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# AI based Heart Disease Predictor using UCI Dataset

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## Abstract

Heart disease remains one of the leading causes of mortality worldwide, and early risk stratification is critical for effective prevention and timely intervention. Conventional clinical scoring systems and traditional machine-learning models often struggle to capture the complex, nonlinear relationships among heterogeneous clinical variables, resulting in sub-optimal predictive performance. This work presents a data-driven heart disease prediction system based on the UCI Heart Disease dataset, integrating routinely collected clinical attributes such as age, sex, blood pressure, cholesterol level, chest pain type, exercise-induced angina, and stress-test results. The dataset is preprocessed through systematic cleaning, encoding of categorical variables, and feature scaling before model development. On this processed data, we design and train a Convolutional Neural Network (CNN) classifier and benchmark it against baseline models, including Logistic Regression, Support Vector Machines (SVMs), and conventional fully connected neural networks. Experimental evaluation demonstrates that the proposed CNN model achieves superior and more accurate performance than existing models such as SVM, with improved overall accuracy and a more balanced confusion matrix for distinguishing between healthy and high-risk patients. These results highlight the potential of CNN-based approaches to support clinical decision making and motivate future work toward user-friendly interfaces and deployment in real-world healthcare environments.

**Keywords:** Heart disease prediction; UCI Heart Disease dataset; Convolutional Neural Network (CNN); deep learning; cardiovascular disease; clinical decision support; predictive modeling; classification.

## 1 Introduction

One of the complicated and complex disease cases in the field of medical science is the prediction of heart disease. The heart is a very important organ for every human body [1]. Heart disease can accurately refer to conditions that exist, when the heart's abnormal function, can be caused by blood clots, heart arteries, or others. Health data is collected from several available sources, one of which is patient electronic devices stored in the format specified in the electronic health record (EHR). To detect or predict using this data and using AI or Machine Learning (ML) algorithms.

Heart disease is said to be the leading cause of death globally, according to the World Health Organization the deathrate from heart disease was around 17.7 million (31in 2015.Every year nearly 20 million people die, showing heart disease as the leading cause of death [2]. The group of diseases relatedto the heart and blood vessels is referred to as cardiovascular disease (CVD). CVD includes coronary heart disease (CHD)or known as coronary artery disease (CAD) which refers to disease of the heart arteries that supply oxygen and blood to the heart and is associated with lifestyle conditions and age.

Machine Learning is a very broad and diverse field and its scope from Supervised, Unsupervised, and Ensemble Learning is used to predict and determine the accuracy of a given data set. Machine learning-based methods have been used in medical science. In healthcare, machine learning can help doctors make more accurate predictions for patients, machine learning can increase the speed of processing and analyzing data. Using machine learning, predictive analytics algorithms can train large datasets and can perform deeper analysis on many variables with minimal changes when applied.

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## 2 Materials and Methods

We first gathered and preprocessed the dataset to remove any necessary inconsistencies, such as replacing null occurrences with average values. We divided the dataset into two distinct groups, named the test dataset and the training dataset, respectively. Next, we implemented several distinct classification algorithms to determine which one achieved the highest accuracy for these datasets

### 2.1 Literature review

In this section, previous heart disease-related study using machine learning methods is discussed, which motivated this work. In this paper, according to Ramalingam et al. [7], a machine learning approach has been employed on some medical datasets and experiments of numerous data. This paper contributes to various model-based algorithms and techniques. Using some supervised algorithms such as Naive Bayes, random forest (RF), decision trees (DT), support vector machine (SVM), and K-nearest neighbor (KNN) are found in these re-searchers. Based on the accuracy, the implementation of various techniques used in the research was compared. The results accuracy of NB was 84.1584% with SVM-RFE (recursive feature elimination) selected in the 10 most significant features. According to Pouriyeh et al. [8] using 13 at-tributes, in this research, the NB algorithm has performed an accuracy of 83.49%. In 1951, Fix and Hodges [9] proposed a non-parametric method for pattern classification which is popularly known as the KNN rule. Accuracy of DT and KNN was 82.17% and 83.16%, respectively. Palaniappan and Awang [10] predict the intelligent heart dis-ease prediction in ML algorithms. The algorithms are collectively proposed to achieve accuracy. Using DT,NB, and NN technique to perdition HD, the accuracy of the DT, NB, and NN was 80.4%, 86.12%, and 85.68%. Rabbiet al. [11] used Cleve-land standard heart disease dataset and classified the three-technique to prove the accuracy. Predicting the accuracy of the computer-based prediction algorithm, SVM, KNN, and artificial neural network (ANN) are used. In the accuracy, KNN (82.963%) and ANN (73.3333%) are used. In the paper, Haq et al. [12] used the UCI dataset to develop using popular algorithms, the cross-validation method, three feature selection (FS) algorithms, and seven classifier performance evaluation metrics such as classification accuracy, specificity, Matthews'correlation, sensitivity, and execution time. Above all those previous studies [7], Ramalingam et al. dida survey which is heart disease prediction using machine learning techniques. The best data will give the best performance of each algorithm [8]. This author worked on the UCI dataset with a comprehensive investigation on the comparison of machine learning techniques on heart disease domain. However, the performance of those techniques depends on feature selection algorithms [9]

Finally, it can be said that they tried to find the best accuracy for predicting heart disease from the UCI dataset's clinical information of patients and correctly predicted below the average of 80% of heart disease patients. They tried to find the best accuracy using all of the features or use some specific feature selection algorithm for a specific machine learning algorithm, and they do not visualize any correlation between features. Also, every other study only shows the prediction score of any algorithm, and they do not describe other performance evaluation matrices like sensitivity, specifcity, logloss, and others.

