Journal of Cardiovascular Disease Research

ISSN: 0975-3583, 0976-2833 VOL14, ISSUE 8, 2023

DEEP LEARNING MODEL FOR AUTOMATED DETECTION OF CARDIAC ARRHYTHMIA

J. Prashanthi[1], G. Saketh[2], K. Meghana[2], Y. Pawan Kumar[2], P. Mastan[2], A. Nandini[2]

[1,2]Department of Computer Science and Engineering

[1,2] Sree Dattha Group of Institutions, Sheriguda, Telangana.

ABSTRACT

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 a number of 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.

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 one-dimension 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.

Keywords: Cardiac arrhythmia, deep learning, ECG signals.

1. INTRODUCTION

1.1 Overview

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

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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.

1.2 Problem statement

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

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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].

The objective of this work is to develop an automated method for the diagnosis of cardiac arrhythmia. We perform a two-class classification of the given ECG signal, whether cardiac arrhythmia is present or not. 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. We employ deep learning-based analysis methods using CNN, CNN-RNN, CNN-LSTM, CNN-GRU. Our work can be an assisting automated tool to cardiologists for the initial screening of people having cardiac arrhythmia.

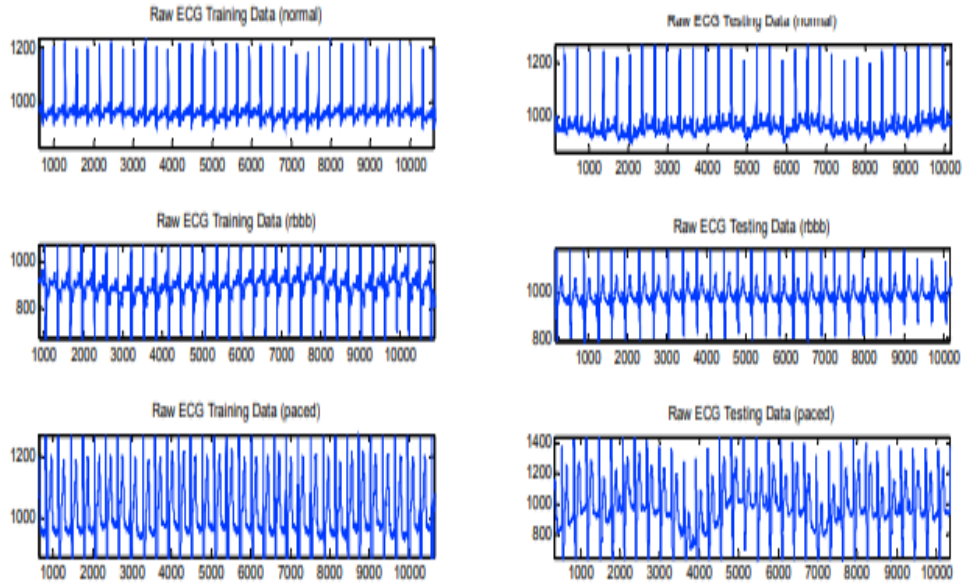

Fig. 1: An example of three different ECG recordings.

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,

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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

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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 METHOD

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 a number of 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.

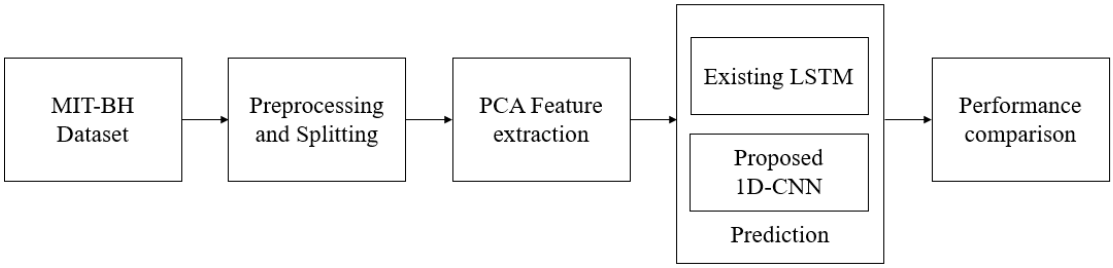

Fig. 2: Proposed block diagram.

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. 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.

Fig. 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.

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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.

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.

The recordings were digitized at 360 samples per second per channel with 11-bit resolution over a 10-mV range. Two or more cardiologists independently annotated each record; disagreements were resolved to obtain the computer-readable reference annotations for each beat (approximately 110,000 annotations in all) included with the database. This directory contains the entire MIT-BIH Arrhythmia Database. About half (25 of 48 complete records, and reference annotation files for all 48 records) of this database has been freely available here since PhysioNet's inception in September 1999.

