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Detection of arrhythmias and myocardial infarction using SVM and ANN algorithms

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Abstract

The heart is one of the most vital organs in humans, and any defect in its function is reflected in the general health of the patient. Therefore, the heart and its diseases have been largely studied in order to help the doctors diagnose heart diseases and reduce errors as much as possible. This study aims to investigate and suggest a method for diagnosing heart diseases from electrocardiogram (ECG) signals. Initially, noise was removed from the signal and the morphological and dynamic features of the ECG signal were extracted by an appropriate feature extraction algorithm and wavelet transformation. A support vector machine (SVM) classifier was then proposed to identify the sound signals from the pathological signals, followed by the use of an appropriate neural classifier in order to classify the pathological signals and extract the results. The system has reached an accuracy of 97 % of the diseased varieties from the healthy ones, out of 150 samples. The proposed system was also able to identify 96% of the number of pathological samples, and attributing them to 3 categories (myocardial infarction, arrhythmias, and other categories).

Keywords: ECG features extraction, myocardial infraction, neural network classifier, SVM, Wavelet transformation.

Introduction

According to the World Health Organization, heart disease is the leading cause of death worldwide. Therefore, many researchers in computer science have focused on the use of algorithms and various innovative techniques in developing systems specialized in detecting and diagnosing heart diseases. An electrocardiogram (ECG) signal is the most efficient and powerful tool for diagnosing heart disease and indicates the heart's electrical activity [1, 2]. Among the difficulties faced in this study were the morphology of the ECG varies from person to person and its diversity, the effect of negative noise on ASHA, Medical errors in diagnosis that occurred as a result of lack of experience or work pressure and Low diagnostic accuracy in traditional diagnostic algorithms.
Therefore, it has been studied in a lot of research in the treatment and extraction of features. The

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proposed study aims to develop an automated system to detect heart disease in humans using ECG signal processing, where the analysis of the ECG signal begins and identifies the types of noise that may be present in the signal and then uses filters that can eliminate the noise while preserving as much of the signal information as possible. Then, the process of extracting the characteristics of the ECG signal, which are useful in diagnosing the studied diseases, such as the locations of the time components of the signal, which are the P, Q, R and S waves, and then the time distances between these waves such as the ST segment, the QRS complex, the PR period and the QT period is extracted using the signal pressure according to the method Suitable (COS- WEVELT – Furrier, etc.). After that, a binary classifier is used as an SVM classifier to determine the pathology from the normal state of the ECG signal, and then an appropriate neurological classifier is used. The pathology was determined from among the following classes (myocardial infarction - arrhythmias - other classes).

Literature Review

Studies presented in the field of heart disease diagnosis, cardiac failure or guess death due to heart disease is very many, and will present in the following the most important of these studies in the last few years.

In the year 2019 the researcher raised up Deb, Pratik [3] in order to classify the ECG signal into a normal or abnormal signal, an automated diagnostic system has been proposed based on the SVM classifier. The SVM classifier was trained and tested on 36 samples from the MIT-BIH Normal Sinus Rhythm Database and 36 from the PTB database, thus the classification accuracy was 98.61%, 97.37% and 97.22 %, respectively. The size of the data adopted by the study is relatively small.

The researcher Dohare, A K [4] did normal and abnormal ECG signals which were categorized using a support vector machine (SVM) classifier. In this study, the Physikalisch-Technische Bundesanstalt (PTB) database was taken and 60 normal cases (N) from 52 people and 60 abnormal cases (A) from 148 people were considered. The accuracy of the performance category was 83.33% (58/60).

In another study by the researcher Anika [5] the study aimed to detect arrhythmia/abnormal and normal ECG signals more accurately as the EKG signal was classified by (SVM) and neural network. The accuracy was around 87% while for the Artificial Neural Network where the classification accuracy ranged between (90 – 93) %.

Research suggest submitted by the researchers Mayapur and Priyanka [6] A classifier was used to classify the signal if it was normal or not, and another classifier was used to classify the pathological samples in terms of three criteria: The origin of the systems, ventricular and supraventricular. Various MIT-BIH, AHA, ESC and UCI databases were used. The proposed study helped in processing, analyzing and classifying EKG signals with an accuracy of 97%.

In a study conducted in 2016 by researchers Maryam Saei and Gina Muhanna [7] the research aims to suggest a new way to discover and classify heart disease in ECG signals using the AFIS nervous infringement system. The algorithm has been applied to an ECG photo database consisting of 147 medical photos attached to the medical report to verify the validity of the discovery and classification and it has achieved a high accuracy of 97 % in the discovery and classification process. With a sensitivity of 94 % classification.

Later the researchers presented Noor Mohammed Ghadi and Nassir H. Salman [8], in this study, was used to the most up-to-date methodologies for medical image analytics that use convolutional neural networks on MRI images. There are several approaches to diagnosing and classifying brain cancers. Inside the brain, irregular cells grow so that a brain tumor appears. The size of the tumor and the part of the brain affected impact the symptoms.

The researchers tried Nadia Adnan Shiltagh Al-Jamali [9] In this paper, a Convolutional Multi-Spike Neural Network (CMSNN) is proposed as a smart system to predict the response of nonlinear dynamical systems. The proposed structure mixed the advantages of a Convolutional Neural Network (CNN) with a Multi -Spike Neural Network (MSNN) to generate a smart structure. The CMSNN has the capability of training weights based on a proposed training algorithm. The simulation results demonstrated that the proposed structure has the ability to predict the response of dynamical systems

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more powerfully than the CNN. The proposed structure is more powerful than the CNN by 28.33%in terms of minimizing the root mean square error.
From previous studies, it conclude that a relatively small number of samples was relied ,the classification of the signal only into two main categories, the normal and abnormal ECG signal category, The studies did not use a standard database, and some studies did not provide information on the classifier it used.
While in this research a standard database was used (MIT-BIH), the signal was classified into normal or abnormal using a classifier SVM, and a number of diseased samples were identified , in proportion to 3 samples (myocardial infarction, arrhythmia and other types).

