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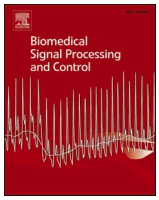

An efficient honey badger based Faster region CNN for chronc heart Failure prediction

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ABSTRACT

If the blood circulation of the heart is not adequate then it causes arrhythmias and Congestive Heart Failure (CHF) which requires immediate medical attention or else it leads to the loss of one's life. An Electrocardiogram (ECG) is a golden standard to diagnose the fatal complications in the heart caused by arrhythmias and it comprises a massive information related to the heartbeat rhythm. The main challenge focused in this paper is to extract the crucial information present in the ECG signal by visual analysis and classify the different abnormalities exhibited in the ECG signal. This paper presents a Honey Badger Algorithm optimized Faster Region-based Convolutional Neural Network (HBA-FRCNN) for CHF prediction with higher diagnostic accuracy. The noisy input ECG signals such as muscle contraction, electrode touch noise, and different noise artifacts are preprocessed using the Delayed Normalized Least Mean Square (DNLMS). The electrocardiographic complex (QRS complex) consisting of the Q, R, and S waves are extracted using the Discrete Cosine Transform (DCT) and fast Fourier transforms (FFT). The target detection box and the anchor parameter for the FRCNN model are tuned using the HBA algorithm to overcome the missed target detection, overfitting, and computational cost. The ECG signals for this study were obtained from Beth Israel Deaconess Medical Center (BIDMC) Congestive Heart Failure Database and the Massachusetts Institute of Technology-Beth Israel Hospital (MIT-BIH) Normal Sinus Rhythm Database. The proposed methodology offers an accuracy, positive predictive value, sensitivity, and specificity score of 98.65%, 97.81%, 98.5%, and 98.2% respectively when evaluated with the ECG signals of the two datasets. For the Cardiac Arrhythmias (ARR), Congestive Heart Failure (CHF), and Normal Sinus Rhythm (NSR) classes present in the MIT-BIH dataset, the proposed model offers an accuracy of 99%, 100%, and 98% respectively and for the classes such as CHF severe and CHF normal in the BIDMC dataset, it offers an accuracy of 98% and 97%. The study mainly demonstrates the effectiveness of the FRCNN technique in predicting arrhythmias and CHF in patients by taking the increased number of features in the ECG signal. It also serves as a promising solution for physicians for long-time surveillance of patients prone to CHF with abnormal heartbeat rhythm.

1. Introduction

The human heart is considered a muscular organ whose expansions and contractions are controlled by using the sequence of electrical impulses for delivering nutrition and oxygenated blood to the entire body parts. In a normal heart, the electrical signals are recorded from the electrocardiogram. The abnormal process of the heart creates cardiovascular disease (CVD) like strokes, cardiac arrhythmias, and heart attacks [1]. The irregular electrical variations from the heart are also known as a cardiac arrhythmia which leads the heart disease. The major factors causing cardiac arrhythmia are stressful lifestyle, smoking, Ischemic heart disease, alcohol intake, and hypertension. The amazing methods are used to predict the electrocardiogram signals that will improve the precision range of heartbeat variations. Deep and machine learning-based classification methods are employed to detect heart disease[2]. Sudden cardiac death (SCD) was caused due to the presents of irregular cardiovascular variations and cardiovascular mortality. When the heart cannot pump blood to the entire part of the body, SCD will occur. Ventricular fibrillation (VF) is the most important fact in causing SCD and ventricular tachyarrhythmia (VT) leads the heart

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failure during the blood pumping of the heart [3].

The electrocardiogram (ECG) is an approach for evaluating electrical signals of the heart and also identifying the irregularities in the heart. The conventional ECG signal processing with hybrid bacterial foraging-particle swarm optimization (BF-PSO) techniques was used to identify the heart diseases such as bundle branch block (BBB), atrial fibrillation (AF), and myocardial infarction (MI). The heartbeat is represented in waveform using QRS complex that is P and T waves are denoted the starting and ending point respectively. Then the ending point is displayed in the U waveform [4]. The standard 12-lead electrocardiogram method is employed for measuring electrical potential from 10 electrodes which are placed at various parts of the human body like four electrodes are placed in the limbs and the other six are in the chest. One of the most common causes of mortality is sudden cardiac death, which is caused by irregular heart rhythms known as arrhythmias. The most deadly arrhythmia is ventricular fibrillation, which is caused by the uncontrolled flow of impulses from the heart's lower chamber. When analyzing the long-term ECG signals of the patients who died of sudden cardiac arrest, these patients have a history of severe cardiac arrhythmia and heart attack. The early diagnosis of these diseases will minimize the mortality of the patients and this study aims to provide the same. The computer-aided ECG classification method follows four major steps such as pre-processing, detection, feature extraction, and selection of classifiers. The classification method is mainly used for reducing the computation time [5,37,38].

Various authors have used machine learning techniques for abnormal ECG identification and some of them are listed as follows. The feed-forward multilayer neural network along with error back-propagation is used for classifying the ECG signals whether it is normal or abnormal. The median filter is utilized for eliminating the unwanted noise in the ECG signal [6]. The deep learning architecture is applied for noise removal and validation purposes. This will be obtained from two stages of the process, one is extraction, and the other is a convolutional neural network (CNN) [7]. Artificial intelligence models such as support vector machine (SVM), adaptive boosting (ADB), convolutional neural network (CNN), artificial neural network (ANN), ensemble classifier, and boosting are used in the literature to detect heart disease. The machine-learning algorithm was used to analyze and investigate the heart disease and imbalance electrocardiogram based on the arrhythmia dataset [8]. The regressive learning-based neural network classifier (RLNNC) also offered higher performance and efficiency for detecting heart diseases [9].

Dai et al. [11] proposed an automatic screening tool to detect Cardiovascular Disease (CVD) based on the deep convolutional neural network by using Electrocardiogram (ECG) signals at different intervals. Here Physiobank ECG dataset, PTB is used. At different intervals such as 1 s, 2 s, and 3 s the ECG signals without wave detection are segmented. In this way, three datasets are obtained. Next, instead of using complex pre-processing, raw ECG signal durations are used in min–max normalization as input. Then, ten-fold cross-validation is used in three obtained ECG signal datasets. Haleem et al. [12] presented a two-stage multiclass algorithm to detect cardiovascular disease (CVD). At first, the ECG beats are extracted through Convolutional Bi-Directional LSTM (Long Short-Term Memory). Then, with the use of Short-Time Fourier Transform the extracted ECG beats are converted into 2D spectrograms. For numerous time intervals, 2D-CNN has been used to produce time-variant spectrograms. The Massachusetts Institute of Technology-Beth Isreal Hospital (MIT/BIH) PhysioNet database is used for the training data. This achieves exceptional outcomes by assisting domain specialists in their job and calculating signal characteristics using an automated CVD diagnostic method.

Hammad et al. [13] developed a classifier to detect abnormal heart conditions by classifying the ECG signals. To extract the characteristics of each ECG signal, an accurate algorithm is utilized. Here four SVM (Support Vector Machine) classifiers, K-NN (K-Nearest Neighbor) classifier, and two Neural networks are used for the classification of ECG signals. These are then compared with the developed classifier. Then, from each ECG signal, a total of 13 features are extracted and fed as input to other classifiers. This algorithm is evaluated with the database of the Massachusetts Institute of Technology-Beth Isreal Hospital (MIT/BIH) arrhythmia. Adam et al. [14] combined Discrete Wavelet Transform (DWT) and non-linear features to detect cardiovascular disease automatically using ECG signal. Hypertrophic cardiomyopathy (HCM), Dilated cardiomyopathy (DCM), and myocardial infarction (MI) ECG signals are exposed to five stages of DWT. The DWT coefficients are used to extract the four non-linear's relative wavelets: sample entropy, signal energy, sample entropy, and fractional dimension. These features are ranked with the use of the Relief method after the features are inserted in Sequential Forward Selection (SFS). This method is used for accurate and faster diagnosis of CVD by the clinical staff.

