

Analysis of ECG Arrhythmia for Heart Disease Detection using SVM and Cuckoo Search Optimized Neural Network

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Abstract

This paper tried to address several topics concerning the analysis, synthesis and compression of the electrocardiogram signal (ECG) using the MIT database. We detect the R-wave by identifying the location of each interval delineating a QRS complex using unbiased and biased estimators. In the second part of the work, we segmented the signal into RR periods constituting the vectors of a data matrix, where we extracted its main components in order to reduce the size of the cardiac information, and then further reduced in addition the size by the use of a threshold on the signal. Then the classification is done for automatic detection of heart disease using Support Vector Machine (SVM) and Cuckoo Search Optimized Neural Network. ECG beats with 4 types of abnormalities (RBBB, APC, PVC and LBBB) from ECG records is retrieved from the MIT-BIH arrhythmia database. Analysis of the different groups shows the overall recognition performance was 99.50%. The worst is 99.63% for the RBBB class.

Keywords: Cuckoo Search; Cardiovascular disease; Electrocardiograms; Neural Network; QRS; Support Vector Machine.

1. Introduction

Cardiovascular disease (CVD) is a major public health problem. They come top of medical causes of death in India. According to WHO (World Health Organization), heart attacks and strokes are responsible for more than 80% of cardiovascular deaths. There are many risk factors: tobacco, sedentary lifestyle, obesity, high blood pressure, diabetes and genetic factors.

The heart, the central organ of the cardiovascular system, can be affected by many diseases that can be either benign, like some tachycardia's for example, or very serious, such as myocardial infarction that causes 10% of deaths worldwide. Due to the scale of the problem, the follow-up of patients at risk becomes essential. Minor arrhythmias inform the physician about the patient's cardiac status. They must be detected in particular to prevent possible degeneration in severe arrhythmias [1].

The ElectroCardioGramme (ECG) is the most commonly performed examination because it is quick to put in place, inexpensive and above all non-invasive and therefore very inconvenient for the patient [2].

The electrocardiogram is a graphical representation of the electrical potential that controls the muscular activity of the heart. This potential is collected by electrodes placed on the surface of the body. It is presented as a series of repetitive (wave) deflections, each representing a phase of functioning of the heart. Each visible distortion

on these waves can be attributed to cardiac dysfunction or arrhythmia.

Cardiac arrhythmias mainly have their origins in the birth of the cardiac stimulus or in the conduction of the depolarization wave through the myocardium (path followed by the depolarization wave from its point of electrical activation).

One way to detect cardiac disorders is to collect the cardiac electrical signal (ECG) by sensors and then analyze it. This analysis presents both practical and theoretical issues for current research in pattern recognition and medicine. The objective pursued through this paper is to propose new methods of recognition of cardiac arrhythmias to help the doctor to read long-term recordings.

The ECG is very often supplemented by a similar 24-hour examination called "Holter", in which the patient can go about his or her usual activities. The main advantage of Holter recording over the short-term ECG is that it allows the detection of sporadic events that do not necessarily occur during the few seconds of ECG recording performed in a hospital setting, when the patient is at rest [3-6]

In the case of the recognition of cardiac arrhythmias, the first step is to treat the raw signal coming from an often noisy Holter recording: to filter it to extract the useful signal, to transform it if necessary in the frequency domain or in the domain time scale to locate and segment areas of interest [1]. These allow us to quantify and describe each beat. Note that these descriptors are those usually used by the cardiologist to make his diagnosis. At this point, each

beat must be represented by a vector of carefully selected characteristics for the discrimination between a normal beat and a pathological beat [7]. Several biomedical signal processing techniques are presented in [22]-[37].

In the second step, we consider that all the beats of the study base are vectors of the same size to be introduced at the entrance of a classifier. Classifier learning is done on a subset of beats previously identified by a doctor. It is clear that the more the first step is carried out rigorously or, in other words, the more the descriptors are relevant to the desired property, the more the second step is seen to be efficient and simplified.

