

# An Approach for Predicting Disease in the Heart Using an Improved Deep Learning Algorithm

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Submitted: 28/01/2024 Revised: 06/03/2024 Accepted: 14/03/2024

**Abstract:** The heart is a vital organ in humans. Deaths from heart disease are common, regularly recorded, and rapidly rising. There is no method to foresee illness or remedy the issue. The research aim is to create a deep learning-based artificial intelligence system for heart disease identification. The deep learning method is a great resource for illness prediction of all types. Better activation functions are used in the convolutional layers of the improved convolutional neural network (ICNN) that is proposed in this paper. A dense or fully connected layer is used to combine the key features. By contrasting the proposed ICNN algorithm with other deep algorithms already in use, its efficiency is verified. This article tests the deep learning algorithm's accuracy in predicting heart disease using data from the UCI repository. The Python Jupyter environment is used for the implementation. The effectiveness of the suggested ICNN model is determined using performance indicators like precision, accuracy, F1 score, along with recall.

**Keywords:** heart disease, Convolutional Neural Network (CNN), accuracy, deep learning, Python

## 1. Introduction

Any serious condition that affects the heart is considered cardiovascular disease. Researchers are making smart systems using electronic health data that can accurately diagnose heart problems using machine learning (ML) algorithms [1, 2, 3, 4, 5]. ML is utilized in medical service areas around the world. In the medical data, ML methods support in the locomotor disorders as well as heart diseases prevention. Researchers' improvement provides valuable insight into how to use their analysis as well as action for a specific patient when such crucial data are discovered [6]. To find out how accurate both ML algorithms are and how often they give false negatives, it is suggested to put patients of similar ages and health conditions into groups [7].

In an extended listing of recent Internet of Things (IoT) advancements across diverse industries, we discovered ML methods. According to other studies, there is only a sparkle of optimism for utilizing ML algorithms to predict cardiac disease. A study compares and analyzes the results of the UCI dataset utilizing a variety of ML methods. Researchers at the "University of California, Irvine" collected the data, which has 75 columns and will only use 14 features [8]. A Python program is produced for medical care work as it is extra dependable along with helps track as well as lay out various sorts of wellbeing checking applications. Working with categorical variables along with converting categorical columns are two aspects of the data processing that we

present. The primary phases of application development are outlined: evaluating the attributes of the dataset, carrying out logistic regression, and collecting databases. A more accurate method for identifying heart diseases is the random forest (RF) classifier algorithm [9].

An existing study uses an artificial bee colony (ABC) and an optimized Adaptive Neuro-Fuzzy Inferences System (ANFIS) to categorize the heartbeat sound. The heartbeat sounds are used to extract MFCC from the cleaned and pre-processed data. Then the ABC-ANFIS model is utilized to track the pre-handled heartbeat sound, along with accuracy is determined [10]. Between the years 2001 and 2021, 270 full-term newborns with complex CHD were joined for postoperative brain MRIs along with preoperative scans, totaling 466 scans. A study looked at clinical factors and white matter injury (WMI) or focal stroke in the brain four times over five years [11]. One study used logistic regression to do this. A previous study used the correlation matrix to find the features that match the most important risk factors to guess how long a patient with HF would live based on pathophysiological parameters [12]. The following are the critical contributions created by the research proposal:

- Initially, a heart disease dataset is split into 80% for training as well as 20% for testing.
- Before it is provided to the convolutional layers, the dataset is reshaped.
- The layers in the proposed ICNN model, are the convolutional layer (ConvL), maxpooling layer (PoolL), flatten layer (FlatL), and dense layer (DenL).
- The ReLU activation layer is used in the proposed model, and it is compared to various other activation

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functions that are already in use, including Tanh and Selu.

The work organization is stated here: Section 2 grants related work on Heart with various deep learning as well as ML algorithms. Section 3 discusses the proposed improved deep learning-based heart disease detection model. Section 4 presents the details regarding the results attained as well as the dataset. Section 5 presents the discussions of the research along with some limitations of the present research. The references come next, and Section 6 completes the work.

## 2. Literature Review

Teixeira et al. [13] created predictive attrition models using various ML techniques and a standard regression model. A baseline model with a fixed count of predictors along with an incremental model with a dynamic count of variables given with every follow-up were both put through their paces. There were eight methods of classification used: J48 Consolidated, J48, Logistic Regression (LR), Functional Trees, K-Nearest Neighbors (KNN), along with Random Forest (RF).