In this study, heart disease (HD) datasets from UCI Machine Learning repository [13] are used. This work is related to the supervised problem of machine learning. Although there has been a lot of research on heart disease, they have tried to solve it using different algorithms. However, it is a complex problem that cannot be solved with a simple machine learning algorithm. This project will be solved by some algorithms such as and 1D Convolutional Neural Network (CNN). For this analysis, some feature selection methods were applied to the datasets. Several classifiers show the best accuracy in heart disease. In addition, machine learning algorithms play vital roles in predicting various health-related diseases in the early stages. The visual representation of the sequential steps for predicting heart dis-ease analysis workflow used in this study is shown in Figure 1.

### 2.2 Data Collection, Processing and Model Selection

In this study, the heart disease data source used was UCI Heart Disease data sourced from the UCI machine learning repository website. The Cleveland dataset is in structured tabular form, which is recognized and frequently employed in research

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focused on diagnosing heart diseases. The data set consists of 297 agencies with 14 attributes. The dataset used in diagnosing heart disease is the Heart Disease Dataset which is a dataset of 4 different combinations of datasets, but in some sources, only the UCI dataset is used in this study. The basis of the data is that there are 76 attributes or features, but in published research, only 14 attributes have been processed [9]. The data is contained in the Dataset repository, namely the UCI dataset. In the dataset, there are 14 attributes and 1 attribute for prediction or known as the dependent variable name, the 'Diagnosis' attribute, and the rest will be entered as input or known as the independent variable. The attribute descriptions are shown in Table I.

Table I. The Attribute Descriptions

| No | Features / Attributes | Type Value | Description Features | Value |
|---|---|---|---|---|
| 1 | Sex | Discreate Variable | Male or female representative of your age | 1: Male<br>0: Female |
| 2 | Age | Continuous Variable | Patient range shown by age | Multiple value in range 28 and 77 (age in years) |
| 3 | CP (Chest Pain) Type | Discrete Variable | Represent to chest pain type: typical angina, atypical angina, non-anginal pain, asymptomatic | 0: typical angina<br>1: atypical angina<br>2: non-anginal pain<br>3: asymptomatic |
| 4 | Rest Blood Pressure (Trestbps) | Continuous Variable | represent the resting heart rate (in mm Hg on admission to the hospital) | Multiple continue value in mmHg |
| 5 | Serum Cholestoral (Chol) | Continuous Variable | represent the resting heart rate (in mm Hg on admission to the hospital) | Multiple Continuous value in mm/dl |
| 6 | Fasting Blood Sugar (FBS) | Discrete Variable | Represent the patient's fasting blood sugar level | 0: false (FBS < 120 mg/dl)<br>1: true (FBS > 120 mg/dl) |
| 7 | Max Heart Rate (Thalach) | Continuous Variable | represent the patient's maximum heart rate | Multiple values from 71 to 202<br>Low: under 50 beats/min<br>Normal: 51–119 beats/min<br>High: 120–180 beats/min |
| 8 | Res Electrocardiographic (Restecg) | Discrete Variable | Represent the ECG's outcome, where each integer represents the level of pain. | 0: normal<br>1: having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV)<br>2: showing probable or definite left ventricular hypertrophy by Estes' criteria |
| 9 | Exercise Induced (Exang) | Discrete Variable | Determine whether or not there is exercise-induced angina by representing. | 1: yes<br>0: no |
| 10 | Oldpeak | Discrete Variable | Show how exercise-induced ST depression compares to rest | Multiple decimal number values between 0 and 6.2. |
| 11 | Slope | Discrete Variable | Describe the patient's state at the height of exercise. There are three sections in this paragraph. | 0: upsloping<br>1: flat<br>2: down sloping |
| 12 | Major Vessels (Ca) | Discrete Variable | The quantity of main vessels that fluoroscopy can colour. This section displays the number of colored vessels. | number of major vessels (0–3) colored by fluoroscopy → (0, 1, 2, 3) value |
| 13 | Thal | Discrete Variable | Patients with chest pain or respiratory distress also need to have this parameter tested. Three different value types displaying Thallium test results are shown in this section. | 0 = normal<br>1 = fixed defect<br>2 = reversible defect and the label |
| 14 | Target / condition | Discrete Variable | The data set's last column. The Class column or Label column are other names for this Target column. Using the preceding 13 parameters for analysis, this column generates prediction results with two classes, i.e. class 0 and class 1. This indicates that the likelihood of avoiding developing heart disease is "0" if the class number. If the class displays the number "1," then the opposite is true, specifically with the potential for developing heart disease. | 0: no disease<br>1: disease |