Materials and Methods

Research Methodology

Fig. 1 shows the stages of completion of the proposed system, where the ECG signal is an input to the system, and it is processed and noise removed using appropriate adaptive filters. Then the signal is prepared and its baseline is determined, and then the signal is compressed using a wafer, extracting the temporal and amplitude features from the signal, and passing the features beam to the SVM classifier in order to determine the sound state of pathology for the signal. As for the pathological signals (unhealthy), they are passed to an appropriate neurological classifier in order to determine the defect in them (myocardial infarction – arrhythmias).

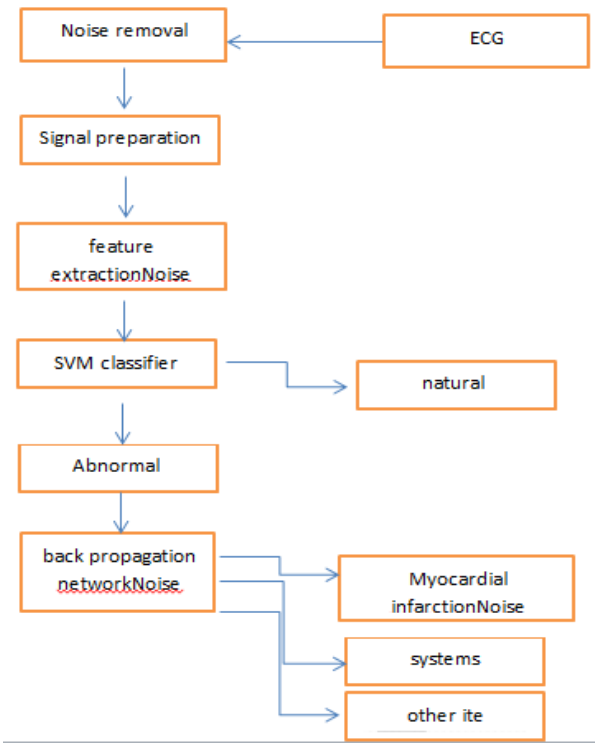

Figure 1. The box diagram of the proposed system

MIT- BIH ECG database on arrhythmias

The Massachusetts Institute of Technology (MIT-BIH) Arrhythmia Database contains 48 half-hour segments of 2-channel ambulatory ECG recordings, obtained from 47 people studied by the BIH Arrhythmia Laboratory between 1975 and 1979 Twenty-three records were chosen at random.
Round-the-clock ambulatory ECG recordings were collected from a mixed group of inpatients (approximately 60%) and outpatients (approximately 40%). The remaining 25 recordings were selected from the same group to include the less common, but clinically significant arrhythmia that would not be well represented in a small random sample. Recordings were digitized at 360 samples per second per channel at 11-bit resolution over 10 millivolts. Signals with a length of 10 seconds were adopted when they were downloaded from the database at a sampling frequency of 360 samples / second, and with a time step of 0.0028s.
The most prominent reference studies that were relied upon in the research were reviewed in terms of their objectives, techniques used, and results. The studies were compared and their results were discussed.

Signal filtering and noise removal

The noise within the signal must be removed by using a suitable filter. The Wiener filter was used with the ECG signal in order to avoid losing some high frequencies in the signal, which contained the most important information, as the Wiener filter depended on the length of a variable filtering window depending on the value of the standard deviation of the samples within the window, and according to the value of the deviation, a filtering process proportional to it was completed. Therefore, the most important information was not lost in the

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signal. Fig. 3 shows the result of applying the filter to the signal in Fig. 2 [10].

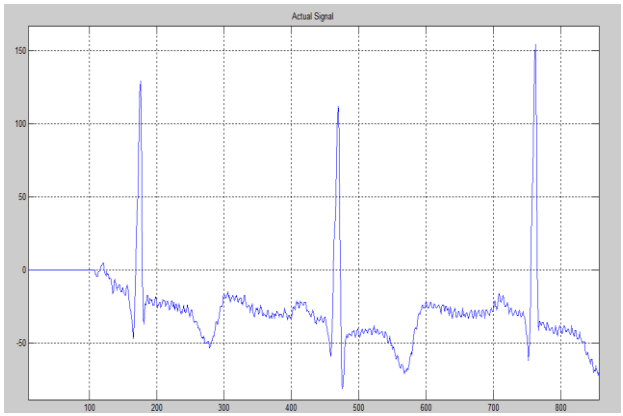

Figure 2. The original signal.

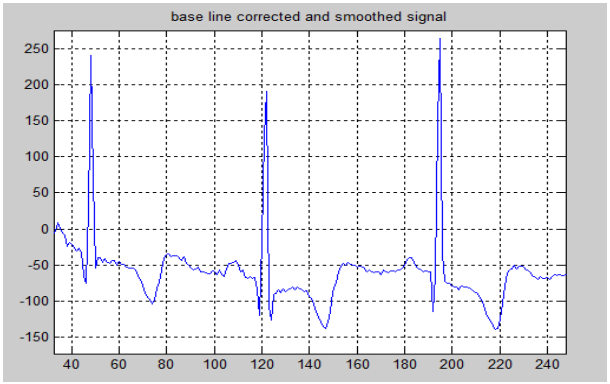

Figure 3. The signal in Figure. 2 after noise processing.

Character Extraction

This stage aimed to determine values that serve as descriptors of the studied samples and determine their belonging to a satisfactory or healthy category. It has been carried out in two stages. The first was to transfer the wafer to the signal, which aimed to compress and reduce the signal data in order to make the second stage easier, which was extracting features.

Wavelet Transform

A wavelet transformation of 1 dimension and four levels of analysis Fig. 4. were carried out using the db4 filter group. The detailed information component was then taken from the signal that contained the most important information in the signal for the four levels. It was noted that the higher-level analysis lost signal information Fig. 5 and lost its information, so the output of this stage was adopted at the second level of analysis as shown in Fig. 6. Thus, the data was reduced by a quarter (from 3800 samples to 955) while retaining the most important information [11].

