

Deep Learning Approach to Cardiovascular Disease Classification Employing Modified ECG Signal from Empirical Mode Decomposition

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ABSTRACT

Multiple cardiovascular disease classification from Electrocardiogram (ECG) signal is necessary for efficient and fast remedial treatment of the patient. This paper presents a method to classify multiple heart diseases using one dimensional deep convolutional neural network (CNN) where a modified ECG signal is given as an input signal to the network. Each ECG signal is first decomposed through Empirical Mode Decomposition (EMD) and higher order Intrinsic Mode Functions (IMFs) are combined to form a modified ECG signal. It is believed that the use of EMD would provide a broader range of information and can provide denoising performance. This processed signal is fed into the CNN architecture that classifies the record according to cardiovascular diseases using softmax regressor at the end of the network. It is observed that the CNN architecture learns the inherent features of the modified ECG signal better in comparison with the raw ECG signal. The method is applied on three publicly available ECG databases and it is found to be superior to other approaches in terms of classification accuracy. In MIT-BIH, St.-Petersberg, PTB databases the proposed method achieves maximum accuracy of 97.70%, 99.71%, and 98.24%, respectively.

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1. Introduction

Cardiovascular Diseases (CVDs) have become the cause of death of millions of people around the globe in recent years. The common CVDs include heart attack, ischemic stroke, hemorrhagic stroke, heart failure, different types of arrhythmia and heart valve problems etc. Almost all of the abnormal conditions of heart due to these diseases, many sinus arrhythmias and also the irregularities in the nervous system can be detected from the electrocardiogram signal of a patient. The electrocardiogram (ECG) signal is a record of the electrical activity of the heart. The standard 12 lead method is used frequently for acquiring ECG signal. Time domain, frequency domain or other signal processing techniques are used to reveal the inherent features of an ECG signal for the purpose of diagnosis of cardiovascular disease of the patient.

Deep learning based approach towards heart disease classification has been a popular choice recently. Atrial Fibrillation detection, ECG arrhythmia detection [1], myocardial infarction detection [2], premature ventricular contraction beat detection [3] and ECG disease classification comparing with the healthy patients using deep

neural networks or general machine learning algorithms have been successful in recent years. ECG signal features such as entropy calculation, standard deviation of beat to beat interval, minimum and maximum of entropy, wavelet analysis [1], R-peak amplitudes, R-R interval time, QRS duration time, ventricular activation time (VAT) [3], dual-tree complex wavelet transformation (DTCWT) [4], etc. have provided a boost to the ECG based heart disease detection and classification. When an ECG signal is recorded using conventional 12 lead ECG recording or any other methods, some noise is added due to signal recording equipment or different lead signal combination algorithms. As a result some preprocessing task such as outlier rejection, amplitude normalization, FIR filter, slope sum function (SSF), signal quality index (SQI) [1], bandpass filtering [2], median filters [5], segmentation [6], denoising, re-sampling and normalizing, R-wave detection [7] have seen a great success in improving the performance of ECG signal analysis. ECG denoising is one of the major tasks before working with this signal. Several techniques like Bayesian filtering [8], Kalman filter method [9], denoising in wavelet domains [10–12] have seen successful efforts in suppressing unexpected signal artifacts in the ECG signal. Learning features based on machine learning algorithms and CNNs have added an extra boost to the literature and successful ECG signal analysis. Feature extraction using CNN architectures, Boltzmann machine [5], deep belief networks with RBM based algorithms

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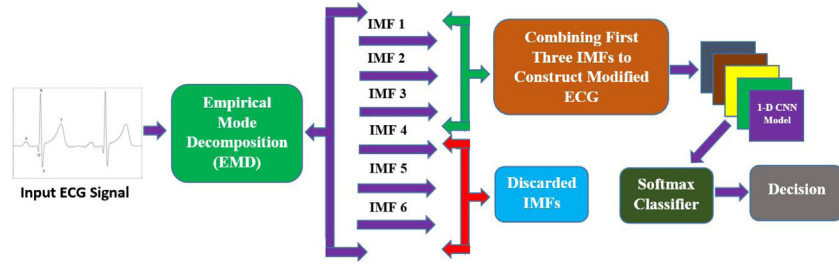


Fig. 1. An illustration of multiple heart disease classification based on the ECG signal. After EMD analysis, the first three higher order IMF signals are recombined to form a modified ECG signal which is fed into a 1-D CNN model. The CNN network classifies the patient by learning the inherent features of the modified ECG signal.

[6], stacked sparse auto-encoder (SAE), multi-scale deep feature learning (MDFL, Softmax-based multiple class classifier) [2], deep dictionary learning (DDL) [13], K-nearest neighbor (KNN), SVM and Multi-Layer Perceptron (MLP) networks [14], recurrent neural networks, density-based clustering technique [4], ensemble methods like incremental bagging, incremental boosting [14], these methods have aided in the effective analysis and classification of ECG signals. Besides, in recent times, the usage of one dimensional CNN has provided some interesting results for time series data [15]. Multiple arrhythmias classification using ECG signal is still a challenge as the ECG signals corresponding to many arrhythmias show similar features which require complex techniques for classifying using traditional signal processing methods. In this paper, we introduce deep learning based multiple heart disease classification method where the features are selected from Empirical Mode Decomposition of ECG signal. The features from EMD analysis are trained in a one dimensional CNN model to learn the inherent features corresponding to each disease. The method is applied to three publicly available databases with various training methodology.

2. Proposed Method

In this section, first, we present a brief overview of our proposed method of classifying multiple heart diseases from ECG signal and in the consecutive sections we present the details of every step. A flow chart of the proposed method is presented in Fig. 1. The ECG signal is processed with Empirical Mode Decomposition (EMD). In this paper, instead of working with the raw ECG signal, a modified ECG signal is formed by summing the first three Intrinsic Mode Functions (IMFs). Although CNN networks have been very successful in recent times for two dimensional or multidimensional signals, we used one dimensional CNN model for heart disease classification based on the modified ECG signal.

2.1. Empirical Mode Decomposition (EMD)

EMD decomposes a signal in time domain into separate Intrinsic Mode Functions (IMFs) [16,17]. The decomposed signals are of the same length and each IMF has an equal number of extrema and zero crossings with its envelopes serving as a simple oscillatory mode. Even though the IMFs are not necessarily orthogonal, they are sufficient to describe the signal. EMD is most useful for natural signals (i.e. ECG) which are non-stationary and non-linear. Unlike Fourier Transforms and wavelet decomposition, EMD provides intrinsic features of a signal using the IMFs. A signal can be denoised in the EMD time domain by discarding lower-order IMF signals on the basis of the assumption that noise and signal are unrelated in frequency bands [16]. Say, from a signal $x(t)$, the upper envelope curve ($x_u(t)$) and the lower envelope curve ($x_l(t)$) are obtained by joining the maxima and minima points of the original signal, respectively.