2. Cardiovascular System

The cardiovascular system also called circulatory system ensures the blood circulation in a continuous way in the body. It allows oxygen and nutrients to be fed to the cellular tissues and waste to the kidneys and carbon dioxide to the lungs. This system is composed of an organ pump, the heart, and a continuous and closed network of ducts that allow the transport of blood, vascular system (veins and arteries) [7].

In summary, it is a question of elaborating the framework in which the present project fits, reviewing the investigations carried out in the study and analysis of the biomedical signals, the electrocardiographic signals in particular, situating, in this way, the context in the will locate the present study.

To this end, and as a summary of the bibliographical references studied regarding the work on ECG signals, it is observed that a scheme commonly accepted in this process is shown in Figure 1, structured in several stages.

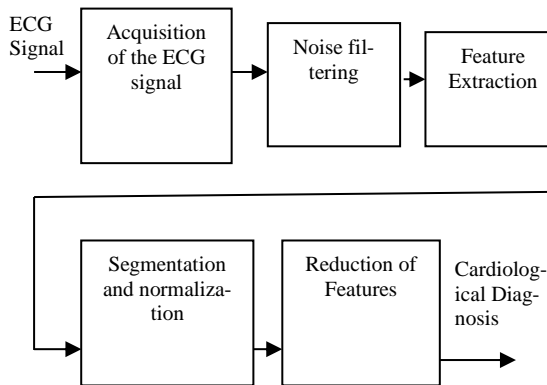


Fig. 1: General process developed in the analysis of the beats of a Holter ECG signal

3. Proposed Method

The method we propose [11] is based on the study of the spectral parameters of QRS complexes and a multiresolution analysis which allows us to consider the frequently content of normal beats and pathological beats.

3.1. QRS Complexes Estimation

To analyze the frequency content of QRS complexes, we selected four types of beats belonging to the most dominant classes of the MITDB database: normal beats (N), ventricular extra systoles (V), right and left branch blocks (RBBB and LBBB). Each class is represented by 200 beats selected in the MITDB database. The QRS complexes are extracted by means of a window of 180 ms length around the annotated positions of the R waves (50 ms before the R peak and 130 ms after the R peak). Each window then contains 64 samples for the sampling frequency 360 Hz.

3.2. Detection Algorithm

1. Decompose the ECG signal $f(t)$ up to 5 resolution levels.
2. Calculate $h = |\prod_{j=4}^5(d_n^j)|$
3. Location of QRS:

$$\begin{cases} \text{if } h(n) \geq 0.3 \cdot \max(h) \text{ then } n = \text{QRS candidate} \\ \text{otherwise } n \neq \text{QRS} \end{cases}$$
4. Suppose n and n' two selected consecutive positions, then:

$$\begin{cases} \text{if } |n - n'| < 36 \text{ then } n \text{ and } n' = \text{even QRS} \\ \text{otherwise } n \text{ and } n' \neq \text{even QRS} \end{cases}$$
 ($36 f_e = 100\text{ms}$ is the standard duration of a QRS complex)
5. A multiple detection in a 200 ms interval shall be deleted. This constraint has a physiological meaning: the refractory period is clearly greater than 200 ms.
6. Omitted beat search: If no beat is detected in a period equal to 1.5 times the current RR interval, the detection threshold is divided by 2 to check for any omitted QRS.

3.3. Classification using Support Vector Machine (SVM)

Our objective is to evaluate the performance of a binary classifier with rejection, we first retained the annotations of the American Heart Association (AHA) [13] and the practical recommendations of the AAMI standard to form two classes of beats (normal beats and ectopic beats)

- The positive class (P) represents ectopic beats, premature beats and some unknown beats.

- Negative class (N) represents the normal beats (about 70% of the study base) and some abnormal beats LBBB (Left Bundle Branch Block), Right Bundle Branch Block (RBBB).

According to the AAMI (American Association for Medical Instrumentation) guidelines, records (102, 104, 107, 217) containing beats from pacemakers are excluded from this study. Recordings not containing PVC beats (11 records) are also excluded [14]. We then have 33 recordings of interest. Note that no selection of signals is based on their quality.

