

Analysis of Electrocardiogram for Heart Performance Diagnosis Based on Wavelet Transform and Prediction of Future Complications

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Abstract

This paper aims to analyze the heart electrocardiograph (ECG) to diagnose the heart performance and predict any future complications. The authors utilize the MIT BIH database to obtain the original data. The discrete wavelet transform (DWT) is used to decompose the ECG signal and to reconstruct it. The means of different performance measures of the heart performance (QRS,RR,ST,QT,PR) are tested for their significance before comparing them to the limits of normal performance. Any abnormal measure is used to diagnose the corresponding disease(s). Prediction techniques are used to expect any future complications regarding the abnormal measure(s). Two methods of prediction are applied: the Linear Prediction Method (LPM) and the Grid Partitioning and Fuzzy c-mean Clustering based on Neuro-Fuzzy prediction.

Keywords: *Electrocardiograph (ECG), Heart Diseases Diagnosis, Wavelet Transform, Linear Prediction Method, Grid Partitioning Method, Fuzzy c-mean (FCM), Neuro-Fuzzy (ANFIS).*

1. Introduction

For the time being, the computerized systems are one of the most important systems for analyzing the biomedical electrical signals. This has become very important especially for understanding the real biological processes such as the electrical activity signal of the heart (i.e., Electrocardiography or ECG) or the electrical activity signal of the brain (i.e., Electroencephalograph or EEG) or the electrical activity signal of the muscles (i.e., Electromyography or EMG). Computerized techniques have many advantages in features extraction of the biomedical signals and this helps in diagnosing the diseases of the mentioned parts [1]. In this paper, we are interested in diagnosing the heart diseases.

Diagnosing the heart diseases depends on processing its beats information to extract some main features which are used in the diagnosis. These features represent the bioelectric signal generated by the processes of the repolarization and depolarization of the heart. Thus, the accurate detection of ECG depends on the values of a trial depolarization (P), the distance between the start of a trial depolarization and the start of ventricular depolarization (PR), the ventricular depolarization (QRS complex), the temporary pause of the ventricular electrical activity before repolarization (ST segment), the ventricular repolarization (T wave) and the

ventricular activity repolarization and depolarization (QT segment). Figure (1) shows these values [1-3].

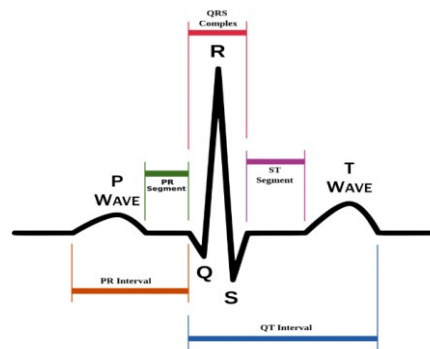


Figure 1. The ECG signal and its features' values

Many researchers have suggested computerized techniques to analyze the ECG signal and to diagnose the heart diseases. These techniques have utilized different tools such as the Neural Networks (NN), the Fuzzy Logic (FL), the Linear Regression (LR), ..., etc.

This paper uses these tools and combines them to analyze the ECG, diagnose the heart diseases, and predict any future complications. MATLAB software is used to simulate the results and the MIT BIH database is used for the processed data of the ECG.

The paper is composed of six sections. Section (1) gives an introduction and section (2) depicts a literature review. Section (3) explains the methodology and section (4) presents the results and section (5) discusses these results and compares them to a set of algorithms from the literature review. Section (6), gives some conclusions and some of the used references are listed at the end.

2. A Literature Review

All previous research on ECG processing focuses on three main stages for diagnosing the heart diseases. These are the preprocessing, the extraction, and the diagnosing stages [2].

The preprocessing stage aims to remove the noise from the original signal and reconstruct the signal values. This is based on using quantized coefficient digital filters [4,5]. Discrete wavelet transform (DWT) is an effective technique which is used for that purpose. It has excellent properties for time-frequency resolution. This means that the signal can be resolved in different frequency bands using different coefficients. This technique will be discussed and used in this paper [2, 6].

Many algorithms focus only on using QRS and/or R peaks for diagnosing the heart diseases. These measures are considered main features. Pan Tompkins suggested an algorithm for microprocessor based real time QRS based on the analysis of slope and amplitude of ECG signal where the width of QRS is used to compute the energy which helps in the diagnosis process [7, 8]

In [9], the authors described a Hilbert transform method for QRS. They discussed how to locate R peaks using the first differentiation of the ECG signal. The algorithm could detect the values of R, T and P with a high level of accuracy (e.g., 99.8%).

In [10], the authors analyzed the ECG signal to detect QRS accurately. They used the first derivative based method, introduced by Hamilton-Tompkins with the Hilbert transform

method (HT) for QRS detection with improving the threshold. The main target of this method is to reach the best performance to detect the normality and abnormality of the beats.

In [11], the authors introduced a survey about the main techniques of features' extraction with different types of algorithms of signal analysis. In [12], the authors discussed six methods of features' extraction of the ECG signal. The authors concluded that Eigenvector technique is the best method for performance analyze in the frequency domain.

Many algorithms have been proposed for prediction and classification of the heart features. In [13], the authors applied the fuzzy clustering algorithm (FCM) and used it for classifying the data. In [14], the authors discussed the prediction of ECG signal features based on neural network using a new method of time series prediction based on Linguistic fuzzy technique.

Adaptive filtering and morphology related analysis of time domain were presented in [15]. Analysis of time domain and frequency domain based on wavelet and other nonlinear transforms were presented in [16, 17]. The principal component analysis (PCA) based on discrete wavelet transform (DWT), and neural network classification were presented in [19].

In this paper, we use, combine, and modify some of the mentioned methods to analyze the heart performance information of its beats, diagnose any diseases, and predict any future complications.

