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Efficient Chronical Disease Prediction Using Improved Convolutional Neural Network Model

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Abstract*:* Accurate analysis of medical data aids with initial illness identification, community services, as well as patient treatment in the healthcare fields. However, when the medical data quality is deficit, the analysis's accuracy suffers. The study's objective is to create an artificial intelligence system for chronic diseases detection that is deep learning-based. The experiment is conducted using various healthcare data that was obtained from Kaggle. Pre-processing is used to fill in the gaps in the data in directive to get around the challenge of imperfect data. This study suggests a novel multimodal disease risk prediction method grounded on convolutional neural networks (CNNs) that uses both structured and unstructured input. The Improved Convolutional Neural Network with Nadam Optimizer (I-NCNN) is the algorithm that is put forth in this paper. As far, there is only some research on multimodal disorders. The implementation takes advantage of the Python Jupyter environment. Performance measures, including precision, accuracy, F1 score, also recall, are make use of to assess the efficiency of the proposed I-NCNN model. The prediction accuracy of the proposed algorithm is 96% when likened to various other existing

Keywords: *Chronic Disease, CNN, optimizer, deep learning (DL), Python.*

1. Introduction

In today's medical research, the diagnosis of chronic disease has become challenging. The patient's health history and the results of their clinical tests must be thoroughly and precisely analyzed in order to make this diagnosis. The tremendous improvements in the field of profound learning try to make wise robotized frameworks that aid specialists together to foresee along with to decide the illness with the Internet of Things (IoT) [1]. Coronary conduit illness is a typical constant infection, otherwise called ischemic coronary illness, which is a cardiovascular breakdown brought about by the deficient blood supply to the heart as well as slays innumerable individuals consistently. As of late, coronary artery disease levels leading among the world's main ten reasons for eave [2].

CNN are utilized to plan a beginning phase expectation and clinical determination framework. CNN obtains 13 clinical features as input. CNN is trained utilizing an amended back propagation training method [3]. A study used a DL algorithm well-known as CNN to guess a likelihood of a patient having cardiovascular disease. This technique is called cardio help. The technique is worried about transient information, as demonstrated by using CNN for HF expectation at its earliest stage [4].

Pre-processing is done with z-score normalization and the maximal overlap discrete wavelet transform (MODWT) smoothing algorithm.

An amalgamation of CNN as well as recurrent neural networks (RNN) grounded on bi-directional long-short-term memory (BiLSTM) was used to reduce the complexity [5].

A CNN model that accurately detects CHF based on a single raw electrocardiogram (ECG) heartbeat is presented to fill this important gap. It also contrasts existing methods, which are typically based on heart rate variability [6].

A loss function called focal loss was introduced as an optimization stage for the deep CNN model. By increasing their importance, this function places an emphasis on minority heartbeat classes [7]. The ordinary and strange heart workings are analyzed by utilizing the Modified Deep CNN (MDCNN). The work was inspected using the University of California, Irvine (UCI) dataset. The MDCNN classifier likewise offers a higher level of exactness than the current methodologies [8]. The ensuing are the contributions of this research:

- Initially, three different chronic disease datasets, like heart disease, kidney disease, and diabetes, are selected and divided into training and testing ratios of 80 to 20%, i.e., 80% for practice along with 20% for analysis.
- Some datasets are structured. Some datasets are not structured; they are structured by using pre-processing. The dataset is reshaped to be sent to the input convolutional layers.

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- In the proposed I-NCNN model, there are two convolutional layers, a batch normalization (BN) layer, a flatten layer, a dropout layer, a max-pooling layer, also two dense layers.
- The training function in this study substitutes the Nadam optimizer for the Adam optimizer that is often utilized. The major aspects are combined using a fully connected (FC) layer.
- The proposed model works with the Nadam optimizer, and comparison is done with some other existing activation functions, such as SGD, RMSprop, and Adam.

The rest of this work is prearranged as follows: Section 2 presents some correlated work review on chronic disease prediction by using various DL and machine learning (ML) algorithms. Section 3 confers the proposed I-NCNN model. Section 4 presents the results achieved and dataset used for simulation, also lastly, Section 5 concludes the work.

2. Literature Review

This section provides a review of some of the recent existing works and methodologies for chronic disease prediction.

Al-Makhadmeh, Zafer, and Amr Tolba [9] present an IoT-based clinical gadget for gathering patients' heart subtleties. The higher-order Boltzmann deep belief neural network (HOBDBNN) was utilized to process the info that is continuously sent to the health upkeep center. By effectively manipulating intricate data, the DL approach efficiently studies heart disease features from previous analysis.