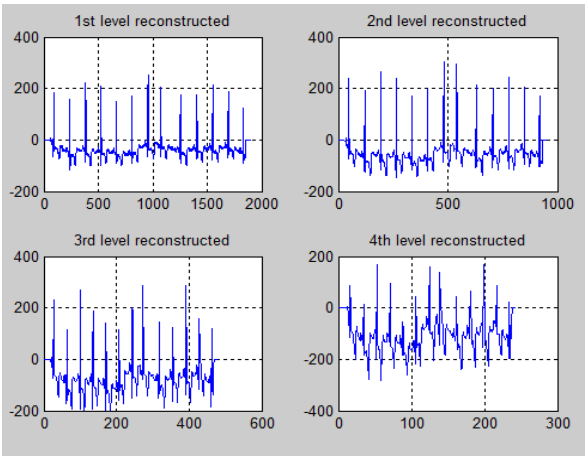

Figure 4. The Four Signal Analysis Levels

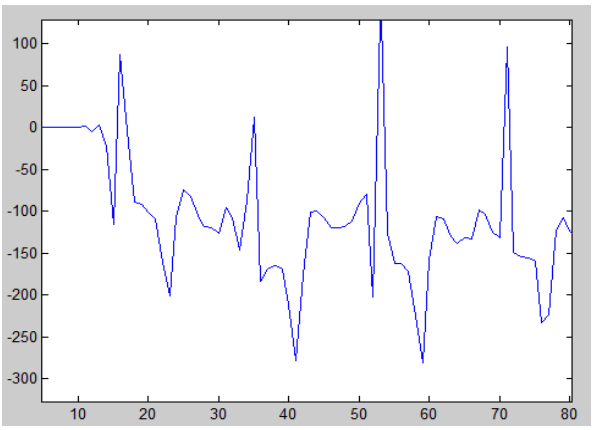

Figure 5. Wavelet transformation of the fourth level of the signal

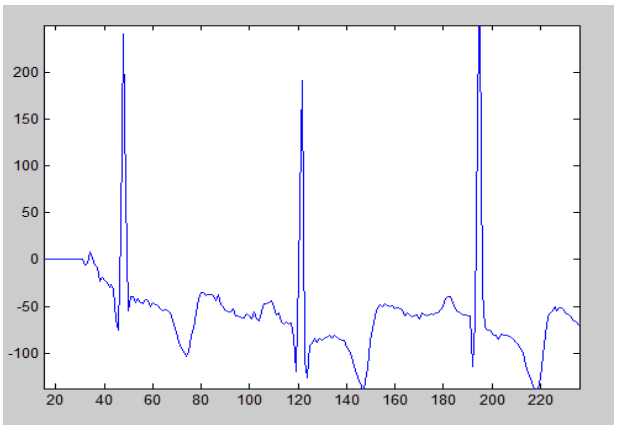

Figure 6. Wavelet Transformation of the Second Level Signal

Time components of the ECG signal

They are values that doctors depend on in deciding their diagnosis of the disease, which were adopted

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to extract the features from them and also in determining the heart rate to know the acceleration or deceleration of the heart and the periodicity of the signal or not. They are: P-wave, Q-wave, R-wave. Table 1 shows the approved features[12].

Table 1. The features used and their importance

Feature	Usage
R-R	Calculating the number of heartbeats and the presence of arrhythmia or not, through the regularity of the spaces between each R and the next.
P-R	Determining the state of the atrioventricular conduction and the extent of the delay in the speed of the electrical signal reaching the ventricles.
QRS	Determining the state of the electrical ventricles.
HR	Determining the heart rate.
Average regularity error squares	Determining the severity of cardiac arrhythmia.
ST	Defining myocardial infarction

Attribute extraction algorithm

R-wave extraction

In some paths (leads), R may be present with large capacitance values and may change in other paths to become a small value, in addition to the fact that the signal may rise or fall from the midline (the 0 volt line) due to the patient's movement during the examination. All of these reasons making the problem of determining the R wave a complex matter, in addition to the fact that determining the R component is the head of a thread for determining the rest of the time components.

The R wave is drawn based on the following steps:

First, it had to be distinguished between the cases of large or small R-wave amplitude, given that the S wave became larger at the expense of R. Therefore, the negative S in this case was considered as R, and then switched later.

Second, separating the reference to the set of negative values R-R and the set of positive values P-R, and the largest value from each group was taken and compared between them. If the positive value Pmax was the largest, it would be R and vice versa, it was considered S (Nmax).

60% of the value of max was taken and considered to be the higher amplitude (R). The points that achieved this value were searched for and put in the matrix P1. However, duplicate values that went back to the same wave were obtained. To solve this problem, it had been jumped from the first value that was found by two large squares, except that in cases accompanied by acceleration of the heart, the R waves formed from each other, so it had been jumped by only one square. At the output of this stage, the R wave is marked with an asterisk as shown in Fig. 7.

In order to calculate the tachycardia characteristic, a calculation was made. The distances between each R and the next are recorded in the R distance matrix:

Calculation of average distances;

The differences between the distances.

Then the number of times of irregularity of the distance R-R was recorded by counting the number of times in which the distance difference between every two successive distances was greater than the permissible value of 0.0392 seconds. Then the mean squares of the regularity error of the distance R-R were calculated from the difference's matrix between the matrices, according to [12]:

$$avg = \frac{\sum_{i=1}^{k}\left(R(i)-R(i-1)\right)}{k} \quad (1)$$

$$e = \sum_{i=0}^{k}\left(\left(R(i)-R(i-1)\right)-avg\right)^2 \quad (2)$$

Where:

avg is the arithmetic mean of the differences between R-R.

i is the pulse index R in the matrix of R.

K is the total number of R pulses extracted.