3. Methodology

Our system is composed of three main units for the diagnosis of heart diseases (e.g., the preprocessing, feature extraction, and the diagnosis units) and a fourth unit is used to predict any future complications. Figure (2) gives the system block diagram and figure (3) gives the corresponding flow chart of the system. The block diagram is briefly described in the following subsections. Notice that our analysis uses the MIT-BIH database [20].

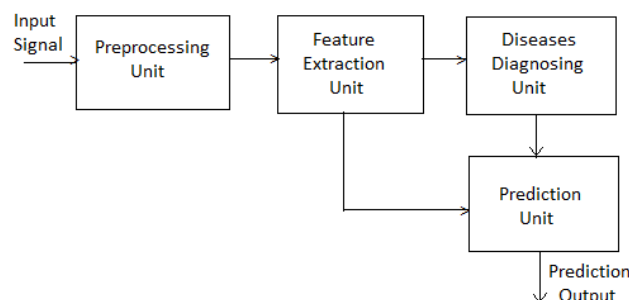


Figure 2. The system block diagram

3.1. The Preprocessing Unit

The ECG recording is affected by different types of noise and interference from other activities of the body. The signal is passed through a series of filters to compute its DWT. The signal threshold is important in denoising it. The main functions and advantages of DWT are [21-25]:

- Recovering the original signal from the noisy signal.
- Analyzing the signal in time and frequency domain.
- Representing the function in case it has discontinuities and sharp peaks more efficiently than using only discrete Fourier transform (DFT) [24-25].

The main procedures of this paper, based on DWT are:

- 1) Decompose the input signal by calculating the levels and number of layers of the wavelet decomposition as shown in figure (3).
- 2) Use the soft thresholding method as follows:
 - a) Choose thresholds for wavelet quantization coefficients.
 - b) Use a threshold for each level of the wavelet to remove every value of coefficient above of threshold value.
- 3) Use the inverse discrete wavelet (IDW) to reconstruct the signal for the decomposition levels[24].

In the following, we explain these processes.

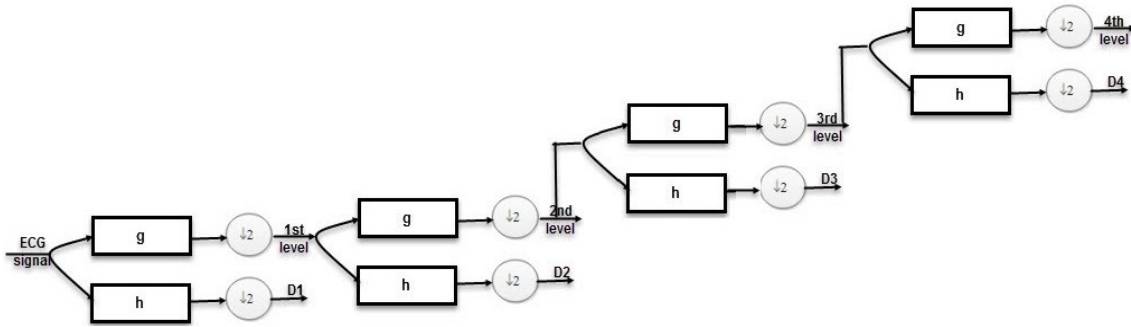


Figure 3. The decomposition process

3.1.1. Signal decomposition

The decomposition process is based on the coefficients of the wavelet (i.e., the details coefficients which are extracted from the high pass filter coefficients and approximation coefficients which are extracted from the low pass filter coefficients), according to equation (1). The signal is processed by dividing the frequency by 2^n times where n is the number of levels. In this paper, we use four levels of decomposition as shown in:

$$DWT(m, k) = \frac{1}{a} \sum_{n=0}^{N-1} s(n) g\left(\frac{k-b}{a}\right) \quad (1)$$

Where $s(n)$ is the ECG original signal, (a, b) are scaling parameters, m is decomposition level, $g(\cdot)$ is the mother wavelet function and N is number of sampling.

3.1.2. Thresholding

We obtain the threshold from the following equation:

$$T = \sigma \sqrt{2 \log N} \quad (2)$$

where T is the threshold, σ is the standard deviation of noise and N is number of samples.[26].

3.1.3. The signal reconstruction:

The signal reconstruction is the inverse process of the signal decomposition process and it also needs the same number of levels which are used in the decomposition process. This is done by using inverse discrete wavelet transform (IDWT) of equation (1). Using a simple description, it is upsampled by 2^n (where n is the number of stages) to obtain the

approximation and detail coefficients. Then, the approximation and detailed coefficients are added after passing them in a low pass filter and in a high pass filter as shown in figure (4) [19,26].

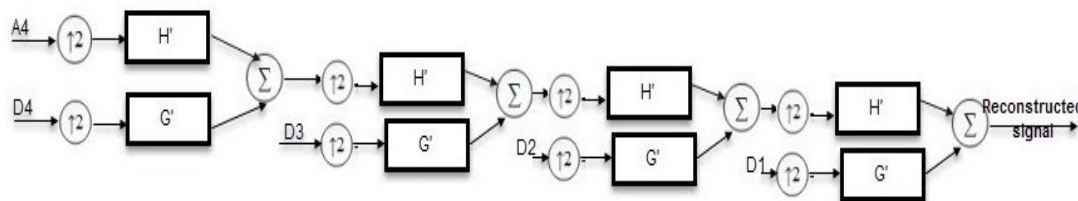


Figure 4. The reconstruction process

3.2. The Features Extraction Unit

This unit consists of two sub-units:

a) The features extraction sub-unit:

The main target of this sub-unit is to extract all features of the ECG signal (RR, QRS,PR,ST,QT). We extract the heart performance features according to the algorithm(s) which will be discussed in a later section [2,23].

b) Significance test sub-unit:

The obtained feature' means are tested for significance to help us to determine if the computed means can be significantly used to diagnose the heart performance or not.