### 2.2.1 Data Description and Analysis

The dataset (Table 1) includes patients of age ranging from 29 to 79, with gender values of 0 representing females and 1 representing males. The slope parameter indicates the inclination of the peak exercise ST segment. Within the patient cohort, we have identified four distinct chest pain types that could potentially function as indicators for cardiovascular disease. The first type, Type 1 angina, is linked to reduced blood flow due to constricted coronary arteries and is typically triggered by mental or emotional stress. On the contrary, non-angina chest pain may have diverse underlying causes and might not necessarily point to an actual heart ailment. The fourth category, no pain, does not manifest as a symptom of heart disease. Thal signifies the presence of Thalassemia, Trestbps indicates the resting blood pressure reading, chol denotes the cholesterol level, restecg represents the outcome of the resting electrocardiogram, thalach signifies the maximum attained heart rate, exang denotes exercise-induced angina, with a value of 1 indicating its presence and 0 indicating its absence. The variable 'ca' represents the count of major vessels identified through fluoroscopy, 'oldpeak' represents the exercise-induced ST depression, 'fbs' signifies the fasting blood sugar level, with 1 indicating a level below 120 mg/dL and 0 indicating a level above, while 'Target' serves as the class attribute, normal patients represented as 0 and patients diagnosed with cardiovascular disease as 1. (Fig. 1) shows the distribution of the dataset according to presence and absence of cardiovascular disease, sex, and age.

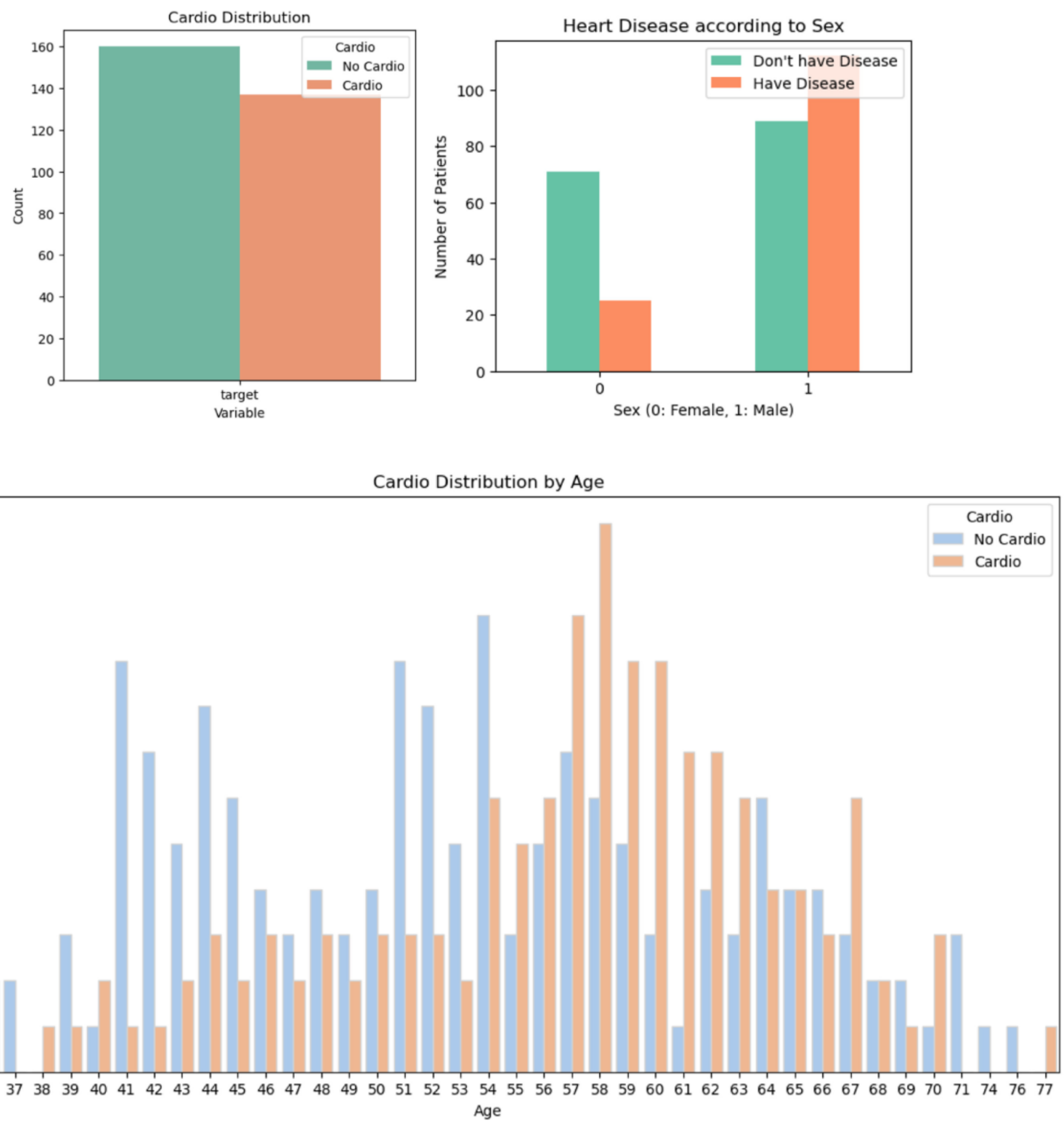


Figure 1: Distribution of dataset according to presence or absence of cardiovascular disease, sex, and age.

