Revolutionizing Cardiac Care: Deep Learning for Arrhythmia Detection

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ABSTRACT

Cardiac arrhythmia is a condition where heartbeat is irregular. The goal of this paper is to apply deep learning techniques in the diagnosis of cardiac arrhythmia using ECG signals with minimal possible data pre-processing. This paper employed one dimensional convolutional neural network (1D-CNN), recurrent structures such as long short-term memory (LSTM) to automatically detect the abnormality. Unlike the conventional analysis methods, the proposed method utilizes the principal component analysis (PCA) for feature extraction. Further, the existing LSTM and proposed 1D-CNN models are trained with PCA features. The optimal parameters for deep learning techniques are chosen by conducting various trails of experiments. All trails of experiments are run for 1000 epochs with learning rate in the range [0.01-0.5]. Moreover, the accuracy obtained by proposed 1D-CNN architecture is compared with existing LSTM method.

Keywords: ECG, cardiac arrhythmia, deep learning, convolutional neural network, long short-term memory.

1. INTRODUCTION

Cardiac arrhythmia is a condition where irregular heart rhythms occur. According to World Health Organization (WHO), about 17 million people in the world die every year due to cardiovascular diseases. This is about 31% of the total deaths globally. According to the statistics of American Heart Association (AHA), one out of every three deaths in US is related to cardiovascular diseases. The deaths due to cardiovascular diseases are more than due to all types of cancer and chronic lower respiratory diseases combined. A 2014 study indicates that approximately 2 to 3% of the people in North American and European countries are affected by atrial fibrillation. A heart rate which is high (above 100 beats per minute in adults) is called tachycardia and a heart rate that is slow (below 60 beats per minute) is called bradycardia. If the beat is too early, then it is called premature contraction. Irregular beat is called fibrillation or flutter. Other than the criteria of heart rate, there are several other classifications for cardiac arrhythmia depending upon different types of criteria. Another type of classification is in terms of the site of origin of the irregular heart rate. Atrial arrhythmias originate in the atrioventricular (AV) node. The AV node is positioned between the atria (each of the two upper cavities of the heart from which blood is passed to the ventricles is referred to as atria) and the ventricles. Atrial fibrillation (AF), atrial flutter, atrial tachycardia, premature atrial contractions, and sinus bradycardia are some examples of atrial arrhythmias. Atrial fibrillation and atrial flutter are examples of arrhythmia which may lead to serious consequences. In AF, the atrium is contracted in a very fast and irregular manner with the heart's electrical signals originating from a different part of the atria or in the adjacent pulmonary veins instead of sino-atrial (SA) node. The walls of the atria fibrillate (quiver very fast) instead of beating in a normal way, making atria unable to pump blood properly into the ventricles. Stroke and heart failure are two complications to which atrial fibrillation can lead to. Conditions like high blood pressure, overactive thyroid gland, coronary and rheumatic heart diseases can lead to AF. Atrial flutter has similar symptoms and complications as AF. But in atrial flutter, the advancement of electrical signals of the heart through the atria happens in a fast and regular manner instead of the irregular way it happens in AF. Ventricular arrhythmias are premature rhythms occurring in an ectopic ventricular focus. Ventricular fibrillation, ventricular tachycardia, premature ventricular contractions are some examples of ventricular arrhythmias. Some arrhythmias are symptomless and not at all life threatening. But some symptomless arrhythmias can even lead to serious complications like blood clotting, stroke, heart failure and sudden cardiac death. Arrhythmias occur when the electrical signals to the heart that co-ordinate heartbeat are not working properly. The first step in the diagnosis of this abnormality is the analysis of electrocardiogram (ECG) and the confirmation that the ECG is not indicative of cardiac arrhythmia. ECG is a bio signal representing the activity of the autonomous nervous system (ANS) controlling heart rhythm. Thus, the electrical activity of the heart is recorded in ECG. It is a non-invasive and efficient tool to study cardiac rhythms and diagnose arrhythmias. The ECG signal is generated because of the following processes. The heartbeat is originated as an electric pulse from the SA node situated in the right atrium of the heart. After contracting both atria, this electric pulse, then activates atrioventricular (AV) node that connects electrically the atria and the ventricles. This is followed by the activation of both ventricles. The complete heart activity is represented in the ECG waveform. Abnormalities in the morphology of ECG waveforms are indicators of cardiac arrhythmias. ECG waveform is analysed to ascertain the risk associated with any type of arrhythmia. Extensive research has been done in arrhythmia detection. The below are works in a serious type of arrhythmia called as myocardial infarction (MI) commonly known as heart attack. Data from a single lead ECG was used for MI detection achieving an accuracy of 94.74% [1]. Multiscale eigenspace analysis was carried out on 12 lead ECG data to achieve the same objective with an accuracy of 96% [2]. Analysis of 12 nonlinear parameters extracted from 12 lead ECG data using discrete wavelet transform (DWT) were used to detect MI to achieve an accuracy of 98.8% [3]. Deep learning techniques are now being increasingly employed in this area. The automated detection of normal and MI was conducted with CNN with an accuracy of 95.22% [4]. An accuracy of 84.54% was achieved in the detection of inferior MI in ECG using CNN [5]. Four types of arrhythmias were classified with an accuracy of 99.38% with MIT BIH data set along with another dataset as input [4]. Classification of MIT Arrhythmia database of ECG into normal and abnormal was conducted using artificial neural network (ANN) achieving an accuracy of 96.77% [5]. There are many works of classifying specific types of cardiac arrhythmia with ECG as normal input data. Often these specific cardiac arrhythmia cases addressed in most of the previous research work will be serious arrhythmia types like myocardial infarction. In short, research was conducted into classifying normal ECG and many types of arrhythmias affected ECG. Cardiac arrhythmia, though identified by the irregularity in cardiac rhythm, is due to the anomalies happening in the heart. These anomalies cause anatomical differences in the structure of atria and ventricles, thus producing changes in its activation, depolarization, and repolarisation. These changes are reflected as deviation of ECG waveform from its normal shape and size. Different types of cardiac arrhythmia are caused by unique factors, thus causing unique changes in the morphology of the ECG wave [6], [7], [8].