This is done by computing the z-test value, based on the mean and standard deviation ratio (equation 3-a). Referring to the normal distribution table, we can obtain the table z_0 value. The computed and the tabulated z values are compared for significance. If the computed z value lies between the minus and positive tabulated values (equation 3-b), it indicates the significance of the mean value. The confidence levels and tabulated z values are shown in figure (5) [27].

$$Z = \frac{\bar{x} - \mu}{\sigma / \sqrt{n}} \quad (3-a)$$

$$\bar{X} - Z_{\alpha/2} \left(\frac{\sigma}{\sqrt{n}} \right) < \mu < \bar{X} + Z_{\alpha/2} \left(\frac{\sigma}{\sqrt{n}} \right) \quad (3-b)$$

Where μ is population mean value, σ is the standard deviations, n is length of data (feature), \bar{X} the mean value of features for test it.

- 1) For a 90% confidence interval: $Z_{\alpha/2} = 1.645$
- 2) For a 95% confidence interval: $Z_{\alpha/2} = 1.96$
- 3) For a 99% confidence interval: $Z_{\alpha/2} = 2.57$

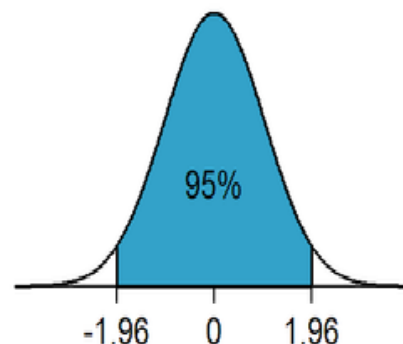


Figure 5. Confidence interval

3.3.The Diagnosis Unit

In this unit, the features' values, which were obtained in the extraction unit, are compared to some limits to determine if they are normal or not. In case, there is any one of these values which is abnormal, we can interpret this abnormality by diagnosing a corresponding disease. Table (1) gives the limit values of the heart features [28] and the algorithm of diagnosing the heart diseases based on its obtained features 'values is given in a separate coming section[20,28,29].

Table 1. Normal standard values of features

Name of Feature wave	Standard normal value (ms)
RR	0.6-1.2
ST	0.08-0.12
QRS	0.08-0.12
PR	0.12-0.2
QT	0.42-0.65

Table 2. Features of some heart diseases

Name of diseases	Rate	PR	QRS
Atrial Fibrillation	>350	Absent	Normal but may be widened
Ventricular Tachycardia	(100-250 bpm)	Not-measurable	Wide (>0.10 sec)
1 st Degree Heart Block	The underlying rate	Prolonged (>0.20 sec)	Normal (0.06-0.10 sec)
Supraventricular Tachycardia	Fast (150-250 bpm)	Normal (0.12 sec)	Normal (.10 sec)
Bundle Branch Block	The underlying rate	Normal (0.12-0.20 sec)	Wide (>0.12 sec)
Sinus Bradycardia	Slow (< 60 bpm)	Normal (0.12-0.20 sec)	Normal (0.06-0.10 sec)
Multifocal Atrial Tachycardia	(>100 bpm)	Variable	Normal (0.06-0.10 sec)

3.4.Prediction unit

It is important not only to diagnose the heart diseases but also to predict any complications in the future. Different remarkable prediction methods have been proposed to predict and classify the future features' values and consequently predict any future complications. From these methods, we discuss and apply: the linear prediction coding (LPC), the Grid partitioning method (GPM) and Fuzzy c-mean Clustering based on Neuro-Fuzzy prediction method [14, 31, 32]. Comparing the three methods, we got almost similar results.

3.4.1. Linear prediction coding method (LPC)

In LPC, predication of the future (estimated value is computed through a linear combination of the present value and history values. The formula of the estimated value is [33]:

$$E(X(n+1)) = -\sum_{i=0}^N a_i X(n-i) \quad (4)$$

Suppose that we want to predict the sample value $x(n+1)$ using a linear combination of the points, $x(n)$, $x(n-1)$, $x(n-2)$, ..., $x(n-N)$ which represent the present and history sample values respectively. It is important to mention here that the estimated sample value $\{E(X(n+1))\}$ and the actual computed future value $\{X(n+1)\}$ are generally not equal. This can be interpreted as a prediction error. The formula gives this error as:

$$\text{Err}(X(n+1)) = \{X(n+1) - E(X(n+1))\} / X(n+1) \quad (5)$$

Where $X(n+1)$ is the actual next value and $E(X(n+1))$ is predicted one. Notice that, we use the first 80% from the data set for training of equation (4) till the a_i coefficients are determined. The rest 20% of the data set are then used to predict the future values. This is repeated for all the features. The prediction LPC algorithm (1) which is applied in our work is given below.

3.4.2. Grid partitioning (GP) method

This method is based on Takagi–Sugeno (T.S.) adaptive neuro-fuzzy inference system (ANFIS) of prediction. ANFIS model is composed of if-then rules as well as couples of input-output. In the ANFIS architecture, both artificial network and fuzzy logic are used. Also, the algorithms of training and learning of the neural networks are applied. The fuzzy systems present problems such as:

- a) The if-then rules must be determined which is a problem of experience and knowledge acquisition and it is also time consuming.

Algorithm 1. The prediction LPC algorithm

Algorithm of LPC

Start

- 1) Input the present and history values of the features (QRS, PR, RR, QT, ST).
- 2) For each feature do the following:
 - Start loop
 - a) Use 80% of data to determine the coefficients of equation (4).
 - b) Use the rest 20% of data to estimate the future value of the feature.
 - c) Extract the next actual value of the feature.
 - d) Calculate the percentage errors between next actual values and the estimation values using the formula :

$$\text{Err} = \frac{\text{actual value} - \text{Estimated value}}{\text{actual value}} * 100\%$$
 - e) Compute the accuracy = 100 - Err
 - 5) print the results
 - End loop

End

- b) The Fuzzy set is determined by what is called the membership function which has its own parameters and these parameters need to be determined. ANFIS learns the rules and membership functions from the used data. Fuzzy partitioning is a technique used for producing fuzzy sets which represent the underlying data. There are three fuzzy partitioning methods. These are the grid partitioning, tree partitioning, and scatter

partitioning. In our work, we use the grid partitioning based on ANFIS prediction Takagi–Sugeno Fuzzy technique.