White-Williams et al. [14] described the patient experience in an interprofessional collaborative practice in this prospective study using both quantitative data as well as qualitative data. Information was gathered from patient experience overviews of 1128 patients found in the Cardiovascular Breakdown Temporary Consideration Administrations for Grown-ups (HRTSA) center. Individuals from the facility staff completed interprofessional cooperative practice reviews. This work identified three significant associations when examining relationships with patient experience. Being single was adversely connected with the patient's experience.

Sutari et al. [15] created a suitability model of 17 people with heart failure, along with four members of their families, who contributed in this distinct case study. Using the experienced-based codesign method, we got participants' stories about heart failure and how they were treated by annotating field notes from individual interviews, healthcare consultations, as well as minutes from stakeholders' feedback. Reflexive topical examination was utilized to foster the subjects' knowledge.

Munagala et al. [16] highlighted that a remote checking model is much better for acknowledging unavoidable medical care administrations. This uses the optimized ensemble fuzzy ranking (OEFR) method, heuristic improvement, deep feature extraction, along with an "optimized ensemble learning"-rooted IoT heart disease detection scheme. Additionally, an improved dingo

optimizer (I-DOX) algorithm is used to optimize each classifier's hyperparameter.

Dhande et al. [17] describe a way to find big features using AI techniques. Their method is based on finding multi-reason illness expectations. The prediction model is used to make predictions about diabetes and heart disease using a variety of well-known classification techniques and various features. Using classification algorithms and feature selection techniques, the method employs an ensemble approach to achieve higher accuracy rates. The suggested approach implements a voting classifier with sigmoid decision tree (DT) algorithms, AdaBoost, along with support vector machines (SVM).

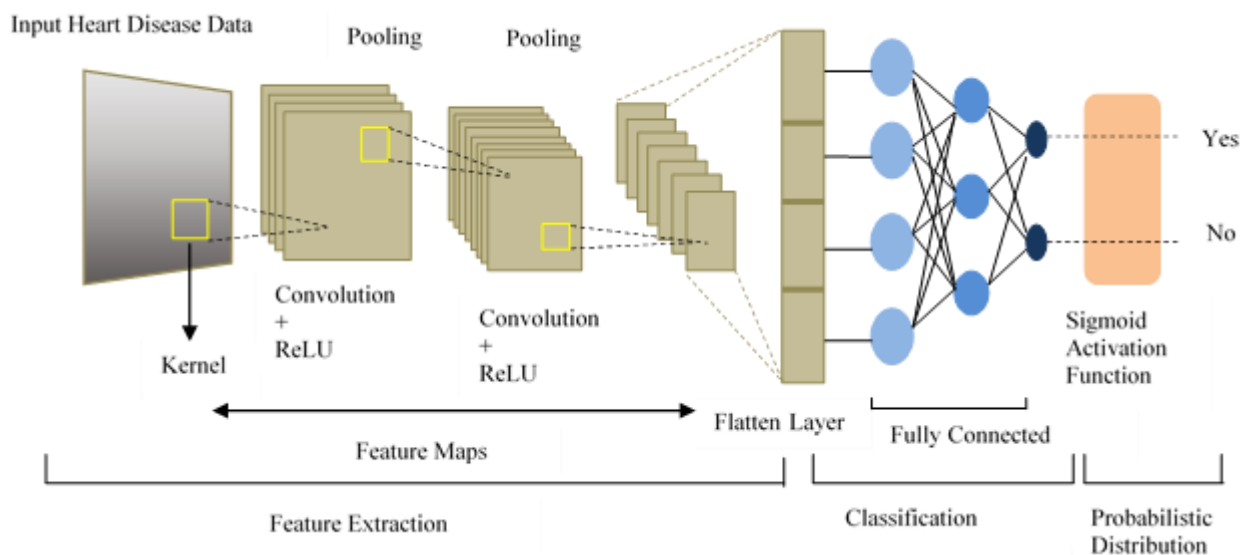
Ninni et al. [18] collected 104 patients' blood DNA for careful aortic valve substitution (AVR) and genotyped it utilizing the Heme PACT board. Four screening strategies were practiced to evaluate HSM, along with postoperative results were investigated. To look at all of the different types of blood and heart cells in a small group of patients before and after surgery, we used mass cytometry and classical monocyte RNA sequencing analysis.