Deng et al. [15] classified cardiovascular disease and human identification by extracting ECG signals' cardiac dynamics. Based on the cardiac dynamics' similarities, the developed recognization system may differentiate and assign EDG patterns dynamically to the specified classes. The efficiency is calculated by the experiments with the use of the FuWai ECG database and public PTB databases. Wang et al. [16] proposed a Deep Multi-Scale Fusion neural network (DMSFNet) to detect multi-class arrhythmia. Here multi-scale feature extraction is used to reduce noise and ECG signals' cross-scale information complementarity is also used to capture the diseases' abnormal patterns effectively. The standard performance is demonstrated by the two datasets: CPSC_2018 and PhysioNet/CinC_2017. For these datasets, the F1 scores are 82.8% and 84.1% respectively. The result shows that the DMSFNet performed well in feature extraction from a wide range of various arrhythmias.

Liu et al. [17] proposed the ECG signals based on the classification methods of heart diseases utilizing long short-term memory (LSTM). To classify the heart diseases on ECG by employing a machine learning technique termed LSTM, which was the state-of-the-art method for evaluating the time sequences with deep learning. The ECG signal data was collected with the UCR time series archive. For data preprocessing, (SAX) symbolic aggregate approximation was also employed for enhancing the accuracy. The experimental results showed that the scheme achieved high classification accuracy in a short time. Xu et al. [18] presented ECG signal classification using a combination of recurrent neural networks (RNN) and CNN. In this paper, the PhysioNet/CinC Challenge dataset and MIT-BIH datasets were used. The RNN-CNN architecture provides a specificity score of 96.34%, a sensitivity score of 95.90%, and an accuracy score of 95.90% in ECG signal classification. The experimental results showed that the combined CNN and RNN achieved higher performance as compared to the other methods. This study only focuses on a single cardiovascular disease and also suffers from the data imbalance.

An efficient data compression technique is usually required to handle the massive information associated with the ECG signal and the technique selected should be capable of reducing the size of the data as much as possible and also capable of retaining the actual features. This paper mainly utilizes the Discrete Cosine Transform (DCT) and fast Fourier transform (FFT) to overcome the complexity associated with handcrafted and manual QRS complex detection. The state-of-art techniques mainly utilized short CHF waveforms instead of long waveforms and achieved satisfactory results. However, their performance often declined when evaluated with larger datasets due to the overfitting and they offered higher performance only when evaluated with a small and balanced dataset. The conventional machine learning classifiers mainly required handcrafted features which are acquired from the trial and error method to offer improved performance.

Hence, this results in the need for an automatic classifier that analyzes the visual features present in the ECG signal accurately and predicts the CHF and arrhythmias with improved accuracy. This is taken as the motivation of this research and we obtained it in this work using the Honey Badger Algorithm optimized Faster Region-based Convolutional Neural Network (HBA-FRCNN) classifier. The ECG signal needs to be fed

as an input to the classifier algorithm by separating the features into different classes via a feature extraction due to the quasi-periodic, non-stationary, and finite duration nature of the ECG signals. The target detection box and the anchor used in the FRCNN model help to locate the abnormalities present in the ECG signals accurately and the missed target detection, overfitting, and computational complexity is overcome by using the HBA algorithm.

The metaheuristic algorithms [10] introduced also serve as an efficient technique for feature extraction from ECG signals to enhance the accuracy of the systems. The DCT and FFT techniques used are efficient in minimizing the computational complexity of this technique. The waveform taken for analysis is obtained from the Beth Israel Deaconess Medical Center (BIDMC) Congestive Heart Failure Database and the Massachusetts Institute of Technology-Beth Israel Hospital (MIT-BIH) Normal Sinus Rhythm datasets. The main aim of this study is to develop an automatic Chronic Heart Failure (CHF) using the ECG signals via a Honey Badger Algorithm optimized Faster Region-based Convolutional Neural Network (HBA-FRCNN). The main contributions of this paper are illustrated as follows:

- Initially, the ECG signals are preprocessed using the motion artifacts, baseline wander, and other disturbances using the Delayed Normalized Least Mean Square (DNLMS) technique which increases the speed of the classifier and minimizes the computational resource usage.
- The DCT and FFT techniques are used to extract the different features present in the ECG signals such as the QRS complex (Combination of Q, R, and S wave) by converting it into a Fourier spectrum.
- The HBA-FRCNN classifier is used to classify the abnormal ECG signals present in the Beth Israel Deaconess Medical Center (BIDMC) Congestive Heart Failure Database and Massachusetts Institute of Technology-Beth Israel Hospital (MIT-BIH) Normal Sinus Rhythm Database with high accuracy.
- The HBA algorithm boosts the FRCNN network convergence and overcomes the overlapping detection box issue.

The rest of this paper is arranged as follows: Section 2 presents the overview of the techniques used for ECG abnormality detection. The working of the proposed methodology is explained in section 3 along with the simulation results in section 4. Section 5 concludes the paper.

2. Methods

2.1. Faster region-based convolutional neural network (Faster R-CNN)

Faster R-CNN, a deep convolutional neural network used primitively for target detection tasks [19]. Unlike other R-CNN models, the faster R-CNN method uses a region proposal network (RPN) in which it generates the detection boxes directly. To speed up the operation of the network, the graphics processing unit (GPU) parallel computation is utilized. The feature map is extracted by means of a feature extraction network after applying the image as input. Then the feature maps are allowed to pass through RPN to acquire initial region proposals. These proposals are acquired by sliding a convolutional kernel across a convolutional feature map with a suitable learning rate. In the middle region of each sliding window, nine default bounding boxes exist that act as a reference point for target detection. These reference bounding boxes are generally named anchors. The convolutional layer's output is subsequently mapped into feature vectors. These vectors are fed into a fully connected layer to perform regression and classification tasks. In order to measure the similarities of output classes, the classification layer utilized the softmax activation function. In RPN, the anchors are labeled as positive and negative samples by the representation of ground truth values. When the overlap rate is greater than 0.7 with ground truth, the anchors are referred to as positive samples; when the overlap rate is below 0.3, the anchors are considered negative samples, and the remaining part which is neither positive nor negative is rejected. After sample division, the total training loss of RPN is computed based on a multi-task function which is defined in the below expression.

$$L_S(\{k_x\},\{d_x\}) = \frac{1}{n_C}\sum_x L_C\left(k_x, k_x^*\right) + \gamma\frac{1}{n_R}\sum_x k_x^* L_R\left(d_x, d_x^*\right) \tag{1}$$

The term $L_C\left(k_x, k_x^*\right)$ indicates classification loss function, γ depicts balance weight, batch training data is represented asn_C, anchor numbers are signified asn_R, and regression loss is implied as$L_R\left(d_x, d_x^*\right)$. The numerical formulation of classification loss is expressed as,

$$L_C\left(k_x, k_x^*\right) = -\log\left[k_x^* k_x + \left(1-k_x^*\right)\left(1-k_x\right)\right] \tag{2}$$

Likewise, the regression loss is also computed based on smooth L1 function as,

$$L_R\left(d_x, d_x^*\right) = \begin{cases} 0.5\left(d_x - d_x^*\right)^2, & |z| < 1 \\ \left|d_x - d_x^*\right| - 0.5, & else \end{cases} \tag{3}$$

From the above equations, the term k_x signifies the prediction probability of anchor as a target, k_x^* implies the predicted output's ground-truth value, $d_x = \{d_p, d_q, d_r, d_s\}$ represents the position of the predicted detection box, and d_x^* denotes the ground truth coordinate. Moreover, the prediction of the anchor as a positive sample means$k_x^* = 1$, else 0. The faster RCNN architecture for ECG abnormality detection is presented in Fig. 1.

2.2. Honey badger algorithm

The Honey Badger algorithm (HBA) [27] simulates the honey badger forage behavior. The honey badger digs and smells or follows the honeyguide birds for placing the source of food. Let us consider two modes namely digging mode and honey mode. In the previous model, it utilizes its smelling capability for approaching the position of prey. Honey badger acquires the honeyguide bird to direct the position beehive in the latter mode.

Algorithmic steps.