The grid partitioning is done by dividing the input area into different fuzzy slices, each of them is used by a membership function to estimate the feature value. The grid partitioning model is of Sugeno fuzzy design that's implemented into the neuro-fuzzy systems [35, 36].

ANFIS has a training step by using the I/O data and back-propagation algorithm or hybrid learning algorithm.

The general ANFIS adaptive network is a network of nodes and directional links, associated with a learning mechanism (e.g. back propagation mechanism). The ANFIS networks learn the relationship(s) between the input(s) and output(s) using one of the many available approaches[34-37].

Notice that the circular nodes are fixed and the squared nodes are learned by the ANFIS. There are forward pass and backward pass in the architecture as shown in figure (6). The ANFIS architecture is as follows [34]:

There are two rules for Sugeno ANFIS:

- 1) If x is A_1 and y is B_1 THEN $f_1 = p_1x + q_1y + r_1$
- 2) If x is A_2 and y is B_2 THEN $f_2 = p_2x + q_2y + r_2$

a) Layer 1: the output for each node is:

$$O_{1,i} = \mu_{A_i}(X) \quad \text{for } i=1,2 \quad (6)$$

$$O_{1,i} = \mu_{B_{i-2}}(Y) \quad \text{for } i=3,4 \quad (7)$$

$$\mu_A(X) = \frac{1}{1 + \left| \frac{x - c_i}{a_i} \right|^{2b_i}} \quad (8)$$

Where $O_{1,i}(X)$ is the membership function, a_i, b_i, c_i are the parameters of learning .

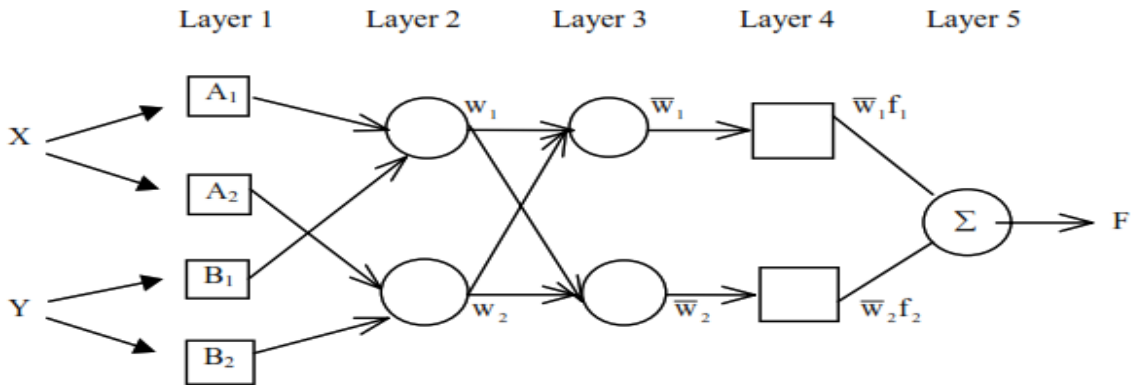


Figure 6. ANFIS Architecture

b) Layer 2: it has fixed node

$$O_{2,i} = w_i = \mu_{A_i}(X) \mu_{B_i}(Y) \quad \text{for } i=1,2 \quad (8)$$

c) Layer 3: it has fixed node which calculates the ratio of the firing strengths of the rules:

$$O_{3,i} = \bar{w}_i = \frac{w_i}{w_1 + w_2} \quad (9)$$

d) Layer 4: consequent of adaptive layer

$$O_{4,i} = \bar{w}_i f_i = \bar{w}_i (p_i x + q_i y + r_i) \quad (10)$$

Where consequent parameter are (p_i, q_i, r_i)

e) Layer 5: the last layer is Output

$$O_{5,i} = \sum_i \bar{W}_i f_i = \frac{\sum_i w_i f_i}{\sum_i w_i} \quad (11)$$

We can estimate the error by

$$RMS = \left(\frac{\sum_{m=1}^K (y_{pred,m} - y_{act,m})^2}{K} \right)^{0.5} \quad (12)$$

Where K is the length of data patterns, m is length of data of next data points, y_{pred} is the predicted output and y_{act} is the next actual value.

The hybrid learning technique is used here because it is frequently used in combination with the methods of Least Square Estimation (LSE) and steepest descent specially to adapt the parameters within the adaptive network[34].

We use 80% of the set of data as training data to determine the model coefficients. Then, we use the rest 20% of the set of data as testing data and then estimate the next mean feature value. We repeat these steps for all the features. The Grid Partitioning ANFIS-TS method is explained in the following algorithm (2):

Algorithm 2. Algorithm of ANFIS-TS (Grid partitioning)

Start

- 1) Input the present and history values of the features(QRS,PR,RR,QT,ST).
- 2) For each feature do the following:
Start a loop
 - a) Apply the "Grid partitioning" MATLAB function with the data set of the feature.
 - b) Select the parameter of Grid partitioning function:
 - 1) Choose the membership function (MF) of our design.
 - 2) Select the type of input function (Gaussian)
 - 3) Select the type of input function (linear).
 - c) To train ANFIS structure, insert the important parameters for this structure:
 - 1) Select type of optimization (Hybrid)
 - 2) Choose the number of epochs.
 - 3) Compute the error

$$Err = \frac{actual\ value - Estimated\ value}{actual\ value} * 100\%$$
 - 4) calculate accuracy
 - 5) Compute the accuracy = 1 - Err
 - d) Print the results

End Loop

End

3.4.3. ANFIS fuzzy clustering mean (FCM) prediction

The FCM is used in ANFIS to improve its performance by classifying data into sets depending on the degree of the member function of each of them. The FCM uses the fuzzy techniques based on K-means and it divides the spaces into a set of chosen clusters, each of them has a corresponding centroid. In this case, all elements of feature space belong to all clusters with different degrees [38]. The FCM algorithm is described as follows:

- 1) Determine the clusters after partitioning the data into fuzzy groups where the vector of data $x_i = 1, 2, \dots, n$
- 2) Determine the center of each cluster $c_i = 1, 2, \dots, c$

3) Determine the membershipfunction from [38]:

$$\mu_{ij} = \frac{1}{\sum_{k=1}^c (\frac{d_{ij}}{d_{kj}})^{2/m-1}} \quad (13)$$

4) Determine the objective function from [38]:

$$J(U, C_1, C_2, \dots, C_c) = \sum_{i=1}^c J_i = \sum_{i=1}^c \sum_{j=1}^n \mu_{ij}^m d_{ij}^2 \quad (14)$$

Where $i=[1,2,\dots,c]$ is the number of clusters selected from data points n , j is number of object $m \in [1, \infty]$, μ_{ij} the member function in object j and cluster i , and $d_{ij} = \|c_i - x_j\|$ is the Euclidean distance between c_i, x_j .

5) Compute the new c-fuzzy cluster from[38]:

$$c_i = \frac{\sum_{j=1}^n \mu_{ij}^m x_j}{\sum_{j=1}^n \mu_{ij}^m} \quad (15)$$

FCM algorithm will be used to obtain the accurate prediction value of next feature based of ANFIS as given by the following algorithm (3):

Algorithm3. Algorithm of ANFIS-FCM (Fuzzy C-mean)

Start

1) Input the present and history values of the features (QRS,PR,RR,QT,ST).

2) For each feature do the following:

Start a loop

a) Apply "FCM" MATLAB function and determine the parameter of FCM function as follows:

1) Choose the number of clusters.

2) Choose number of iteration.

3) Choose Partition Matrix Exponent.

4) Choose the minimum value of improvement

b) To train ANFIS structure use the first 80% of the data and:

1) Select the type of optimization (Hybrid)

2) Choose the number of epochs.

3) Estimate the predicted value using the rest 20% of data.

4) Calculate the actual next value

5) Compute the error as follows:

$$Err = \frac{\text{actual value} - \text{Estimated value}}{\text{actual value}} * 100\%$$

6) Calculate the accuracy = 100 – Err.

7) Print the results.

End Loop

End

Accuracy of this method is found 99% - 100% for all features (RR,PR, ST, QRS, QT).

3.5. The Whole System Algorithm

The block diagram, given in figure (1), is programmed using MATLAB and the user is given the chance to choose the method of prediction. In the following, the general algorithm of the system is described in algorithm (4) and figure (7) gives the corresponding flow chart.

Algorithm 4. The main algorithm of System block diagram

Start

- 1) Read the samples from the MIT database file and divide them in periods corresponding to one minute each.
 - 2) For each period of samples, apply the DWT as it was explained in the preprocessing section above.
 - 3) The values of P, Q, R, S, and T are extracted as follows:
 - a) The peak R is taken as a reference for the signal detection with a threshold of 60%.
 - b) The position of the peak R is taken as a reference for the following peaks of (Q, P, R, S, T) [23].
 - 4) Extract the features values.
 - 5) Compute the averages of the feature values.
 - 6) Test for significance of the means of the feature values.
 - 7) Use the significant means of the feature values to diagnose the heart performance.
- Notice that the MIT database is using a sampling frequency of 120 samples per second. Thus, the sampling period $T_s = 1/F_s$ [21].
- 8) For all the features, compare the feature values to their limit values according to table (1).
 - 9) If heart features' values are within the limits, then the heart performance is normal.
 - 10) If the heart features values are out of the limits, they are abnormal.
 - 11) For each abnormal feature:
 - a) Determine the corresponding disease according to table (2).
 - b) Choose the prediction methods (LPC, ANFIS-FCM or ANFIS-TS) to estimate its future value.
 - c) Compute the next actual values of the features and calculate the errors and accuracies of prediction.
 - 12) Print the results