Rani et al. [10] proposed a crossover choice emotionally supportive network that can aid the early discovery of coronary illness in view of the clinical boundaries of the patient. The authors dealt with the missing values by employing the chained equations multivariate imputation algorithm. A hybridized highlight determination calculation joining the Genetic Algorithm (GA) as well as recursive element end has been utilized for the choice of reasonable elements from the accessible dataset. More, for the pre-handling of information, the destroyed synthetic minority oversampling technique (SMOTE) also standard scalar strategies have been utilized.

Wang et al. [11] highlighted a CNN approach to automatically classify arrhythmia in the heartbeat. First, the original signals are separated from each heartbeat. In this structure, bits of various extents are utilized in every convolution layer, which makes the most of the highlights at various scales. A max-pooling layer came next. The past pooling layer's outputs are combined as well as used as input for FC layers.

Nagarajan et al. [12] find that the prevalence of heart disease has emerged as a major focus of current research, and numerous models have been given in the past year. The improvement calculation assumes a fundamental role in finding coronary illness with high precision. The creation of a hybrid GCSA, for feature selection along with classification utilizing deep CNN, is a significant objective of this work.

Li et al. [13] differentiate congestive heart failure (CHF) patients from healthy individuals by using entropy calculation to combine a CNN also a distance distribution matrix (DDM). Fuzzy local measure entropy (FuzzyLMEn), Sample entropy (SampEn), also fuzzy global measure entropy (FuzzyGMEn) were the three entropy procedures that were utilized.

Deperlioglu and Omer [14] detail the PASCAL training data set that categorises three distinct heart sound data types: normal, murmur, and extrasystole. Classification was done with phonocardiograms taken from the data set's heart sounds. To compare the outcomes, classification was carried out using both CNN and a Neural Network (ANN).

Dutta et al. [15] developed an effective neural network with convolutional layers to classify clinical data with significant class disparities. The information is arranged from the Public Wellbeing and National Health as well as Nutrition Examination Survey (NHANES), determined to foresee the event of coronary heart disease (CHD).

Alotaibi and Fahd Saleh [16] tested the accuracy of HF predictions with the UCI heart disease dataset. In directive to comprehend the data as well as predict the likelihood of heart failure in a medical database, various ML methods were used. The mix of the AI model introduced in this study with clinical data frameworks would be helpful to anticipate HF or some other infection utilizing the live information gathered from patients.

Ramalingam et al. [17] applied Artificial Intelligence (AI) calculations and strategies to different clinical datasets to computerize the examination of enormous and complex information. In current years, many researchers have utilized a variability of ML procedures to assist professionals and the healthcare industry in the diagnosis of heart-related illnesses. This different model is presented in light of such calculations and strategies and analyzes their presentation. The researchers found that ensemble models and models grounded on supervised learning algorithms like Decision Trees (DT), Support Vector Machines (SVM), Random Forest (RF), Naive Bayes (NB), and K-Nearest Neighbour (KNN) are very popular.

Nancy et al. [18] discuss profound learning, which has the groundbreaking potential for precisely examining immense information at uncommon speeds, inspiring shrewd bits of knowledge, and effectively addressing complex issues. Preventive care and initial intervention for those at risk depend on the timely and accurate prediction of diseases. In light of the widespread use of electronic medical records, developing more accurate prediction models is essential for utilizing DL variants of RNNS that are capable of managing sequential time-series data.

3. Proposed Methodology

Predicting if a patient has chronic disease is difficult since it requires binary categorization. Deep neural networks with several application-specific hidden layers have recently shown remarkable advancement due to the explosion of structured data [15]. If a subject's chronic disease is incorrectly diagnosed, they may go untreated or receive the wrong possible treatment medicine. As a result, one of the main goals of this research is to escalation classification accuracy, or the ability to predict whether an individual has chronic disease or not. This research proposes an improved Nadam convolutional neural network (I-NCNN) to solve these restrictions and is motivated by the success of deep networks. The proposed model contains two convolution layers, a BN layer, a dropout layer, a max-pooling layer, followed by a flatten layer, along with two dense layers, as illustrated in Figure 1.