The mean of the two signals ($M = (x_u(t) + x_l(t))/2$) is subtracted from the original signal ($x(t)$) to obtain a first proto IMF signal $G_1(t)$,

$$G_1(t) = x(t) - M(t) \quad (1)$$

This sifting process is applied on the proto IMF signal $G_1(t)$ until a threshold point is reached where the conditions for an IMF are fulfilled [16]. In this paper the maximum limit for the number of sifting iterative process is set to 3000. The threshold values for stopping criterion of this sifting iterative method, corresponding to θ_1 [18] is 0.05, θ_2 [18] is 0.5 and the tolerance for stopping criterion corresponding to α [18] is 0.05. After this operation first IMF signal (I_1) is obtained. The residue signal ($R_1(t)$) is,

$$R_1(t) = x(t) - I_1(t) \quad (2)$$

The sifting process is again applied on the residue signal ($R_1(t)$) for second, third and etc IMFs. Generally,

$$R_{i-1}(t) - I_i(t) = R_i(t); i = 1, 2, 3, 4, \dots, N \quad (3)$$

In this paper, the total number of IMFs is $N = 6$. Finally a residue signal ($R_N(t)$) and 6 IMFs ($I_1(t), I_2(t), \dots, I_6(t)$) are obtained such that,

$$x(t) = \sum_{i=1}^N I_i(t) + R_N(t) \quad (4)$$

here, $N = 6$, and $I_i(t)$ is the i th order IMF. In the above method of EMD analysis, lower order IMFs are fast oscillatory modes and higher order IMFs are slower oscillatory modes [16]. Fig. 2 shows the IMF signals and the residual signal of an ECG signal from two databases.

2.2. Formation of Modified ECG

The raw ECG signal is empirically mode decomposed and first three IMF signals are summed to construct a modified ECG signal shown in Fig. 3. Combination of first three IMFs after EMD analysis removes most of the noise and artifacts and constructs a denoised ECG signal [16,19,20].

The modified and denoised ECG signal (x) is defined as,

$$x_{\text{mod}} = I_1(t) + I_2(t) + I_3(t) \quad (5)$$

here, $I_1(t)$, $I_2(t)$ and $I_3(t)$ are the first three IMFs. In the raw ECG signal, the P, Q, S, T peaks of the ECG are not clearly separable due to noise. But, the modified ECG signal can be explored easily to separate Q, R, S peaks as shown in Fig. 3. The lower order IMFs thus contain noise information. Hence, summing only the first three IMFs removes most of the noise artifacts from the raw ECG signal. The noise between two ECG cycles has also been minimized as illustrated in Fig. 3 for two different ECG signals from two databases. Moreover, it has been reported in [10] that the combination of the first three IMFs are better suited for denoising performance. Furthermore, the denoising performance of the modified ECG is investigated in this paper following the algorithm reported in [21]. Section 3.3 illustrates the detailed analysis.

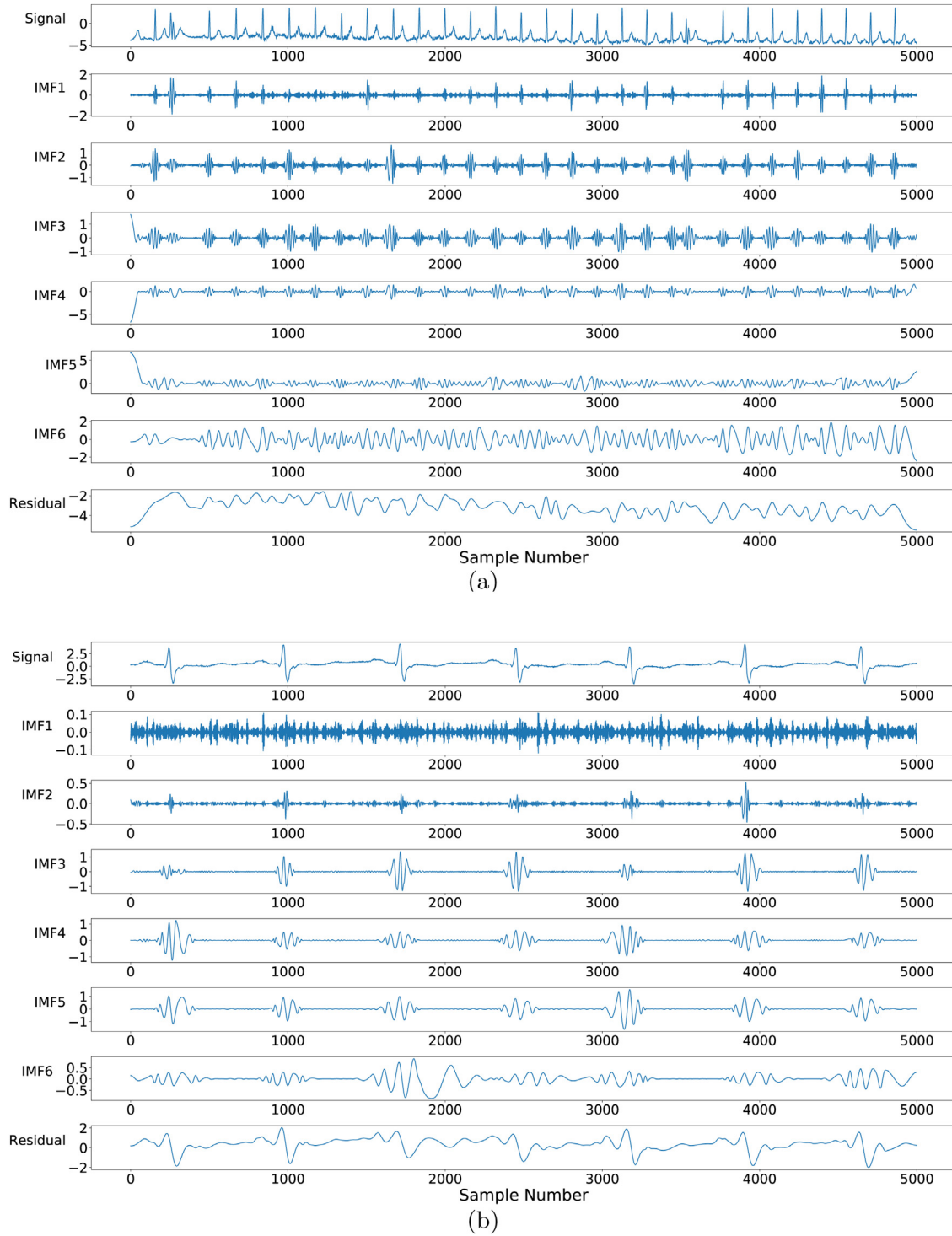


Fig. 2. Empirical Mode Decomposition (EMD) of an ECG signal from database [24] in (a) and from [22] in (b). The topmost plot of each sub-figure is the original raw signal followed by six IMF signals and the residual portion after EMD.