HBA is furnished with both exploitation and exploration stages, and then it is stated as the global optimization method. As a result, the population of the candidate solution in HBA is stated as follows:

$$\begin{bmatrix} y_{11} & y_{12} & y_{13} & \cdots & y_{1E} \\ y_{21} & y_{22} & y_{23} & \cdots & y_{2E} \\ & \cdots & \cdots & \cdots & \\ y_{o1} & y_{o2} & y_{o3} & \cdots & y_{oE} \end{bmatrix} \tag{4}$$

The honey badger *jth* position is represented as$y_j = \left[y_j^1, y_j^2, \ldots\ldots, y_j^E\right]$.

Step1: Initialization stage.

Initializing the numbers of a honey badger and their different positions are expressed in the below equation;

$$y_j = Jc_j + s_1 \times \left(vc_j - Jc_j\right), \tag{5}$$

where the candidate solution of the population O in the *jth* honey badger location is represented byy_j, s_1 are the random values among 1 and 0, and search domains upper and lower bounds are represented by vc_j andJc_j.

Step 2: Defining Intensity(J).

The intensity is corresponding to concentrate the strength of the prey and the distance between it and *jth* $_{\text{the}}$ honey badger, the small intensity of prey is denoted byJ_j; in case the smell is higher, then the motion will be vice versa and fast, it is expressed by inverse square law as;

$$J_j = s_2 \times \frac{T}{4\Pi e_j^2}, \tag{6}$$

$$T = \left(y_j - y_{i+1}\right)^2 \tag{7}$$

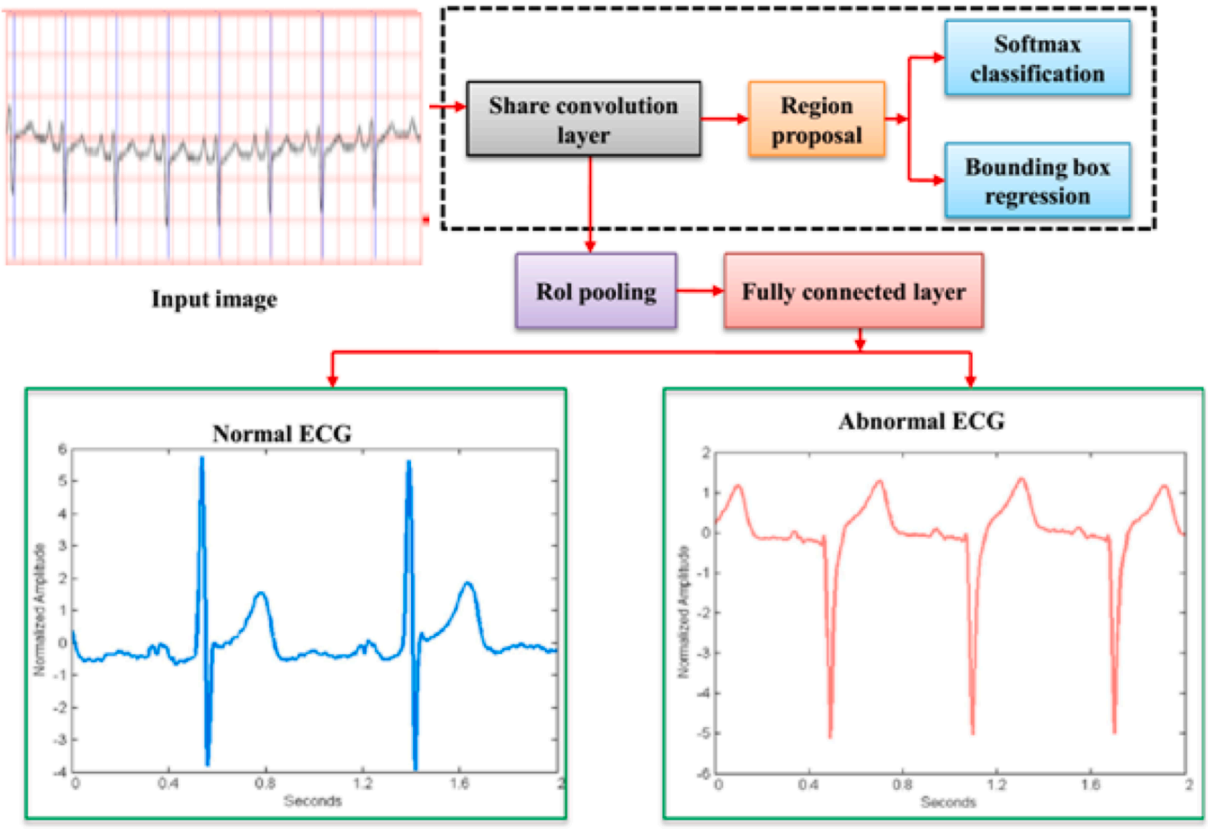

Fig. 1. ECG abnormality detection using Faster RCNN.

$$e_j = y_{pr} - y_j \tag{8}$$

where s_1 is the random value among 1 and 0, T is the concentration strength or source strength, and the distance between *jth* badger and the prey is denoted bye_j.

Step 3: Update density factor.

The density factor (β) is used to control the randomized time variation for ensuring the gradual transition from both phases (exploration to exploitation). Update the density factor β which reduces through iteration to reduce randomization through the period. That is expressed in the below equation;

$\beta = D \times ex\left(\frac{-u}{u_{MAX}}\right)$, u_{MAX} = maximum iterations (9).where D is the constant⩾1.

Step 4: Escape with local optima regions.

This stage and the next two stages are utilized for escaping from the regions of local optimum. In this case, the flag G is utilized that changes the direction of the search for assisting great opportunity for operatives to search the space scanning.

Step 5: Agents location update.

HBA location update method y_{NEW} is separated into two phases the honey stage and the digging stage and its detailed explanation is given below;

Step 5–1: Digging stage.

In the digging stage, the honey badger executes action which is identical to the Cardioid shape. The Cardioid action is expressed as;

$$y_{NEW} = y_{pr} + G \times \beta \times J \times y_{pr} + G \times s_3 \times \beta \times e_j \times |\cos(2\Pi r_4) \times [1 - \cos(2\Pi r_5)]| \tag{10}$$

The prey location is denoted byy_{pr}. In other words that is the best global location. The honey badger's capability to obtain food is represented by (default = 6)γ⩾1. The distance between *jth* honey badger and the prey is denoted bye_j. s_3, s_4, s_5 are the three distinct random values among 1 and 0.G operated as a flag which changes the direction of search, it is expressed in the below equation;

$G = \begin{cases} 1 & if\ s_6 \leqslant 0.5 \\ -1 & else \end{cases}$, The random value between 1 and 0 iss_6. (11).

In this stage, the honey badger greatly depends on the prey y_{pr} of smell intensity$J$, the distance between the badger and prey is denoted bye_j, and the search influence of the time-varying factor is denoted byβ. In digging action, the badger received any disturbance G enables to detect a better prey position.

Step 5–2: Honey stage.

In this case, the honey badger followed the honeyguide bird for reaching the beehive is expressed by;

$$y_{NEW} = y_{pr} + G \times s_1 \times \beta \times e_j, \tag{12}$$

where the new location of the honey badger is denoted by y_{NEW} then the prey position is y_{pr} and the random value among 0 and 1 are denoted bys_7. Based on the information distance e_j the honey badger performed a search close for the prey locationy_{pr}. In this stage, the search behavior influences the search at varying timesβ. However, the honey badger can detect any disturbance$G$.

3. Proposed methodology

This paper mainly aims to identify the abnormalities present in the ECG signals of the BIDMC and MIT-BIH datasets. Initially, the DLNMS algorithm is applied for signal preprocessing and the features such as the QRS complexes are extracted via the DCT and FRT techniques. These signals are then normalized before feeding them into the Faster RCNN classifier and the abnormalities in the ECG signal are identified. The HBA algorithm executes the different steps such as initialization, defining intensity and update density factor, escaping from local optima, updating agent position via the digging and honey phase, and returning

the best position. The HBA algorithm is mainly used to tune the target detection box and the anchor parameter of the faster RCNN architecture. At last, the efficiency of the classifier is verified in terms of different performance metrics such as accuracy, positive prediction rate, sensitivity, and specificity. Fig. 2 presents the proposed overall architecture and the steps in the methodology are elaborated in the subsections.