End

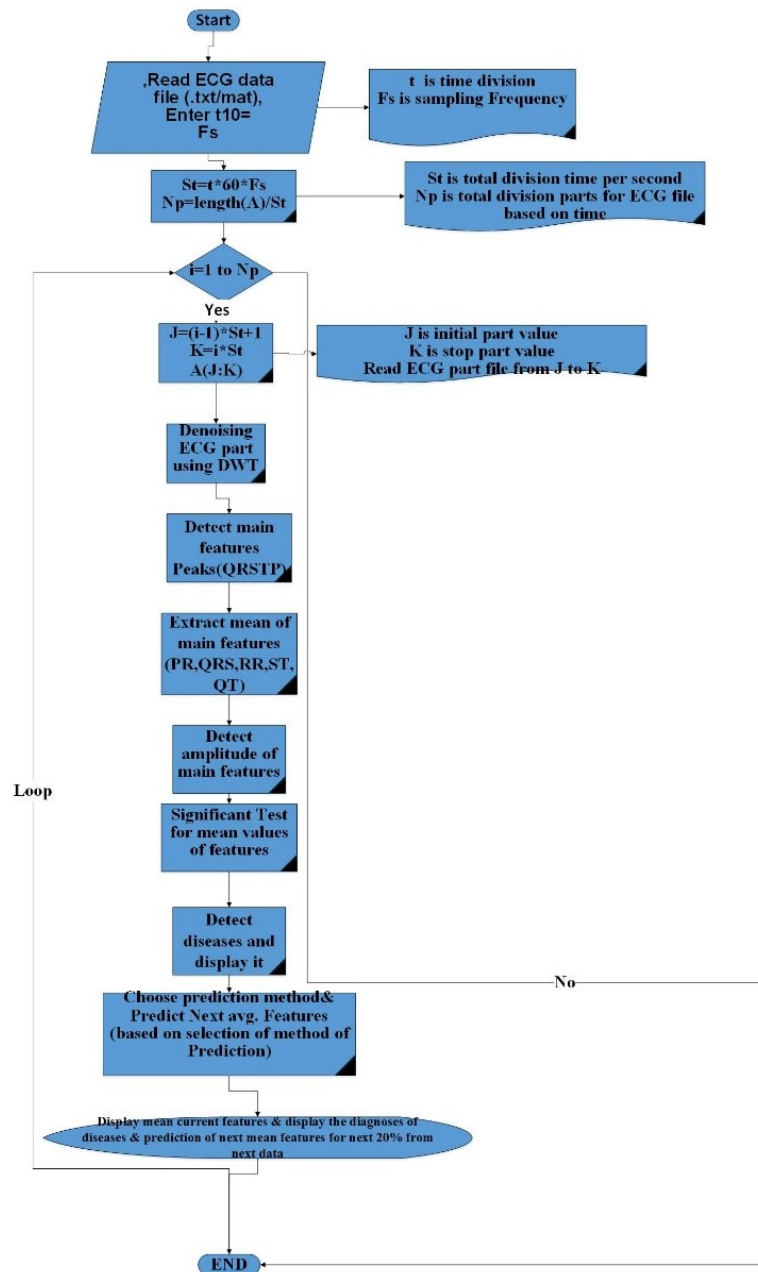


Figure7. The system flow chart

4. Results

In this section, we present the results which were obtained based on the previous sections. For that purpose, the MATLAB 2016a is used to write and run a code corresponding to the general system algorithm. The following initial data are used for running the code and obtaining the results.

- 1) The original heart performance data are taken from the MIT HIB database. We used 1000000 samples, with a sampling frequency of 250 samples per second. We divided the samples in groups, each of them corresponds to 10 minutes, such that we process the samples of the first minute (15000 samples) of the period and hold the results on the screen for the remaining 9 minutes. Figure (8) shows a train of samples of the used data.

- 2) The ECG samples are processed using DWT as explained in pervious sections and the results are shown in figures (9,10).
- 3) The main peaks of (Q,R,S,T,P) are extracted as shown in figure(11).
- 4) The obtained means of the features are tested for significance as shown in table (3).
- 5) The mean values are compared to the normal limits of the heart performance given in table (1).
- 6) From the obtained values of the features, we notice that PR is abnormal (according to table 1). Thus, the corresponding disease from table (2) is "Multifocal Atrial Tachycardia".
- 7) For the abnormal feature PR, we applied the prediction methods as described before to expect any future complications. We applied three methods: the LPM and the GPM ,FCM based on TAP. The results of the two methods are shown in figures (12 – 16).
- 8) To collect all the results and figures on the screen to help doctors to follow up the patient situation, we designed a Guide User Interface (GUI) as shown in figure (17). Table (4) gives the description of the obtained tables and figures from our work.

Table 3. Results of features detections

Features	Mean values	Significant _estimation %
RR	0.45	99.5%
ST	0.24	97.5%
QRS	0.08	95.05%
PR	0.35	97.5%
QT	0.32	95.05%

Table 4. Description of figures and tables obtained from our system

Figures/tables	Description
From figure (8) to figure (10) give the original signal of ECG and the processing results of applying the DWT	
Figure (8)	The original signal of current ECG.
Figure (9)	The reconstructed signals at the different levels in figure (4).
Figure (10)	The base line correct with smoothing signal
Figure (11)	Detected peaks of the ECG signal
Table (1)	Limits of the normal features of the ECG signal
Table (2)	Diseases corresponding to the abnormal features.
Table (3)	Extracted features from the detected peaks
From figure (12) to figure (16) compare between the three prediction methods (LPC, FCM, and FTS) for each feature	
Figure(12)	A comparison between LPC, FCM, and FTS methods for obtaining the RR value. It is clear that the LPC Method is the best. The FCM and FTS methods are nearly the same in performance for RR prediction.
Figure (13)	A comparison between LPC, FCM, and FTS methods for obtaining the PR value. The three methods are nearly the same
Figure (14)	A comparison between LPC, FCM, and FTS methods for obtaining the QRS value. The FCM and FTS are clearly better than the LPC.
Figure (15)	A comparison between LPC, FCM, and FTS methods for obtaining the QT value. The three methods are nearly the same but the LPC is a bit better than FCM and FTS methods
Figure (16)	A comparison between LPC, FCM, and FTS methods for obtaining the ST value. The three methods are almost the same.
Figure (17)	A GUI for our system to help the users to effectively use the system.

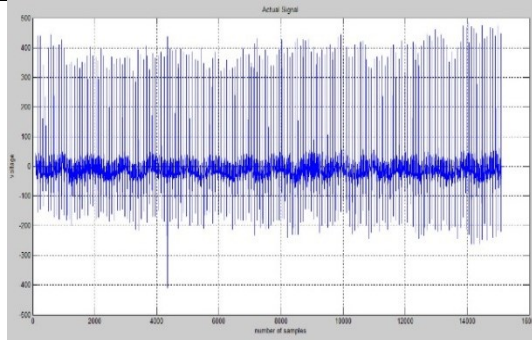


Figure 8. Original sampled signal

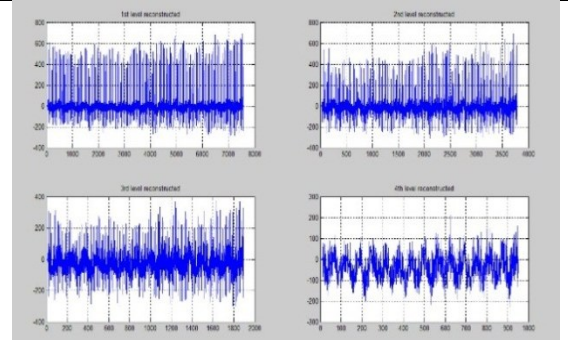


Figure 9. Reconstructed signals at different levels in figure (4)

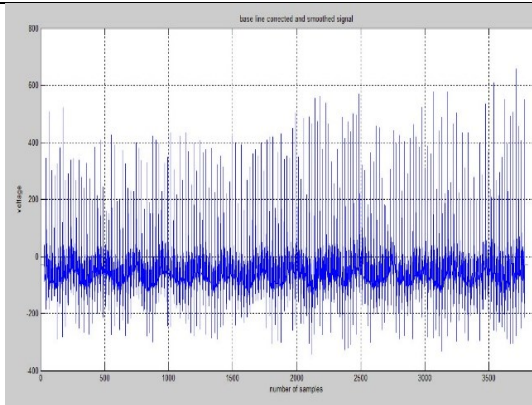


Figure 10. Base line corrected with smoothing signal.