2.3. Convolutional Neural Network Architecture

The complete network architecture for modified ECG signal classification is illustrated in Fig. 4. The Convolutional Neural Network (CNN) architecture is designed to handle one-dimensional data and all the convolution operations in the convolutional layers are performed on the 1-D sequence. The kernel size in each layer is modified to be applied on the 1-D sequence. The first five layers of the network are convolutional layers and are followed by three

fully connected layers. The final output of the network has a soft-max regressor with a specific number of classes which vary among different databases.

The first convolutional layer is fed by a 1000×1 sequence and the layer modifies the input sequence with 96 kernels of size 11×1 with a stride of 4. Consequently, a feature space of size 248×96 is produced. Then a Maxpooling layer converts the feature vector space to 124×96 space. The second convolutional layer converts the feature space to a shape of 124×256 with 256 kernels of shape

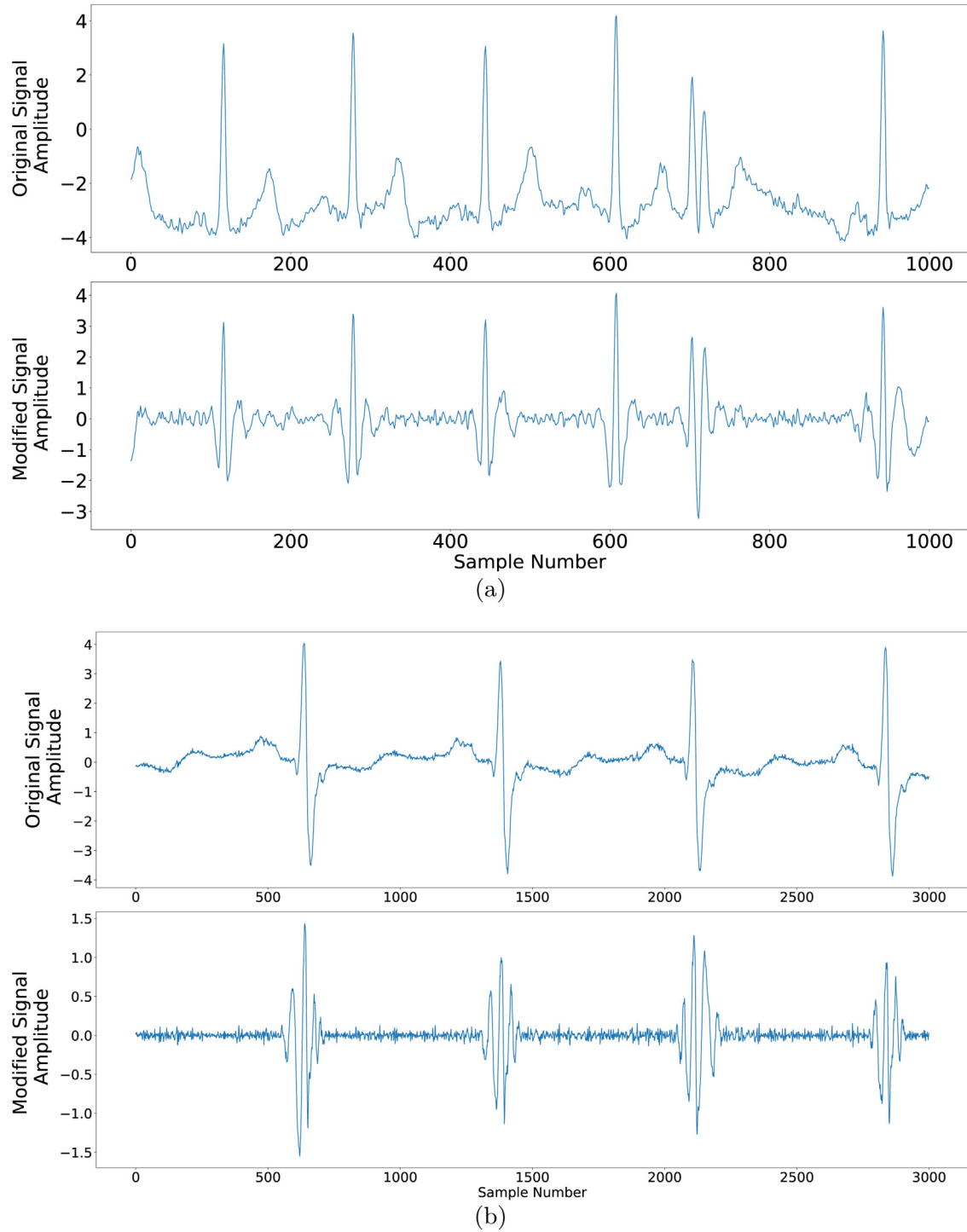


Fig. 3. Modified ECG signal is formed by summing the first three IMF signals after EMD. The peak amplitudes of a typical ECG signal are better detectable in the modified ECG signal from [24] in (a) and from [22] in (b).

5×1 and a stride of 1. The third, fourth and fifth convolutional layers convert the respective input feature vector space to a shape of 61×256 , 61×384 , 61×256 respectively. The corresponding kernel numbers, kernel shapes, and strides are shown elaborately in Fig. 4. The third, fourth and fifth convolutional layers do not have any intermediate pooling layers or normalization layers in between them. After the first and second convolutional layers, batch normalization layers are introduced. Throughout the architecture, ReLU is acting as the non-linear activation function. The final pooling layer converts the feature space of last convolutional layer into a shape of

30×256 and then flattened to feed to the first fully connected layer containing 4096 neurons. The second fully connected layer does also contain 4096 neurons. Finally a 'softmax' activation function classifies the signal to desired classes.

The convolutional layers use bias vectors and initialized with zero values. The kernels are initialized uniformly. No kernel regularizer, bias regularizer or activity regularizer are used in separate convolutional layers. Additionally, the kernels and biases have no constraint function applied to them. The batch normalization layers have a momentum of moving mean and variance equal to 0.99.