Experimental Protocol: The conditions under which the classification tests are carried out must meet certain criteria. Thus all tests must be carried out in the same way.

Standardization of data: The learning and test data are structured as matrices. The number of rows represents the number of beats (or examples x_i) and the number of columns represents the number of characteristics y_j quantifying each beat. Each line thus represents a vector characterizing a beat.

These characteristics can be very different from one example to another. Their standardization is therefore necessary. This operation consists in bringing each characteristic (each column of the data matrix) to follow a reduced Gaussian distribution, that is to say of zero mean and of standard deviation equal to unity. The normalization formula is given by:

$$\tilde{y}_{ij} = \text{tansig} \left(\frac{y_{ij} - \bar{y}_j}{\sigma_{y_j}} \right) \quad (1)$$

Where y_{ij} is the characteristic component of the j^{th} characteristic. \bar{y}_j and σ_{y_j} are the mean and standard deviation of the j^{th} component of the feature vector and $\text{tansig}(n) = \frac{2}{[1 + \exp(-2n)] - 1}$.

3.4. Selection of Hyper-Parameters by Cross-Validation

The performance of an SVM technique is to a great extent subject to the determination of penalization parameters and kernel parameters. The optimal parameters are called hyper-parameters. In our case, the parameters to be optimized are: the penalty parameter C and the width of the Kernel expressed by σ . They are determined by a cross validation technique. Cross-validation is available in several sub-methods. The most common is the "k-Fold" method with typically $k \in [4, 10]$. It consists in sharing a validation set

composed of n examples in k equal parts. We then proceed to k learning experiments from examples. The remaining examples are used to test the rules learned and to evaluate the result. A cross-validation is applied according to the following algorithm:

1. Divide the validation set (VS) into k under balanced sets (same number of positive examples and even number of negative examples).
2. Solve the optimization problem (Learning) on the union of $k-1$ subsets.
3. Test on the k^{th} subassembly and calculate the mean squared error.
4. Repeat k times steps 3 and 4.
5. The division of VS generating the minimum error must be tested on a grid of values C and σ .

The pair (C, σ) corresponding to the minimum error is retained as a pair of hyper-parameters.

3.5 Cuckoo Search Optimized Neural Network

Back propagation neural network is a type of multi-layer feed forward network in which each layer is connected by transfer functions and can fulfils arbitrary nonlinear mapping [15]. It is widely applied in stock price, petroleum price, economic time sequence, network flow and other nonlinear areas and attained satisfactory performance. The structure of back propagation neural network is shown in Figure 2 [16].

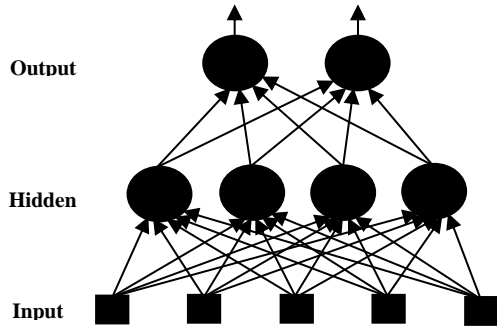


Fig. 2: Structure for back propagation neural network [16]

The basic learning process of the back propagation neural network algorithm is as follows [17]:

1. Initialize the connection weights w_{ij} , v_{jt} and threshold θ_j in the back propagation neural network.
2. Input the first learning sample couples to the back propagation neural network.
3. Compute the input u_j of each neural unit and the output h_j in the hidden layer. The equation is:

$$u_j = \sum_{i=1}^n w_{ij}x_i - \theta_j \quad (2)$$

$$h_j = f(u_j) = \frac{1}{1+\exp(-u_j)} \quad (3)$$

4. Compute the input l_t of each neural unit and the output y_t in the output layer. The equation is:

$$l_t = \sum v_{jt}h_j - \gamma_t \quad (4)$$

$$y_t = \frac{1}{1+\exp(-l_t)} \quad (5)$$

5. Compute the weights error δ_t which is connected to the neural unit t in the output layer.

$$\delta_t = (c_t - y_t)y_t(1 - y_t) \quad (6)$$

In the equation (6), c_t represents the expectation of the sample.