Sonia et al. [19] used effective feature choice methods like Recursive Feature Elimination (RFE) to select significant features. In addition, ML classifiers were utilized for performance evaluation. DTs, KNNs, LRs, Artificial Neural Networks (ANNs) [20], and RFs were put through their paces, and the results were compared. Common classifiers like neural networks, KNNs, LR classifiers, DTs, as well as RFs are joined into a single model to address the classification issues. LR was predicted with the highest accuracy.

Wagner et al. [21] used model-grounded meta-analysis to produce a connection network that comprised both normal signs of dyslexia, including translating, phonological alertness, and oral language, as well as response to intervention (RTI) as well as the chance of having dyslexia in the family.

## 3. Proposed Methodology

It is challenging to determine if a patient has a heart illness since it involves binary categorization. In recent months, deep neural networks that include multiple application-specific hidden layers have advanced significantly due to the abundance of structured data available [22]. If a patient's cardiac condition is misdiagnosed, they could not get any therapy at all or the wrong kind of treatment. Because of this, improving classification accuracy—or the capacity to determine whether a person has a cardiac illness or not—is one of the primary objectives of this study.



**Fig.1.** Proposed ICNN Model Layer Organization

This research was motivated by the success of deep networks and suggests an improved CNN (ICNN) to get around these issues. The model proposed in this research has consecutive convolution layers of a count 2, trailed by a FlatL, a PoolL, as well as two DenL, as depicted in Figure 1.

CNN's main benefit is that it provides an analytical way to directly extract input data's raw form features. Its classification and learning skills surpass those of conventional neural networks. In place of the more traditional 2D kernel, a 1D convolution kernel was utilized to exploit the input data properties. A 1D-CNN model must first train on the heart disease data in order to obtain the predicted value. The forward propagation process goes from the input layer to the output layer. When the results of the forward propagation do not match the expectation, the cross-entropy loss function is employed to regulate the error that lies between the expected as well as actual values. Then, in order for Adam's optimizer to adjust the weight, the error is sent back to each layer. Until the smallest loss function value is obtained and the network is finished with the new parameters, the procedure is repeated [23].

### 3.1. Convolutional Layer

Using a 1D-CNN model, spectral information was extracted. The 1D-CNN layer is used as the primary layer using the dataset input size. Local feature extraction is accomplished on the ConvL, which is positioned below the sequential layer, to obtain feature data with fewer dimensions. 1D-CNN is used to perform convergence throughout the local input data region in order to provide the matching feature. Each kernel has unique attributes at every location on the feature map. 1D-CNNs employ weight sharing to converge with fewer parameters. This guarantees an early and faster convergence of 1D-CNN. Every input layer and output layer stride will make use of every weight

with 3 as the kernel size. In the kernel window, weights are applied to the input values. The values are added together to generate the feature map value. The output of the ConvL functions as the next layer's input and output at the same time. Two convolutional layers are used in this research, one after the other [24].

### 3.2. Pooling Layer

The PoolL comes after the ConvL layer also can get lower-resolution feature data, make the network more resilient, and reduce the number of dimensions in the feature vector even more. PoolL layers are critical for CNNs. To expedite the succeeding phase, PoolL lowers the parameters count while maintaining the vital properties. Therefore, at this point, every feature map is analyzed employing the max method. The max-PoolL technique is employed to select the extreme parameters. PoolL methods are likewise projected to overcome the overfitting problem. The output values will be reduced in size, along with the maximum values for the network layer that comes after will also be carefully chosen as well as directed as input to the layer that will be compressed.

### 3.3. Fully Connected Layer

To obtain the complete data features, the output data from the flatL layer is passed into the fully connected (FC) layer, also known as the dense layer. The ReLU is used as the activation function in this study, which aid in learning the inspiring data of the network, advance its nonlinear modeling abilities, and provide more accurate predictions. The FC layer of CNN is a crucial component. The CNN method splits the input into a feature vector also then looks at all feature distinctly. This stage initial phases are pooling along with convolution. The procedure yields a final decision that is fully connected. Reshaping (flattening) the network's earlier stages output produces a single vector. They all represent the probability that a particular attribute

is assigned to a class. To select the suitable label, weights as well as the feature map are inputted. FC's output layer provides the final probabilities for all labels. The different activation functions checked were Tanh. The Tanh function has an S-shape and an output range difference of -1 to 1. When the input is larger, Tanh's output value approaches 1.0, which is more positive, whereas when the input is smaller, it approaches -1.0, which is more negative. The tanh mathematical expression is given in (1)