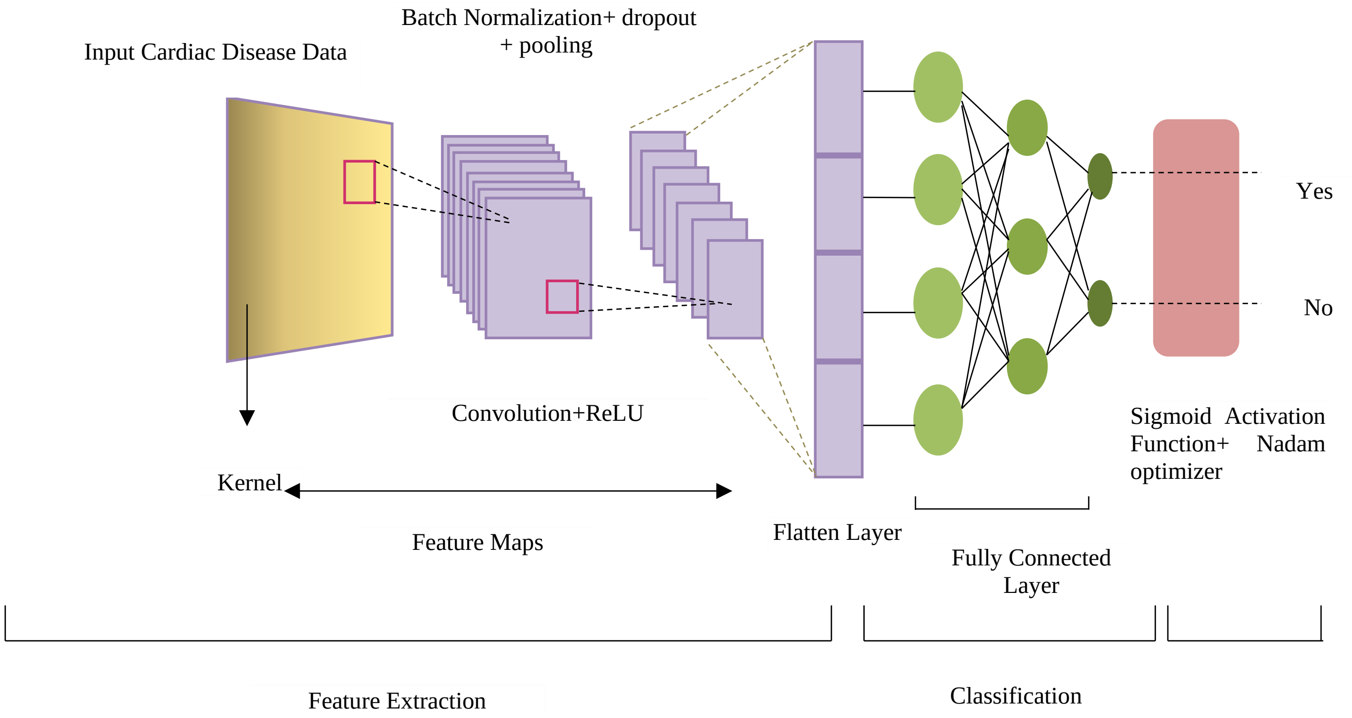


Fig 1. Proposed I-NCNN Model Architecture

When the outcomes of the onward propagation don't match the expectancy, it is then utilized to identify the error between the predicted values along with the real value utlizing the cross-entropy loss function. The error is then returned every layer so that Adam's optimizer can change the weight. The process is repeated till the minimum loss function value as well as the network is complete using the new parameters [19, 20].

3.1. Pre-Processing

Before the DL learning algorithm is applied to the raw data, it must be transformed through the preprocessing procedure. The standard of the data and functional information that may be derived from it might have an impact on the quality along with accuracy of the proposed model, making the preprocessing of the data a crucial stage. After preprocessing, the input data is given to the proposed convolutional layer.

3.2. Convolutional Layer

The preprocessed input data is the input to the convolutional layers. A 1D-CNN model was employed to extract spectral information. The 1D-CNN model is initially imported with the preprocessed data's original input size. To acquire dimensionality-reduced feature data, local feature extraction is carried out on the convolutional layer (Conv), which is located beneath the sequential layer. Convergence across the local area of input data is carried out using 1D-CNN to provide the matching feature. On the feature map, every kernel has distinct properties at every place. Weight sharing is used by 1D-CNNs, which converge with fewer parameters. This ensures that 1D-CNN will converge early along with more quickly. Since the kernel size is set to 3, each input layer and output layer stride will share all weights. Weights added to the input values in the kernel window. The feature map value is created by adding up the values. The convolution layer's output serves as both the input and the output for the subsequent layer. In this study, two convolutional layers are followed by one another [21]. The output from the convolutional layer is given to the batch normalization layer.