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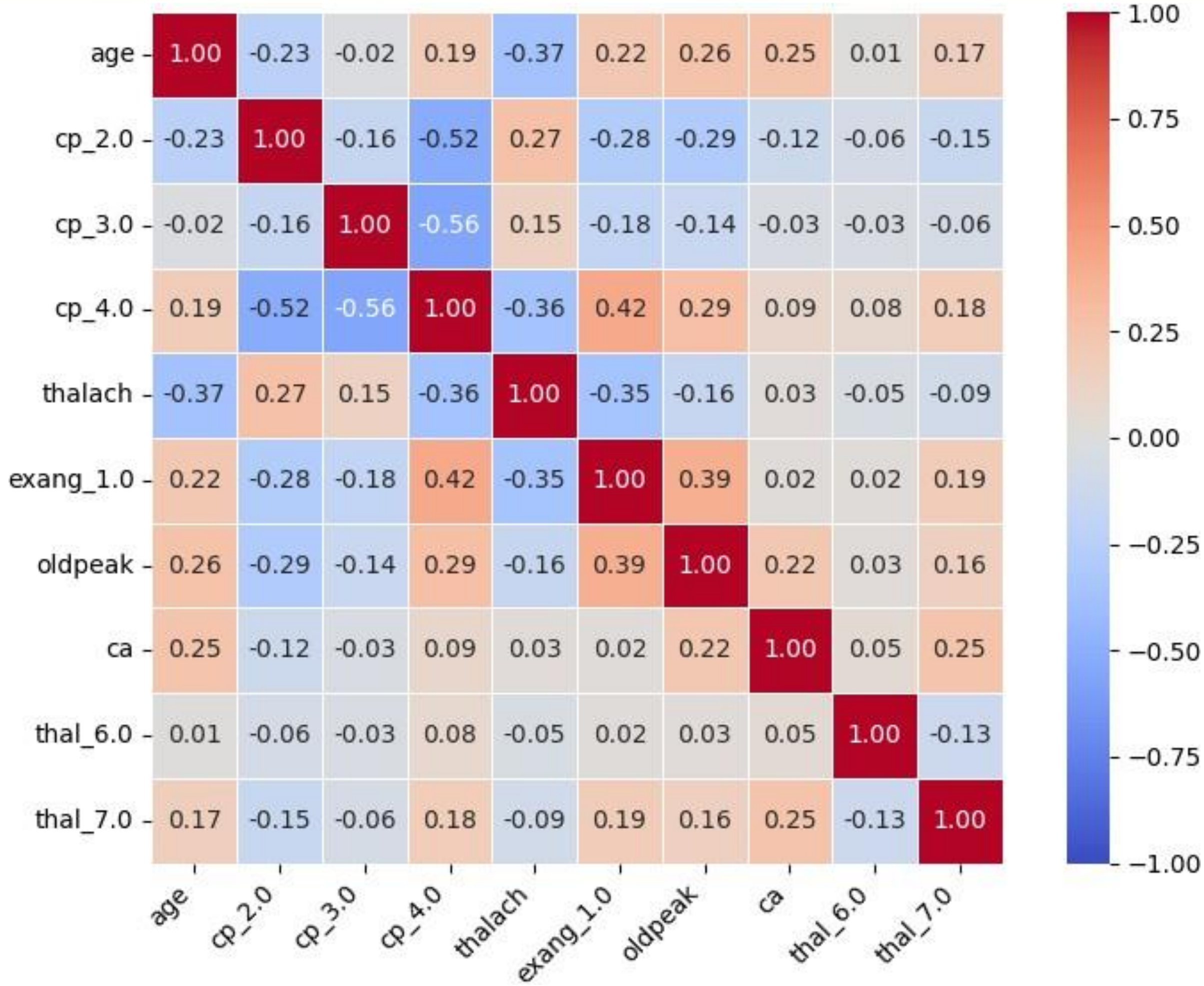


Figure 2: Correlation heatmap of the heart disease dataset attributes.

The Correlation Matrix in Fig. 2 shows the relationship between two attributes. Attribute ca is highly correlated with the target variable, followed by thalach, exang, and oldpeak. Thalach is highly correlated with age, exang, and oldpeak. Other correlations between the attributes can be visualized from the figure.