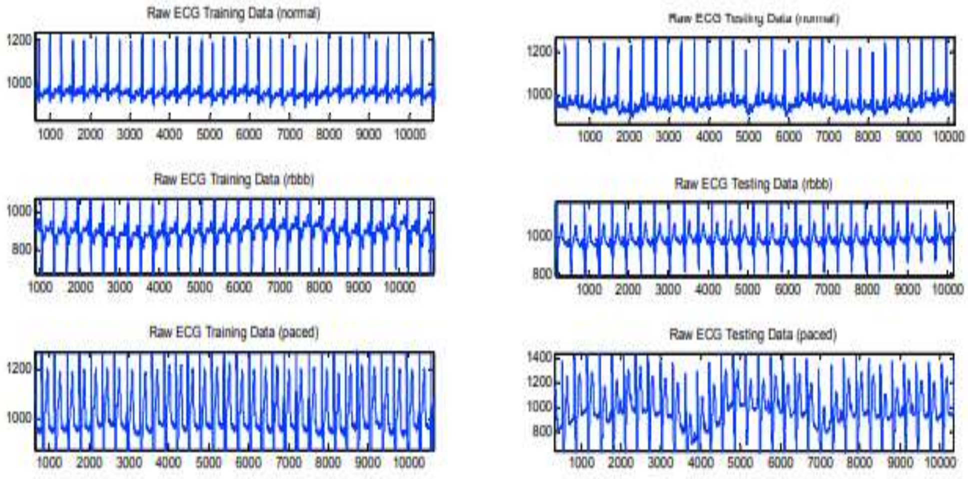

Fig. 1: An example of three different ECG recordings.

The objective of this work is to develop an automated method for the diagnosis of cardiac arrhythmia. We use ECG recordings from the publically available MIT-BIH arrhythmia database in Physionet. The MIT-BIH arrhythmia database is the first generally available dataset which is widely used for ascertaining the efficiency of cardiac arrhythmia detection algorithms.

2. LITERATURE SURVEY

Jafarnia et al. used two new features i.e., T-wave integral and total integral as extracted feature from one cycle of normal and patient ECG signals to detection and localization of myocardial in-fraction (MI) in left ventricle of heart. And used the T-wave integral because this feature is important impression of T-wave in MI. The second feature in this research is total integral of one ECG cycle, because that the MI affects the morphology of the ECG signal which leads to total integral changes. Also, this work can improve the accuracy of classification by adding more features in this method. A simple method based on using only two features which were extracted from standard ECG is presented and had good accuracy in MI localization.