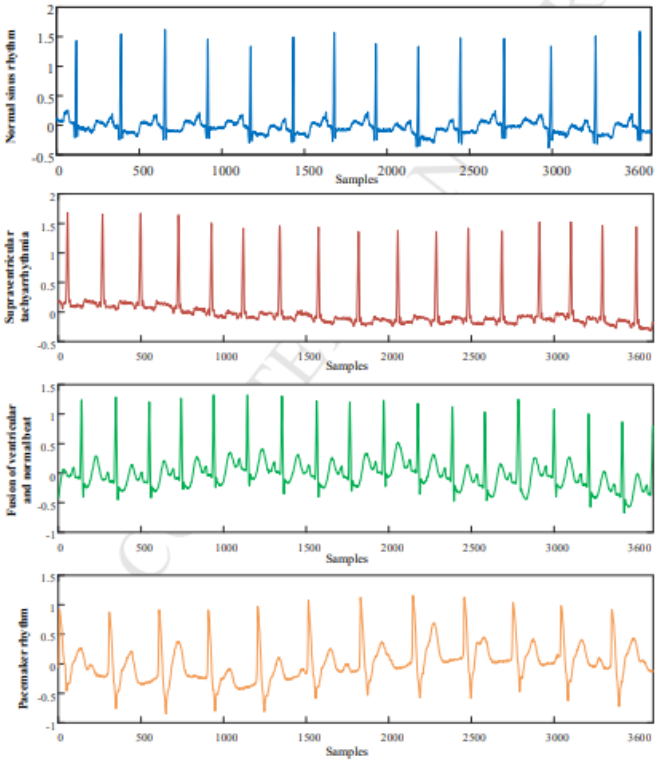

Fig. 3: Typical signal samples of different classes.

Finally, the dataset contains ‘Normal heart', 'Ischemic changes (coronary artery disease)', 'Old Anterior Myocardial Infarction', 'Old Inferior Myocardial Infarction', 'Sinus tachycardy', 'Sinus bradycardy', 'Right bundle branch block' as disease classes.

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3.2 Preprocessing

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.

3.3 Splitting the Dataset

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. Here, we can define these datasets as:

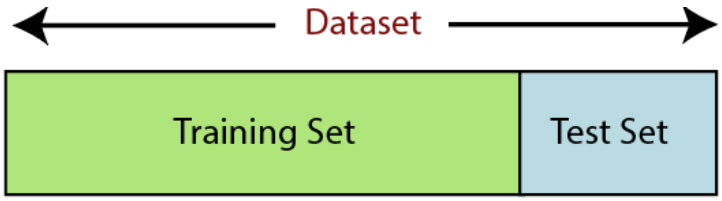

Fig. 4: Splitting the dataset.

Training Set: A subset of dataset to train the machine learning model, and we already know the output.

Test set: A subset of dataset to test the machine learning model, and by using the test set, model predicts the output.

For splitting the dataset, we will use the below lines of code:

```
from sklearn.model_selection import train_test_split

x_train, x_test, y_train, y_test= train_test_split(x, y, test_size= 0.2, random_state=0)
```

3.4 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.

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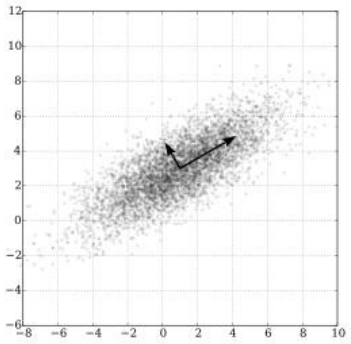

Fig. 5: PCA of a multivariate Gaussian distribution.

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.

In data analysis, the first principal component of a set of variables, presumed to be jointly normally distributed, is the derived variable formed as a linear combination of the original variables that explains the most variance. The second principal component explains the most variance in what is left once the effect of the first component is removed, and we may proceed through iterations until all the variance is explained. PCA is most used when many of the variables are highly correlated with each other, and it is desirable to reduce their number to an independent set.

PCA is used in exploratory data analysis and for making predictive models. It is commonly used for dimensionality reduction by projecting each data point onto only the first few principal components to obtain lower-dimensional data while preserving as much of the data's variation as possible. The first principal component can equivalently be defined as a direction that maximizes the variance of the projected data. The principal component can be taken as a direction orthogonal to the first principal components that maximizes the variance of the projected data.