#### 2.2.2 Data Preprocessing

The dataset was cleansed by eliminating rows with missing values. For preprocessing the dataset, standard scaling was employed. This preprocessing step helped in eliminating biases towards features with larger magnitudes and facilitated fair comparison among the models.

$$z = \frac{x - \mu}{\sigma} \qquad (1)$$

$K$

$j = 1$

$$\mu = \frac{1}{K}\sum_{j=1}^{N} Y_i \qquad (2)$$

$$\sigma = \sqrt{\frac{1}{K}\sum_{j=1}^{K}(y_i - \mu)^2} \qquad (3)$$

Where $\mu$ is the mean, $\sigma$ represents the standard deviation, while K stands for the count of occurrences within each column. Most ML models work strictly with numerical features. It is possible to convert categorical features into numerical features. The trick is to use one-hot encoding, an all-zeros

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vector with a single element being one correspond-ing to the index of the category.

**Missing values:** This work replaces any missing value with the mean if it was a new class label "Un-known" if it was categorical, and the target classes are balanced by repeating randomly selected cases.

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**Data split:**Training a complex model on simple data can result in overfitting. Informally, it is when the model can memorize the dataset entirely with-out learning how to classify it correctly. It is the model's inability to detect the underlying patterns in the data. Whereas training a simple model on complex data might result in underfitting (learning trivial rules). For example, a model classifies pa-tients based on age only (sick if old and healthy otherwise). To avoid both problematic outcomes, the data is split into two chunks. The first split will be used to train the model, and the second to test it. Both splits should be representative enough of the entire dataset (the same ratios of healthy to sick cases; stratified). A trained model is overfitting if its performance in training surpasses the testing and underfitting if it could not improve over a fixed classifier; it always predicts the same thing (healthy or sick) regardless of the input.

### 2.2.3 Proposed System

The proposed diagnosis model selection system (Fig. 3) comprises five phases, such as data col-lection, data pre-processing, classification using deep learning and machine learning algorithms, performance evaluating metrics, assessment of the efficiency of the various algorithms, and finally selecting the best model for cardiovascular disease classification based on a comparative study of performance metrics.

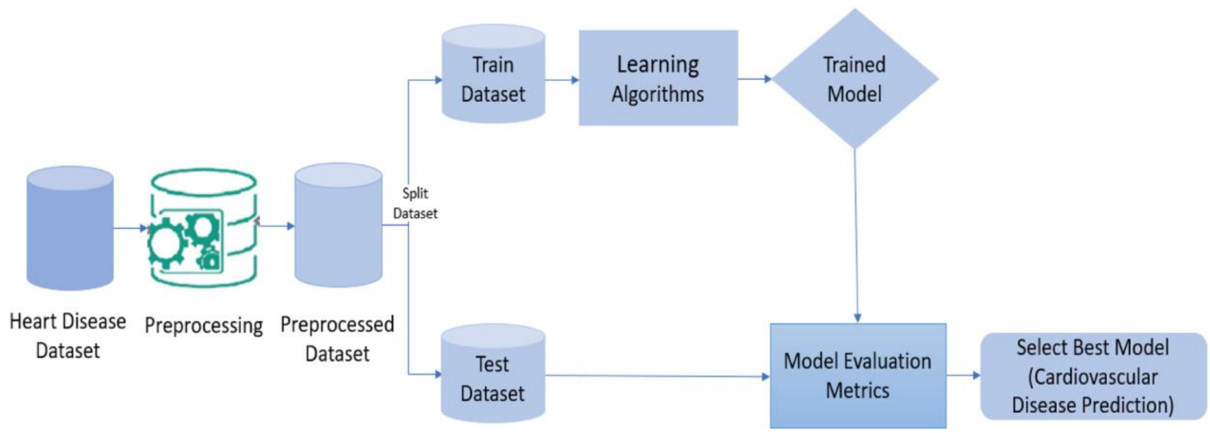


Figure 3: Proposed diagnosis model selection system for cardiovascular disease prediction.

### 2.2.4 Classification using Deep Learning Techniques

Deep learning is a form of ANN which is struc-tured similarly to the human brain, with numer-ous layers of interconnected nodes, or neurons. Ev-ery neuron receives inputs, processes them through a mathematical operation, and generates an out-put as shown in Fig. 4. Classifier in general use the data that had been processed earlier. The classification algorithm tested in this paper is the 1D-convolutional neural network (CNN). CNN ar-chitecture consists of convolution layers for fea-ture extraction, pooling layers for dimensionality reduction and a fully connected layer for classifi-cation. In CNN dropout and batch normalization are used to prevent overfitting and improve stabil-ity. DenseNet improves CNN by connecting each layer to every previous layer by ensuring better gradient flow and parameter efficiency. DenseNet re-quires fewer parameters than traditional CNN. The 1D-CNN model is trained and tuned using different hyperparameters and finally, from the top model parameters, we should evaluate the model we made based on the accuracy of its prediction and its per-formance algorithm using the performance metrics or metrics indicators.

**Hyperparameter tuning:** Deep learning mod-els in general have a few configurable hyperparam-eters, a set of properties that changes its training behavior and final performance. Usually, they de-pend on each other (e.g., a particular hyperparam-eter setting has a different meaning and effect if the value of another hyperparameter is changed). So, to achieve the best results for a model, it needs to be trained under all combinations of possible assigned values for its hyperparameters if feasible. This is what is known as hyperparameter tuning through grid-search.

