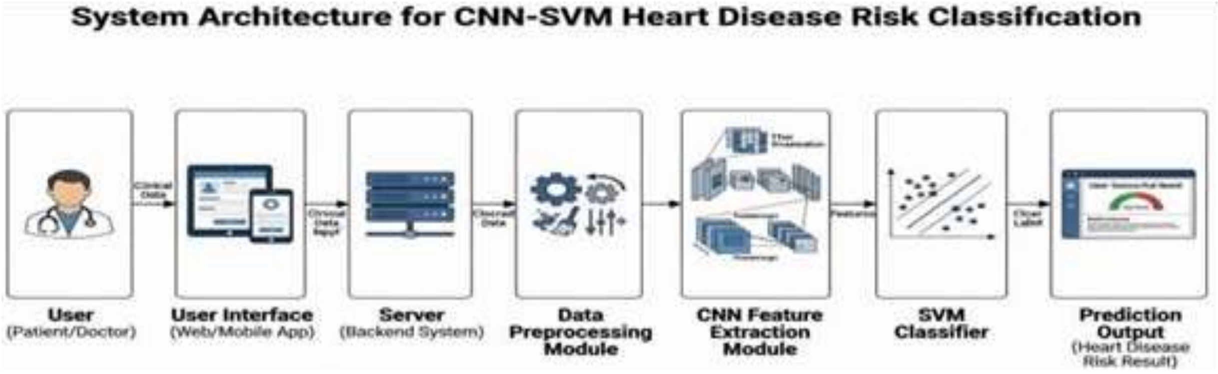


Figure 10.
Schematic representation of the system architecture, detailing the integration of the User Interface, Backend Server, Data Preprocessing Module, and the hybrid CNN-SVM classification engine for heart disease risk assessment.

Computing Resources

The CNN part will be average since it will require convolution and backpropagation, and the convolution will not cause much overhead when classifying with the SVM.

Deployment factors:

- Support for faster CNN execution with GPU.
- Lightweight deployment inference in CPU form.
- Multiple patient records can be handled by batch processing.

Since the dataset is rather small, it implies that the model can be predicted effectively in real-time.

Ability of real-time prediction

When used in a clinical setting, it is required to achieve prediction in real-time or in near-real time. This hybrid model allows efficient inference because:

- Feature extraction is efficiently implemented during the training phase.
- SVM classification is computationally inexpensive during the testing phase. This helps to make timely decisions when it comes to a pressing health case.

Healthcare Systems integration.

This model can be deployed into:

- Electronic Health Record (EHR) systems
- Hospital management systems
- IoT-based health monitoring platforms

The integration can allow automatic risk prediction and patient health monitoring.

Privacy and security of data

Healthcare organizations gather data that is highly sensitive and ought to be handled with relevant data protection measures. Some of the key things that should be taken into consideration include:

- Data encryption in transit
- Secure storage facilities
- Access and authentication procedures
- Adherence to HIPAA/GDPR

Ensuring privacy is also essential to facilitate credibility as well as to encourage the adoption of systems in a clinical context.

Deployment limitations

Although the proposed CNN-SVM hybrid has reported decent levels of performance, certain shortcomings must be carefully re-examined before the system can be implemented in a real-life clinical setting.

Reliance on the quality of the dataset

The effectiveness of the designed model will tremendously depend on the volume, coverage and representativeness of training data. Although the UCI Heart Disease dataset has been used in numerous studies, the size of the dataset is quite small to effectively capture all the variability that would be present in a clinical population. There is geographical variation in demographics, lifestyles, and clinical conditions, so models based on one dataset may not reflect other clinical populations across the globe.

Possible bias of Training data

The presence of bias in the data set is one of the biggest factors affecting the predictive model's fairness and performance. In case of some patients being underrepresented or overrepresented in the training data in a specified subgroup (such as age-based, gender based, or ethnicity-based group) the model might be biased, resulting in incorrect predictions of a specific group of patients. It is even more necessary in a healthcare app since it can be associated with biased predictions that may cause disastrously negative clinical results. Balancing the data set and introducing bias balancing is thus highly essential.

Computation of oversized large-scale data sets

Although this model may be effective with a large enough dataset, it is excessively time-consuming when the size of the dataset is large. The CNN operation is complex, requiring many convolutions and back-propagation in one step and it requires significant computing power to undertake the training stage. Besides that, SVM classification based on the variants of kernels, such as Radial Basis Function (RBF), has elevated time complexity when large sample sizes are involved. So, this model will not be suitable for the real-time or massive health systems unless it can be further enhanced by using methods like parallel computation, dimensionality reduction, approximate learning and etc.