Calculating the number of heartbeats

As mentioned previously, the calculation of the Heart Rate varied according to the regularity or

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irregularity of the distance between R_R. If the distance was regular, the number of large squares formed by the distance R-R was calculated, where each square had been 0.2 seconds long, and then divided the value 300 by the result according to (3) [12].

Heart Rate = 300/((mm*0.0028*4)/0.2) 3

Where:

- mm is the average distance between R-R.
- mm*0.0028 Converts the value to seconds.
- mm*0.0028*4 to return the value to level zero (actual signal).
- (mm*0.0028*4)/0.2 to calculate the number of squares.

The value of the heart rate was 73.8068 beats / minute, as indicated in (Fig. 7).

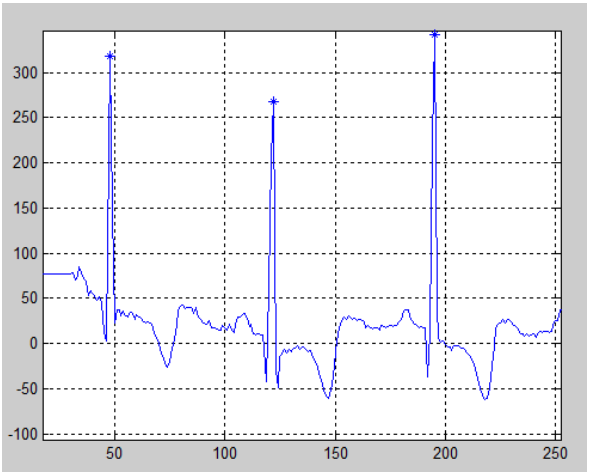

Figure 7. Shows the R wave marked with a star

Extracting the S wave:

To determine the S-wave, the following steps were followed:

1- Placing an initial domain in which S was likely to reside.
2- If the field exceeded the limits of the time-vector matrix of the signal, the last S-field was terminated with the value 1800;
3- The calculations for determining the field in the case of acceleration were different from the calculations in the normal case, a smaller field in the case of acceleration was chosen;
4- The first value that corresponded to the value of R within the initial range was set to be the beginning of the new range, which was determined from this value up to 70% of the value of one large square.

If (as mentioned in extracting R) the amplitude of S was greater in absolute terms than the amplitude of R: The assumed value of S was the largest value in the range. In contrast, S was the smallest value in the range. R became S. This can be seen from Fig. 8 that the value of S, marked by Δ, was extracted.

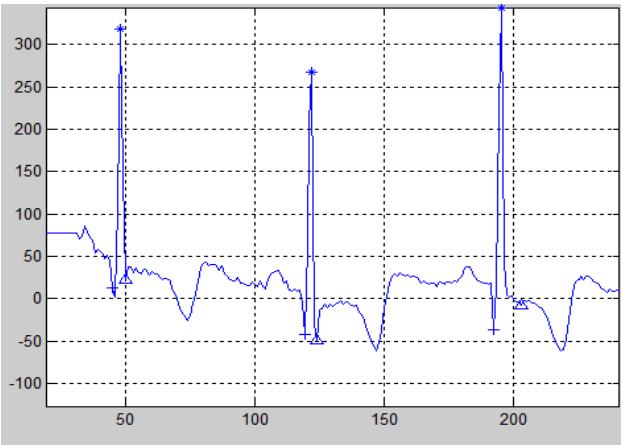

Figure 8. Extraction of the value S marked by Δ.

Determine the Q-wave:

As for the location of those waves, they were the lowest value before R, and their appearance in deep indicated a heart infarction that occurred at an earlier time. Determining that wave was similar to the steps of extracting the previous compounds in terms of determining the field with different field lengths. However, when the amplitude S was greater in absolute value than the amplitude of R, Q became R, the Q wave appeared in Fig. 8 was marked by the symbol. Extracting the P-wave: It was extracted as before; the P wave was shown in Fig. 9.

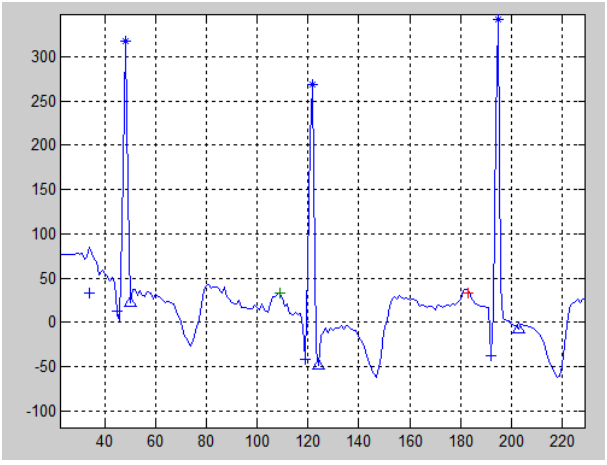

Figure 9. Characteristics of an ECG signal

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Position the piece ST: The entire piece was taken with a pressure coefficient of 4. A sample was taken out of every four successive samples from the piece, Fig. 10.

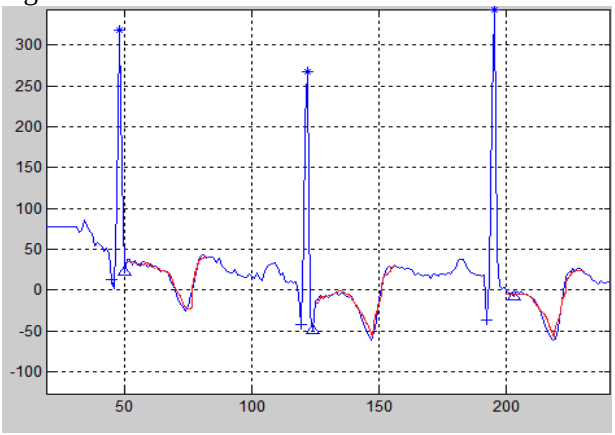

Figure 10. Placing the ST Piece

Algorithm for detecting pathological conditions in the ECG signal

The algorithm for detecting pathological conditions in ECG was determined according to the following steps as shown in Fig. 11.

