Detection of Cardiac Hypertrophy by RVM and SVM Algorithms

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Abstract

The meaning of the term 'hypertrophy' is the increasing size. Heart hypertrophy is a symptom of increase in the thickness of the heart muscle and the left ventricular hypertrophy is the most common type. The causes of hypertrophy heart disease are high blood pressure, aortic valve stenosis and sport activities, respectively. The assessment of this amount by using ECG signal analysis is essential because the risk of heart disease. Ventricular hypertrophy increases the timely diagnosis. The ECG signal demonstrates heart electric activities and includes some characteristic points such as P wave, QRS complex, and the T wave is formed. In this study an algorithm has been presented for the assessment of diagnosis of ventricular hypertrophy. In The presented algorithm, first picks of ECG signal have been assessed and then a high degree of statistical information such as skewness, kurtosis, R peak height, and cumulants has also been used.

Keywords: Left Ventricular Hypertrophy, Higher Order Statistics, Skewness, Kurtosis, Cumulants, Support Vector Machines, Relevance Vector Machine

1- Introduction

The electro cardiogram signals are among the erotica cardiac signals and through estimation and processes of these signals we can prevent many different cardiac problems. At the first step of processing the noise signals should be canceled and at the second step the pick signals should be identified and at the final step the correct algorithms with adequate accuracy should be used. An ECG signal includes some characteristic points such as p wave, QRS complex, and T wave. Some of ECG has another wave named U that appears after T wave and the waves presented in Fig.1.

QRS complex is one of the important components of ECG and with its usage many of disorders could be diagnosed while other waves of signal are identical with use of QRS complex [1, 2].

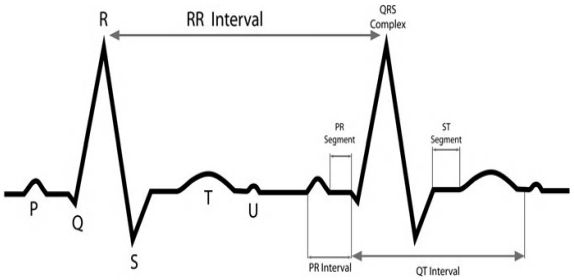

Fig.1. Different parts of the ECG signal

In this study an algorithm is provided for hypertrophy illness diagnosis as shown in the Fig.2.

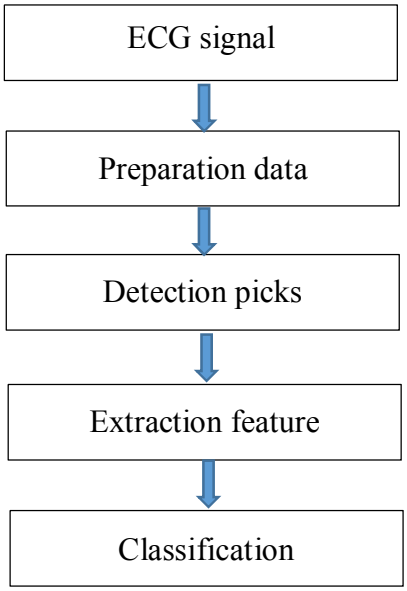

Fig.2. The algorithm presented

2- Detection of Picks

In this study a well-known Algorithm of Pantompekins is used for the detection of (R) peak as it is presented in Fig.3.

In this algorithm the Savitzky-Golay filter is used for the detection of noise to increase the ratio of signal to noise. For this installation, filter windows of 17 sampling is used by adopting a polynomial order 7. The outcome signal of this filter passed from a Butterworth filter with cut frequency of 6 and upper cut frequency of 30. Butterworth filter output is applied to a derivative [3].