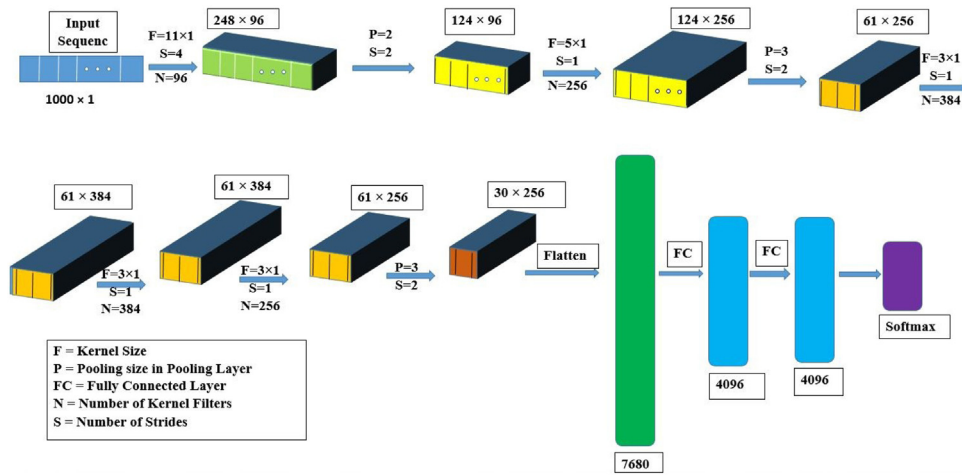


Fig. 4. Illustration of the proposed neural network architecture with a total of 5 convolutional layers, 3 fully connected layers, total trainable parameters of 49,434,376. The input of the network is 1000×1 dimensional. The number of neurons in the subsequent layers are 23808–31744–23424–15616–4096–4096–Number of classes.

Table 1
 Train and test data-sets specifying the number of sequences per class.

| Database | PTB diagnostic ECG database (7 classes) [22] | MIT-BIH arrhythmia database (4 classes) [23] | St.-Petersburg arrhythmia database (9 classes) [24] |
|----------|--|---|--|
| Training | Bundle branch block = 26,980 Valvular heart disease = 26,980 Myocarditis = 26,980 Healthy control = 26,980 Dysrhythmia = 26,980 Myocardial infarction = 26,980 Cardiomyopathy = 26,980 | Sinus bradycardia = 22,702 Normal sinus rhythm = 19,901 Paced rhythm = 22,676 Atrial fibrillation = 15,287 | Healthy = 20,225 Acute MI = 18,648 AV nodal block = 18,642 Coronary artery disease = 18,564 Transient ischemic attack = 18,543 Earlier MI = 18,531 WPW = 18,468 Sinus node dysfunction = 18,466 Atrial fibrillation = 18,466 |
| Testing | Bundle branch block = 11,485 Valvular heart disease = 12,532 Myocarditis = 12,805 Healthy control = 12,454 Dysrhythmia = 12,343 Myocardial infarction = 11,993 Cardiomyopathy = 12,799 | Sinus bradycardia = 9730 Normal sinus rhythm = 6082 Paced rhythm = 4471 Atrial fibrillation = 2564 | Healthy = 8650 Acute MI = 7986 AV nodal block = 7989 Coronary artery disease = 7956 Transient ischemic attack = 7945 Earlier MI = 7938 WPW = 7912 Sinus node dysfunction = 7912 Atrial fibrillation = 7912 |

Besides, the beta weights and moving means are initialized to zeros while gamma weights and moving variances are initialized to ones. No beta regularizer or gamma regularizer are used separately in each batch normalization layer separately. Also, beta and gamma weights are free of any kind of constraints. Moreover, the weights are scaled by the gamma initializer.

The slope of the negative part of activation function ReLU is set to zero and the threshold value for threshold activation is set to zero as well. The activation function returns element-wise maximum value compared to zero value, i.e. ($\max(x, 0)$; here x = output data from the previous layer). The pooling layers have different stride number and pooling size in different layers specified in Fig. 4. The dense layers use bias vectors and initialized to zeros. Also, the kernels are initialized uniformly. No regularizer (i.e., kernel regularizer, bias regularizer or activation regularizer) is used in any densely connected layer. Besides, the biases and kernels are free from any kind of constraint function. The final two densely connected layers are followed by dropout layers with a dropout percentage of equal to 50% of the incoming nodes from the previous layer.

3. Results and Discussion

In this section the database used in the experiment, denoising performance of the modified ECG, classification results of different

training approaches, comparison among the training methods and the learning procedures are described in detail.

3.1. Database

The proposed method is evaluated on ‘The PTB Diagnostic ECG Database’ [22], ‘MIT-BIH Arrhythmia Database’ [23], ‘St.-Petersburg Institute of Cardiological Technique’s 12-Lead Arrhythmia Database’ [24] in the PhysioNet [25]. Each database has a different number of classes and data recording criteria. The PTB database contains 549 records digitized at a frequency of 1000 Hz. The MIT-BIH database contains 48 records, each of which is 30 minutes long and digitized at a frequency of 36 Hz. The St.-Petersburg database contains 75 annotated recordings sampled at 257 Hz. A comprehensive database description is shown in Table 1 along with the considered disease labels and the corresponding number of segmented data. The CNN architecture requires a sequence of shape 1000×1 as input to the first layer. Therefore, a sequence of 1000 data points is sampled from the modified ECG signal for feeding into the neural network model. There is overlapping between two consecutive sequences for preserving inter-sequence and intra-sequence features. The overlapping is done in a random manner in different records. This fulfills two purposes. First, the data augmentation task is completed. Second, the training procedure does