3.3. Batch Normalization Layer

The BN layer enhances the stability and effectiveness of the proposed model while preventing gradient vanishing along with over-fitting. In addition, BN is applied to feature maps to address issues with internal covariance shift. The distribution of hidden unit values changes due to the change in internal covariance, which delays convergence and necessitates careful setup of network parameters. By removing the batch mean and separating by the batch standard deviation, BN normalizes the output of the prior activation. As a result, each proposed model layer will gain some independence from the lower tiers. BN serves as regularize as well. The BN output is forwarded to a dropout layer.

3.4. Dropout Layer

Overfitting during the training phase may frequently be solved by using the dropout layer. Weights are adjusted and modified during training, whereas in the dropout layer, neurons are chosen at random. During training, neurons should be turned off so that any randomly turned-off neurons have their output values set to no value or zero. Disabled neurons also momentarily lose connections. The proposed model can still continue to work effectively. The random "dead neuron" selection method is an efficient way to deal with over-fitting. The dropout output is forwarded to a max pooling layer.

3.5. Pooling Layer

The pooling layer sits after the convolutional layer and has the ability to further reduce the feature vector's dimensionality, improve the network's resilience, and retrieve lower-resolution feature data. For CNNs, pooling layers are essential. Pooling reduces the count of parameters while keeping the important features to swiftness up the following step. As a result, the max approach is used to analyze each feature map at this stage. The maximum parameters in the default window are chosen using the max-pooling approach. The problem of over fitting is also expected to be resolved via pooling techniques. The output values will be scaled down, along with the maximum values for the following network layer will be chosen and sent as input to the layer that will be flattened. The flattened output is forwarded to the final dense, or FC layer.

3.6. Fully Connected Layer

The flatten layer output data are fed into the dense layer in order to retrieve the data's overall feature. This layer is the essential layer in a model. In this learning, the Nadam function is utilized as the activation function, which can assist the network in learning difficult data, enhance its nonlinear modelling skills, and provide predictions that are more accurate. Some different optimizer's results are evaluated, such as the SGD, RMSprop, and Adam [22]. At every time step t in the SGD optimization approach, the parameter is updated. In Equation (1), the SGD weight update rule is shown.

$$\theta_{t+1} = \theta_t - l d_t \tag{1}$$

Where l the learning is rate, and d_t denotes the objective function incline grounded on the time step. RMSprop is an optimization method created to slow the learning rate's monotonic decline. The learning rate is divided by the average of squared inclines' exponential decay rate $R[d^2]_t$ square root as per the RMSprop weight update rule. In Equation (2), the weight update rule is presented.

$$\theta_{t+1} = \theta_t - \frac{l}{\sqrt{R[d^2]_t + \epsilon}} d_t \tag{2}$$

Where $\in$ is a smaller vector count to prevent division by zero. In Adam, the first moment (mean) along with the second moment (variance) are represented by the past squared gradient (u_t) and past gradient (a_t), respectively. This is how the a_t and u_t are calculated in equations (3) and (4)

$$a_t = \beta_1 a_{t-1} + (1 - \beta_1) d_t \tag{3}$$

$$u_t = \beta_2 u_{t-1} + (1 - \beta_2) d_t^2 \tag{4}$$

When decay rates are low (i.e., β_1 and β_2 are close to zero), the a_t along with u_t are skewed towards zero. The first moment as well as second moment with bias-adjusted terms are computed and is equated in (5) and (6)

$$\hat{a}_t = \frac{a_t}{1 - \beta_1^t} \tag{5}$$

$$\hat{u}_t = \frac{u_t}{1 - \beta_2^t} \tag{6}$$

Then, Equation (7) provides the Adam weight update rule.

$$\theta_{t+1} = \theta_t - \frac{l}{\sqrt{\hat{u}_t + \epsilon}} \hat{a}_t \tag{7}$$

A variation of the weight updating rule is Nadam. Equation (7)'s equation of a_t and $\hat{a}_t$ is used to extend Equation (8) to compute it.

$$\theta_{t+1} = \theta_t - \frac{l}{\sqrt{\hat{u}_t + \epsilon}} \left(\frac{\beta_1 a_t - 1}{1 - \beta_1^t} + \frac{1 - \beta_1}{1 - \beta_1^t} d_t \right) \tag{8}$$