For either objective, it can be shown that the principal components are eigenvectors of the data's covariance matrix. Thus, the principal components are often computed by eigen decomposition of the data covariance matrix or singular value decomposition of the data matrix. PCA is the simplest of the true eigenvector-based multivariate analyses and is closely related to factor analysis. Factor analysis typically incorporates more domain specific assumptions about the underlying structure and solves eigenvectors of a slightly different matrix. PCA is also related to canonical correlation analysis (CCA). CCA defines coordinate systems that optimally describe the cross-covariance between two datasets while PCA defines a new orthogonal coordinate system that optimally describes variance in a single dataset. Robust and L1-norm-based variants of standard PCA have also been proposed.

CNN Classifier

According to the facts, training and testing of CNN involves in allowing every source data via a succession of convolution layers by a kernel or filter, rectified linear unit (ReLU), max pooling, fully connected layer and utilize SoftMax layer with classification layer to categorize the objects with probabilistic values ranging from.

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Convolution layer is the primary layer to extract the features from a source image and maintains the relationship between pixels by learning the features of image by employing tiny blocks of source data. It's a mathematical function which considers two inputs like source image $I(x, y, d)$ where x and y denotes the spatial coordinates i.e., number of rows and columns. d is denoted as dimension of an image (here d=3 since the source image is RGB) and a filter or kernel with similar size of input image and can be denoted as $F(k_x, k_y, d)$..

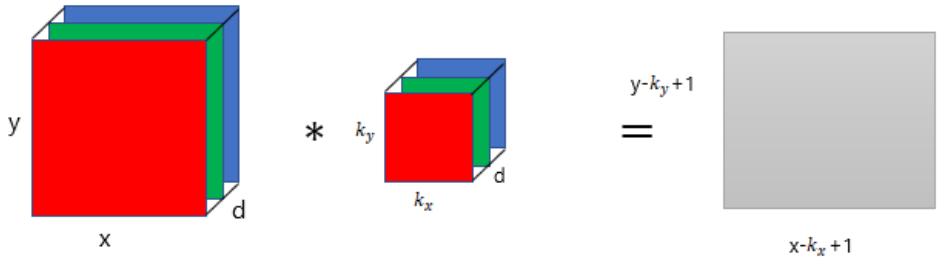
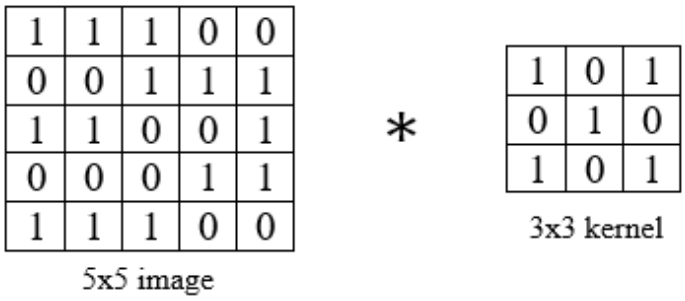
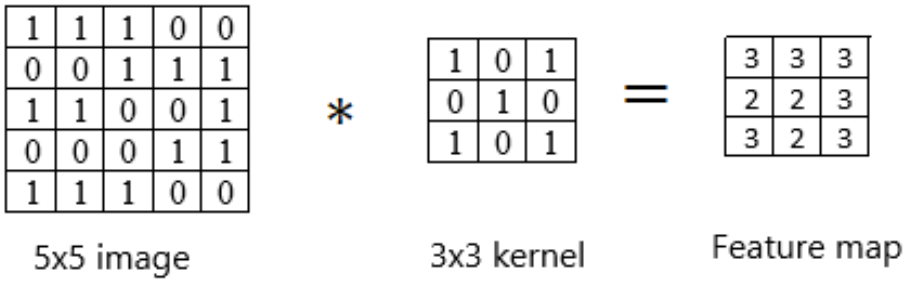


Fig. 6: Representation of convolution layer process.

The output obtained from convolution process of input image and filter has a size of $C\left((x - k_x + 1), (y - k_y + 1), 1\right)$, which is referred as feature map. Let us assume an input image with a size of 5×5 and the filter having the size of 3×3. The feature map of input image is obtained by multiplying the input image values with the filter values.



(a)



(b)

Fig. 7: Example of convolution layer process (a) an image with size 5×5 is convolving with 3×3 kernel (b) Convolved feature map.