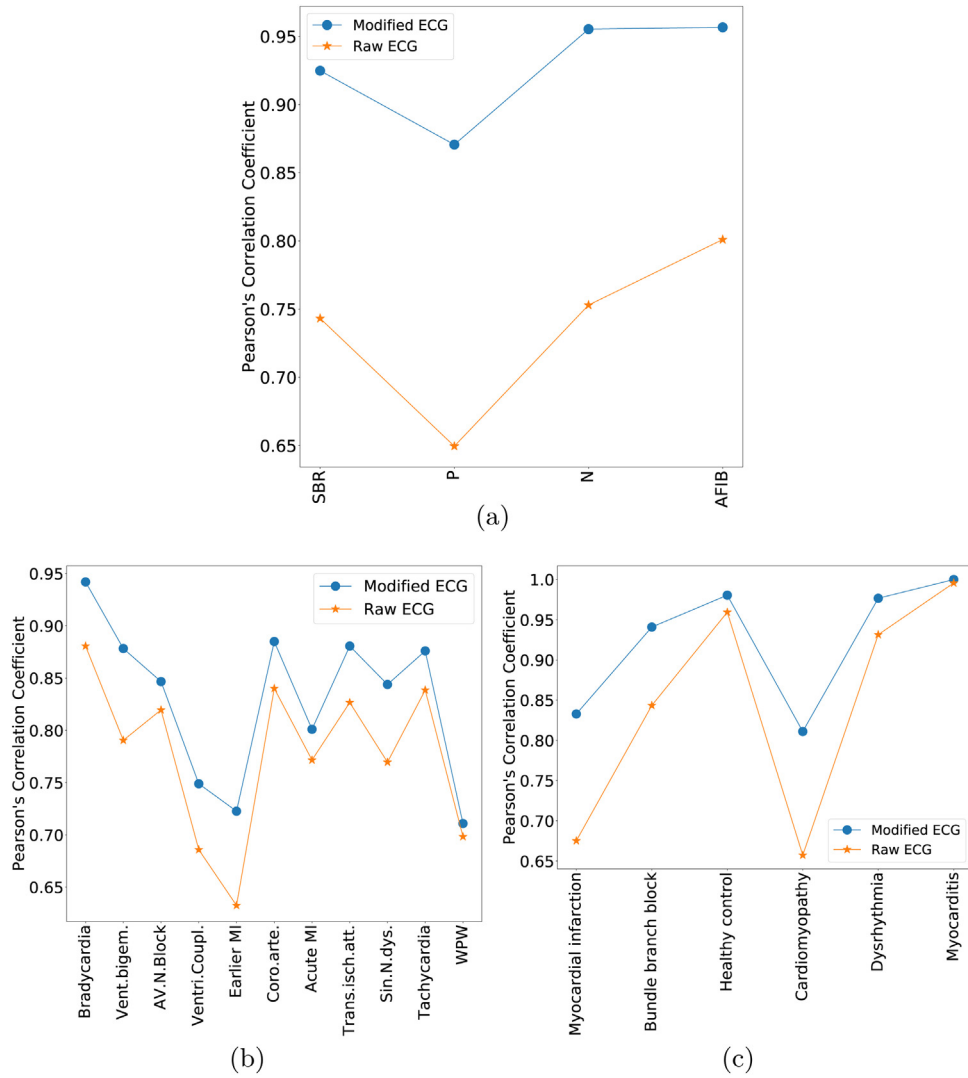


Fig. 5. Average Pearson's Correlation Coefficient of raw ECG signal and proposed modified ECG signal for each disease class in (a) MIT-BIH database [23], (b) St.-Petersburg database [24], (c) PTB database [22]. The coefficient value is higher for modified ECG signal than that of raw ECG signal signifying better signal quality and regularity throughout the database.

not become dependent on a specific overlapped sampling method throughout the entire database. A single segmented sequence contains four to five periodic rhythms (depending on the sampling rate of the database) so that any sequence fed into the network can learn both periodic and inter periodic features.

3.2. Learning Methodology

The model is trained using stochastic gradient descent (SGD) [26] algorithm with a batch size of 32 sequences, momentum of 0.9. The SGD is followed to optimize the neural network weights during training. The weights are updated after each sample passes through the network during the training rather than changing the gradient based on all of the available training samples. The algorithm has been reported in [26].

Learning rate scheduler is applied for faster learning the features of interest. In the scheduler, the initial learning rate is set to 0.01 and dropped by 50% from its previous value with a step of 5 epochs. Fig. 6 shows the details of this scheduling scheme. The final learning rate, at which the training accuracy is almost at its peak point, is approximately 0.0007 which is achieved at near 20th epoch. At this epoch, the validation accuracy is almost saturated as illustrated in Fig. 7. The kernels are initialized uniformly in all of the convolu-

tional layers. The neuron biases are initialized with constant zero. The learning rate is same for all the layers. The model is run on the TESLA K40 Graphics Processing Unit (GPU).

Fig. 7 shows the data validation accuracy improvement over the training process using different signals as input to the CNN. The usage of the learning rate scheduler makes the training time much shorter than that without a scheduler. Too low learning rate makes the training process slower. Hence, initially, the learning rate is 0.01 and gradually decreased according to the scheduler as the model approaches near the optimized position following the gradient descent algorithm. The model trained with the proposed modified ECG learns the features of interest faster compared to other signals such as the raw ECG or individual IMF. The time needed to reach the highest accuracy is the shortest for proposed modified ECG.

3.3. Denoising Performance of Modified ECG

The template matching algorithm using Pearson's correlation coefficient, reported in [21], is utilized to investigate the denoising capability of the modified ECG signal. According to [21], a denoised ECG signal has higher correlation coefficient than that of a noisy ECG signal. The algorithm is applied to both raw and modified ECG.

Table 2

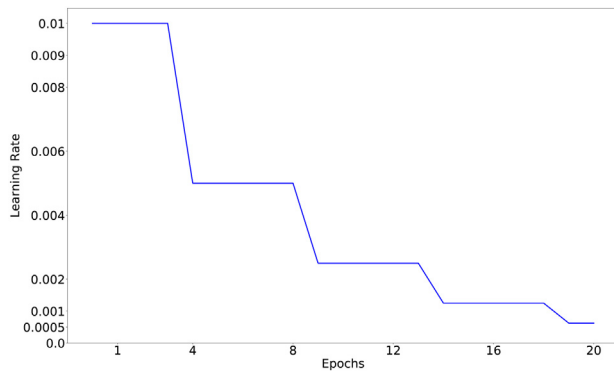
Comparison of classification accuracy of the proposed method in Fig. 1, raw ECG signal training scheme and individual IMF training scheme.

| Training methodology | PTB diagnostic ECG database(7 classes) (%) | MIT-BIH arrhythmia database (4 classes) (%) | St.-Petersburg arrhythmia database (9 classes) (%) |
|----------------------|--|---|--|
| Raw ECG signal | 95.03 | 97.08 | 99.29 |
| IMF 1 | 83.08 | 96.35 | 98.29 |
| IMF 2 | 90.01 | 91.97 | 94.70 |
| IMF 3 | 81.46 | 88.88 | 91.00 |
| IMF 4 | 64.92 | 84.57 | 89.38 |
| IMF 5 | 51.85 | 82.62 | 86.58 |
| IMF 6 | 44.11 | 76.22 | 76.31 |
| Proposed method | 98.24 | 97.7 | 99.71 |

Table 3

The total number of records corresponding to true and false predictions of the proposed method for St.-Petersburg database [24].