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

However, Tanh must contend with vanishing gradients in addition to the substantially higher gradient of the Tanh function. Next, the Selu activation function is checked. The Scaled Exponential Linear Unit (SELU) was created to handle internal normalization in self-normalizing networks. This keeps the mean and variance of each layer the same. By modifying the mean and variance, SELU makes this normalization possible. The Selu mathematical expression is given in (2)

$$f(\alpha, x) = \lambda \begin{cases} \alpha(e^x - 1) & \text{for } x < 0 \\ x & \text{for } x \geq 0 \end{cases} \quad (2)$$

Given that SELU is a novel activation function, it is not yet commonly utilized in practice. Hence, in this research, the Relu activation function is used and is equated in (3)

$$f(x) = \max(0, x) \quad (3)$$

The ReLU function is more computationally effective than the other functions since only a small portion of neurons are active. Adam is a tool used for optimization. Adam has lately been mentioned in the majority of scholarly articles since it converges much more quickly than other adaptive approaches. The result from the prediction output is then utilized to determine the heart disease.

## 4. Results

### 4.1. Description of the Dataset

The dataset employed in this work is from the UCI ML Repository [25]. The dataset features are employed to identify individuals who have a high risk of heart illness. Age, cp, trestbps, fbs, chol, sex, exang, restecg, oldpeak, thalach, slope, ca, thal, and target. Figure 2 depicts the heatmap for the dataset.



Fig. 2. Heatmap for the Dataset

Table 1. ICNN model parameters

Layer	Layer Type	Parameter
Conv1D	Convolutional	32 is the filter size with 3 as kernel size, activation = relu, dataset size = (13,1)
Conv1D	Convolutional	16 is the filter size with 3 as kernel size, activation = relu
Maxpooling1D	Pooling	Size of the pool is 2
Flatten	Flatten	-
Dense	Dense	10-unit, activation = relu
Dense	Dense	1 unit, activation = sigmoid

The proposed ICNN model parameters are listed in Table 1. The ConvL layers are the first and second. With a pool size of two, the PooliLis the third layer. The fourth layer is the FlatL. The fifth layer is the FC, with Relu activation function and 10 units. Since the proposed study involves binary classification, the final layer is also dense with a single unit, and the sigmoid activation function is chosen since it is thought to be the best for binary classification. The Adam optimizer, 50 epochs, as well as binary cross entropy are the additional training parameters.

Defining how fine the model would perform with input data requires evaluating its performance. The proposed ICNN model with four other existing DL models uses eight different metrics to check the efficiency. These metrics allow comparisons between many models and the evaluation of the data's importance for each classification label. The metrics include support, weighted average, confusion matrix (CM), f1 score, precision, accuracy, recall, along with macro average. An indicator of accuracy is the proportion of acceptably recognized data over all data. It

gives data on the inputs percentage that are properly detected. Equation for accuracy is provided in (4).

$$\text{accuracy} = \frac{\text{Properly detected data}}{\text{Total data}} \quad (4)$$

The CM includes a list of each prediction the model made. This matrix's columns indicate the actual class classifications, while each row shows the forecasts for every class. Relations such as true negative (TN), false negative (FN), true positive (TP), as well as false positive (FP) are used for a comprehensive analysis.

The term "TP" denotes to the total count of properly detected inputs. This value is present in the matrix's leading diagonal for every class. TN is the samples count that are correctly recognized as not being members of a certain class. FP is the samples count for which the model wrongly forecasts a certain class. FP patients' prediction without heart disease happens during the model receives an input intended for a patient with heart disease but instead provides it to a person without heart disease. This count is calculated for a class by totalling all the row values, excluding the TP. FN is the models from one class count that the model incorrectly forecasts as models from extra class. When the model incorrectly forecasts a person without heart disease given an input that resembles to a heart disease patient.