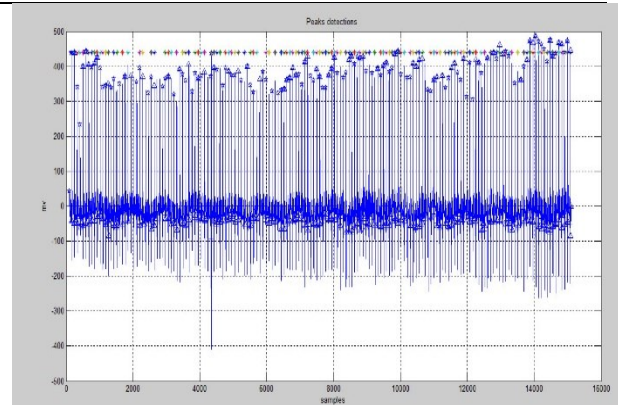


Figure 11. Peaks detection

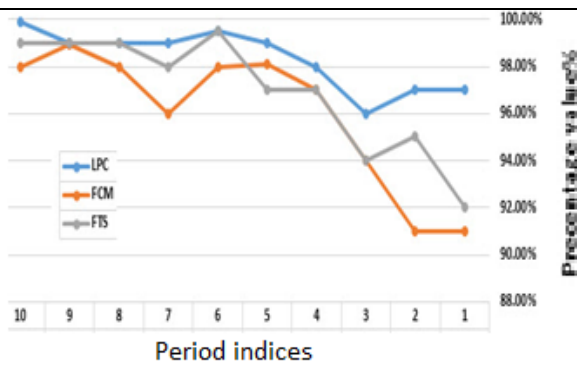


Figure 12. Results of the three prediction methods in regard with the RR feature

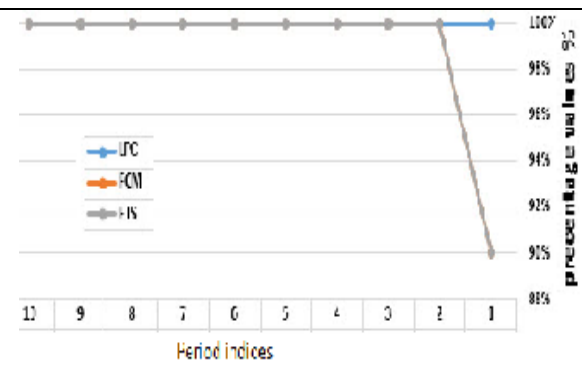
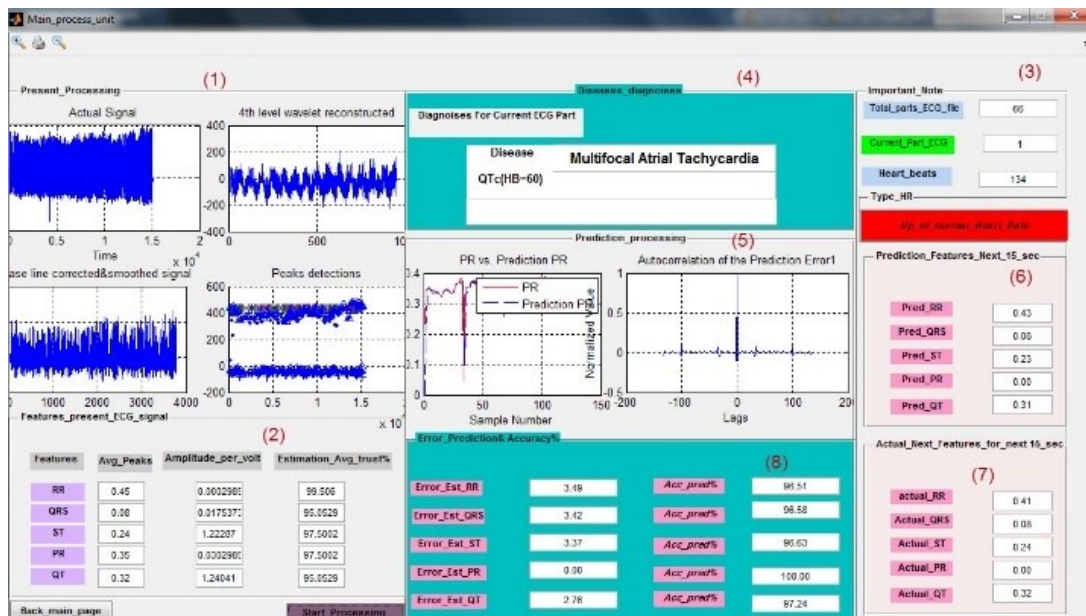
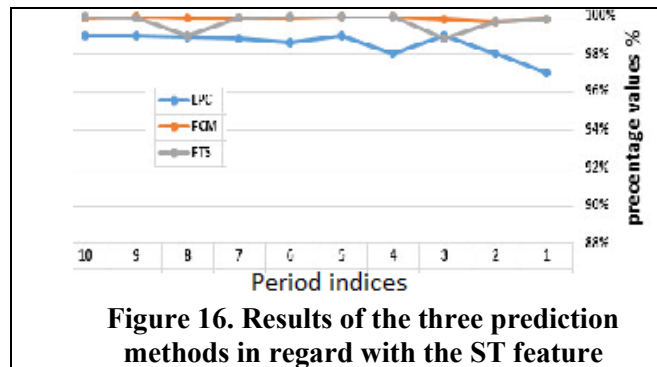
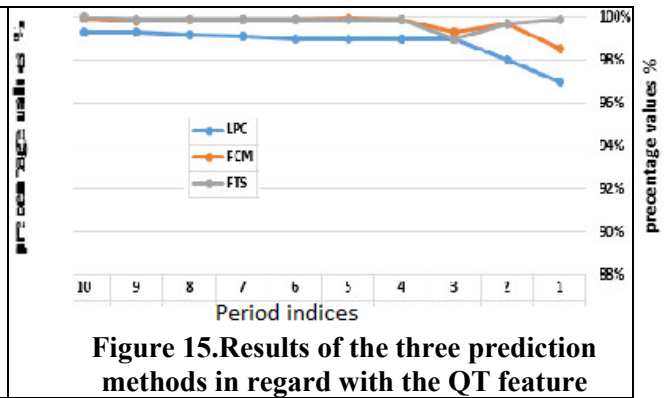
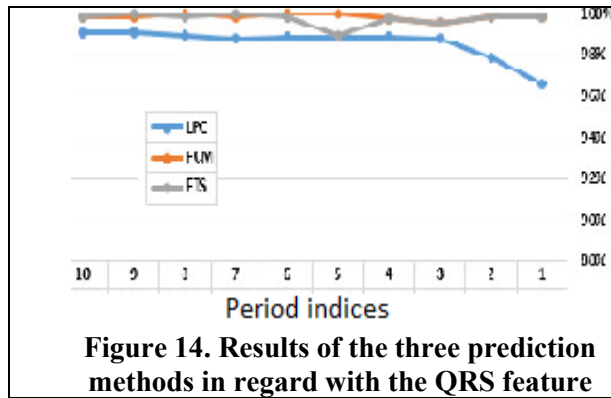