6. Compute the weights error δ_j which is connected to the neural unit j in the hidden layer.

$$\delta_j = \sum_{t=1}^q \delta_t v_{jt} h_j (1 - h_j) \quad (7)$$

7. Update the connection weights v_{jt} and threshold γ_t in the back propagation neural network.

$$v_{jt}(N + 1) = v_{jt}(N) + \alpha \delta_t h_j \quad (8)$$

$$\gamma_t(N + 1) = \gamma_t(N) + \beta \delta \quad (9)$$

8. Update the connection weights w_{jt} and threshold θ_j in the back propagation neural network.

$$w_{jt}(N + 1) = w_{jt}(N) + \alpha \delta_j x_i \quad (10)$$

$$\theta_j(N + 1) = \theta_j(N) + \beta \delta_j \quad (11)$$

9. Input the next learning sample and go to the step 3 until all of the samples are trained.

10. Back propagation neural network go to a new round of learning. If it meets the equation (12), the training of the back propagation network can be ended.

$$|\sum_{k=1}^q E_k| \leq \varepsilon \quad (12)$$

In the equation (12), ε represents the accuracy requirement of back propagation neural network, E_k represents the mean square error and the definition are as follows [18]:

$$E_k = \frac{1}{2} \sum_{t=1}^q (c_t - y_t)^2 \quad (13)$$

Before training the back propagation neural network, proper connection weights w_{ij} and v_{jt} of the back propagation neural network should be chosen. Normally the initialization is randomly which can cause the convergence is slow and the defect of local optimal solutions.

Optimization of Neural Network

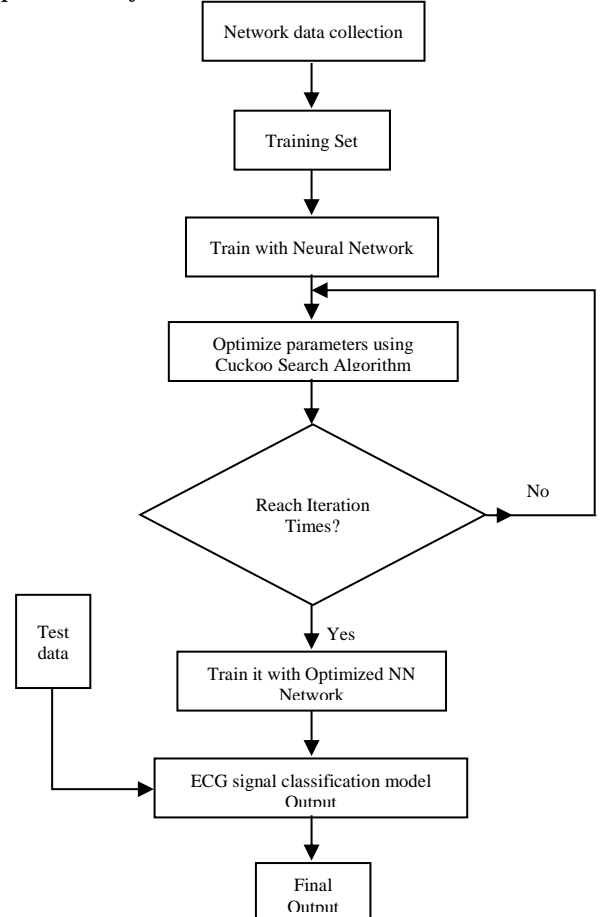


Fig. 3: Flow diagram for Cuckoo Search Optimized BP Neural Network based model

Cuckoo Search (CS) Algorithm

Cuckoo Search (CS) is a recent metaheuristic [19] that is inspired by the reproduction pattern of some cuckoo species. In fact, their reproductive strategy is characterized by the fact that females lay their eggs in the nest of other species (whose eggs are similar). These eggs can then be hatched by surrogate parents. On the other hand, when cuckoo eggs hatch in the host nest (they hatch more quickly), cuckoo chicks have the reflex to eject the host species eggs out of the nest and even mimic the cry of the host chicks for the purpose of being fed by the host species.