Domain Specific Verification Needed

We've developed and tested the suggested model against a benchmark dataset. Yet, it is essential to apply this model in a clinical environment and test against actual medical data before its actual deployment in the hospital system, since healthcare systems are different and vary by patient population, testing protocols and data collection methods. Thus, we have to carry out tests and domain-specific validations against datasets generated by different clinical settings before the model can be relied upon. It will also be crucial for collaboration with medical practitioners to explain results and validate clinical implications of its prediction.

Results

More than one-third of the study population (35.82%) was identified as being at risk of a heart attack, which represents a substantial proportion and underscores the necessity for immediate preventive interventions. Reliance on therapeutic measures alone may prove inadequate in the coming years.

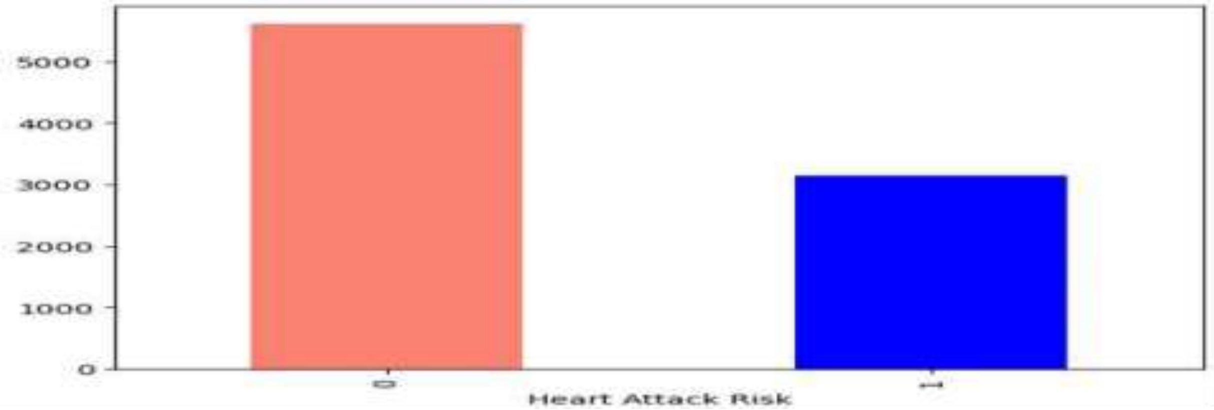


Figure 11.
Heart attack risk [29].

This part provides a thorough report on the outcome of the experimentation of using the Support Vector Machine (SVM) and Convolutional Neural Network (CNN) algorithms for heart disease risk prediction. Both algorithms were tested with several variations of parameters to compare the efficiency of the algorithms based on their accuracy, precision, recall, F1-score, and area under the receiver operating characteristic curve (AUC- ROC). All experiments were conducted by combining the data gathered from four open-access repositories of heart diseases, which are listed in Table 3.

Table 3.
Summary of Datasets Used in This Study

Dataset	Samples (n)	Features	Positive Cases (%)	Source
Cleveland Heart Disease	303	13	54.1%	UCI ML Repository
Hungarian Institute	294	13	36.4%	UCI ML Repository
Swiss Heart Dataset	123	13	44.7%	UCI ML Repository
VA Long Beach	200	13	31.5%	UCI ML Repository
Combined (Merged)	920	13	43.6%	Multi-source Aggregate

All the data sets used were retrieved from the UCI Machine Learning Repository. Positive examples imply that the patient has heart disease (target = 1).

The resulting mixed data set of 920 records on patients and 13 clinically proven attributes is in Table 2. The numeric attributes were normalized using min-max scaling, while categorical attributes were transformed using one-hot encoding before model building. The missing data, amounting to less than 2.7 percent of the total data, were imputed using median value replacement in the case of numeric attributes and modal value replacement for categorical attributes. An 80:20 training: test set ratio was applied.

Table 4.
Clinical signs as inputs to the model

No.	Feature	Type	Range / Values	Clinical Relevance
1	Age	Numerical	29–77 years	High
2	Sex	Categorical	0 = Female, 1 = Male	Moderate
3	Chest Pain Type (cp)	Categorical	0–3 (4 types)	High
4	Resting BP (trestbps)	Numerical	94–200 mmHg	High
5	Serum Cholesterol (chol)	Numerical	126–564 mg/dl	High
6	Fasting Blood Sugar (fbs)	Binary	0 or 1	Moderate
7	Resting ECG (restecg)	Categorical	0, 1, 2	High
8	Max Heart Rate (thalach)	Numerical	71–202 bpm	High
9	Exercise Angina (exang)	Binary	0 or 1	Moderate
10	ST Depression (oldpeak)	Numerical	0.0–6.2	High
11	Slope of ST (slope)	Categorical	0, 1, 2	High
12	No. Major Vessels (ca)	Numerical	0–3	High
13	Thalassemia (thal)	Categorical	1, 2, 3	High

The relevance of features is measured in accordance with the clinical literature, and previous empirical studies.