| True label | Predicted label | | | | | | | | |
|------------|------------------------|---------------|--------------------------|-------------------------------|------------------|---------------|------------------------------|------------------------------------|---------------|
| | AV nodal block (AV NB) | Acute MI | Atrial fibrillation (AF) | Coronary Artery Disease (CAD) | Earlier MI (EMI) | Healthy | Sinus Node Dysfunction (SND) | Transient Ischemic Attack (TIA)WPW | True Label |
| AV NB | 7985 (99.96%) | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Acute MI | 0 | 7967 (99.76%) | 0 | 4 | 2 | 7 | 1 | 0 | 5 |
| AF | 0 | 0 | 7827 (99.87%) | 1 | 0 | 0 | 0 | 9 | 0 |
| CAD | 0 | 2 | 6 | 7899 (99.37%) | 4 | 36 | 2 | 0 | 0 |
| EMI | 1 | 0 | 0 | 5 | 7930 (99.90%) | 0 | 0 | 2 | 0 |
| Healthy | 1 | 0 | 0 | 9 | 8 | 8604 (99.50%) | 1 | 24 | 0 |
| SND | 0 | 0 | 0 | 0 | 0 | 1 | 7911 (99.99%) | 0 | 0 |
| TIA | 0 | 0 | 0 | 21 | 1 | 18 | 0 | 7903 (99.50%) | 0 |
| WPW | 0 | 0 | 0 | 1 | 0 | 29 | 0 | 3 | 7879 (99.58%) |

**Fig. 6.** Learning rate scheduler implementation in the training procedure. The training accuracy is at its maximum at a learning rate approximately equal to 0.0007.

The analysis has been performed by taking windows of 5000 samples from the database records. The values of average correlation coefficients per disease are shown in Fig. 5 on three databases. It can be observed from the figure that the modified ECG shows a higher correlation coefficient than the raw ECG signal for all the diseases in each database. Hence, it can be concluded that the modified ECG has better denoising performance compared to the raw ECG signal.

3.4. Results of Proposed Modified ECG Training Method

First, the classification results on the test set of all databases are shown using the proposed method. In the next section, classification accuracy is presented employing other training approaches.

Individual IMF obtained after EMD are trained separately to find out the performance of each IMF in the classification of ECG signals. The resultant testing accuracies corresponding to each IMF

are reported in Table 2, where it is evident that the higher order IMFs (IMF 1, IMF 2, IMF 3) provide better results than the lower order IMFs. Based on the observation, we realized that the higher order IMFs are comprised of signal features that are crucial for the classification of ECG signals and it is expected that the combination of these higher order IMFs might boost the classification accuracy rather than the individual performances. This leads us to consider a modified ECG by combining the first three IMF signals expecting better results. Hence, the modified ECG signal is fed into the CNN model for classification. The overall procedure is illustrated in Fig. 1. Table 2 shows the detailed classification result on three databases. The modified ECG signal, the raw ECG signal, and 6 IMF signals are trained separately using the methodology in Fig. 1. The proposed modified ECG outperforms individual IMF accuracies as anticipated. Besides, the proposed method performs better than the raw ECG signal as shown in Table 2. The detailed classification results using the modified ECG signal are reported in Table 3–5 for databases [24,22,23], respectively indicating true and false predictions. As demonstrated in Table 3, the proposed method predicts with almost 100% accuracy for most of the test classes except the ‘Coronary artery disease’, ‘Transient ischemic attack’, and ‘Healthy’ patients. This results in a total accuracy of 99.71%. In Table 4, the maximum false prediction is only 3.75% for the class ‘Dysrhythmia’. This class is being falsely predicted with the other three major diseases. Consequently, this class had a significant effect on the overall accuracy of the whole database reaching a value of 98.24%. However, in Table 5, there is a maximum of 5.34% false predictions for the class ‘AFIB’ and the overall accuracy is 97.70%.

One interesting study could be to investigate the performance of different combinations of IMFs. For a total 6 IMFs at hand, there are 63 different possible combinations. Performance for all of the possible combinations has been investigated for the PTB database. The IMF combinations with accuracies greater than 80% are presented

Table 4

The total number of records corresponding to true and false predictions of the proposed method for PTB diagnostic database [22].

| True label | Predicted label | | | | | | |
|-----------------|---------------------------|-----------------|-----------------|-----------------|----------------------------|-----------------|------------------------------|
| | Bundle branch block (BBB) | Cardiomyopathy | Dysrhythmia | Healthy control | Myocardial infarction (MI) | Myocarditis | Valvular heart disease (VHD) |
| BBB | 12,177 (98.1%) | 18 | 174 | 27 | 14 | 2 | 1 |
| Cardiomyopathy | 83 | 12,633 (96.85%) | 219 | 11 | 97 | 1 | 0 |
| Dysrhythmia | 23 | 40 | 12,182 (96.25%) | 75 | 327 | 4 | 5 |
| Healthy Control | 3 | 1 | 17 | 12,681 (99.40%) | 51 | 3 | 2 |
| MI | 56 | 37 | 101 | 118 | 11,820 (97.24%) | 20 | 4 |
| Myocarditis | 3 | 0 | 2 | 9 | 3 | 12,967 (99.87%) | 0 |
| VHD | 1 | 0 | 0 | 1 | 3 | 0 | 12,539 (99.96%) |

Table 5

The total number of records corresponding to true and false predictions of the proposed method for MIT-BIH database [23].

| True label | Predicted label | | | |
|------------|-----------------|---------------|---------------|---------------|
| | AFIB | Normal | P | SBR |
| AFIB | 5071 (94.66%) | 104 | 180 | 2 |
| Normal | 317 | 7423 (95.37%) | 36 | 7 |
| P | 150 | 9 | 7987 (98.05%) | 0 |
| SBR | 0 | 3 | 0 | 9732 (99.97%) |

Table 6

Experimental result of separate training methodology according to Fig. 8. (Five best combinations (rows 1–5) along with the group of all IMFs (row 6) and the proposed method (row 7) accuracy.)

| PTB diagnostic ECG database (7 classes)(%) | MIT-BIH arrhythmia database (4 classes)(%) | St.-Petersburg database (9 classes)(%) |
|--|--|--|
| IMF(1, 2, 3) = 90.98 | IMF(1, 2, 3) = 94.96 | IMF(1, 2, 4) = 97.47 |
| IMF(1, 2, 4) = 87.79 | IMF(1, 2, 4) = 94.55 | IMF(1, 2, 5) = 97.30 |
| IMF(1, 2, 5) = 85.60 | IMF(1, 2, 5) = 94.58 | IMF(1, 2, 3) = 97.08 |
| IMF(2, 3, 4) = 85.36 | IMF(1, 2, 6) = 93.58 | IMF(1, 2, 3, 4, 5) = 96.24 |
| IMF(1, 2, 3, 4, 6) = 84.42 | IMF(1, 3, 5) = 92.87 | IMF(1, 3, 5) = 95.72 |
| IMF(1, 2, 3, 4, 5, 6) = 70.36 | IMF(1, 2, 3, 4, 5, 6) = 87.67 | IMF(1, 2, 3, 4, 5, 6) = 92.75 |
| Proposed_method = 98.24 | Proposed_method = 97.70 | Proposed_method = 99.71 |