ReLU layer

Networks those utilizes the rectifier operation for the hidden layers are cited as rectified linear unit (ReLU). This ReLU function $\mathcal{G}(\cdot)$ is a simple computation that returns the value given as input directly if the value of input is greater than zero else returns zero. This can be represented as mathematically using the function $max(\cdot)$ over the set of 0 and the input x as follows:

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$$\mathcal{G}(x) = \max\{0, x\}$$

Max pooing layer

This layer mitigates the number of parameters when there are larger size images. This can be called as subsampling or down sampling that mitigates the dimensionality of every feature map by preserving the important information. Max pooling considers the maximum element form the rectified feature map.

4. RESULTS AND DISCUSSION

Modules

To implement this project to designed following modules

1) Upload Arrhythmia Dataset: using this module will upload dataset to application. Finally, the dataset contains ‘Normal heart', 'Ischemic changes (coronary artery disease)', 'Old Anterior Myocardial Infarction', 'Old Inferior Myocardial Infarction', 'Sinus tachycardy', 'Sinus bradycardy', 'Right bundle branch block' as disease classes.
2) Pre-process Dataset: this module will read all dataset values and then replace missing values with MEAN and then normalize training values and then selected important features from dataset by applying PCA algorithm. Dataset contains more than 270 columns and all these columns are not required so PCA selected relevant features from dataset. After features selection dataset splitted into train and test where application using 80% dataset for training and 20% for testing.
3) Run LSTM Algorithm: the 80% training data is applied input to LSTM to trained a model and then model will be applied on 20% test data to perform prediction and then calculate accuracy.
4) Run CNN Algorithm: the 80% training data is applied input to CNN to trained a model and then model will be applied on 20% test data to perform prediction and then calculate accuracy.
5) LSTM & CNN Training Graph: this module plots CNN and LSTM training graph
6) Performance Table: this module displays both algorithms performance in tabular format.

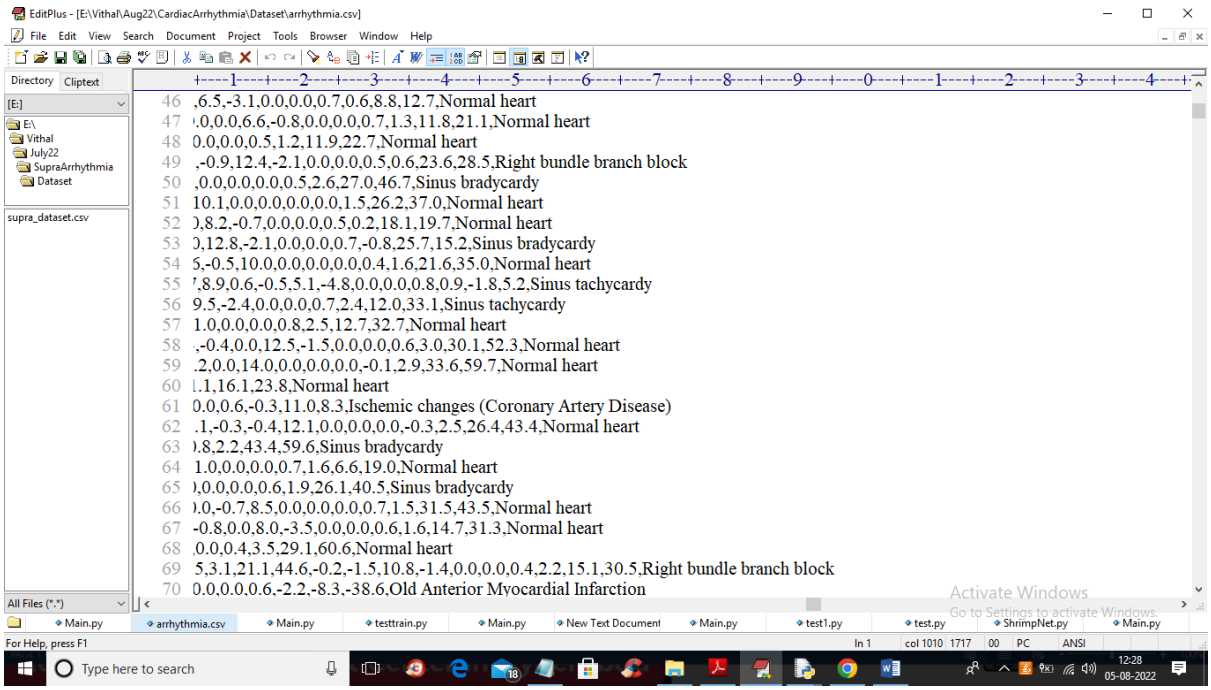

Fig. 8: Sample dataset.