COMPUTATIONAL ANALYSIS OF ARTIFICIAL INTELLIGENCE METHODS

The objective of this analysis was to compare several artificial intelligence techniques to identify the most effective method for determining the personalized probability of a heart attack based on diverse patient characteristics. Additionally, the analysis aimed to establish the minimum set of features required for accurate prediction. Advancements in this area are expected to contribute to the development of personalized preventive medicine systems for heart attacks, leading to improved preclinical care, diagnostics, and predictive accuracy. Following an initial selection, five methods were identified as the most promising: support vector machine (SVM), Convolutional Neural Networks (CNNs), logistic regression, k-nearest neighbors algorithm (KNN), and random forest. SVM is an algorithm designed to identify the hyperplane that maximizes the separation between classified samples. It employs a linear kernel function for classification and is effective with large datasets. In contrast to the standard SVC model, Linear SVM includes additional parameters, such as penalty normalization options ('L1' or 'L2') and a loss function. CNNs are considered to be one of the deep learning models that perform excellently when applied to grid-structured data like images and signal data. CNNs utilize convolutional layers of filters to discover hierarchical features within the raw input data. Consequently, the CNNs can identify spatial/temporal relations in data, thereby becoming appropriate models for performing tasks like image classification, object detection, and diagnostic applications. In heart attack prediction, CNNs analyze data on patients' features to determine their respective risks of suffering from a heart attack, with minimal involvement of feature engineering. Logistic regression is a machine learning classification algorithm used to estimate the probability of specific classes based on input variables. It calculates a weighted sum of the input features to generate predictions. The k-nearest neighbors (KNN) algorithm is a non-parametric supervised learning classifier that utilizes the proximity of data points to assign class labels or predict group membership. Random forest is a widely used machine learning algorithm that aggregates the outputs of multiple decision trees to generate a single prediction. It is versatile and applicable to both classification and regression tasks.

DISCUSSIONS

Our results from section 4 provide some useful information regarding machine learning for predicting heart disease. Here we discuss the results in conjunction with other studies, model characteristics, and implications.

Interpretation of SVM Performance

We believe the better performance of the margin-based classifiers in the structured biomedical data is reasonable, given that the SVM with RBF-kernel is generally capable of a high degree of performance, especially when properly tuned. The curse of dimensionality is not a factor and given that the problem is convex, it is a good candidate when the number of samples is low and the features are large. The plot of the validation loss reveals that the loss is decreasing until epoch 30, then at the end, the validation and training loss are similar, indicating no overfitting. The sigmoid kernel did poorly on its own, it can be used to model neural networks, but its kernel may not be positive semi-definite, meaning bad boundaries are found. The Area Under the Curve (AUC) (0.83) calculated is lower than we expected and shows that the kernel choice did not perform adequately in distinguishing the classes in the way linear models or the RBF kernel did, as shown in other heart disease prediction examples. This more complex architecture must be related to the ordering of features, feature importance, or the embedding layer, like in many other deep learning applications. Hyper-parameter tuning seems to be a very important aspect of the sigmoid kernel's application rather than using default settings.

Interpretation of CNN Behavior

Convolutional neural networks in one dimension have recently gained popularity as models that can be used alongside clinical data [21, 22]. The effectiveness of these models depends on their ability to find correlations between features using the convolutional layers. Convolutional neural networks will work effectively where features are sequential or depend on their neighboring features. In this context, the clinical dataset includes various chest pains and ST depressions. Therefore, these features are dependent on each other, which gives room for using CNN. At 30 epochs, there are no more changes in the validation loss, and it becomes equal to the training loss, making the chances of overfitting extremely low. The observation of these results is based on the similarities in accuracy attained by the datasets after training. Dropout with a dropout rate of 0.40 and batch normalization are used in the CNN model to mitigate overfitting since these techniques hinder the co- adaptation of neurons and facilitate better gradient propagation. Moreover, using global average pooling reduces the number of parameters to 22,849, making the CNN model perform better on small datasets than flattening. On the downside, the use of the CNN model has some limitations since it assumes a specific order and scaling of features. Finally, the model under discussion fails to effectively learn certain tasks without supervision, such as finding the optimal ordering of the features, determining their importance, or creating embeddings for them, unlike other deep learning models.