1. The feature matrix extracted in the feature extraction phase was used to train the SVM;
2. Separated test matrices for normal and abnormal (diseased) ECG signals were generated for the SVM test;
3. If the SVM output was "0", the test signal was classified as an abnormal ECG signal by the SVM classifier. On the other hand, If the output was "1", the test signal was classified as a normal ECG signal by the SVM classifier;
4. The accuracy was calculated, as it was already known which signal was normal and which was not.

In this study, however, a Supporting Vector Machine (SVM) was used. Vapnik was the first to suggest this approach, and since then it has shown excellent outcomes to garner more interest in ML research [13]. It can be presented as a supervised learning method that analyses data and recognizes patterns, used in classification (machine learning) and regression analysis. Standard SVM is a binary line classifier. The purpose of the binary classifier was to predict which of the two classes the input belonged to. Hence, for a set of training examples, each of them was classified as belonging to one of two classes; the SVM training algorithm creates a model that predicts the class to which the studied samples belong. Intuitively, the examples used to build an SVM model can be thought of as points in space, set in such a way that the sample classes were divided by a margin that could be as wide as possible. For each new sample, it was then mapped to the same space and the class to which the sample belonged was predicted by using the information on which side of the margin they fall.

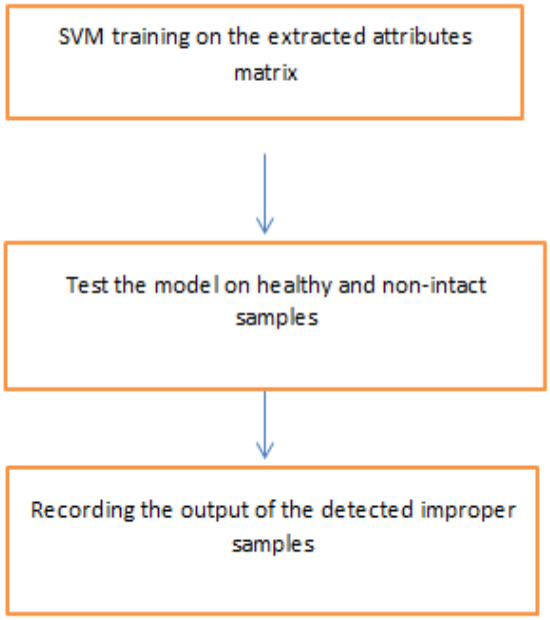

Figure 11. Steps of the pathological specimen identification algorithm

The output of this stage was to determine whether the sample was healthy or satisfactory. Then the pathological sample will be backpropagation.

Algorithm for determining myocardial infarction / arrhythmias

80% of the samples collected from MIT-BIH containing pathological defects (cardiac infarction, arrhythmias, other types) were entered into a neural network that adopts the backpropagation method to find the separation line between the three classes (myocardial infarction, arrhythmias, other items). The structure of the generated neural network was illustrated in Fig. 12. It consisted of an input layer that contained 20 neurons for each of the features, one neuron except for the two QRS attributes, which were entered on two neurons in order to increase the effectiveness of the feature as an important feature and 13 associated attributes. By placing the ST segment, which was very important in the diagnosis of myocardial infarction (cardiac

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ischemia). It was made up of the following components: the hidden layer 1 containing 8 neurons connected to each neuron, including all the neurons of the input layer; the hidden layer 2 containing 6 neurons connected to each neuron, including all the neurons of the hidden layer 1. Finally, the output layer consisting of one neuron gave one output, which was the item number to which the pathological sample belonged (0 for the rest of the cases, 1 for the case of infarction, 2 for the case of cardiac arrhythmias). All activation methods in all classes were of type Togsig.

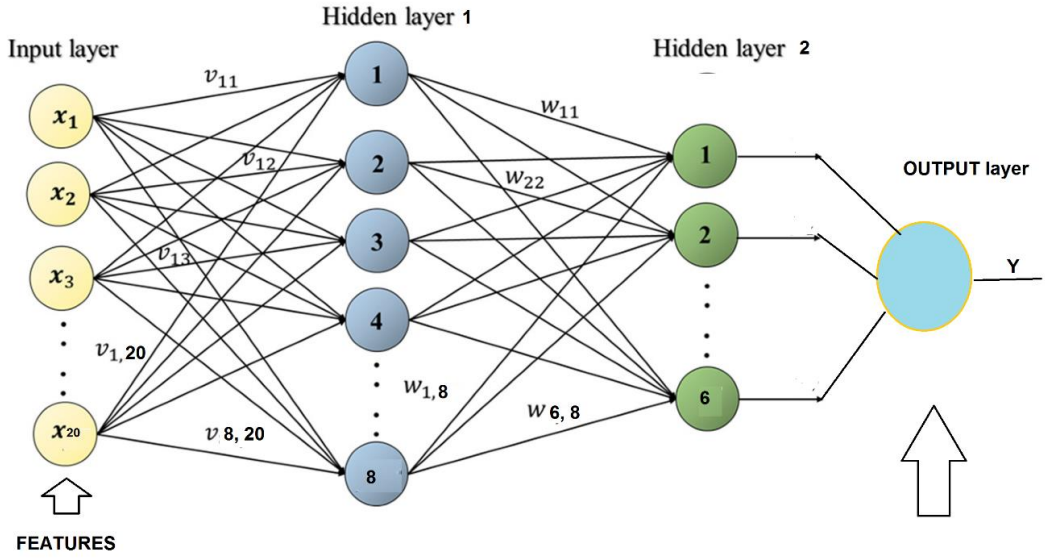

Figure 12. The structure of the neural network.

Results and discussion

The system was tested on 150 signals from the MIT-BIH database. The system succeeded in identifying pathological samples using SVM classifier by 96% of the total number of samples. However, all the special cases of the various forms of the ECG signals (almost unique to each person) were not addressed in this study.