Where $\frac{\beta_1 a_t - 1}{1 - \beta_1^t}$ is an estimation of the momentum vector from the prior time step that has been bias-corrected? Therefore, we may change it to (9).

$$\theta_{t+1} = \theta_t - \frac{l}{\sqrt{\hat{u}_t + \epsilon}}\left(\beta_1 \hat{a}_{t-1} + \frac{1-\beta_1}{1-\beta_1^t} d_t\right) \tag{9}$$

Therefore, as indicated in Equation (10), the Nadam update rule is providing by substituting the bias-corrected assessment of the prior momentum vector, $\hat{a}_{t-1}$, with the bias-corrected assessment of the present momentum vector.

$$\theta_{t+1} = \theta_t - \frac{l}{\sqrt{\hat{u}_t + \epsilon}}\left(\beta_1 \hat{a}_t + \frac{1-\beta_1}{1-\beta_1^t} d_t\right) \tag{10}$$

Thus, this research uses the Nadam optimizer for the classification of chronic diseases. The results of this work are deliberated in the next section

4. Results and Discussion

A study of several characteristics connected to various chronic disorders is provided in this section. Based on a DL classification approach, this experimental investigation is done. Three online UCI datasets are used in this study such as heart disease dataset, diabetes dataset as well as kidney dataset. Python programming using the Anaconda distribution has been used to build several DL approaches.

4.1. Dataset

The heart illness dataset was obtained from the ML Repository at the UCI [23]. This dataset contains characteristics that can be utilized to recognize people who are at high risk for mounting heart illness. The features in the dataset are age, restecg, trestbps, cp, chol, sex, oldpeak, fbs, exang, thalach, ca, slope, thal, as well as target. The heatmap of the heart illness dataset is illustrated in figure 2.

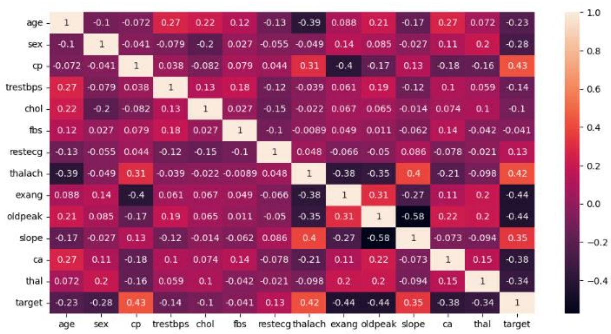


Fig 2. Heat map for the Heart Dataset

A data set generated for attendees of the 1994 AAAI Spring Symposium on Artificial Intelligence (AI) in Medicine is contained in the diabetes dataset [24]. The heat map of the diabetic dataset is illustrated in figure 3.

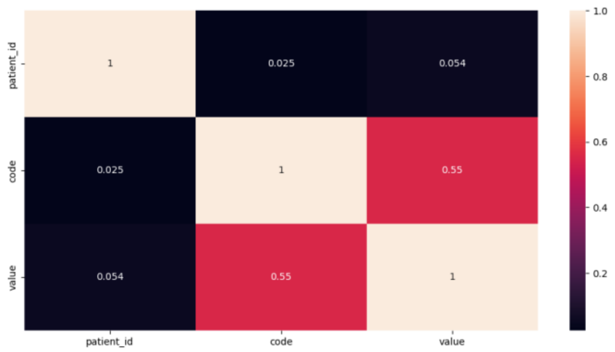


Fig 3. Heatmap for the Diabetic Dataset

The kidney dataset [25] consisted of 25 features and was collected during a 2-month period in India. The classification, can be either one "ckd" or "notckd" (ckd stands for chronic kidney disease), is the goal. 400 rows are present. Because it contains NaNs and has to be converted to floating, the data needs to be cleaned. Hence, preprocessing is done with this dataset. The heatmap of the kidney dataset is illustrated in figure 4.