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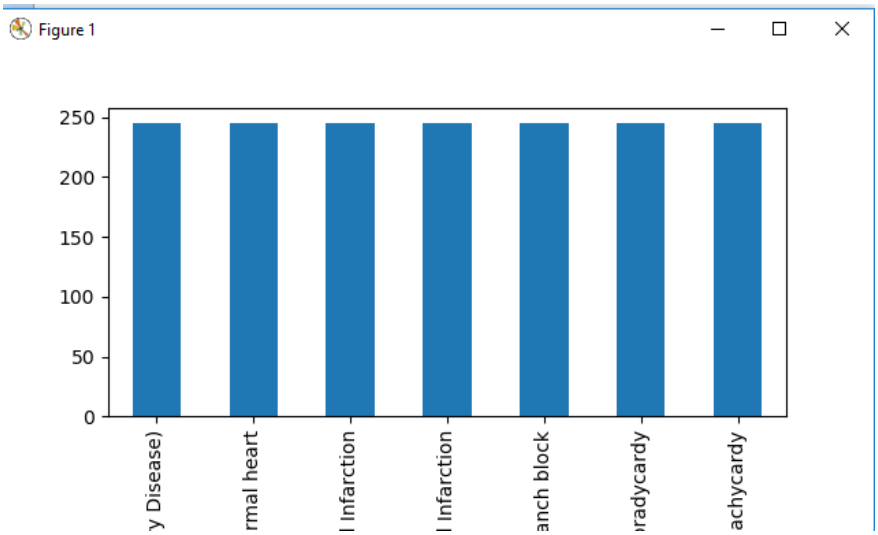

Fig. 9: Records found for each class.

In Fig 7, 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.

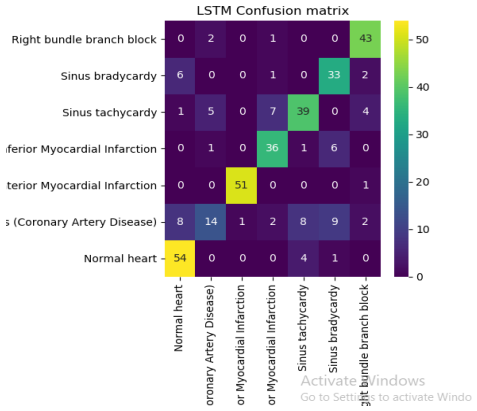

Fig. 10: Confusion Matrix of LSTM.

In above screen 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.

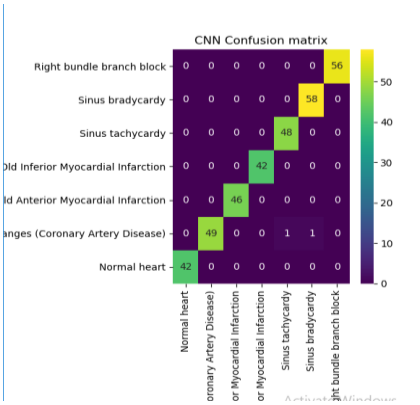

Fig. 11: 1D-CNN Confusion matrix.

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In above screen 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.

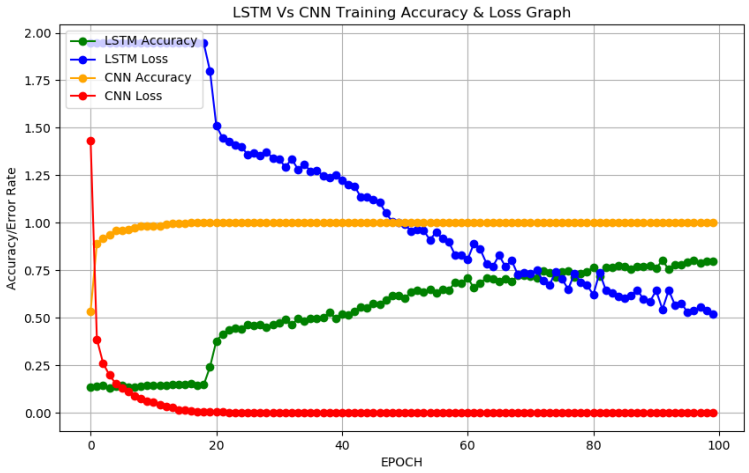

Fig. 12: Accuracy and Loss performance graph.

In above graph 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.

Table 1. Performance comparison.

Metric	Existing LSTM	Proposed 1D-CNN
Accuracy	83.38	99.54
Precision	83.075	99.24
Recall	83.0074	99.56
F-Score	82.32	99.24
Sensitivity	100	100
Specificity	91.66	97.28

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 public ally available MIT-BIH arrhythmia database.

We compared the performance using a variety of deep learning architectures of LSTM, 1D-CNN. 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

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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 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.

Future scope

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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