Sharma et al. studied the multiscale wavelet energies and eigenvalues of multiscale covariance matrices are used as diagnostic features. Support vector machines (SVMs) with both linear and radial basis function (RBF) kernel and K-nearest neighbor are used as classifiers. Datasets, which include healthy control, and various types of MI, such as anterior, anteriolateral, anterioseptal, inferior, inferiolateral, and inferioposterio-lateral, from the PTB diagnostic ECG database are used for evaluation. The results showed that the proposed technique can successfully detect the MI pathologies.

Acharya et al. proposed a novel method of automated detection and localization of MI by using ECG signal analysis. In this study, a total of 200 twelve lead ECG subjects (52 normal and 148 with MI) involving 611,405 beats (125,652 normal beats and 485,753 beats of MI ECG) are segmented from the 12 lead ECG signals. Firstly, ECG signal obtained from 12 ECG leads are subjected to discrete wavelet transform (DWT) up to four levels of decomposition. Then, 12 nonlinear features are extracted from these DWT coefficients. The extracted features are then ranked based on the t value. This proposed method has achieved the highest average accuracy of 98.80%, sensitivity of 99.45% and specificity of 96.27% in classifying normal and MI ECG (two classes), by using 47 features obtained from lead 11 (V5).

Mohammadzadeh and Setarehdan used a neural network classifier to automatic classification of cardiac arrhythmias into five classes. HRV signal is used as the basic signal and linear and nonlinear parameters extracted from it are used to train a neural network classifier. The proposed approach is tested using the MIT-BIH arrhythmia database and satisfactory results were obtained with an accuracy level of 99.38%.

Vishwa et al. proposed an automated Artificial Neural Network (ANN) based classification system for cardiac arrhythmia using multi-channel ECG recordings. In this study, producing high confident arrhythmia classification results to be applicable in diagnostic decision support systems. The classification performance is evaluated using measures; sensitivity, specificity, classification accuracy, mean squared error (MSE), receiver operating characteristics (ROC) and area under curve (AUC). Experimental results give 96.77% accuracy on MIT-BIH database and 96.21% on database prepared by including NSR database also.

Swapna et al. discussed the characteristics and different methods (and their measures) of analyting the heart rate variability (HRV) signal, derived from the ECG waveform. The HRV signals are characterised in terms of these measures, then fed into classifiers for grouping into categories (for normal subjects and for disorders such as cardiac disorders and diabetes) for carrying out diagnosis.

Sujadevi et al. explored and employed a deep learning method such as RNN, LSTM and GRU to detect the Atrial Fibrillation (AF) faster in the given electrocardiogram traces. This study used one of the well-known publicly available MIT-BIH Physionet datasets. This is the first time Deep learning has been employed to detect the Atrial Fibrillation in real-time. Based on this work experiments RNN, LSTM and GRU offer the accuracy of 0.950, 1.000 and 1.000 respectively. This methodology does not require any de-noising, other filtering, and preprocessing methods. Results are encouraging enough to begin clinical trials for the real-time detection of AF that will be highly beneficial in the scenarios of ambulatory, intensive care units and for real-time detection of AF for life saving implantable defibrillators.

Pathinarupothi et al. applied a deep learning technique called LSTM-RNN (long short-term memory recurrent neural network) for identification of sleep apnea and its severity based only on instantaneous heart rates. This tested this model on multiple sleep apnea datasets and obtained perfect accuracy. Furthermore, this work has also tested its robustness on an arrhythmia dataset (that is highly probable in mimicking sleep apnea heart rate variability) and found that the model is highly accurate in distinguishing between the two.

Goldberger et al. of cardiovascular and other complex biomedical signals. The resource has 3 interdependent components. PhysioBank is a large and growing archive of well-characterized digital recordings of physiological signals and related data for use by the biomedical research community. It currently includes databases of multiparameter cardiopulmonary, neural, and other biomedical signals from healthy subjects and from patients with a variety of conditions with major public health implications, including life-threatening arrhythmias, congestive heart failure, sleep apnea, neurological disorders, and aging. PhysioToolkit is a library of open- source software for physiological signal processing and analysis, the detection of physiologically significant events using both classic techniques and novel methods based on statistical physics and nonlinear dynamics, the interactive display and characterization of signals, the creation of new databases, the simulation of physiological and other signals, the quantitative evaluation and comparison of analysis methods, and the analysis of nonstationary processes. PhysioNet is an on-line forum for the dissemination and exchange of recorded biomedical signals and open-source software for analyzing them. It provided facilities for the cooperative analysis of data and the evaluation of proposed new algorithms.