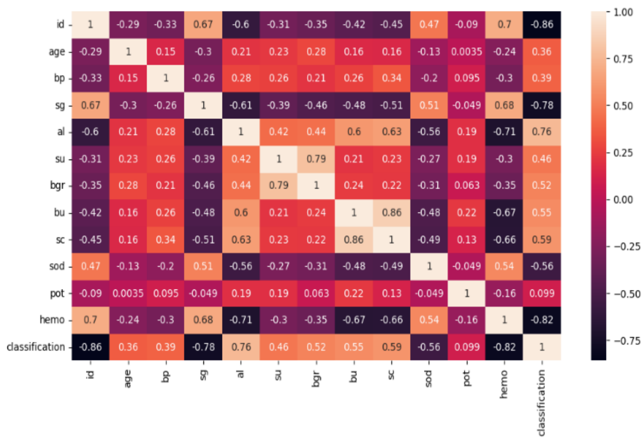


Fig 4. Heatmap for the Kidney Dataset

4.2. Discussions

Table 1 describes the parameters utilized in the proposed I-NCNN model. The first and the second are the convolutional layers. The batch normalization layer is the third layer. The dropout layer is a fourth layer with a dropout rate of 0.4. The pooling layer is a fifth layer with a pool magnitude of 2. The flatten layer is the sixth layer. The dense layer is the seventh layer, with 10 units as well as a Relu activation function. The last layer is also a dense layer with one unit since the proposed work is a binary classification, and the activation function is sigmoid since it is considered best for binary classification. The other training parameters are binary cross entropy, the optimizer used in the Nadam, and the epochs are 50.

Table 1. Parameters for the proposed I-NCNN model

Layer	Type	Parameter
Conv1D	Convolutional layer	kernel size =3, Filters = 16, activation = relu, input shape = (13,1) (heart) (2,1) (diabetics) (15,1) (kidney)
Conv1D	Convolutional layer	Filters = 32, kernel size =3, activation = relu
Batch Normalization	Batch Normalization layer	-
Dropout	Dropout layer	Drop rate = 0.4
Maxpooling1D	Pooling layer	Pool size =2
flatten	Flatten layer	-
Dense	Dense layer	Unit =1, activation = sigmoid
Dense	Dense layer	Unit =10, activation = relu

The model's performance evaluation is a crucial step in figuring out how well it would perform with hypothetical data. Four distinct measures have been used in this study to compare the proposed I-NCNN model with four existing DL models. These metrics make it possible to assess the significance of the findings for each categorization label and to compare several models against one another. The measures are the F1 score, accuracy, precision, and recall.

The proportion of properly identified observations over all observations is a measure of accuracy. It provides information on the proportion of inputs that are properly identified, making it a preliminary indicator of model performance. Accuracy is mathematically given in (11).

$$accuracy = \frac{Proporly\ identified\ observations}{All\ Observations} \quad (11)$$

All of the model's predictions are tabulated in the confusion matrix. The columns of this matrix correspond to the real class classifications, and each row represents predictions made for each class. The leading diagonal shows the model's accurate predictions since both the rows and the columns denote classes. For thorough examination, terms like true positive (TP), true negative (TN), false positive (FP), as well as false negative (FN), are utilized.

The number of successfully identified inputs is referred to as TP. The leading diagonal of the matrix has this value for each class. The number of samples that are accurately identified as not belonging to a specific class is referred to as TN. The count of samples for which the model predicts the particular class wrongly is referred to as FP. A case of FP prediction for patients with no heart disease occurs when the model wrongly predicts the patient with no heart disease class for an input that corresponds to a patient with heart disease. For a class, this number may be computed by adding up all of the values in the row except the TP case. The count of models from a certain class that the model mistakenly predicts as models from another class is referred to as FN. For instance, FN prediction for a patient with heart disease occurs when the model wrongly predicts a patient with no heart disease for an input that corresponds to a patient with heart disease.

Precision is a metric utilized to assess the accuracy of the model's predictions for a specific class. It details how many times the model's prediction that the output would belong to a certain class was accurate out of all the predictions. As a result, this statistic provides information on the model's accuracy for each class. For each class, it may be computed by calculating the ratio of TP to the overall of TP and FP. Precision is equated in (12).

$$precision = \frac{TP}{FP+TP} \quad (12)$$

The proportion of samples properly classified by the model to all samples belonging to that class is known as recall. It also goes by the name "sensitivity," since it describes how sensitive the model is to the existence of a specific class. Recall is equated in (13)

$$recall = \frac{TP}{FN+TP} \quad (13)$$

A harmonic ratio called the F1 Score measure aids in achieving a balance between recall and precision. F1 score is equated in (14)

$$F1\ score = 2 * \left(\frac{precision*recall}{precision+recall}\right) \quad (14)$$