It may happen, however, that cuckoo eggs are discovered; in this case, the surrogate parents take them out of the nest, or abandon the nest and start their brood elsewhere. This metaheuristic is thus based on this parasitic behaviour of the species of cuckoos associated with a logic of displacement of the "Levy flight" type specific to certain birds and certain species of flies [19].

The CS algorithm is based on the following rules:

- Each cuckoo lays only one egg at a time and places it in a nest chosen randomly.
- The best nests with eggs (solutions) of high quality are kept for the next generations.
- The number of host nests is fixed and the egg laid by a cuckoo can be discovered by the host species with a probability $p_a \in [0, 1]$. In this case, the host bird either takes the egg out of the nest, or leaves the nest and builds a new one. For simplicity, this last hypothesis can be approximated by the replacement of a fraction p_a of n nests by new ones.

Levy Flight is a random walk class in which jumps are distributed according to the Levy distribution which consists of a power law with infinite variance and mean of the type:

$$Levy(\beta) \sim y = x^{-\beta}, 1 < \beta \leq 3 \quad (14)$$

In the case of CS, the use of Levy Flight improves and optimizes the search: new solutions are generated by a random walk of Levy around the best solution obtained so far, which accelerates the overall search Figure 3.

The generation of a direction can be made from a uniform distribution, while the generation of steps is more delicate. There are several methods to achieve this, but one of the simplest and most effective is to use Mantegna formulas to determine the pace [20]:

$$S = \frac{u}{|v|^{1/\beta}} \quad (15)$$

Where u and v are centered Gaussian distributions such as:

$$u = N(0, \sigma_u^2), \quad v = N(0, \sigma_v^2) \quad (16)$$

With,

$$\sigma_u^2 = \frac{\Gamma(1+\beta) \sin(\pi\beta/2)}{\Gamma((1+\beta)/2) \beta 2^{(\beta-1)/2}}, \quad \sigma_v^2 = 1 \quad (17)$$

Where $\Gamma(z)$ is the Gamma function.

$$\Gamma(z) = \int_0^{+\infty} t^{z-1} e^{-t} dt \quad (18)$$

Initialization of the Algorithm

The initial population consists of an N_H number of host nests generated randomly in the search space. Recall that the number of host nests, cuckoos and eggs are equal.

Assuming that the i^{th} host is represented by $X_i = (x_{i1}, \dots, x_{ij}, \dots, x_{in})$. Where n is the dimension of the problem, so each nest is generated by:

$$x_{ij} = X_{\min_j} + rnd(0,1) (X_{\max_j} - X_{\min_j}), j = 1, \dots, n, i = 1, \dots, N_H \quad (19)$$

The values of the corresponding cost functions are evaluated.

Description of the algorithm

Step 1: Global search

The first step is to do a global search. For this, we generate new cuckoo (solutions) tests from existing cuckoo (solutions) by making Levy Flight. This is to use the following evolution law for each cuckoo:

$$\left. \begin{aligned} X_{new\ i} &= X_i + \alpha \otimes Levy(\beta) \\ F_{new\ i} &= f(X_{new\ i}) \end{aligned} \right\}, i = 1, \dots, N_H \quad (20)$$

Where $\alpha > 0$ is the size of the displacement step which depends on the problem considered and such that $\alpha \approx O(L/10)$, where L is the characteristic scale of the problem considered. The \otimes product is the term product term.

In order to know where / if the new i^{th} cuckoo is going to drop an egg, he chooses randomly a host nest $X_j (j \neq i)$ of cost function F_j . The new cuckoo pond if:

$$F_{new\ i} < F_j \quad (21)$$

In this case, the solution $X_{new\ i}$ replaces the solution X_j in the population.

Step 2: Local search

New cuckoo eggs have a probability of being discovered.