Table 7

Comparison between the accuracy of the proposed method and accuracies after parallel training according to the scheme in Fig. 9.

| IMF signal parallel training methodology | PTB diagnostic ECG database (7 classes)(%) | MIT-BIH arrhythmia database (4 classes)(%) | St.-Petersburg database (9 classes)(%) |
|--|--|--|--|
| IMF(1, 2, 3) parallel train | 91.77 | 97.58 | 97.98 |
| IMF(1, 2, 4) parallel train | 89.18 | 97.55 | 97.75 |
| IMF(1, 2, 3, 4, 5, 6)parallel train | 85.14 | 95.39 | 97.70 |
| Proposed method | 98.24 | 97.7 | 99.71 |

in Fig. 10 as a bar chart. It is evident from the figure that the combination of the first three IMFs, which is considered in the proposed method, performs better than all other combinations considered.

The average time complexity added to the system due to decomposing the raw ECG through EMD and constructing the modified ECG is approximately 0.1593 s which is effective enough for real-time diagnosis of a broad range of ECG signals of cardiovascular patients. This processing time is calculated on a system of Intel (R) Xeon (R) 64 bit CPU E5-2680 v4 @ 2.40GHz with a capacity of 3300MHz.

3.5. Results of Other Training Approaches

Beside the proposed method analysis, all IMFs have been trained in a group using different training schemes. In this section, these approaches are analyzed and compared with the proposed method.

It is investigated if training any combination of IMF signals through the method shown in Fig. 8 can provide better results than the proposed method in Fig. 1. The best 6 combinations with greater accuracies than the others are shown in Table 6 for this methodology along with the accuracy of the proposed method. The proposed methodology shows a better result in this case too. However, as

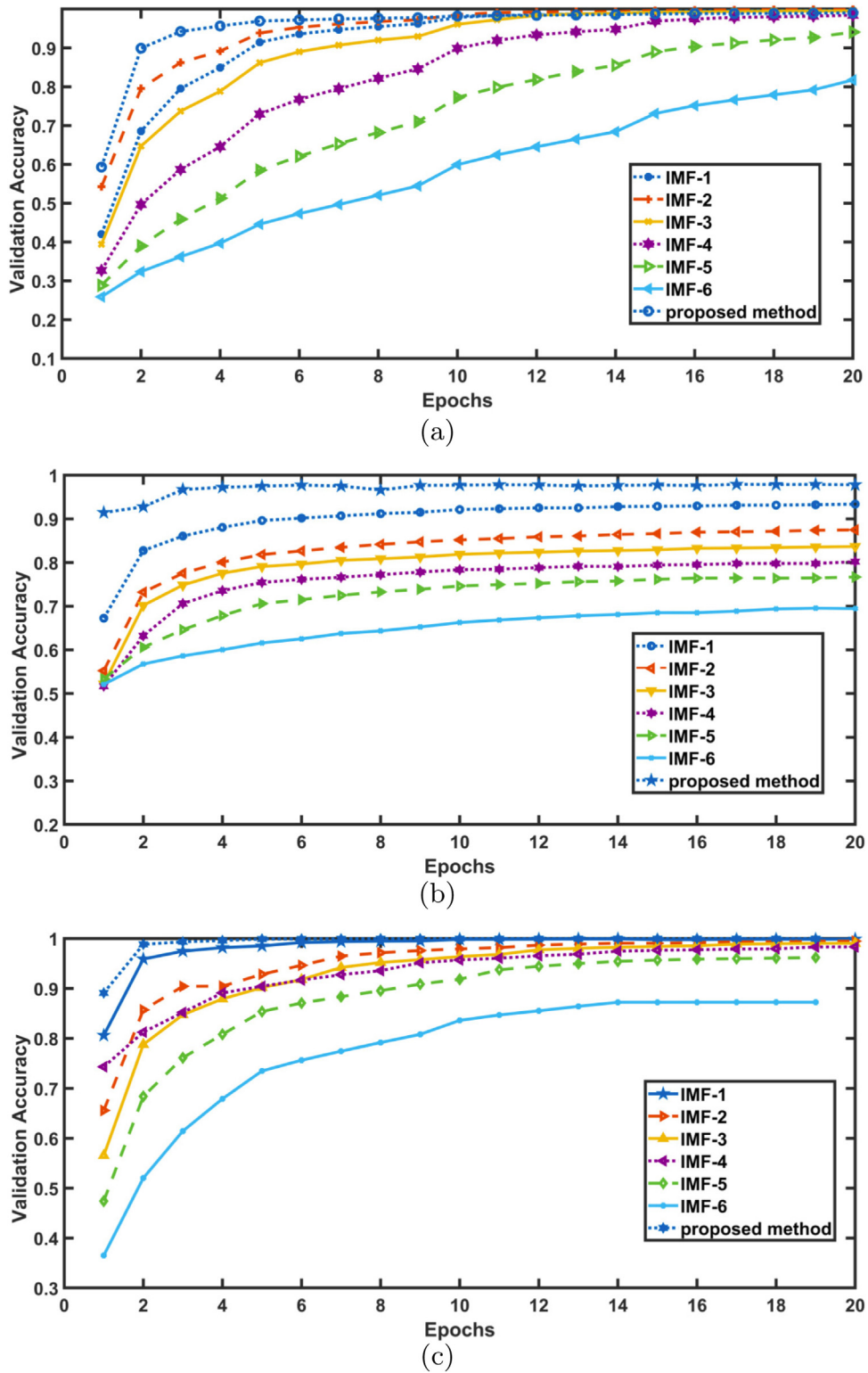


Fig. 7. Database validation accuracy improvement throughout the training procedure for (a) PTB diagnostic ECG database [22], (b) MIT-BIH Arrhythmia database [23], (c) St.-Petersburg Arrhythmia database [24]. In every case, the CNN learns the features of the proposed modified ECG signal faster than the individual IMF signal during the training phase.