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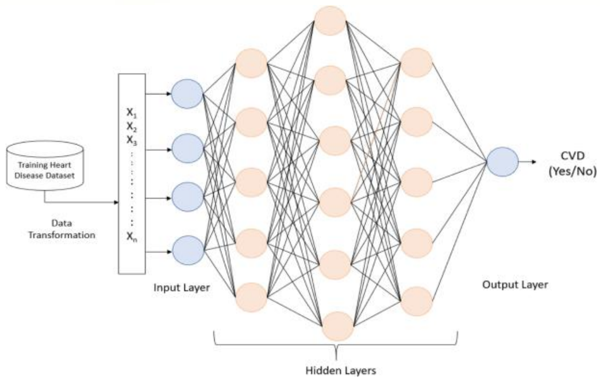


Figure 4: Deep learning model.

**Model Evaluation:** After building and training the DL model with different hyperparameters, one can compare their classifying power and see which one performs better. The following metrics are utilized to evaluate the performance or quality of the model implemented for heart disease classification:

- ***Accuracy:*** It expresses the model's accuracy in predicting, as a percentage of all predictions. However, accuracy alone may not be the best metric to use for heart disease prediction, as the dataset may be imbalanced, meaning there may be more cases of one class than the other. The accuracy lies in the range of [0, 1].

$$Accuracy = \frac{t_p + t_n}{t_p + t_n + f_p + f_n} \quad (4)$$

- ***Recall:*** It is the proportion of genuine true cases of heart disease in the dataset that are true positives. It assesses how many actual heart disease cases the model correctly pre-dicted.

$$Recall = \frac{t_p}{t_p + f_n} \quad (5)$$

- ***Precision:*** Precision deals with the amount of true positives heart disease cases that were accurately predicted to all other positive predictions generated by the model, including false positives. In other words, it counts the number of times the optimistic forecasts came true.

$$Precision = \frac{t_p}{t_p + f_p} \quad (6)$$

- ***F1-score:*** It is a harmonic mean of recall and precision, offers a single metric that strikes a compromise between the two metrics. When recall and precision are equally crucial to solving the problem, it is frequently used.

$$F1\ score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (7)$$

Where tp represents the instances where the model correctly predicts that an individual has a heart dis-ease when they do, fp represents the instances where the model incorrectly predicts that an individual has a heart disease when they do not, fn repre-sents the instances where the model incorrectly pre-dicts that an individual does not have heart disease when they do, tn represents the instances where the model correctly predicts that an individual does not have heart disease when they do not.

## 2.3 Computational Requirements

All the experiments were conducted in a Google Colab environment which provided a cloud-based dual NVIDIA Tesla T4 GPU with 16GB of VRAM. Our 1D CNN model's lightweight architecture fa-cilitates quick training, accomplished in its entirety (50 epochs with early stopping) in around 2–3 min. The models average inference time is under 10 milliseconds, which makes it a prime candidate for real-time clinical application. The design of the 1D CNN structure allows the usage of the networks on normal clinical computers and clinical cloud services. This is because the networks do not need complex super computers which is a great help in low-resource healthcare settings. The model is designed in Python 3.10 in the Google Colab which also runs TensorFlow 2.15 with the Keras API for the deep learning part. The other Python packages used were NumPy for arrays and numerical operations, Pandas for data frames, Scikit-learn for data preprocessing (StandardScaler) and evaluation metrics, and Seaborn with Matplotlib for data graphics.

We assigned the loss function as categorical cross-entropy as the target variable is binary, it becomes a classification problem. For this model, the num-ber of epochs was set to 50 with the batch size of 32. To combat overfitting, early stopping was implemented, which halted the training phase without improvement of the validation loss over a span of 15 epochs. Furthermore, we applied the ReduceLROn-Plateau callback, designed to lower the learning rate when the validation loss remains flat for a set dura-tion of 5 epochs.

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## 3 Results

In this research, we undertook multiple experiments that evaluated. The studies centered on the proposed method for the prompt recognition of diseases. We will first cover the various iterative models being studied and then a quantitative comparative analysis of our technique against contemporary methods in the field of Medical Records Big Data. Ultimately, performance graphs are used to analyze the results, concentrating on and extracting the critical insights about enhanced treatment, in doing so, clarifying the main contributions of this section. Considering various model architecture and training configurations to enhance the final accuracy for Disorder Prediction. Table II shows the different model versions that were assessed. This also includes the associated accuracy metrics.