Gers et al. reviewed an illustrative benchmark problem on which standard LSTM outperforms other RNN algorithms. All algorithms (including LSTM) fail to solve a continual version of that problem. LSTM with forget gates, however, easily solves it in an elegant way.

3. PROPOSED SYSTEM

Cardiac arrhythmia is a condition where heart beat is irregular. The goal of this paper is to apply deep learning techniques in the diagnosis of cardiac arrhythmia using ECG signals with minimal possible data pre-processing. We employ deep learning convolutional neural network (1D-CNN), and long short-term memory (LSTM) to automatically detect the abnormality. This work is focused on the design of CNN and LSTM algorithms to predict Arrhythmia diseases with 7 different stages. To train both algorithms, the MIT-BH dataset is used with 7 different disease stages. Further, existing LSTM resulted in low accuracy. So, this work adopted the CNN model for training and testing Arrhythmia disease.

Figure 1 shows the block diagram of proposed. Here, MIT-BH dataset is considered for evaluating the performance of overall system. Initially, the dataset is splitted into 80% for training and 20% for testing. Then, the entire operations are going to be perform on both training and testing datasets. Further, pre-processing operation is carried out to remove the missing symbols and unknown characters, special characters. The pre-processing operation also normalizes the number of rows and columns presented in the dataset. Further, both LSTM and 1D-CNN models are applied to evaluate the prediction of MITBH dataset. So, through this prediction it is going to identify the cardiac arrhythmia presented in overall dataset. Finally, performance comparison is takes place between both LSTM and 1D-CNN models.

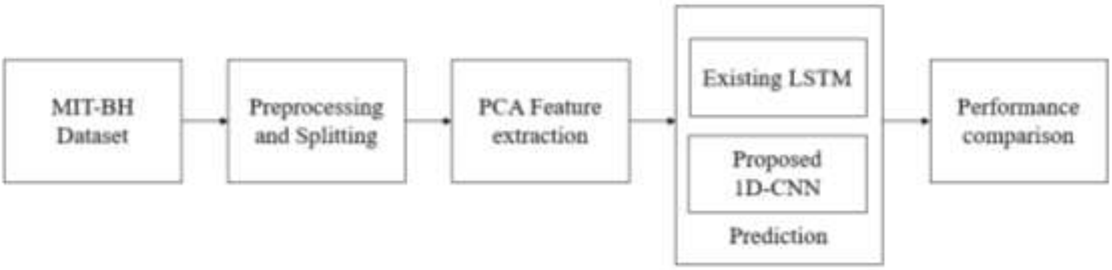

Fig. 1: Proposed architecture of cardiac arrhythmia detection.

3.1 MIT-BH Dataset

The MIT-BIH Arrhythmia Database contains 48 half-hour excerpts of two-channel ambulatory ECG recordings, obtained from 47 subjects studied by the BIH Arrhythmia Laboratory between 1975 and 1979. Twenty-three recordings were chosen at random from a set of 4000 24-hour ambulatory ECG recordings collected from a mixed population of inpatients (about 60%) and outpatients (about 40%) at Boston's Beth Israel Hospital; the remaining 25 recordings were selected from the same set to include less common but clinically significant arrhythmias that would not be well-represented in a small random sample.

3.2 Preprocessing and splitting

Data preprocessing is a process of preparing the raw data and making it suitable for a machine learning model. It is the first and crucial step while creating a machine learning model. When creating a machine learning project, it is not always a case that we come across the clean and formatted data. And while doing any operation with data, it is mandatory to clean it and put in a formatted way. So, for this, we use data preprocessing task.

In machine learning data preprocessing, we divide our dataset into a training set and test set. This is one of the crucial steps of data preprocessing as by doing this, we can enhance the performance of our machine learning model. Suppose if we have given training to our machine learning model by a dataset and we test it by a completely different dataset. Then, it will create difficulties for our model to understand the correlations between the models. If we train our model very well and its training accuracy is also very high, but we provide a new dataset to it, then it will decrease the performance. So we always try to make a machine learning model which performs well with the training set and also with the test dataset.