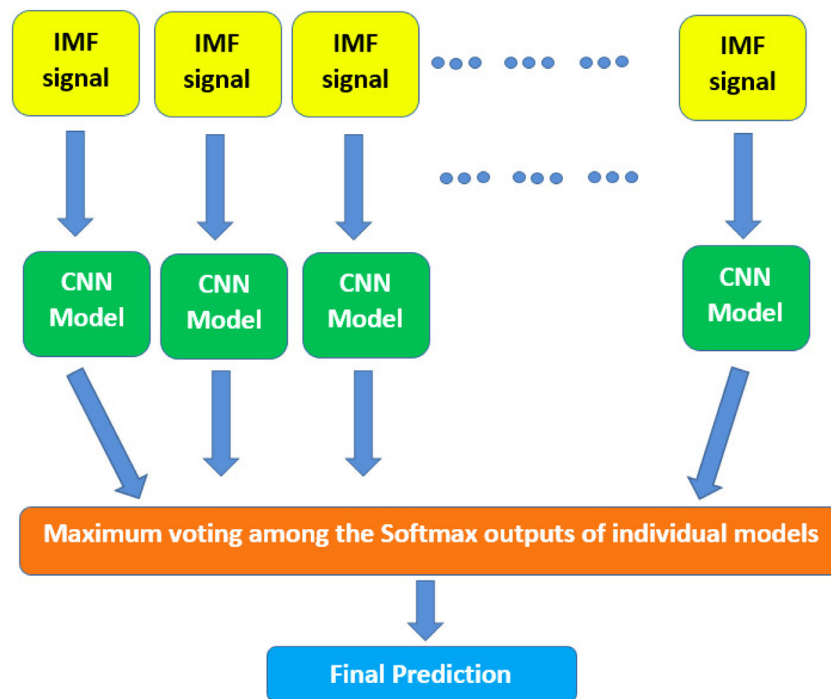


Fig. 8. Separate training of IMF signals. The prediction of individual CNN model is combined using the maximum voting criterion to predict the final class. Each of the CNN models is depicted in Fig. 4.

the lower order IMFs are included in any group, the classification accuracy drops. After comparing the results of each IMF signals in Table 2 and the accuracies of combined IMFs in Table 6, it is indicating that combining all IMFs according to Fig. 8 provides a worse result than individual IMF. The lower order IMFs degrade the result if combined with the higher order IMFs.

Next, we considered parallel training of IMF signals to experiment if learning interdependence of IMF signals can provide better results. The IMF signals are trained in parallel mode simultaneously and concatenated at the last softmax classifying layer as shown in Fig. 9. This layer is followed by three fully connected layers with a dropout rate of 20%. These fully connected layers have kernels initialized uniformly with a maximum weight constraint of 3 in each hidden layer. The activation function used in these three fully connected layers is ReLU. Three different combinations of IMFs such as (IMF1, IMF2, IMF3), (IMF1, IMF2, IMF4) and (IMF1, IMF2, IMF3, IMF4, IMF5, IMF6) are trained in parallel mode. The results are shown in Table 7. By comparing Table 6, and Table 7 it is evident that the parallel mode of training according to Fig. 9 provides better results than the separate mode of training as in Fig. 8. But still, it cannot surpass the result of the proposed method.

Table 8 compares the result of the proposed method with the reported results in the literature using similar databases. Even though it is reported by Wu et al. [2] an MI detection accuracy of 99%, the proposed method achieves an accuracy of 97.24% in PTB database depicted in Table 4. On the other hand, both 'Acute MI' and 'Earlier MI' have been recognized almost perfectly in database [24] as shown in Table 3. Consequently, the combined accuracy of detecting 'Myocardial Infarction(MI)' is 99% which is similar to

what is reported in [2]. But the proposed method utilizes multiple databases and multiple classes in each database. The use of different sources of databases makes the proposed methodology more robust and generalized than other methods in the literature. Hence, the proposed modified ECG based method has a broader range of cardiovascular disease classification capability.

4. Conclusion

In conventional multiple heart disease classification schemes, the raw ECG signal is employed in feature learning and classification. But in this paper, a modified ECG signal is formed using EMD analysis and then forwarded to the classification task. First, the modified ECG is formed by summing the first three IMF signals obtained through EMD analysis and it is shown that the modified ECG has better denoising property. Next, a one dimensional CNN network is developed to learn the features of the modified signal for classification purpose. Apart from this, the proposed method is compared with other approaches to training with different combinations of IMF signals. It has been shown that the proposed method achieves a better result than all other approaches. The proposed approach is evaluated on three publicly available databases and so this makes the method robust and capable of classifying a broader range of cardiovascular diseases. Through detailed investigation it has been shown that the modified ECG exhibits superior performance in terms of classification accuracy (98.24% in PTB database, 97.70% in MIT-BIH and 99.71% in St.-Petersberg database) and training time [30].

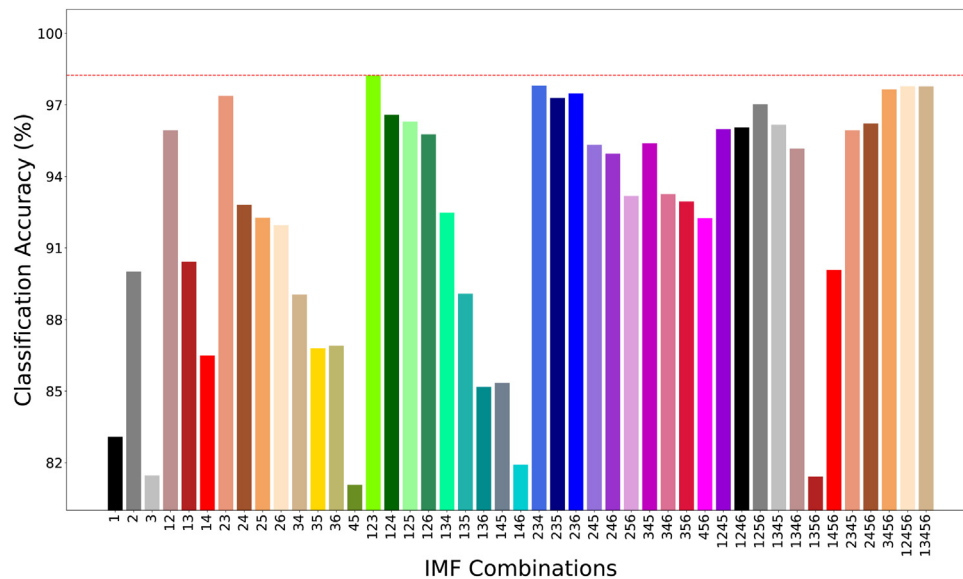


Fig. 10. Effect of different combinations of IMFs on the model performance in the PTB database [22]. The proposed combination of the first three IMFs (IMF 1, IMF 2, IMF 3) performs better than other combinations considered. The x-axis labels denote the IMF combinations.

Conflicts of interest

None.

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