A statistic called precision is used to evaluate how well or accurately a model predicts a given class. Out of all the forecasts, it indicates the number of epochs the model's forecast that the output would fit to a certain class was correct. Consequently, this statistic offers details on the correctness of the model for every class. It is determined for each class by dividing the sum of TP and FP by the TP ratio. Precision is equivalent to (5).

$$\text{prec} = \frac{\text{TP}}{\text{FP}+\text{TP}} \quad (5)$$

Recall is the ratio of samples suitably categorized by the model to the total samples in that class. It is also termed as "sensitivity." In (6), recall is equated

$$\text{recall} = \frac{\text{TP}}{\text{FN}+\text{TP}} \quad (6)$$

A harmonic ratio known as the F1 Score measure makes finding the ideal balance among recall as well as precision. The equation for an F1 score is in (7).

$$\text{F1 score} = 2 * \left( \frac{\text{prec} * \text{recall}}{\text{prec} + \text{recall}} \right) \quad (7)$$

Support provides information on the total frequency of models from a specific class. This reveals the count of samples utilized in the study, allowing for the analysis of the dataset's class-wise distribution. There are two ways to summarize all of these metrics: macro as well as weighted average. All of the classes are combined together to obtain the total values of a measure, including accuracy, recall, f1 score, for calculating a macro-average. Divide the amount

by the total classes count after that. After that, divide the total by the total classes count. This is mathematically expressed in (8)

$$\text{Macro avg} = \frac{\text{score of first class} + \text{score of second class}}{2} \quad (8)$$

An averaging method that takes into consideration the dataset's uneven sample distribution of classes is called a weighted average. This is written in math as (9), which is the result of adding every class metric score to the number of samples that belong to that class also then dividing that number by the entire number of samples.

$$\text{Weighted avg} = \frac{\sum(\text{ith class score} * \text{ith support class})}{\text{total dataset count}} \quad (9)$$

## 5. Discussion

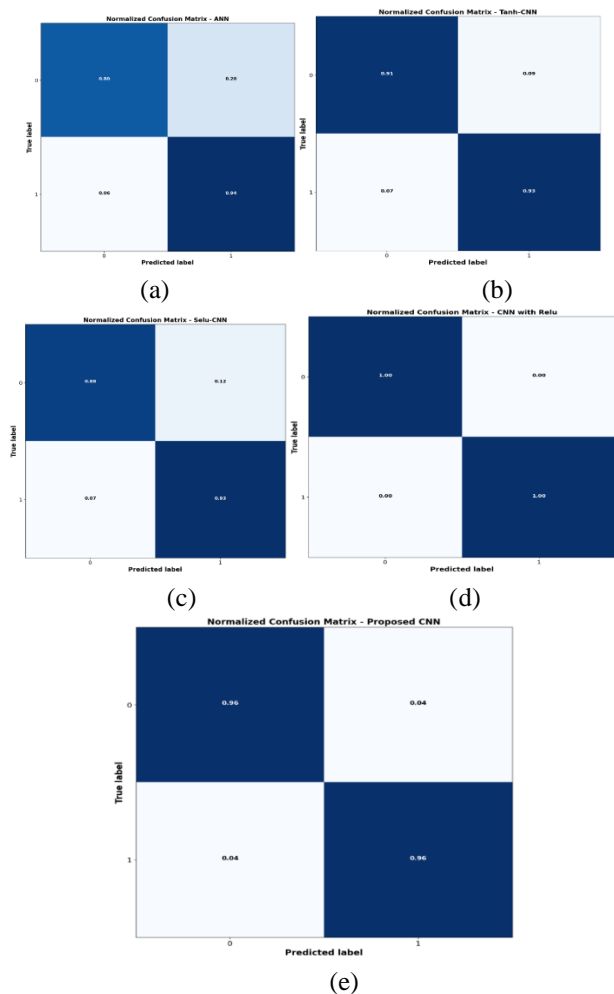
The proposed ICNN model for classifying heart disease is compared to an existing ANN, CNN using different activation functions such as Tanh, Selu, as well as Relu. An ANN transforms the input data through consecutive hidden layers, as well as at the output layer, it computes the error. The error is transmitted back to update the layer weights continuously using the gradient descent technique.