3.3. PCA Feature extraction

Principal component analysis (PCA) is a popular technique for analyzing large datasets containing a high number of dimensions/features per observation, increasing the interpretability of data while preserving the maximum amount of information, and enabling the visualization of multidimensional data. Formally, PCA is a statistical technique for reducing the dimensionality of a dataset. This is accomplished by linearly transforming the data into a new coordinate system where (most of) the variation in the data can be described with fewer dimensions than the initial data. Many studies use the first two principal components in order to plot the data in two dimensions and to visually identify clusters of closely related data points. Principal component analysis has applications in many fields such as Population Genetics, Microbiome studies, Atmospheric Science etc.

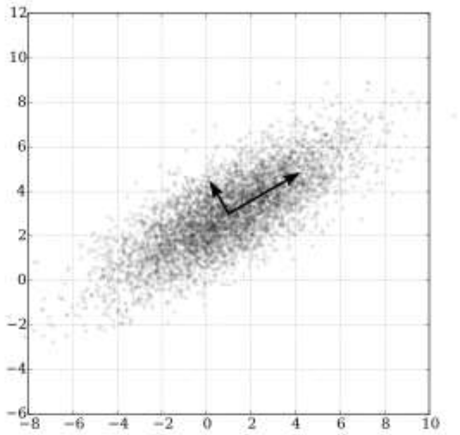

Fig. 2: PCA of a multivariate Gaussian distribution.

The principal components of a collection of points in a real coordinate space are a sequence of unit vectors, where the vector is the direction of a line that best fits the data while being orthogonal to the first vectors. Here, a best-fitting line is defined as one that minimizes the average squared perpendicular distance from the points to the line. These directions constitute an orthonormal basis in which different individual dimensions of the data are linearly uncorrelated. PCA is the process of computing the principal components and using them to perform a change of basis on the data, sometimes using only the first few principal components and ignoring the rest.

3.4 Existing LSTM model structure

Because there are connections between neurons in the RNN layer, the network can learn the change law of sequence data before and after, and the internal sequence rules of data is easy to be mined. Thus RNN is widely used in the field of sequence data processing such as speech recognition and machine translation. However, this structure also has some problems. When data is transmitted backward, the problem of gradient disappearance or gradient explosion is unavoidable, which limits its processing of long-term dependencies. The LSTM network changes the way of gradient transmission during backpropagation by adding multiple special computing nodes in the hidden layer of RNN, which effectively slows the problem of gradient disappearance or gradient explosion. Its model structure is shown in Figure 2. Where h_{t-1} represents the output of the previous cell, and x_t represents the input of the current cell. σ represents the sigmoid function. The difference between LSTM and RNN is that it adds a ‘‘processor’’ to the algorithm to determine the usefulness of the information. The structure of this processor is called a cell. Three gates are placed in a cell, which are called *Input gate*, *Forget gate*, and *Output gate*. A piece of information enters the LSTM network, and it can be judged whether it is useful according to the rules. Only the information that meets the algorithm authentication will be left, and the non-conforming information will be forgotten through the *Forget gate*.

Forget gate: The first step for data entering the LSTM is to decide what information should be lost and what retained. This decision is made by the Forget gate, which reads h and x and outputs a value between 0 and 1, where 1 means ‘‘complete reserved’’, 0 means ‘‘completely discarded’’. Forget gate is calculated as:

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

In the formula, f_t is the calculation result of the Forget gate which is mainly used to control the retention of the information transmitted from the unit state at the previous moment to the unit state at the current moment. The system indicates that the two vectors are spliced, h_{t-1} is the output of the unit at the previous moment, and are the weight and bias of Forget gate, W_f and b_f are Sigmoid activation functions.

Input gate: Input gate determines the addition of new information, and its operation process includes sigmoid layer and tanh layer. The sigmoid layer determines the information that needs to be updated. The calculation formula is:

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

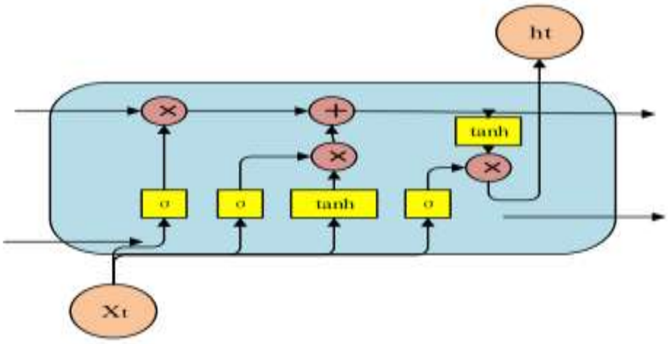

Fig. 2: LSTM model structure.