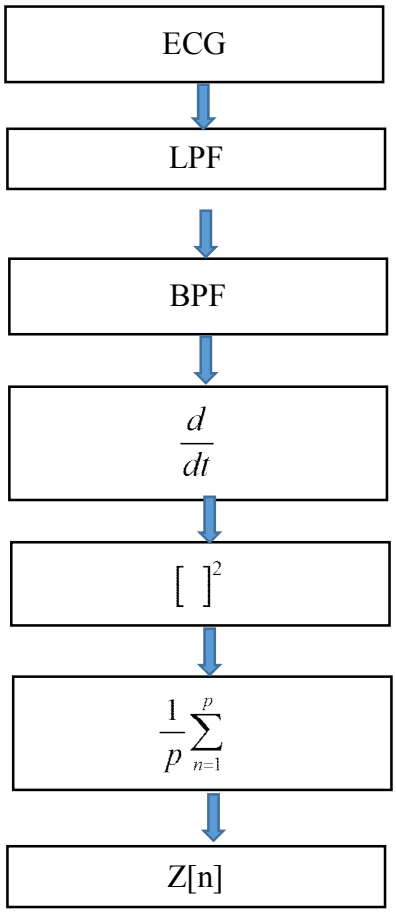

Fig.3. The Algorithm of pantompekins

After derivation the output of derivative will go to power and then will be averaged with equal distance and this stage is presented in fig.4.

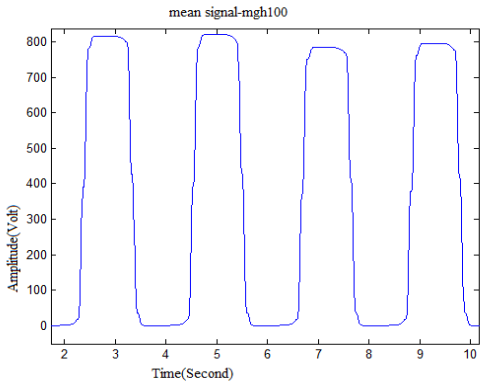

Fig.4. Output of the Algorithm of pantompekins

For finding the peaks of R after calculation of 1/3 of average signals and recording the position of these numbers on the purging sleep and lower going of the average matrix peaks at the result we will identify the maximum part of signal according to fig. (5).

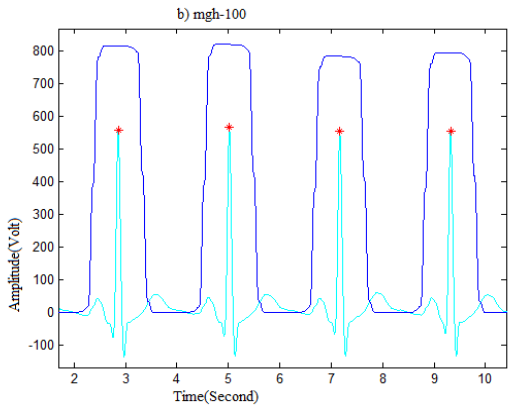

Fig.5. The R picks diagnosed

3- Detection of Q Picks

For this identification of Q picks the lowest amount of signal at the 150 MS before picks of will be identified according to fig. (6)[4].

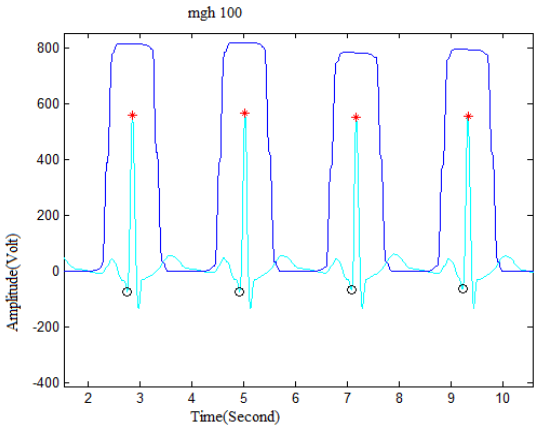

Fig.6. The Q picks diagnosed

4- Detection of S Picks

As the minimum of signal at 200 MS period after R pick caption, S pick was diagnosed according to fig. (7) [5].