3.1. ECG signal preprocessing using the DENLMS algorithm

The ECG signals are more susceptible to various forms of intrusions and data artifacts during the data acquisition process [20]. Several data interfering factors are baseline drifts, power line interference, muscle contraction, electrode touch noise, etc. These kinds of artifacts and noises are removed from ECG signal data by initial processing. Preprocessing of ECG signals is an indispensable task that eliminates the data noises and paves the way to detect heart abnormalities effectively. Furthermore, the DENLMS method is utilized to evaluate non-stationary ECG data. The LMS algorithm is an ideal candidate for adaptive filters due to its ease of implementation [21]. The FIR filter coefficients are modified depending on the weight update equation as shown below:

$$W(M+1) = W(M) + \sigma\, y(M) f(M) \tag{13}$$

where,$W(M+1)$,M,$W(M)$, represents updated weight, time step, and old weight respectively.σ,$y(M)$, $f(M)$ indicates step size, filter input, and error signal respectively.

The adaptive filter output $x(M)$ is measured by using input and updated weight and is expressed by,

$$x(M) = W^T(M)\, y(M) \tag{14}$$

where, $W^T(M)$ is the filter weight. The filter error output is given below,

$$f(M) = c(M) - W^T(M)\, y(M) \tag{15}$$

In an adaptive LMS filter, the input ECG signal is measured as a distorted signal. The MSE value is reduced when adaptive algorithms are used, and the filter produces a reasonable least-squares estimation of the

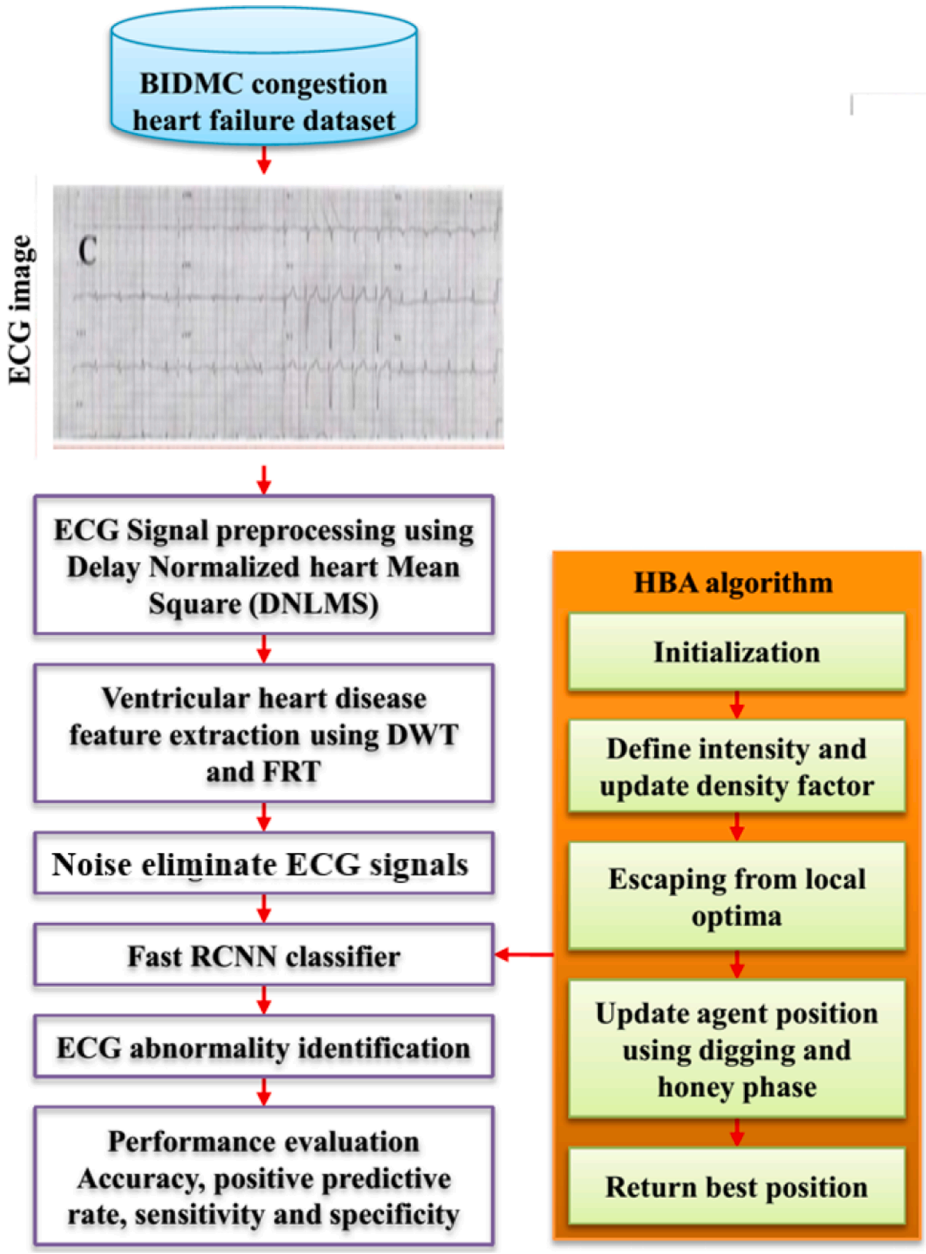

Fig. 2. Proposed overall architecture.

signal. The MSE is calculated by using the equation shown below.

$$F\left[f^2(M)\right] = F\left[(y(M) - x(M))^2\right] + F\left[w^2(M)\right] \tag{16}$$

The pipelining filter is a difficult task when the feedback structure is present in the filter. The pipelined filter and filter without pipelining were gathered with the same number of coefficients. Because of its feedback nature, the impulse invariant response (IIR) filter is used in pipelines. The LMS algorithm has $2M+1$ multiplications and $2M$ additions, So this algorithm is applied for various adaptive filtering applications. The three major steps of delayed LMS algorithms are the evaluation of the updated weight, error signal computation, and output signal calculation, which are determined by the equations (17)-(19).

$$W(M+1) = W(M) + \sigma f(M-KE)y(M-KE) \tag{17}$$

$$f(M-KE) = c(M-KE) - x(M-KE) \tag{18}$$

$$x(M-KE) = W^t(M-KE)y(M-KE) \tag{19}$$

whereσ, KE indicates step size and number of delays respectively. The stable step size can decide the steady-state behavior and convergence rate of the filter. The convergence of the LMS algorithm is calculated from the below equation,

$$0 < \sigma < \frac{2}{(M-2K-2)\ (p_{tl})} \tag{20}$$

The NLMS algorithm was written using the coefficient update equation as shown in equation (21).

$$W(M+1) = W(M) + \sigma_N f(M)\, y(M) \tag{21}$$

Here, σ_N represents normalized step size and is expressed as,

$$\sigma_N = \left[\frac{\sigma}{P + y^s(M)\, y(M)}\right] \tag{22}$$

The term P is to eliminate big step size and small denominator value.

3.2. Feature extraction using DCT and FFT

The ECG is mainly recorded in different ways and the conventional ECG signal records the 12 different ECG signals acquired from the ECG leads placed in the body of a resting patient. In certain methodologies, the cardiac excitation is computed by placing a set of body surface potentials in the patient which is applied as an input to the three-dimensional vector model. To analyze the life-threatening sequences in the heartbeat rhythm of the Intensive Care Unit (ICU) patients, two leads of the ECG signals are continuously monitored to notice the differences. This process of measuring the heartbeat is called arrhythmia analysis [31,32]. The width and height of the QRS complex interval and QRS complex area are the time domain features of the ECG signal which are most prone to noise.

The energy ratio window for both high and low frequencies along with the energy measured for a specific frequency band together forms the ECG signal frequency domain features. With an 8–12 bit resolution, a total of 200–500 ECG signals are samples that arise the need to store and transmit a large amount of data. Hence, this arises the need to minimize the data storage space and preserve the crucial information for successful signal reconstruction. Chronic heart failure is mainly recognized by reconstructing the signal and hence it rises the necessity to selectively compress the ECG signals. The real-time data processing applications mainly require an effective data reduction and data compression technique to satisfy the objective. The ECG signal is mainly transformed to another domain for compression and for this purpose we utilized the Discrete Cosine Transform (DCT) and fast Fourier transform (FFT).