Fig. 13, 14, 15 and 16 show the feature schematic for all database signals, from which it can be found that the selected features were distinctive and none of them were unpromising features depending on the shape of the zigzag schema.

Fig. 13 plots the characteristic P-R, which is the time interval between the P-pulse and the R-pulse, and the figure shows the changes in the values of this characteristic within the range 0.1 sec to the range 0.25 sec for all database samples.

All samples had their heart rate calculated and attributed to three main categories (acceleration - deceleration - normal), all of which were correct (100%).

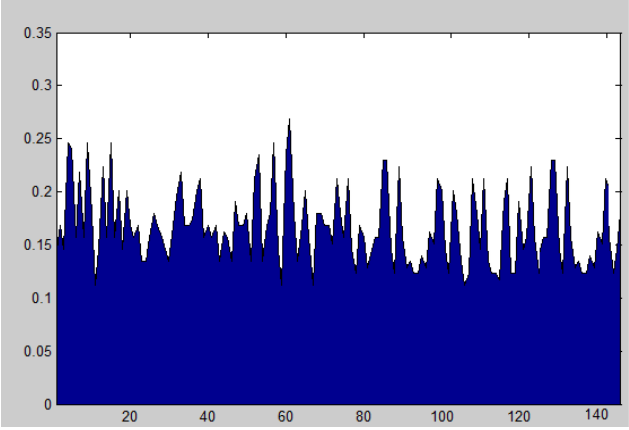

Figure 13. P-R Theme Diagram

Fig. 14 is plotting of the feature length QRS, which is the time interval between the Q pulse and the S pulse. The figure shows changes in the values of this feature within the range 0.1 sec to 0.25 sec for all database samples, we find that these changes can distinguish the samples.

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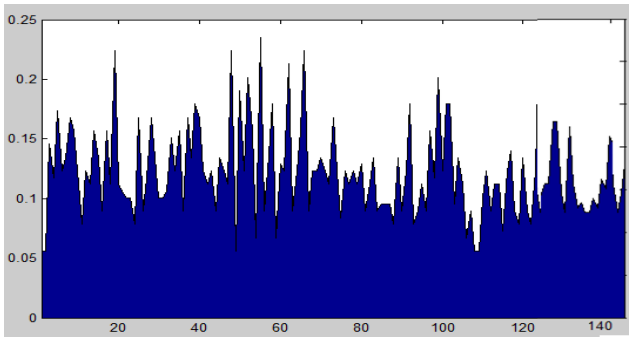

Figure 14. QRS Period Length Attribute Diagram

Fig. 15 is a plotting of the feature of mean squares error of regularity, whose values ranged from 0 (that the sample has normal systems) to 10 (that the sample suffers from severe irregularities). It was found that these changes might distinguish the samples.

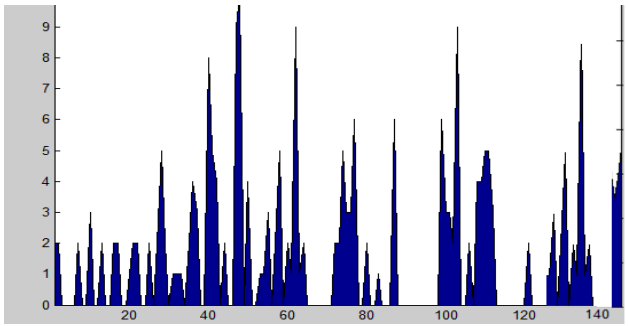

Figure 15. Mean squared regularity error

Fig. 16 plots the characteristic of the heart rate, the values of which range from 45 (the sample has a slow rhythm) to 150 (the sample suffers from an acceleration of the heartbeat), we find that these changes can distinguish the samples.

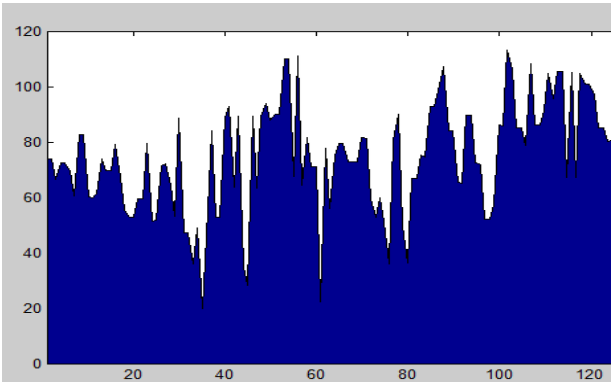

Figure 16. Heart rate characteristic chart

From fig. 13, 14, 15, and 16, we can deduce the important features (PR, QRS, mean squared regularity error, HR) respectively for each cardiac signal from the database. Table 2 shows some of the most important values for the characteristics that we got from the figures, and these values are considered input to the neural network designed to detect arrhythmias and myocardial infarction.

Table 2. Statistical measurements (feature beam) for each cardiac signal.

signal number	P-R	QRS	mean squared regularity error	HR
1	0.1456	0.056	0.018073	73.80679
2	0.168	0.056	0.017818	73.89163
3	0.1456	0.1456	0.006844	66.54836
4	0.2464	0.1176	0.00592	72.55937
5	0.2408	0.1736	0.00616	72.305
6	0.1568	0.1232	0.006533	69.57328
7	0.2184	0.1344	0.10565	60.40809
8	0.1568	0.168	0.0049	82.71123
9	0.2464	0.1568	0.0047	82.79552
10	0.1792	0.112	0.03645	60.18188
11	0.112	0.0784	0.01155	59.89352
12	0.1456	0.1232	0.009067	61.28452
13	0.224	0.112	0.095709	73.97666
14	0.1568	0.1568	0.01004	69.80877
15	0.2464	0.1344	0.0084	69.73795
16	0.1568	0.0896	0.040473	79.07222
17	0.2016	0.1568	0.124133	67.32496
18	0.1456	0.112	0.0172	55.65863
19	0.2016	0.224	0.0096	52.65005
20	0.168	0.112	0.024743	52.64081

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Fig. 17 shows one of the samples that was wrongly classified as abnormal, due to the presence of motion patterns noise that led to the absence of some signal parameters.