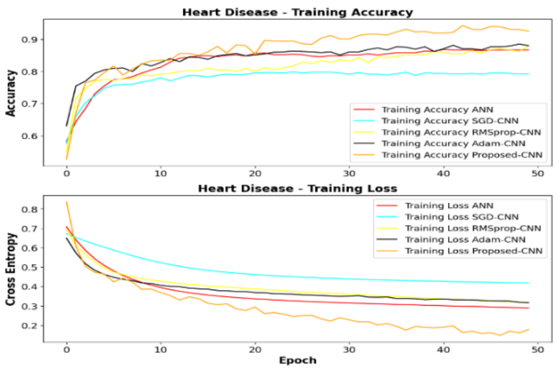
The comparison of the proposed I-NCNN model for chronic disease classification is done with existing ANN, CNN with SGD activation function, CNN with RMSprop activation function, and CNN with Relu activation function. An ANN transmutes the input data through successive unseen layers, along with at the output layer, it calculates the error. Using the gradient descent process, the mistake is propagated back in order to update the layer weights repeatedly.

Table 2. Comparison of Different Models

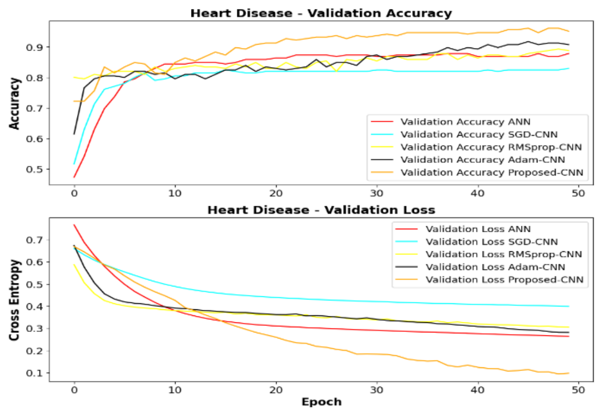
Methods	Classes	Precision	Recall	F1-score
Heart Disease Dataset				
ANN	0	0.93	0.8	0.86
	1	0.83	0.94	0.89
	Accuracy			0.87
CNN with SGD	0	0.92	0.91	0.91
	1	0.92	0.93	0.92
	Accuracy			0.92
CNN with RMSprop	0	0.92	0.88	0.9
	1	0.89	0.93	0.91
	Accuracy			0.91
CNN with Adam	0	0.98	0.91	0.94
	1	0.92	0.98	0.95
	Accuracy			0.95
Proposed I-NCNN	0	0.96	0.96	0.96
	1	0.96	0.96	0.96
	Accuracy			0.96
Diabetes Dataset				
ANN	0	1	0.75	0.85
	1	0.41	1	0.58
	2	0	0	0
	3	0	0	0
	4	0	0	0
	Accuracy			0.7
CNN with SGD	0	0.66	1	0.8
	1	0	0	0
	2	0	0	0
	3	0	0	0
	4	0	0	0
	Accuracy			0.66
CNN with RMSprop	0	0.66	1	0.8
	1	0	0	0
	2	0	0	0
	3	0	0	0
	4	0	0	0
	Accuracy			0.66
CNN with Adam	0	0.99	0.77	0.87
	1	0.43	0.99	0.6
	2	0	0	0
	3	0	0	0
	4	0	0	0
	Accuracy			0.72

Proposed I-NCNN	0	1	0.8	0.89
	1	0.44	0.99	0.61
	2	0	0	0
	3	0	0	0
	4	0	0	0
	Accuracy			0.73
Kidney Dataset				
ANN	0	0.96	1	0.98
	1	1	0.88	0.93
	Accuracy			0.97
CNN with SGD	0	0.89	1	0.94
	1	1	0.62	0.77
	Accuracy			0.91
CNN with RMSprop	0	0.89	1	0.94
	1	1	0.62	0.77
	Accuracy			0.91
CNN with Adam	0	0.92	1	0.96
	1	1	0.75	0.86
	Accuracy			0.94
Proposed I-NCNN	0	1	1	1
	1	1	1	1
	Accuracy			1

Table 2 details the comparison of performance parameters between different methods with the three different datasets. When comparing all the parameters, the proposed model seems to show better results than the existing models like ANN, CNN with SGD, CNN with RMSprop, and CNN with Adam. In this case, the proposed I-NCNN model has nearly 96% accuracy for heart dataset. This is 7.87% better than the ANN model, 4.35% better than CNN with SGD, and 5.49% better than CNN with RMSprop, and 1.05% better than CNN with Adam. Likewise for the other datasets also the proposed model is showing improved accuracy also loss when compared to other existing models. This is illustrated in figure 5, 6 and 7.