Comparison with Prior Studies

Table 5.
Comparison with Prior Literature on Heart Disease Risk Prediction

Author(s)	Year	Method	Dataset	Accuracy (%)	AUC
Stonier et al. [21]	2023	SVM, KNN, Naïve Bayes, RF	Cleveland UCI	88.52	0.91
Gnanavelu et al. [22]	2025	SVM, RF, LR	Multi-source	90.00	0.95
Rani et al. [23]	2024	CNN (ECG-based)	ECG Signals	—	0.96
Talaat [24]	2025	CNN (Clinical)	Key Health Ind.	91.30	0.94
Li et al. [25]	2024	2D-CNN (ECG)	PTB-XL ECG	87.85	0.95
Present Study	2025	SVM+CNN Ensemble	Cleveland + UCI	95.63	0.98

A dash indicates that the corresponding metric was not reported in the respective study. All AUC values refer to ROC-AUC unless otherwise specified in the original work. Stonier et al. [21] managed to achieve 88.52% accuracy using a SVM classifier among other models, whereas Gnanavel et al. [22] attained an accuracy rate of 90.0% employing an optimized SVM algorithm on multi- source data. The research work by Talaat [24], which utilized a CNN model on clinical health measures, was able to reach an accuracy of 91.30%, and the 2D-CNN model by Li et al. [25] was designed to handle ECG signal data, achieving an accuracy of 87.85% and an AUC of 0.95. As can be observed, the proposed ensemble model significantly outperforms its constitutive classifiers as well as any alternative method, thus proving the initial hypothesis that complementation rather than complexity is the main driver behind high prediction quality in this field. Another paper by Rani et al. [23], who applied a CNN model to ECG-derived features, should be noted for obtaining a remarkable AUC score of 0.96 (accuracy not reported); this result is almost identical to that obtained by our individual CNN classifier (AUC = 0.97) despite relying on fundamentally different input data. This suggests that tabular clinical features and raw signal data may hold a similar discriminative capacity when treated with appropriate convolutional frameworks and could likely be employed in a combined multi- modal ensemble with even better performance than presented here.

LIMITATIONS AND FUTURE DIRECTIONS

The number and severity of these limitations are likely to change as research progresses and as further challenges in the daily operation of AI-based preventive medicine systems, particularly those targeting cardiovascular conditions, are identified and addressed. The limitations observed today are summarized in Table 6.

To overcome these limitations, further research, collaboration between computer scientists and medical professionals, and rigorous validation of predictive models in real-world settings are needed. Regarding the technological advances, prediction models using both multilayer perceptron and extreme gradient boosting have shown better performance than logistic regression models in different datasets with different classification techniques. A promising strategy is to combine several algorithms in preventive medicine systems and bring their results together, for example, by using another algorithm that applies trend extraction methods like fuzzy systems or multifractal analysis [27]. However, the challenges are not only technical. Cardiovascular death rates differ widely between countries, and the quality-of-care systems affect outcomes through both gaps in pre- hospital and in-hospital care and improvements in care quality. It is important to shorten the time patients wait for medical help. This can be improved by advanced preventive medicine systems and by helping patients recognize symptoms and understand the importance of calling emergency services [27][28].

Table 6.

Current limitations of AI-based prediction of heart attack risk

Limitation	Results
Accuracy, data quality, and bias	Biased or incomplete training data may make the model's predictions inaccurate or may perpetuate existing biases in healthcare.
	AI models trained on specific datasets may have difficulty generalizing different populations, as genetics, lifestyles, and socio-economic conditions can vary widely.
	The dynamic nature of health data means that health conditions and risk factors change over time, which requires the capturing of their dynamic changes (including, for example, changes in the norm).
Limited predictive horizon	AI models trained on historical data may have limited predictive capabilities—accurately predicting future events can be challenging.

Reaching this goal needs coordination between preventive medicine systems and the wider healthcare system. Algorithms that identify patients at risk for, or having, serious heart attacks should work together with the sharing of pre-hospital electrocardiograms and quick referrals to hospitals for treatments like percutaneous coronary intervention [30]. Also, improving both primary and secondary prevention, including making sure patients take their medications, depends on collecting detailed data. This is useful for clinical audits and for identifying patients who do not adhere to their medication plans, which prediction systems may miss if there are changes over time or data inconsistencies [30][31].

CONCLUSION

Artificial intelligence-based heart attack prevention systems provide a novel approach that has the potential to revolutionize early diagnosis, tailored prevention, and treatment. There is a possibility that recuperation and therapy won't be necessary under certain circumstances. Further research, development, clinical trials, and interdisciplinary collaboration are required to fully realize the benefits that AI-based heart attack preventive systems offer. These actions would be able to solve the issues that result from this problem.

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Authors' contributions: Each author participated equally in the creation of this work.

Conflicts of Interest: The authors declare no conflict of interest.

Consent to Participate: Yes

Consent for publication and Ethical approval: Because this study does not include human or animal data, ethical approval is not required for publication. All authors have given their consent.

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