Table II. CNN model ablations to forecast cardiovascular disease.

| Model variant | Config | Activation | Batch | LR | Accuracy (%) |
|---|---|---|---|---|---|
| Model A (initial configuration) | 2 Conv1D, 1 Dense | ReLU | 32 | 0.001 | 78.35 |
| Model B (increased depth) | 3 Conv1D, 2 Dense | ReLU | 32 | 0.001 | 79.10 |
| Model C (dropout added) | 3 Conv1D, 2 Dense + Dropout | ReLU | 32 | 0.001 | 80.55 |
| Model D (reduced learning rate) | 3 Conv1D, 2 Dense + Dropout | ReLU | 32 | 0.0005 | 81.40 |
| Model E (L2 regularization) | 3 Conv1D, 2 Dense + Dropout + L2 | ReLU | 32 | 0.0005 | **82.53** |

To understand the performance of DL models, we use the confusion matrix. The confusion matrix is a performance measurement for machine learning classification problems. The confusion matrix in this case is a table with 4 different combinations of predicted values and actual values. The terms or values of the confusion matrix are TP, FP, TN, and FN shown in Table III. Figure 5 provides the predictive performance of the model:

- **True Negatives:** 59 (identified correctly as not having heart disease).
- **False Positives:** 15 (no healthy patients were misclassified as having heart disease).
- **False Negatives:** 14 (patients with heart disease were misclassified as healthy).
- **True Positives:** 78 (identified correctly as having heart disease).

The results from the test set indicate that the model did not overfit and robust generalization was achieved.

Table III. Confusion Matrix.

| | | Predicted | |
|---|---|---|---|
| | | has heart disease (Positive) | no heart disease (Negative) |
| Actual | has heart disease (Positive) | TP | FN |
| | no heart disease (Negative) | FP | TN |

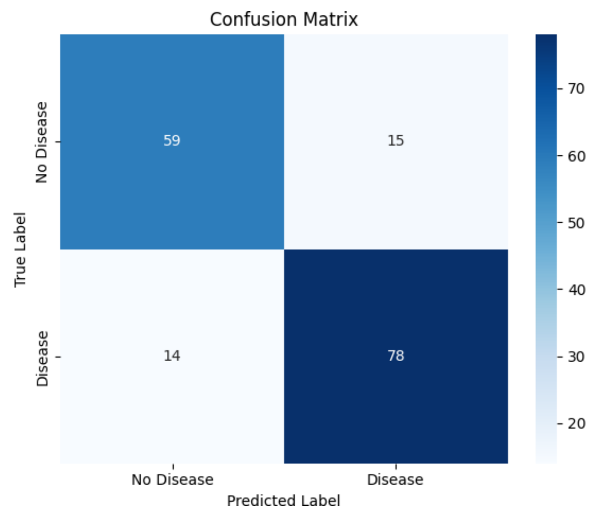


Figure 5: Confusion matrix of the proposed CNN model.

From the confusion matrix, the following performance metrics can be obtained:

*Accuracy:* The total value of the true results which comprise the true positives and true negatives out of total results is what is referred to as accuracy.

$$\text{Result:} \quad \frac{59+78}{59+15+14+78} = 0.8253 \ (82.53\%) \tag{8}$$

*Precision:* Precision is the ratio of correctly predicted positive cases to the total predicted positive cases. That would express the strength of the model in avoiding false positives.

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$$\text{Result:} \quad \frac{78}{78+15} = 0.8387 \tag{9}$$

*Recall:* Recall, or sensitivity, is the ratio of correctly predicted positive cases against the total of actual positives and represents the ability of the model to identify true positives.

$$\text{Result:} \quad \frac{78}{78+14} = 0.8478 \tag{10}$$

*F1-score:* When accuracy and recall differ greatly, the F1-score, which is the harmonic mean of the two measures, offers a single score that balances both.

$$\text{Result:} \quad 2 \cdot \frac{0.8387 \cdot 0.8478}{0.8387 + 0.8478} = 0.8432 \tag{11}$$

Figure 6 illustrates the learning progress over epochs for the training and validation sets. The learning progress can be summarized in the following observations:

- **Rapid initial improvement:** The first two epochs show both the training and validation accuracies improving significantly, indicating that the most relevant features are being learned.
- **Validation performance:** With respect to validation performance, though the validation accuracy is lower than the training accuracy, it demonstrates significant progress, getting to about 83% by the end.
- **Minimal overfitting:** The training and validation accuracy curves are very close to one another, which indicates that the model is able to generalize well, it indicates slight overfitting in the model.

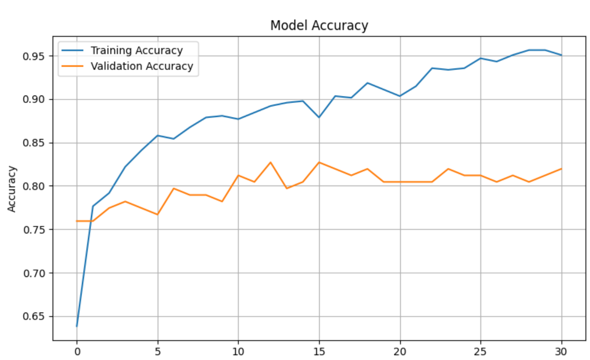


Figure 6: Training and validation accuracy

Figure 7 gives more insights into the model train-ing process.

- **Convergence:** The training and validation loss curves exhibited a consistently declining trend, which suggests that learning and optimization processes were effective.
- **Generalization:** The training and validation loss curves diverged very little in the later epochs, which means that the model is likely generalizing without overfitting.
- **Last achievement:** The model was able to predict well since both loss values had converged to approximately 0.65 by the 8th epoch.