**Table 2.** Diverse Models Comparison

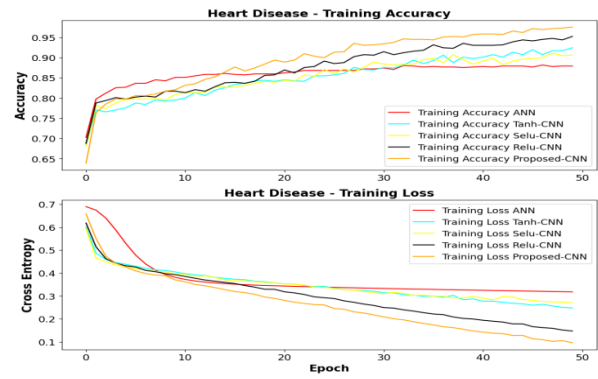
Methods	Classes	Prec	Recall	F1-score	Support
ANN	0	0.93	0.8	0.86	98
	1	0.83	0.94	0.89	107
	Acc			0.87	205
	Macro avg	0.88	0.87	0.87	205
	Weighted avg	0.88	0.87	0.87	205
CNN with tanh	0	0.92	0.91	0.91	98
	1	0.92	0.93	0.92	107
	Acc			0.92	205
	Macro avg	0.92	0.92	0.92	205
	Weighted avg	0.92	0.92	0.92	205
CNN with Selu	0	0.92	0.88	0.9	98
	1	0.89	0.93	0.91	107
	Acc			0.91	205
	Macro avg	0.91	0.91	0.91	205
	Weighted avg	0.91	0.91	0.91	205
CNN with Relu	0	0.98	0.91	0.94	98
	1	0.92	0.98	0.95	107
	Acc			0.95	205

	Macro avg	0.95	0.94	0.95	205
	Weighted avg	0.95	0.95	0.95	205
Proposed ICNN	0	0.96	0.96	0.96	98
	1	0.96	0.96	0.96	107
	Acc			0.96	205
	Macro avg	0.96	0.96	0.96	205
	Weighted avg	0.96	0.96	0.96	205

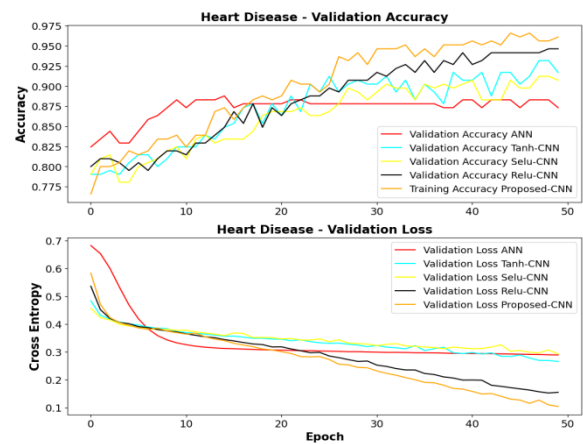
The comparison of performance parameters between numerous approaches is tabulated in Table 2. The proposed model performs better than the models, such as ANN and CNN, with diverse activation functions like Tanh, Selu, and Relu. The proposed ICNN model has an accuracy of around 96% in this instance. This outperforms the ANN model by 7.87%, CNN with Tanh by 4.35%, CNN with Selu by 5.49%, and CNN with Relu by 1.05%. Also, the CM graph for these models is illustrated in Figure 3.



**Fig. 3.** Confusion Matrix (a) ANN (b) CNN with Tanh (c) CNN with Selu (d) CNN with Relu (e) Proposed ICNN Model



**Fig. 4.** Training Accuracy and Loss Comparison Graph



**Fig.5.** Validation Accuracy and Loss Comparison Graph

The training accuracy as well as training loss improvement graph is illustrated in figure 4. The validation accuracy along with the validation loss improvement graph are explained in Figure 5. The proposed ICNN model in the figures is shown by the orange-colored line. The proposed ICNN model outdoes the previous models by accuracy along with loss. The proposed ICNN model therefore outperforms other current methods for detecting cardiac disease.

### 5.1. Limitations

Though the proposed work has better predicted heart disease until now, there are limitations in accuracy. Moreover, in this work, other than ML algorithms, DL algorithms are used to detect heart disease effectively. So as long as DL algorithms show some defects in accuracy, this work can be extended by working with a combination of both ML and DL algorithms.

### 6. Conclusion

This study uses the ICNN model to identify cardiac illness. In order to conduct a comparison assessment and achieve true positive performance, the proposed model's efficacy is examined in conjunction with existing DL methods. The proposed ICNN model outperformed statistical techniques in this study, according to the findings. The results of several



studies, which show that this model is the finest means to forecast as well classify cardiac disease, are given by this article. Various performance parameters, including precision, F1 score, accuracy, recall, and others, have been compared for every recently available DL classification models on the UCI data set. The future research aims to improve the algorithm further by combining machine learning and DL techniques.

**Conflict of Interest:** None

**Funding:** None

**Data Availability Statement:**

<https://archive.ics.uci.edu/ml/datasets/Heart+Disease>

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