If this is the case ($rnd(0,1) < p_a$), new eggs are generated. Several methods can be envisaged for this. For CS, the following is the case where hybridization between elements of the randomly selected population is carried out:

$$\left. \begin{aligned} X'_{new\ ij} &= x_{ij} + rnd(0,1)(x_{pj} - x_{mj}), j = 1, \dots, n, i = 1, \dots, N_H \\ F'_{new\ i} &= f(X'_{new\ i}) \end{aligned} \right\} \quad (22)$$

Where $m \in \{1,2,3, \dots, N_H\}$ and $p \in \{1,2,3, \dots, N_H\}$ such that $p = m$ are randomly chosen.

A selection identical to that of the previous step is then performed.

3.6. Pseudo-code of the Algorithm

The simplified pseudo code of the algorithm is given below.

Generation of an initial population of N_H host nests X_i

As long as the stopping criterion is not satisfied, repeat:

 Generate a cuckoo by Levy Flight (20) and evaluate its cost function F_i ,

 Randomly choose a nest X_j among the N_H host nests, if $F_i < F_j$

 Replace F_j with this new solution,

 End If

 A fraction p_a of the worst nests is dropped and others are generated instead (22), and make a selection.

 Identify the best X_{best} solution

End As long as

4. Simulation Results

4.1. Database Explanation

Since 1975, the laboratories of the Beth Israel Hospital in Boston and MIT have developed an MIT / BIH database, which was started to be distributed in 1980. This database contains 48 records extracted from a half hour of ambulatory records with two ECG pathways obtained from 47 subjects studied by the BIH arrhythmia laboratory between 1975 and 1979. Twenty-three registrations were randomly selected from a set of 4000 outpatient 24-hour records (60%) and non-hospitalized patients (40%) at the Beth Israel Hospital in Boston, the remaining 25 records were selected from the same registrations but of rarely observed arrhythmias that have clinical significance. The recordings were sampled at a frequency of $f = 360$ Hz with an 11-bit resolution over a range of 10 mV. Two or more cardiologists independently annotated each record, about 110,000 annotations were included with the database [21].

Table 1 and Table 2 represent the accuracy for each class using SVM and CS-Optimized Neural Network respectively.

Table 1: Result for SVM

Class	Sensitivity = $\frac{TP}{TP+FN}$	Specificity = $\frac{TN}{TN+FP}$	Accuracy = $\frac{TN+TP}{TP+FN+TN+FP}$
Normal	91.75%	100%	97.54%
RBBB	99.81%	95.07%	96.75%
APC	98.81%	99.21%	98.83%
PVC	97.59%	99.71%	99.59%
LBBB	98.27%	99.75%	99.46%

Table 2: Result for CS-Optimized Neural Network

Class	Sensitivity = $\frac{TP}{TP+FN}$	Specificity = $\frac{TN}{TN+FP}$	Accuracy = $\frac{TN+TP}{TP+FN+TN+FP}$
Normal	92.58%	100%	98.01%
RBBB	99.94%	97.13%	99.63%
APC	98.97%	99.57%	99.95%
PVC	98.44%	99.91%	99.96%
LBBB	98.73%	99.87%	99.98%