In the formula, i_t is the calculation result of the input gate, and the input gate also has independent weight and bias. The role of the tanh layer is to generate a vector of candidate update information. Its calculation formula is:

$$\tilde{C}_t = \tanh\left(W_c * [h_{t-1}, x_t] + b_c\right)$$

$\tilde{C}_t$is the unit state of the current input, the unit state of the current moment is C_t, and its calculation formula is:

$$C_t = f_t * C_{t-1} + i_t * \tilde{C}_t$$

Output gate: Output gate is roughly the same as the Input gate, and its operation flow includes sigmoid layer and tanh layer. The sigmoid layer determines the output part of the information, and the calculation formula is:

$$o_t = \sigma\left(W_o\,[h_{t-1}, x_t] + b_o\right)$$

Finally get the output of the current moment h_t:

$$h_t = o_t * \tanh\left(c_t\right)$$

The forward propagation of LSTM calculates the cell state C_t and h_t the output of the current moment and completes the forward propagation calculation of the network. The backpropagation of LSTM is like the back-propagation principle of RNN. Finally, the weights and biases of all parts of the network are updated to complete the model training.

3.5 Proposed 1D-CNN

A 6-layer deep convolutional network was designed for the classification of ECG signals according to cardiac arrhythmia. This deep network model provides automatic classification of input fragments through an end-to-end structure without the need for any hand-crafted feature extraction or selection steps. The structure of the deep network model consists of the classical CNN layers, but the structure of 1D-CNN is predominant. In 1D convolution layers, feature maps that are representations of ECG fragments are subjected to convolution processing with weights of various sizes.

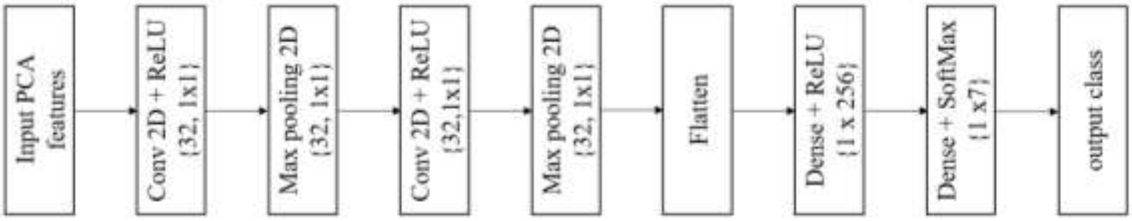

Fig. 3: Block diagram of the proposed 1D-CNN model.

Table.1: Layers description.

Layer Names	No. of filters	Kernel size
Conv 2D +ReLU	32	1x 1
Max pooling 2D	-	1 x 1

Conv 2D+ReLU	32	1 x 1
Max pooling 2D	-	1 x 1
Flatten	-	-
Dense +ReLU		1 x 256
Dense + SoftMax		1 x 7

In the first layer of the model, 1D convolution is performed with 128 weight vectors on the input ECG signals. The activation outputs of this layer are normalized using batch normalization layer for each batch. In the 1D max pooling layer, new feature maps are generated by taking the maximum values in the region specified on the feature maps obtained from the previous layers. This layer reduces the size of feature maps from the previous layer according to the region size. The reducing feature map sizes is an important step in reducing the computational cost of deep learning structures. For this purpose, different methods such as average values are used instead of maximum values in 1D Max layer. In the fourth layer, the convolution process is repeated on the input feature maps with 32×7- size weights. By performing batch normalization process again, the feature maps whose region width is set to two are reduced by half using pooling method on the 6th layer. These operations are repeated in the next 1D convolution and 1D max pooling layers.

The proposed deep network has a flattened layer on the 14th layer so that the feature maps obtained from the 13th layer can be transformed to the appropriate size as an input to the subsequent layers of the network. This layer transforms multidimensional input feature vectors into one-dimensional output data. The features obtained from the flattened layer are fed to a dense-connected neural network layer of 512 units. In the last layer of the network, there is a layer of softmax which is the unit of the number of the output classes. Using the softmax layer, the prediction of the class to which the input data belongs is realized. In addition to all of these, some layers have a dropout parameter to prevent the overfitting during the learning phase. After developing the model, the layer numbers, types and parameters of the deep algorithm are changed by brute force technique and the performances of the validation sets are observed. Our developed 6-layer model yielded the highest classification results for long duration ECG signals.