Figure 13. Results of the three prediction methods in regard with the PR feature



5. Discussion of the Results

Our discussion here is done in two parts: a) discussion of the results and b) comparing our results with other results from the previous work.

The original heart performance data are taken from the MIT HIB database. We used 1000000 samples, with a sampling frequency of 250 samples per second. We divided the samples in groups, each of them corresponds to 10 minutes, such that we draw the beats and

process them in the first minute (15000 samples) of the period and hold the results on the screen for the remaining 9 minutes. This gives the doctors a chance to read the results and they can change the scale of the drawings to see them more clearly. The GUI includes all the results in values and drawings, as shown in figure (17). This includes the different present and predicted features' values.

The wave let transform is used to decompose and reconstruct the signal. It gives low pass and high pass filter coefficients. The signal details coefficients are extracted from the high pass filter coefficients and the signal approximation coefficients are extracted from the low pass filter coefficients. This means that the wave let transform is an excellent tool for time and frequency domain analyses.

The means of the obtained values are tested for significance before using them in the diagnosis process. High confidence levels are obtained for RR = 99.5%, QRS = 95.05%, ST = 97.5%, PR = 97.5%, QT = 95.05%. This assures the validity and reliability of the analysis and diagnosis.

The obtained mean values RR, QRS and PR are used for diseases diagnosis. The results show that these values are abnormal and this means we need to apply the prediction techniques to predict any future complications. The other two features St and QT are also found abnormal which assures that the used data are taken from a patient. The heart rate is computed using RR as: $60/RR = 133.33$ bpm. Looking at table (2), we notice that this value is greater than 100 bpm which means that the patient has a "Ventricular Tachycardia". Also the computed rate may be taken for the "Multifocal Atrial Tachycardia". The value of PR can't be measured for the first disease and it is variable for the second disease. Thus, we conclude that the patient has a "Multifocal Atrial Tachycardia". This conclusion is confirmed by the result of QRS ($=0.08$) which is in the range (0.06 – 0.1).

For the abnormal feature PR, we applied the prediction methods (LPC, GPM and FCM based on TAP). The results of the three methods are shown in figures (12 – 16). From these figures, we notice that they change closely, and give very close values, except in the start (the first processing period) where no history points are available for the prediction process.

The prediction process divided the data into two parts: 80% from the data is used for training and 20% is used for testing. The accuracy of the features mean values of PR, QRS, ST, and QT are found to be between 97 to 100%.

We can conclude from the results that for a big change on the RR interval, The LPC prediction algorithm is found to be the best accurate one.

In [23], the analysis of ECG signal is based on only the value of ST while our results take the values of RR, PR, and QRS into consideration. When we applied the same technique of [23], the value of ST was found normal while it is found in our results to be abnormal and its confirmed by the value of QRS. We could reach the same conclusion of the abnormality of ST by using the technique of [39].

We agree with [39] in using the same concepts and values of RR, PR, and QRS to diagnose the heart diseases. Our results agree with the its results of the means of features but we added to the detection operation two steps: the first is to test the significance of the mean values, and the second is to predict any future complications using the LPC, GPM and FCM based on TAP methods.

6. Conclusion

This paper aimed to analyze the heart electrocardiograph (ECG) to diagnose the heart performance and predict any future complications. The MIT BIH database is used to obtain the original data. The discrete wavelet transform (DWT) is used to decompose the ECG signal and to reconstruct it. The means of different performance measures of the heart performance (QRS,RR,ST,QT,PR) are tested for their significance before comparing them to the limits of normal performance. Any abnormal measure is used to diagnose the corresponding disease(s). The Linear Prediction Coding (LPC), the Grid Partitioning and Fuzzy c-mean Clustering based on Neuro-Fuzzy prediction are used for prediction. High confidence levels are obtained for significance. This assure the validity and reliability of the analysis and diagnosis. Our results showed that the patient suffered from a "Multifocal Atrial Tachycardia" disease. This is different from the results of some previous work [23] and matching with the results of another pervious work [39]. The three used prediction methods give very close values but for a big change in RR interval, the LPC method is the best accurate one.

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