4.2. Results

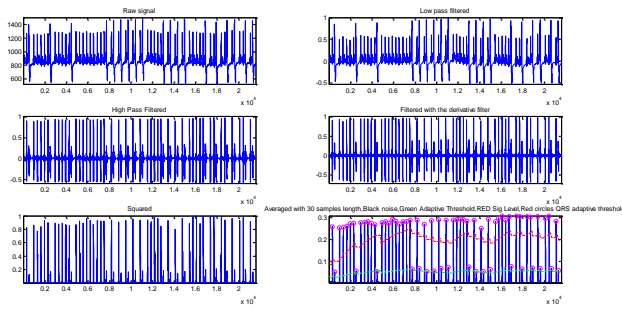


Fig. 4: Filtering of original Signal

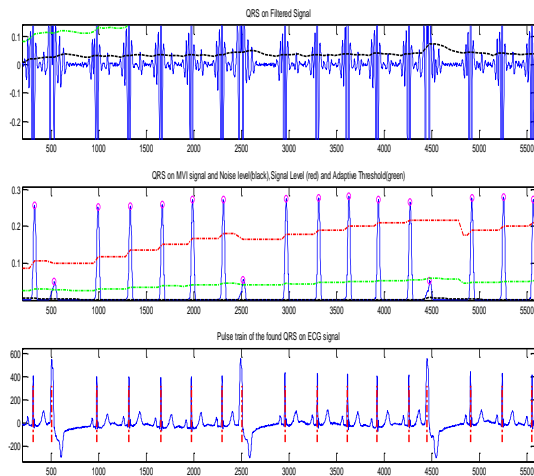


Fig. 5: QRS on filtered signal

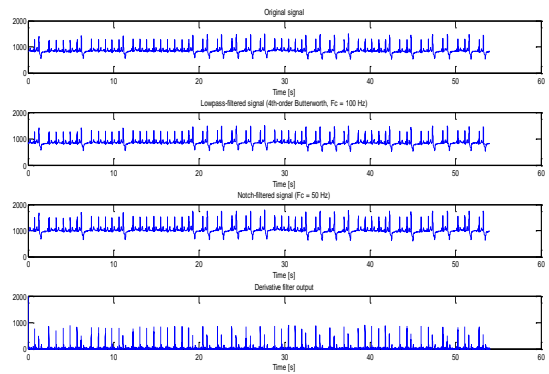


Fig. 6: Filter output

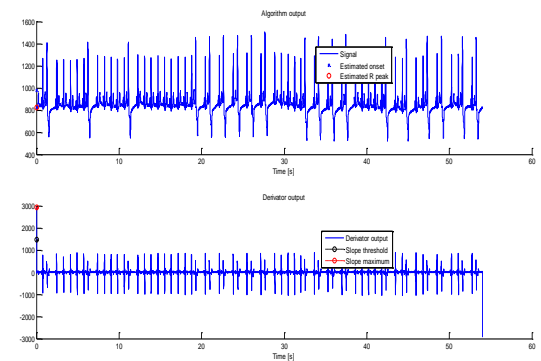


Fig. 7: Algorithm output

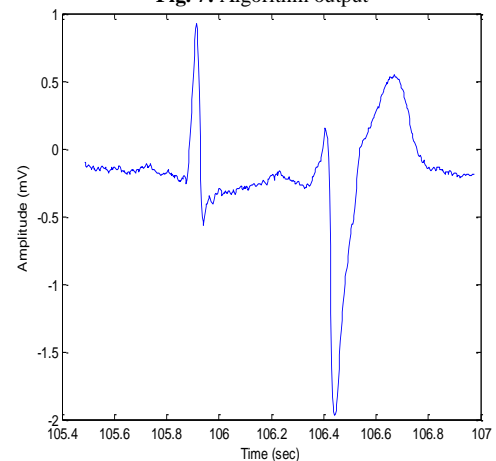


Fig. 8: Extracted QRS signal

5. Conclusion

The work presented in this paper consists mainly of two domains: signal processing and statistical learning. Signal processing techniques have allowed us to segment and represent each heartbeat by a vector of characteristics. Around these vectors, we constructed a decision rule that allows us to distinguish an ectopic beat from a normal beat. To do this, we chose to work with Neural Network method, a proven algorithm in terms of discrimination performance and generalization power. The algorithms developed were validated on the American Heart Association basis and the MIT-BIH database was severely noisy. A pre-processing step was then unavoidable. These pre-treatments have been performed in the time-scale domain because the signals suffer from non-stationary, particularly during the arrhythmia phases.

In the segmentation of cardiac beats, the presence of arrhythmias and a variety of atypical beats was constraining for the detection of R waves and the localization of QRS complexes. The detected QRS is further used as a feature extraction by using wavelet transform.

These features are trained with both the classifiers and accuracy achieved is 99.46% for SVM and 99.98% for CS-Optimized Neural Network.

We can also conclude that a large number of parameters do not necessarily provide the best result, but it is enough to use the most appropriate parameters, whatever they may be, to have a good performance. It may also be inferred that there is no better type of parameter for the classification of all heart diseases but each group of arrhythmias may have its appropriate parameters.

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