For the reconstruction process, we extract a set of parameters from the actual signal. The transform methods such as DCT and FFT are efficient in terms of achieving a higher compression ratio. The Fourier transformation results in a coefficient sequence that minimizes the data complexity associated with the actual signal representation. The DCT and FFT methods are effective in minimizing the energy of the signal with minimal samples in the frequency domain when compared to the time domain. In this way, the small transform coefficients are also eliminated.

Feature extraction using the DCT method determines the heart rate variability (HRV) by the effective detection of R-peaks in ECG signals [20,21]. The abnormalities in ECG signals are determined using the arrhythmic beat classification method. Based on the heartbeat rate, the R-peak detection methods estimate the RR (beat-to-beat) intervals on ECG. These intervals are calculated by measuring the instantaneous heartbeat rate per minute. This measurement system uses a correlation method with time resolution ±1 ms. The measuring accuracy of RR intervals is increased by means of the digital signal processor; moreover, the baseline wanders in ECG signal are eliminated by using the DENLMS-based adaptive filtering method. Features are RR interval metrics that are produced from the deflection positional information. Two R peak values in consecutive beats and their differences are calculated for determining the RR interval [22]. The heart rate is calculated by using the below equation as,

$$H_{rate} = \frac{60}{RR_{interval}} \ \text{beats per minute} \tag{23}$$

Right bundle branch block (RBBB), which is a delay in conduction inside the right bundle branch, is one of the cardiovascular arrhythmias detected using these criteria. The presence of a right bundle branch block is shown by the presence of a conduction delay. The right bundle branch block is generated when the QRS duration is beyond 0.14 sec. Bradycardia is occurred due to the heartbeat going under 60 beats per minute (bpm). The rapid beating of the heart is greater than 100 bpm which leads to causing Tachycardia. The normal heartbeat range is 60–100 bpm with QRS width from 0.04 to 0.10 sec. The Ventricular Tachycardia has a heartbeat rate of 101–250 bpm with QRS width greater than 0.12 sec. The perfect RBBB has greater than 0.12 sec of QRS width and the imperfect RBBB has QRS width of 0.10 to 0.12 sec.

3.2.1. Procedure to extract QRS complex from the actual ECG signal

The ECG signal normally comprises three main components such as the P-wave, T-waver, and QRS complex. The QRS complex mainly contains crucial information regarding the heart state. The QRS complex identification is also an important problem in the proposed research. The noises such as poor electrode contact, muscle contraction, power line interference, body movement, and baseline wandering due to respiration are corrected by selecting appropriate filters. The subsequent ECG signals are first partitioned into a window frame of 10 s and it is normalized to obtain the amplitude value. Utilizing the first derivative zero crossings, the local maximum sets are found and they are normalized by applying a threshold value of 0.9.

After the P-wave, there is a downward deflection known as the Q wave and the immediate upward deflection is labeled as the R wave. The downward deflection that occurs after the R wave is said to be the S wave. The QRS complex mainly appears for 0.06–0.10 s in a person's heartbeat and it appears in shorter intervals for an exercising patient and a child. The baseline wander noise is enhanced via a high pass filter which is a second-order Butterworth filter with a cutoff frequency set as 0.83 Hz. The power line interference is attenuated by passing this filter through a stop band filter and the signal is passed via a low pass and high pass cascaded band pass filter. The low pass cut-off frequency is set as 11 Hz. The energy in the range of 10 Hz is extracted via the high pass filter and the QRS energy mainly lies in the 5–15 Hz interval. The 50 Hz power interference and the higher frequency ranges are eliminated via the low pass filter. After the QRS complex is detected by setting an appropriate threshold value, the signal is processed by the DCT and FFT techniques.

3.2.2. Discrete Cosine Transform (DCT)

A set of N samples is used to compute the DCT (Discrete Cosine Transform) [23] of an ECG waveform.

$$D(v) = \beta(v)\sum_{n=0}^{N-1} y(n)\cos\left[\frac{\prod(2n+1)v}{2N}\right] \quad for\ \ v = 0, 1, 2, ..., N-1 \tag{24}$$

The mathematical representation of inverse DCT is.

$$y(n) = \sum_{V=0}^{N-1} \beta(v)D(v)\cos\left[\frac{\prod(2n+1)v}{2N}\right] \quad for\ \ n = 0, 1, 2, ..., N-1 \tag{25}$$

$\beta(v)$ is expressed as.

$$\beta(v) = \begin{cases} \frac{1}{\sqrt{N}} & for\ v = 0 \\ \frac{2}{\sqrt{N}} & for\ \ v \neq 0 \end{cases} \tag{26}$$

In equation (26),$D(v = 0)$ is the mean of the ECG beat recordings, which is called the DC coefficient. DCT, like other transforms, produces energy compaction. DCT's cosine basis is orthogonal to each other.

3.2.3. Fast Fourier Transform

In R Peak detection [22] the first stage involves extracting the signal of interest is formed using appropriate metrics. Each beat's Q, R, and S deflections were detected before these could be separated from the ECG signal. This is done with the following methods using an algorithmic script. The fundamental challenge is to identify the R Peak because once located, the R-peak may be used to easily locate the S and Q points. The R peak may be easily identified due to the distinctiveness of the QRS complex and unique properties even in the most distorted ECG readings. As a result, it provides a starting point for identifying ECG features. The deflections were calculated using a digital signal processing approach. The below-given equation is used to apply Fast Fourier Transform (FFT) to the ECG signal.

$$Y_l = \sum_{n=0}^{N-1} ynf^{\frac{-2\prod_j}{N}nl},\ l = 0, ..., N-1 \tag{27}$$

The below equation is used to apply the inverse FFT to the generated signal.

$$Y_l = \frac{1}{N}\sum_{n=0}^{N-1} ynf^{\frac{-2\prod_j}{N}nl}, l = 0, ..., N-1 \tag{28}$$

l represents the discrete-time index, and N represents the total number of ECG signal samples that will be processed. The accuracy of the R-point, as estimated above is determined to be reasonable. "A negative wave at the commencement of the QRS complex, and the valley is characterized as Qpoint," according to the Q wave. Therefore, the Q point is located as the local minimum in a small (about 0.05 sec) window to the left of the R-point calculated in the equation below.

$$\frac{dx}{dy} < 0\forall y < y(t) \quad and \quad \frac{dx}{dy} > 0\forall y > y(t) \tag{29}$$

The S-point is initially calculated as the point at which the slope crosses from negative to positive zero after the R-point in equation (29). It was discovered that it may be more precisely put as the local minimum in a 0.05-sec window before the aforementioned estimate.

$$\frac{dx}{dy} < 0\forall y < y(s) \quad and\ \frac{dx}{dy} > 0\forall y > y(s) \tag{30}$$

This must be true for a 0.05 sec s window length.

3.3. Modified Faster R-CNN structure using the HBA algorithm

Based on the original Regions with Convolutional Neural Networks (R-CNN) target detection algorithm, which is quicker, to increase the detector's performance certain changes have been done such as establishing anchors the HBA algorithm is introduced and removing the overlapping detection boxes using soft non-maximum suppression. The anchor of the Faster R-CNN target detector is a crucial parameter. The number and shape of the anchors have an impact on the detector's accuracy and efficacy. The default aspect ratio for the Risk Priority Number (RPN) is 512^2, 256^2, and 128^2, with default aspect ratios of 2:1,1:2, and 1:1.This may be combined to create nine different types of anchors. The default size of anchors, however, does not satisfy the real scenario for dissimilar data sets. Incorrect anchors not only slow down network integration speed but also have an impact on the computation of the error function. In this part, the typical Faster R-CNN technique of manually setting the anchor is replaced by the K-means clustering algorithm. The majority of actual ECG images are of comparable shape and size. The dispersion of actual ECG image dispersed. Hence, manually determining the suitable anchor is quite challenging.