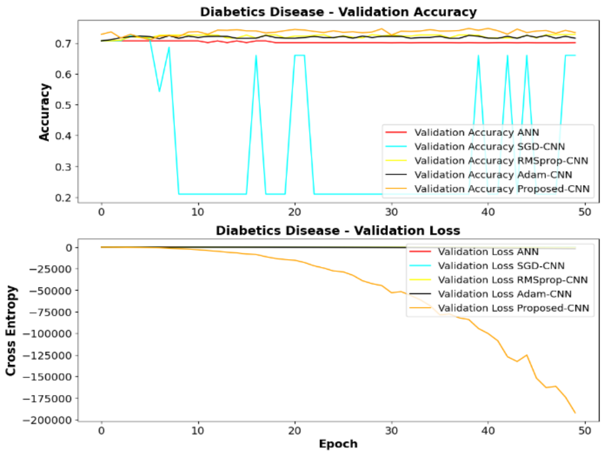
(a)



(b)

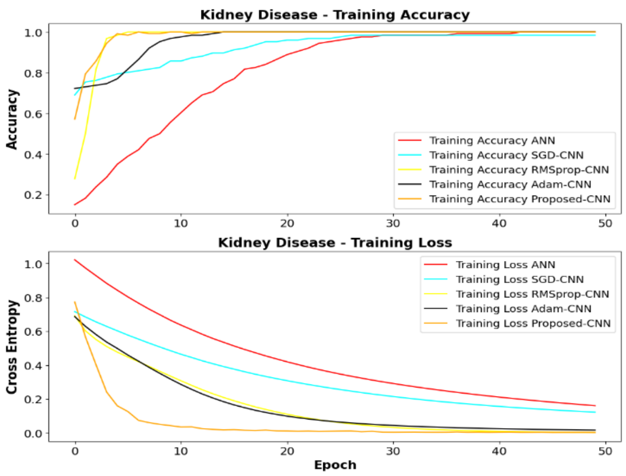
Fig 5. (a) Training Accuracy along with Loss Comparison Graph for Heart Dataset (b) Validation Accuracy along with Loss Comparison Graph for Heart dataset

(a)

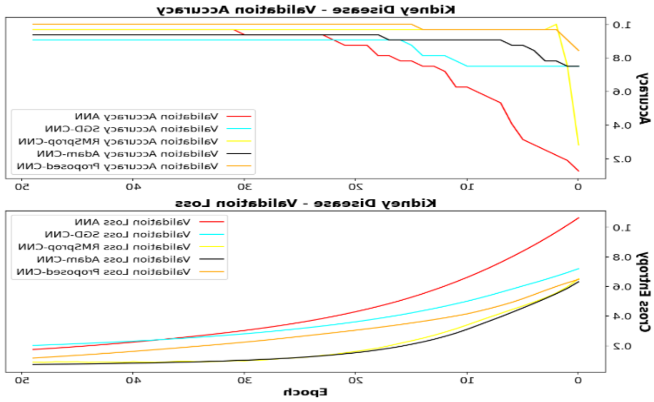


(b)

Fig 6. (a) Training Accuracy also Loss Comparison Graph for Diabetics Dataset (b) Validation Accuracy also Loss Comparison Graph for Diabetics dataset



(a)



(b)

Fig 7. (a) Training Accuracy as well as Loss Comparison Graph for Kidney Dataset (b) Validation Accuracy as well as Loss Comparison Graph for Kidney dataset

In the figures, the orange color line describes the proposed I-NCNN model. For accuracy, the proposed I-NCNN is higher than the other existing models, and for loss, the proposed I-NCNN model is lower than the other existing models. Thus, it is proven that the proposed I-NCNN model detects heart disease better than other existing models.

5. Conclusion

This research detects chronic disease by using the I-NCNN model. The proposed model efficiency is explored with other DL approaches to doing comparative evaluation and achieving genuine positive performance. In this research, it was concluded that the proposed I-NCNN model performed much improved than statistical methods. This article supports the findings of several studies indicating that this model is the most effective technique for predicting and categorizing heart disease. On the UCI online chronic disease datasets, several performance metrics, such as F1 score, precision, accuracy as well as recall have been compared for all existing DL classification models. The goal of further study will be to further refine the algorithm by using by hybrid ML and DL approaches

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