4. RESULTS AND DISCUSSION

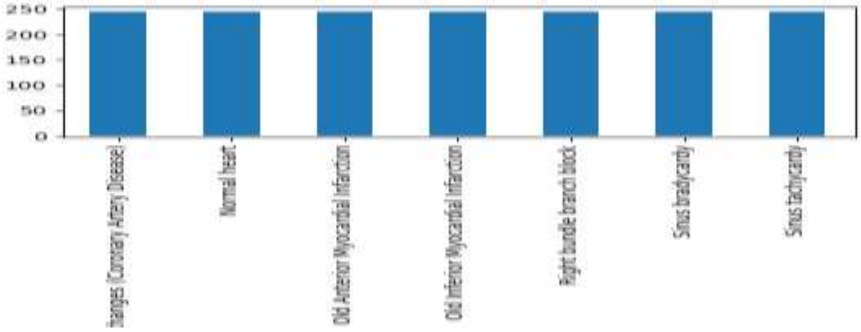

Fig. 4: Dataset descirption.

In Figure 4, we can see dataset loaded and in graph x-axis represents 7 different disease stages and y-axis represents number of records found for that disease in dataset. In Figure 5 with LSTM we got 78% accuracy and in confusion matrix graph x-axis represents Predicted classes and y-axis represents TRUE classes and all blue colour boxes count are wrong prediction and different colour boxes count are correct prediction and we can see LSTM predicted so many wrong classes. In Figure 6 with CNN, we got 99% accuracy and in confusion matrix graph only 2 counts in blue colour boxes are wrong prediction and rest are correct prediction. In Figure 7, x-axis represents training epoch and y-axis represents training accuracy and loss values and green colour line represents LSTM accuracy and orange colour line represents CNN accuracy and red colour line represents CNN loss and blue line represents LSTM loss and in above graph we can see both algorithms accuracy got increase in every epoch and loss get decrease.

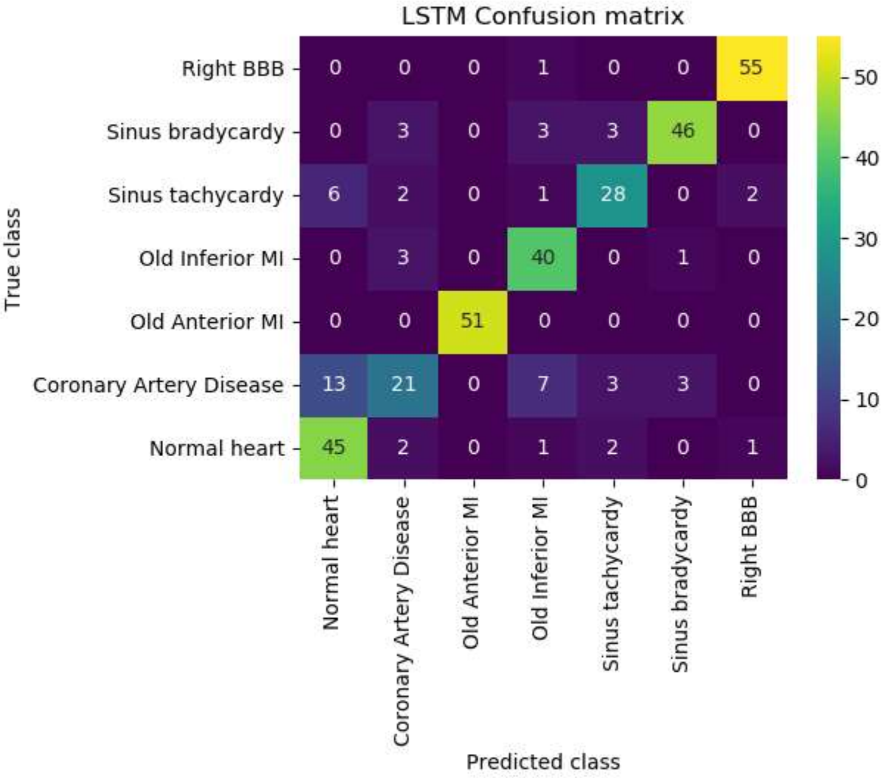

Fig. 5: Confusion matrix obtained using LSTM model.