The bounding box and the anchor are present in the dataset as they may be overlapped if the IoU mean value is larger than 0.5. The measurement values of IOU are enhanced due to the increasing number of anchors. Moreover utilizing more anchors which will increase the cost of calculation and causes overfitting that will lead to detector performance degradation. The anchor position is unpredictable. Therefore, the height and width are only utilized for the computation. The eight anchoring values obtained by the HBA algorithm is (30, 25), (55, 44), (37, 35), (31, 53), (28, 37), (34, 87), (25, 21), and (25, 29).The anchors are based on targeting the features and verifying the k-means clustering algorithm effectiveness. In the final detection results, a similar ship target is included in the multiple target detection boxes (DB). The distance among the targets is extremely close, the existing algorithm will remove the overlapping DB is greater than the threshold of IoU which leads to misplaced target detection. For extracting the most appropriate target detection the Honeybadger algorithm (HBA) is used and it is expressed as;

$$t_j = \begin{cases} t_j, & IoU\left(N, c_j\right) < O_u \\ t_j \times e^{\frac{IoU\left(N,c_j\right)^2}{0.5}}, & IoU\left(N, c_j\right) \geqslant O_u \end{cases} \tag{34}$$

The current category of DB is represented by t_j the highest score in the DB is denoted by$N.IoU\left(N, c_j\right)$ indicates their IoU and HBA threshold is represented byO_u.

4. Result and discussion

A ten-fold cross-validation strategy is utilized in this phase, with the datasets being divided into ten segments. This is repeated for 10 rounds, with the testing proportion varying each time. The results of all rounds are aggregated and reported as the system performance. Also, the validation loss is minimized by setting the learning rate to 2 × 10–5. A random uniform method is applied to set the biases value to zero and initialize the weights. The proposed model is implemented on HP All-in-One 24-dp0888in PC with an Intel Core i5 processor along with 32 GB RAM and it was implemented based on Keras. Table 1 lists the

Table 1
Experimental settings.

Parameter	Description
Learning rate	0.001
Total number of epochs	70
Detection threshold value	0.5
Number of the honey badger	0.5
Honey badger ability	6
Constant	2
Number of epochs in each iteration of the training process	300
Batch size	32
Learning rate	2 × 10–5

parameters and their descriptions.

4.1. Dataset Description

4.1.1. BIDMC Congestive heart Failure Database

BIDMC Congestive Heart Failure Database is taken from the physio net [24,25,34]. This database contains 15 participants' long-term ECG records. Here, 4 women ranging in ages from 54 to 63 and 11 males ranging in ages from 22 to 71. The dataset mainly contains the information of patients affected with severe congestive heart failure and grades them based on the classes present in the New York Heart Association (NYHA) related functional classification of Heart Failure. The heart disease classes in the dataset are mainly NYHA class 3(moderate) and class 4 (severe). This set of participants was part of a wider study group that milrinone, an oral inotropic drug, was administered before normal medical treatment. More information regarding the bigger study group is available in the first reference mentioned above. Several other studies have used these records and additional notes are given below. Individual recordings are approximately 20 h long and consist of two ECG signals, each with a sample of 250 samples per second in the range of ± 10 millivolts with 12- bit resolution. Beth Israel Hospital in Boston made the initial analog recordings with a bandwidth of 0.1 Hz to 40 Hz recorded using ambulatory ECG recorders. Annotation files with ECG suffix are generated using auto detector are not manually corrected.

4.1.2. MIT-BIH normal Sinus Rhythm Database

The normal ECG recordings are obtained from this dataset [26,35] which comprises a total of 18 long-term ECG recordings. This dataset consists of the samples of persons who do not have high arrhythmias and they are both men and women within the 20–50 age limit. To increase the size of the dataset we also utilized 30 ECG recordings obtained from a nearby hospital. The dataset is partitioned into two parts where 80% of the data is used for training while the remaining 20% is used for testing.

4.1.3. Randomized clinical cohort dataset

This dataset [33,36] consists of a total of 800 recordings acquired from a 24-hour dynamic 12-lead ECG. The 800 recordings consist of 200 whole courses of atrial fibrillation(AF), 200 paroxysmal AF (PAF), and 400 NAF readings.

4.2. Performance metrics

Some of the performance metrics such as accuracy (A), positive predictive value ($Positive_{PV}$), specificity (SP), sensitivity (S), are applied to evaluate the efficiency of the proposed classifier. The mathematical expression for each metric is given below. The term $True_P$, $True_N$, $False_P$, $False_N$ in the equations represents true positive, true negative, false positive, and false negative respectively.

$$A = \frac{True_P + True_N}{True_P + True_N + False_P + False_N} \tag{35}$$

$$Positive_{PV} = \frac{True_P}{True_P + False_P} \tag{36}$$

$$SP = \frac{True_N}{False_P + True_N} \tag{37}$$

$$S = \frac{True_P}{True_P + False_N} \tag{38}$$

$$DER = \frac{False_N + False_P}{True_P + False_N} * 100 \tag{39}$$

4.3. Comparative analysis

Table 2 shows a comparison of various methods, as well as the proposed method, in terms of accuracy, positive predictive value, specificity, and sensitivity. The memory consumption is computed in terms of size and the memory consumed by different techniques to execute the operations is presented in Table 2. The proposed method is compared with Deep Convolutional Neural Network (DCNN), Deep Multi-Scale Fusion neural network (DMSFNet), Convolutional Bi-Directional LSTM (Long Short-Term Memory), and Support Vector Machine (SVM) respectively. The proposed method has attained higher accuracy of 98.65% than existing methods. A higher sensitivity rate is achieved by the proposed method compared to existing methods like DCNN, DMSFNet, CBDLSTM, and SVM respectively. A lower sensitivity rate is achieved by SVM. When compared to other approaches, the proposed method has a high PPV rate of 97.81%. The PPV rate of the SVM algorithm is just 83%. The DCNN method has a high PPV rate when compared with DMSFNet, CBDLSTM, and SVM methods. Among all methods, the proposed method has a high specificity rate of 98.5% and the SVM method has a very low specificity rate. The memory consumption of the proposed model is also low due to the usage of DCT and FFT for compression.

Table 3 compares the proposed method's convergence time to that of different existing approaches such as DCNN, DMSFNet, CBDLSTM, and SVM. The convergence time of the proposed method is 0.024 s which is low compared to others. The convergence time of DCNN, DMSFNet, CBDLSTM and SVM are 0.869 s, 0.065 s, 161.87 s and 0.033 s respectively.

Fig. 3 represents the testing and training accuracy curve of the proposed method. The graph is plotted between Epoch and accuracy rate. From the figure, when the epoch value increases, the testing, and training data also increase thereby error is minimized. Therefore, the proposed method offers higher performance than the conventional techniques. Both training and testing curve increases with respect to an increase in Epoch value.

The values of different parameters such as mean, mean square value, power spectral density, and standard deviation are tabulated in Table 4. The obtained values in the BIDMC Congestive Heart Failure dataset are as follows: mean value is $2.9347e^{-015,}$ the mean square error rate is 0.0081, power spectral deviation is 2.9934 and the standard deviation is

Table 3
Analysis of convergence time.

Techniques	Convergence time
Proposed	0.024 s
DCNN	0.869 s
DMSFNet	0.065 s
SVM	0.033 s
CBDLSTM	161.87 s

Table 2
Comparative analysis of various methods.