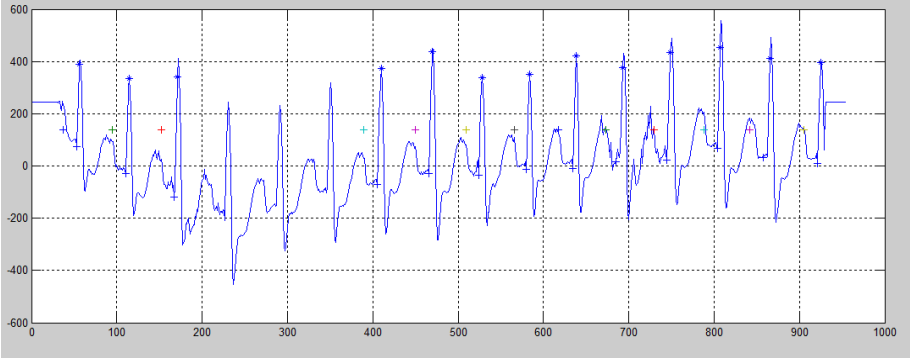

Figure 17. The noise of movement patterns leading to the absence of some features

Results of the pathological sampling algorithm

Table 3 contains the final results, which represent the ability of the SVM classifier to separate the healthy samples from the pathological ones, as the system recognized 98% of the samples that belonged to the abnormal variety and, therefore, it misclassified 2% of the samples that belonged to the various natural. The system classified 96% of the samples that belonged to the natural variety, and, therefore, it misclassified 4% of them. The accuracy of the system proved that it was usable in practical applications.

Table 3. Results of determining the pathological status of ECG

Number of ECG signals	Diagnosis	Number of samples classified as abnormal	Number of samples classified as normal
100	Abnormal	98	2
50	Normal	2	48

To illustrate the results, we plotted a confusion matrix, which shows the percentage of cases in which the model predicted correctly, as well as cases in which the model failed to predict the correct output. Table 4 shows the confusion matrix, where the confusion matrix allows us to obtain the accuracy resulting from the classification process, by determining all of the following (the number of correct positive diagnoses (TP), the number of correct negative diagnoses (TN), the number of false positive diagnoses (FP), and the number of false negative diagnoses(FN).

Table 4. Confusion Matrix.

		Actual	
		Abnormal	Normal
Predicted	Abnormal	TP	FP
	Normal	FN	TN

Table 5 shows the result of each calculation:
Accuracy: It is the number of samples correctly predicted over the total number of samples and is given by the relation (4) [14].

$$Acc = \frac{Tp + Tn}{Tp + Tn + Fp + Fn} \quad 4$$

Recall or sensitivity: It is the number of valid samples detected over the total number of valid samples, and is given by the relation (5) [14].

$$SN = \frac{Tp}{Tp + Fn} \quad 5$$

Specificity: The number of false samples detected over the total number of false samples, and is given by the relationship (6) [14].

$$SP = \frac{Tn}{Tn + Fp} \quad 6$$

F1-score: It expresses the harmonic relationship between the two measures (precision) and (recall), and is given by the relationship (7) [15].

$$F1 - score = \frac{2 * Tp}{2 * Tp + Fn + Fp} \quad 7$$

Finally, Matthew's correlation coefficient range 15, allows one to gauge how well the classification model/function is performing.

$$MCC = \frac{(TP * Tn) - (Fp * Fn)}{\sqrt{(Tp + Fp)(Tp + Fn)(Tn + Fp)(Tn + Fn)}} \quad 8$$

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Table 5. Results of the performance of the algorithm using the data presented in the confusion matrix

Algorithm	ACC	SN	SP	F1-Sorce	MCC
SVM	97%	98%	96%	98%	94%

Results of the algorithm for detecting arrhythmias and myocardial infarction

In order to train (to reach the desired error value), the neural network needed about 2,200 iterations, as it reached an error rate of 0.00073, which was a reasonable error rate. The network was fixed to it with a number of iterations less than the maximum number. 29 out of 31 samples belonging to the category "myocardial infarction", i.e. a rate of 93%, were classified, while 49 samples were classified as "cardiac arrhythmias" out of 50 samples, representing 98% of the number of samples belonging to this class. 18 samples were correctly classified out of 19 belonging to the category "other diseases", with a recognition rate of 94% of the total number of samples, and therefore the total identification rate reached 96%, which is a suitable percentage for practical applications. The reason for the relatively low percentages in the two classes "myocardial infarction" and "others" was due to the small number of samples associated with them.
Fig. 18 shows the system performance error curve according to the MSE and the number of times the system is trained (epochs). It is concluded from the figure that the greater the number of training times the system has, the lower the error until it reaches it's peak in iteration 2200.

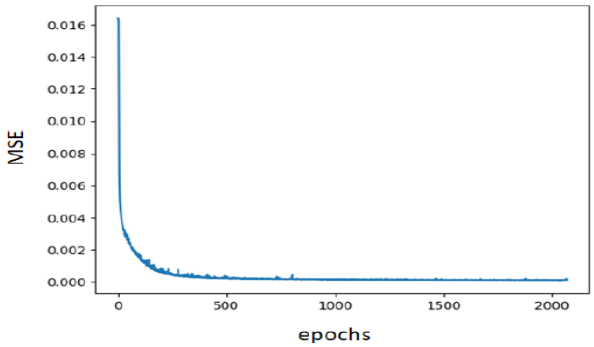

Figure 18. Training Back Propagation Network

100 samples were entered from the database that the network was not trained on. Fig. 19 shows the analysis of the network's performance through the ROC curve. It is a curve that connects the number of samples attributed by the system to it even though they do not belong to it (False positive) and the number of samples that the system recognized correctly (True positive).