The model demonstrates generalization with no overfitting, shown by the use of early stopping criteria, dropout, and L2 regularization, as well as data augmentation. An accuracy of 82.53% on the test set shows strong generalization on unseen data.
The loss function, which is categorical cross entropy loss, can be expressed as follows.

$$L = -\frac{1}{N}\sum_{i=1}^{N}\sum_{j=1}^{M} y_{ij} \log(\hat{y}_{ij}) \tag{12}$$

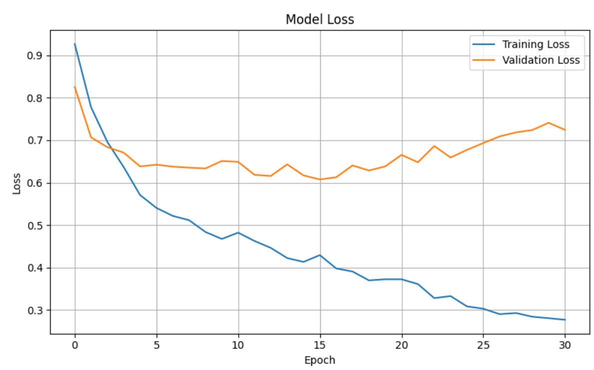


Figure 7: Training and validation loss

Figure 8 presents the model's diagnostic discrimination ability. The model's AUC is 0.87, which shows exceptional diagnostic discrimination for heart disease classification. Such a near-perfect AUC value implies that the model, at differing thresholds for classification, successfully differentiates between cases that are positive and those that are negative.

$$AUC = \sum_{i=1}^{n-1}(x_{i+1} - x_i) \cdot \frac{y_i + y_{i+1}}{2} \tag{13}$$

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where ($x_i$, $y_i$) represents the coordinates of points of the ROC curve.

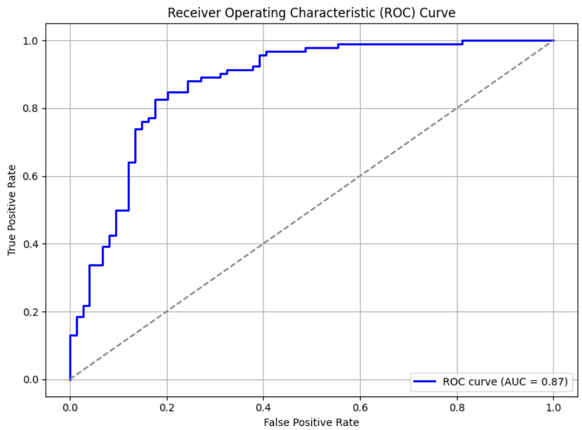


Figure 8: ROC curve

# 4 Conclusion

A CNN-based model for heart disease prediction demonstrates significant progress in diagnostic medicine. Achieving 82.53% diagnostic accuracy, 83.87% precision, 84..78% recall, and an F1-score of 84.32% indicates strong improvement com-pared with many conventional approaches reported in the literature. These results serve to underscore the value of deep learning technologies, especially convolutional neural networks, in capturing complex and intricate patterns within Medical Imaging Data that other, more conventional machine learning tools, would likely miss.

One of the main advantages of the proposed model is its ability to automatically extract important features from the input data. This distinguishes the CNN architecture from conventional methods that rely on manual feature extraction. By learning hierarchical representations of the data, the model increases the likelihood of identifying early signs of heart disease that might otherwise be overlooked. This capability is particularly valuable in the medical field, where many conditions have complex and not fully understood causes.

The loss and accuracy curves further demon-strate stable and effective learning throughout the training process. The steady reduction in loss, along with the improvement and stabilization of both training and validation accuracy, suggests that the model successfully learned meaningful patterns from the dataset. In addition, the close agreement between training and validation performance indi-cates strong generalization ability and limited over-fitting. This is especially important in medical applications, where a model must perform reliably not only on training data but also on unseen real-world cases.

The confusion matrix provides further insights into the model's performance. the convolutional architecture from the burden of explicit statistical feature engineering. This innovative approach enables models to learn sophisticated, non-linear relationships that tritional statistical methodologies might overlook showing a fairly even split between those with heart disease (78 positive) and those without (59 negative).

Real-world implementation of our CNN model in healthcare surroundings will face many obstacles. Many healthcare businesses run simple computer networks which may be too slow to support our model to streamline patient care. Staffing and investment in sufficient computer networks will be necessary to support the implementation.

Another noteworthy issue is the varying approaches different institutions take toward patient record documentation. The model was trained on a single dataset, but in real-life scenarios, different hospitals may have different techniques for capturing blood pressure readings or recording cholesterol levels. To deal with the variability, some degree of model customization may be needed in order to keep up real-world performance.

Overall, the proposed CNN model shows strong potential as a decision-support tool for early heart disease prediction. Future work may focus on validating the model on larger and more diverse clinical datasets, improving interpretability, and developing user-friendly deployment systems for real-world healthcare settings.

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