Methods	Accuracy (%)	Positive Predictive Value (%)	Specificity (%)	Sensitivity (%)	Memory consumption in terms of Size
Proposed	98.78	97.81	98.5	98.2	625 KB
DCNN	96.2	95.25	93.53	97.1	50.2 MB
DMSFNet	92.65	92.05	90.75	93.53	1976 KB
SVM	88.5	89.53	87.53	90.05	8 MB
CBDLSTM	85.35	86.5	84.05	87.77	24.4 MB

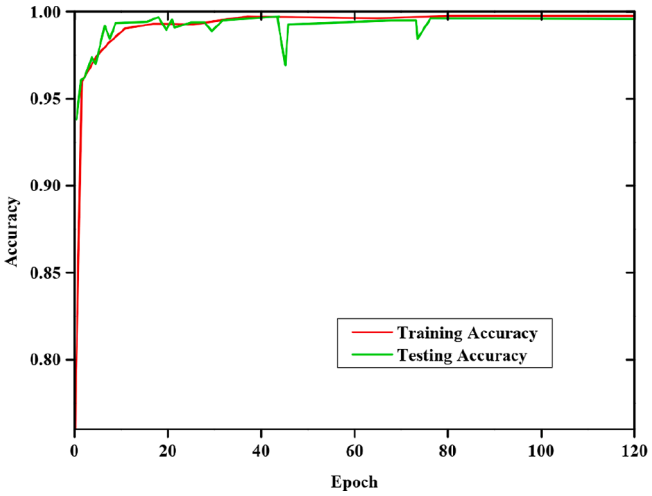

Fig. 3. Testing and training accuracy curve.

Table 4
Parameter settings of the ECG samples in the BIDMC Congestive Heart Failure dataset.

Parameters	BIDMC Congestive Heart Failure Database
Mean	$2.9347e^{-015}$
Mean Square Error	0.0081
Power Spectral Deviation	2.9934
Standard Deviation	0.0293

0.0293.

The classification performance of the proposed method for 10-fold is evaluated and tabulated in Table 5. The metrics like accuracy, positive predictive value, specificity, and sensitivity are calculated for each fold.

Figureeee 4 Fig. 4(a)-(j) represents the loss curve obtained for 10fold cross-validation. The graph is plotted between the number of iterations and the number of loss values.

4.4. Discussion

The state-of-art techniques show the advancement of the deep learning techniques in visual analysis. The main advantage of these techniques is their capability of simplifying a feature extraction process and presenting an end-to-end classifier without any manual intervention. The deep learning techniques are also capable of solving the multiple arrhythmia detection from the ECG signals. CHF is often a complicated disease that affects the lifespan of a human by minimizing the heart pumping rate and blood filling capacities. The main challenge associated with recognizing the CHF in ECG is that they require long or short-term RR interval data. Hence this paper presents a novel architecture named HBA-FRCNN to clearly distinguish the normal and abnormal heartbeat rhythms. The ECG signal comprises noise which increases the complexity of identifying the QRS complex. Hence this paper utilizes the FFT and DCT techniques to increase its robustness toward the noise. In this way, the proposed HBA-FRCNN model is trained without noise.

Table 5
Comparative analysis of the proposed HBA-FRCNN in terms of different evaluation metrics.

10-fold	Accuracy (%)	Positive Predictive Value (%)	Specificity (%)	Sensitivity (%)
1	98.84	98.94	98.04	98.41
2	98.93	98.57	98.39	98.09
3	98.67	96.82	98.86	98.97
4	98.33	98.71	98.67	98.15
5	98.19	98.15	97.10	98.59
6	98.96	98.73	98.88	98.38
7	97.46	97.21	98.57	98.78
8	98.86	98.89	98.48	98.29
9	98.61	98.67	98.79	98.14
10	98.78	98.07	98.75	98.87

The proposed model offers a high sensitivity value of 98.47% which is crucial for a screening tool. The PPV value is also high for every heart disease class thus minimizing the needless fear of the patients in their ongoing diagnostic procedure and the high cost associated with different procedures. The performance of the proposed HBA-FRCNN model is evaluated using the confusion matrix for the two datasets' namely MIT–BIH arrhythmia database and the BIDMC dataset. The confusion matrix is mainly an N × N matrix used to evaluate the performance of the classifier where N is the total number of classes in the dataset. Initially, the classes such as Cardiac Arrhythmias (ARR), Congestive Heart Failure (CHF), and Normal Sinus Rhythm (NSR) are classified using the proposed model and the results are shown in Table 6. The ARR mainly denotes the abnormal heart rate which is caused due to various etiologies such as abnormal impulse origination, etc. CHF is congestive heart failure due to a high level of triglyceride or cholesterol in the blood. The NSR is the normal heartbeat of a healthy person and it is the rhythm that emerges from the sinus node. The proposed model classifies a total of 99% of ARR classes accurately and only 1% of ARR classes are misclassified as CHF. As per the details shown in Table 6, the proposed model offers an accuracy of 100% for the CHF class and it shows our model's reliability in predicting congestive heart failure accurately. The confusion matrix for the BIDMC dataset is presented in Table 7, where the proposed model offers an accuracy of 98% and 97% for the CHF severe and CHF moderate classes.

The performance of the proposed HBA-FRCNN model is compared with different optimization algorithms such as hybrid Grey Wolf optimized Artificial Bee Colony (HGWOABC) algorithm [28], Bidirectional LSTM optimized using the Bayesian optimization (BiLSTM-BO) [29], and Coy-Grey Wolf optimization-based deep convolution neural network (Coy-GWO-based Deep CNN) [30] in terms of positive predictive value (PPV) and DER. The results shown in Table 8 demonstrate the effectiveness of the proposed model in terms of PPV and DER when evaluated using the MIT-BIH dataset and compared with different techniques. The reason for the higher accuracy when compared to the state-of-art classifiers is the usage of the FFT and DCT techniques in eliminating the noise of the ECG signal and accurate placement of the target detection box and anchor via the FRCNN.

5. Conclusion

This paper presents an HBA-optimized Faster R-CNN architecture for heart disease prediction from the ECG signals. Heart disease mainly occurs from abnormalities in the ventricular filling, myocarditis, congenital heart disease, and abnormal blood ejection for systematic circulation. Heart disease patients have different symptoms such as fluid retention, low exercise tolerance, fatigue, dyspnea, etc. The input ECG signals are initially preprocessed using the Delayed Normalized Root Mean Square (DNLMS). DCTand FFTare used to extract the features such as ventricular heart rate. The HBA algorithm is used to optimize the Faster RCNN architecture for removing the overlapping detection boxes and minimizing the number of anchor boxes used to enhance the detection accuracy. The performance metrics such as accuracy, positive predictive value, specificity, and sensitivity are calculated and compared to detect the normal and abnormal ECG signals (chronic heart failure). The proposed methodology offers improved performance in terms of accuracy, sensitivity, positive predictive rate, and specificity values than existing methods like DCNN, DMSFNet, CBDLSTM, and SVM. The convergence time of the proposed method was compared with existing methods where the proposed method has a very low convergence time. The simulation results conducted on the BIDMC Congestive