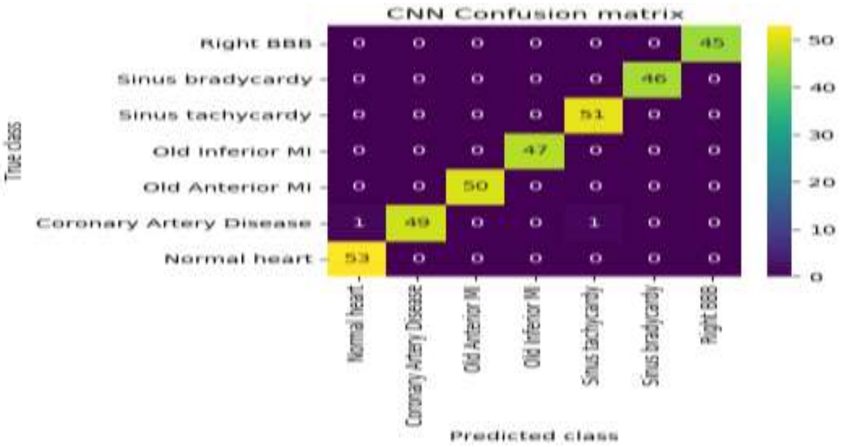

Fig. 6: Confusion matrix obtained using proposed 1D-CNN model.

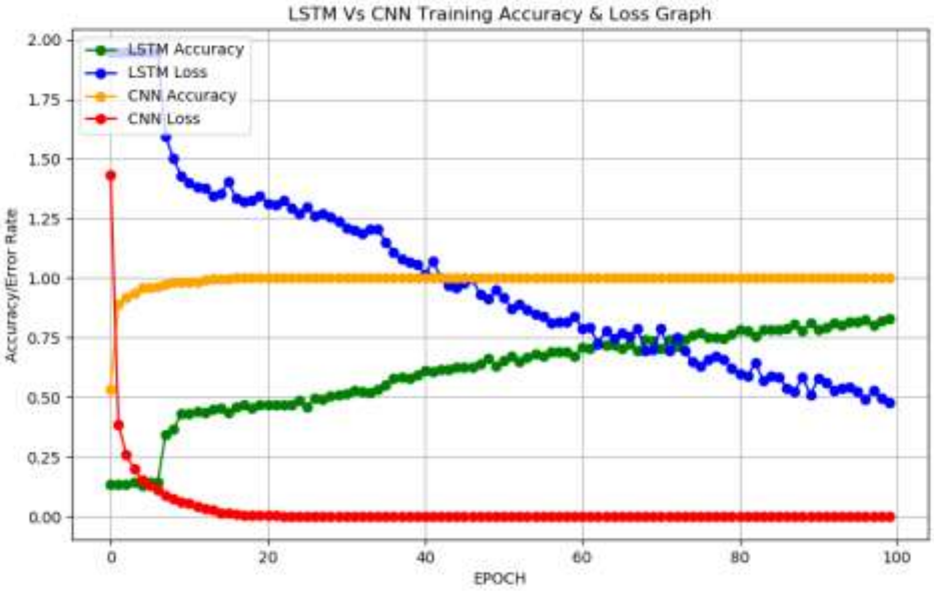

Fig. 7: Accuracy and loss obtained using LSTM and 1D-CNN models.

5. CONCLUSION

Cardiac arrhythmia is an irregularity in heart rhythm. Some types of cardiac arrhythmia can lead to complications like stroke, heart attack and may even lead to sudden cardiac death. So, timely detection and diagnosis of arrhythmia is especially important. Once arrhythmia is detected, next stage of identification of category of arrhythmia can be done. We developed an automated non-invasive system based on deep learning networks to perform the basic classification of a given ECG data as belonging to normal ECG or abnormal (having arrhythmia) ECG using the most popular publicly available MIT-BIH arrhythmia database. With concern on computational cost, we are not able to train more complex architecture. The reported results can be further improved by using more complex deep learning architecture. The complex network architectures can be trained by using advanced hardware and following distributed approach in training that we are incompetent to try. We have discussed the role of deep learning techniques such as 1D-CNN and LSTM structures in the task of arrhythmia classification. The highlight of the proposed method is that it does not need any noise filtering and feature engineering mechanisms. The results obtained prove that the performance of our method is better than other published results in effectively classifying ECG as belonging to normal or arrhythmia class. Though deep learning networks produces excellent results, the disadvantage lies in the insufficient understanding of the complex inner mechanisms of the deep learning networks. This could be overcome by remodelling the nonlinear deep networks to a linear form by computing eigenvalues and eigenvectors in different time steps. The future work can be the collection of real-world datasets from hospitals having cardiac care units and the application of the same methodologies to the real datasets.

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