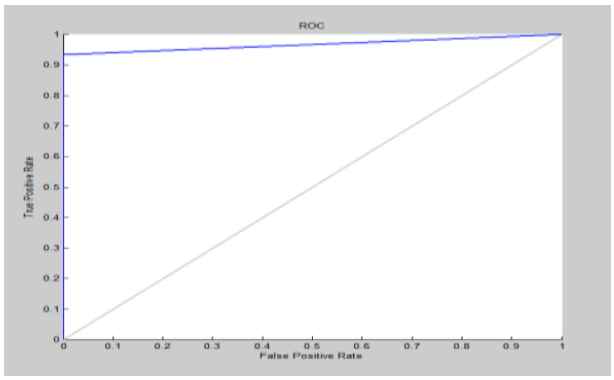

Figure 19. Roc curve for the proposed neural network

It can be seen from the figure that the area under the curve is maximum, which means that the system performance is excellent, Table 5 shows the confusion matrix of the proposed network and Table 6 shows the network performance evaluation.

Table 6. Results of the disease detection stage

Number of ECG signals	Diagnosis	Number of samples classified as infarction	Number of samples classified as arrhythmia	Number of samples classified as other
31	Infarction	29	1	1
50	Arrhythmia	1	49	0
19	Other	0	1	18

Table 7. Performance evaluation of the back propagation algorithm

Algorithm	ACC	SN	SP	F1-Sorce	MCC
Back propagation	96%	96%	98%	96%	94%

Comparing the current study with Marj Studies

In order to know the location of the current study between previous studies, the current study has been compared to the most important and other similar studies in the field of medical decision support systems, and the results are summarized in Table 8.

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Table 8. Comparing the current study with Marj Studies

The Study	Aim of the study	Algorithm	Result
Deb, Pratik [3]	Classify the signal as normal or not	SVM	98.61% on the MIT-BI and 97.37% on the PTB
Dohare, A. K [4]	Classify the signal as normal or not	SVM and Composite Lead Features	83.33%
Alim, A[5]	Classify the signal as normal or not	SVM and ANN	87% for SVM and (90-93)% ANN
Mayapur and Priyanka [6]	Classifying the signal if it is normal or not, and determining the arrhythmia in the abnormal case	The study did not mention the type of classifier used	97%
Maryam Saei and Gina Muhanna[7]	Photo classification ECG	ANFIS	97%
The current study	Detection and identification of pathological conditions in ECG	Adaptive filters, SVM and Back propagation	97% -96%

Conclusion

Automated diagnosis in the medical field raises the level of medical services, as it helps doctors detect and diagnose diseases with high accuracy and reliability, signal processing techniques and artificial intelligence methods play a pivotal role in advancing this goal.

In this research, a model was presented for detecting heart diseases (arrhythmias - myocardial infarction) and classifying them using ECG signals, the system has been implemented and tested on a set of ECG signals obtained from the MIT-BIH database.

The noise was first removed from the signals by applying a Winner filter, after that, the basic features that distinguish diseases were extracted, as the number of extracted features reached 4 features (PR – QRS – mean squared regularity error – HR) capable of distinguishing between diseases to form the input beam of the neural network that was built using the MATLAB program, and this study provided accurate results as high as 97% regarding the extracting traits. Thus, the identification of natural and pathological varieties was accurately met via the SVM classifier. These results were higher than those achieved by previous studies, which used neural networks with an SVM classifier. The system also succeeded in classifying the heart rate into the categories to which it belonged (normal - deceleration and acceleration). Therefore, the proposed system was practically valid for use.

Author's Declaration

- Conflicts of Interest: None.
- We hereby confirm that all the Figures and Tables in the manuscript are ours. Besides, the Figures and images, which are not ours, have been given the permission for re-publication attached with the manuscript.
- Ethical Clearance: The project was approved by the local ethical committee at University of Al Andalus.

Author's Contribution

Title of manuscript: Detection of arrhythmias and myocardial infarction using S.V.M. and A.N.N. algorithms. The authorship of the title above certify that they have participated in different roles as follows:

Conceptualization, analysis, Resources, Study, M.I. and M.A.; Preparation, analysis of the results , Study, Editing Writing, G.S.; Preparation, Analysis, Curation of data, Study, Writing –main draft, A.M.
The Final Paper was read and authorized by all Writers.

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الكشف عن اللانظيمات واحتشاء العضلة القلبية باستخدام خوارزميتي SVM و ANN

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الخلاصة

يعد القلب من أهم الاعضاء الحيوية عند الإنسان وأي خلل في وظيفته فإنه ينعكس على الصحة العامة للمريض لذلك تمت دراسة القلب وأمراضه في العديد من الأبحاث من أجل مساعدة الطبيب في تشخيصه للأمراض القلبية وتقليل الأخطاء قدر الإمكان. يهدف هذا البحث الى تقديم طريقة لتشخيص أمراض القلب بالاعتماد على اشارات مخطط كهربائية القلب ECG، حيث تم في البداية إزالة الضجيج من الإشارة واستخلاص السمات المورفولوجية والديناميكية لإشارة ECG عن طريق خوارزمية استخلاص سمات مناسبة و تحويل (Wavelet) للمويجات، ومن ثم تم استخدام مصنف SVM لتحديد الاشارات السليمة من الاشارات المرضية يتبع ذلك تدريب شبكة عصبونية من أجل تصنيف الاشارات المرضية واستخلاص النتائج. وقد أظهر النموذج دقة تعرف على الاصناف المريضة من الاصناف السليمة بلغت 97 % من أصل 150 عينة . كما استطاع النموذج التعرف على 96 % من عدد العينات المرضية وذلك بنسبها الى 3 اصناف هي (احتشاء العضلة القلبية واللانظيمات واصناف اخرى).

الكلمات المفتاحية: سمات إشارة ECG، احتشاء العضلة القلبية، مصنف الشبكة العصبونية، مصنف SVM، تحويل Wavelet للمويجات.