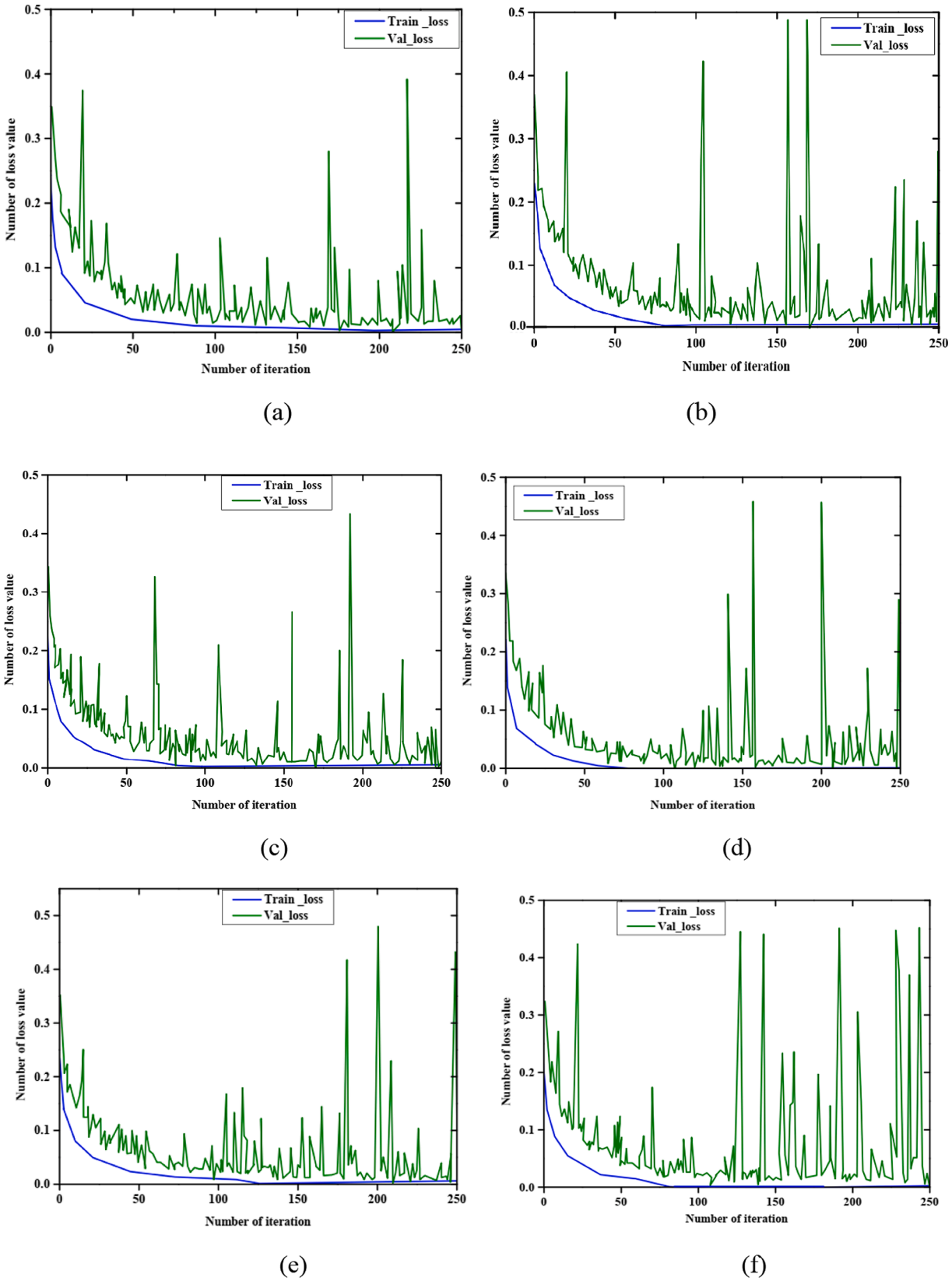

Fig. 4. (a)-(j): Loss curve obtained for 10fold cross-validation. (a)-(j) Fold1- Fold 10. Cardiac Arrhythmias (ARR), Congestive Heart Failure (CHF), and Normal Sinus Rhythm (NSR).

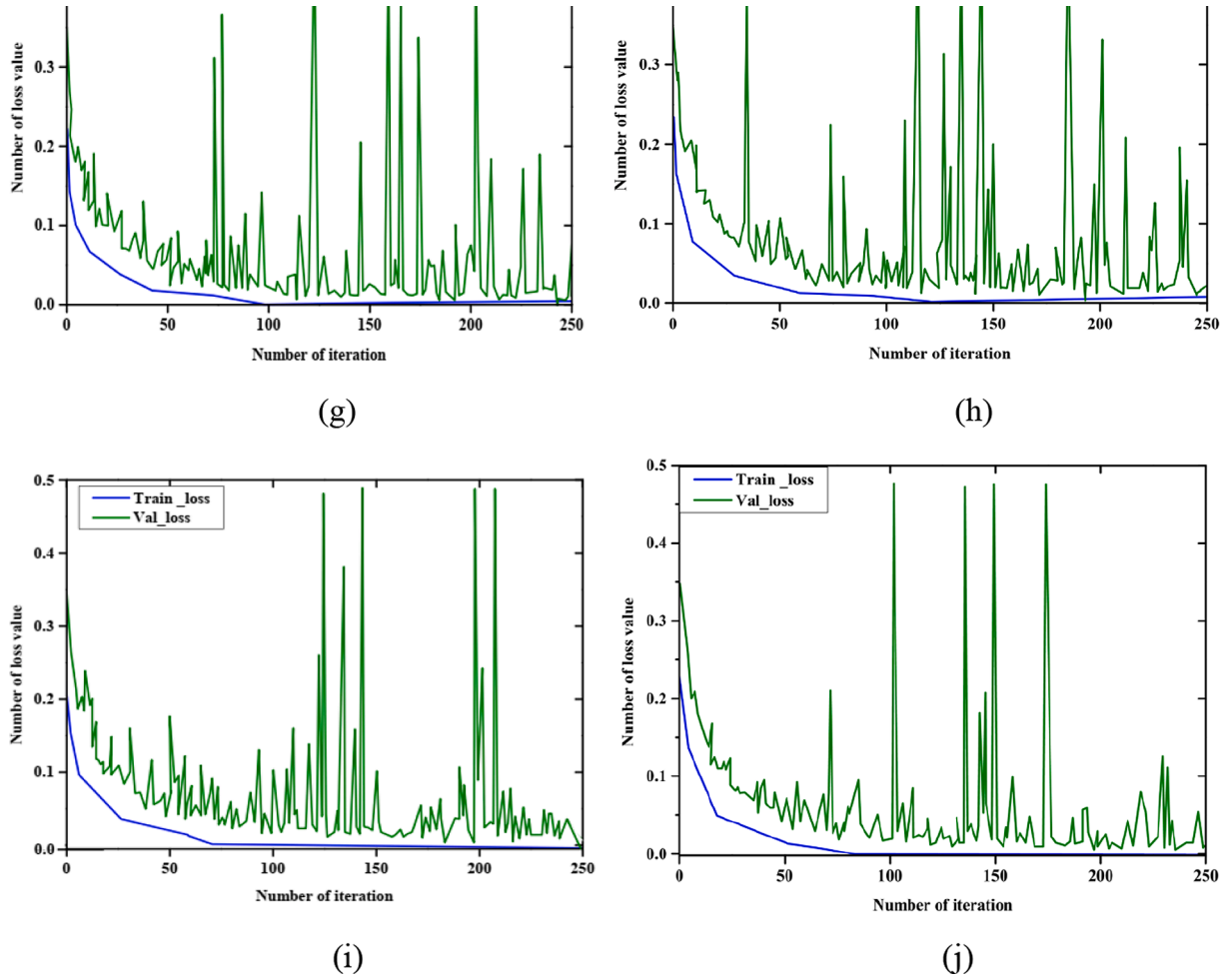

Fig. 4. (*continued*).

Table 6
Confusion matrix for the MIT-BIH dataset.

Class Name	ARR	CHF	NSR
ARR	99%	1%	0%
CHF	0%	100%	0%
NSR	2%	0%	98 %

Table 7
Confusion matrix for the BIDMC dataset.

Class Name	**CHF** (severe)	**CHF** (moderate)
CHF (severe)	98%	2%
CHF (moderate)	3%	97%

Table 8
Performance evaluation using DER and PPV rate.

Techniques	PPV (%)	DER(%)
BiLSTM-BO [29]	97.15	0.39
HGWOABC [28]	98.12	0.38
Coy-GWO-based Deep CNN [30]	98.54	0.34
proposed HBA-FRCNN model	99.11	0.24

Heart Failure Database demonstrate the effectiveness and the feasibility of the proposed methodology in congestive heart failure detection. In the future, we plan to implement this work in smartwatches to monitor the irregular heartbeat of the patients in real-time and offer a timely diagnosis. The proposed model classifies 99% of the ARR class correctly and only misclassifies 1% of ARR classes incorrectly. The convergence time of DCNN, DMSFNet, CBDLSTM, and SVM are 0.869 s,0.065 s, 161.87 s and 0.033 s respectively. The proposed model offers a faster convergence rate of 0.024 s The limitation of this model is that its generalizability is not evaluated in terms of photoplethysmography signals and slow arrhythmias. We plan to overcome this limitation in the future, by analyzing the model's accuracy in a large photoplethysmography dataset which comprises different arrhythmia types.

Availability of data and material

The data that support the findings of this study are openly available in [MIT-BIH Normal Sinus Rhythm Database and Randomized Clinical cohort dataset], reference number [27, 38 and 36, 39].

CRediT authorship contribution statement

S. Irin Sherly: Conceptualization, Methodology, Software. **G. Mathivanan:** Data curation, Writing – original draft.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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