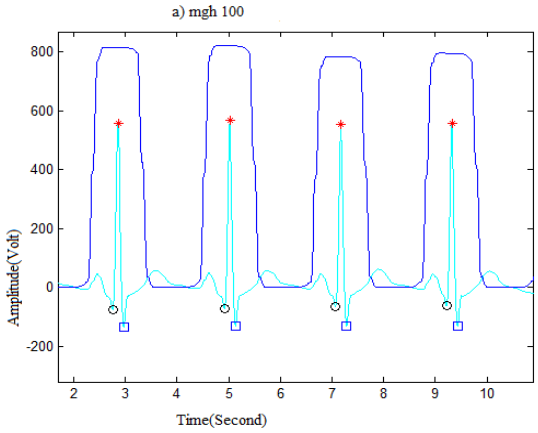

Fig.7. The S picks diagnosed

5- Detection of T Picks

For identification of T pick part of signal at %65 from %8 of peak of stop Q the next beat at the caption T pick was diagnosed according to fig. (8)[6].

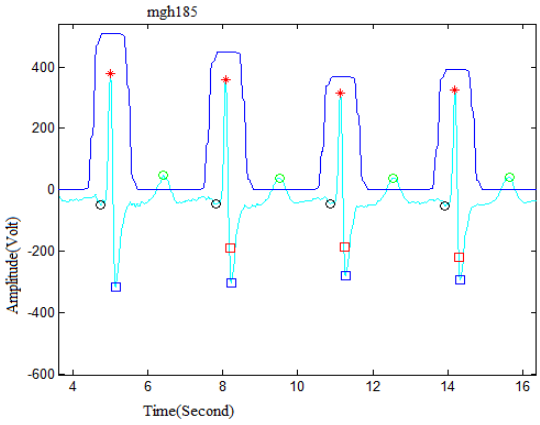

Fig.8. The T picks diagnosed

6- Extraction of Features

6.1. Time Features

Since the height of R picks is the main indication of hypertrophy, R picks will be considered as the time indication for the diagnosis of left ventricular hypertrophy.

6.2. Statistical Features of high degree

Since the increase of the time of QT part indicates ventricular hypertrophy for the calculation of high degree of statically characters, those parts in QT signal will be used [7,8]. There is a high degree of statistical information such as: skewness, kurtosis, R peak height and cumulants. We have n samples of variables. Cumulants' level R will be calculated as follow:

$$\hat{m}_r = \frac{1}{n}\sum_{i=1}^{n} x_i^r \qquad (1)$$

6.2.1. Skewness

Probability theory In statistics, skewness is a measure of the asymmetry of the probability distribution of a real-valued random variable about its mean. The skewness value can be positive or negative, or even undefined. This is defined as follows:

$$Y_1 = \frac{\hat{m}_3}{\left(\hat{m}_2\right)^{\frac{3}{2}}} \qquad (2)$$

6.2.2. Kurtosis

In probability theory and statistics, kurtosis represents a peak height probability distribution. The kurtosis criterion is used for amount of the Gaussian probability distribution functions [9, 10]. Kurtosis is defined as follows:

$$B_2 = \frac{\hat{m}_4}{\left(\hat{m}_2\right)^2} \qquad (3)$$

For classification of extracted characters we use Support Vector Machines and Relevance Vector Machines.

One of the approaches recently used for classification is support vector machine. A support vector machine is a two class categorizer that classifies data by using separating hyper planes. After training SVM using training data along with its class labels, support vector machine classifies new data that are test data and give a hyper plane for testing the data.

The SVM algorithm works by finding the hyper plane which is at the largest possible minimum distance to the training samples. Two times of this distance is also known as margin, since the goal of SVM is to maximize this margin of training samples as much as possible [11].

7- Relevance Vector Machines

The Relevance Vector Machine (RVM), was introduced by Tipping (2001). The RVM Algorithm is the first and most important step on modeling data according to the linear composition of basic derivatives that enable the possible structure for judgment of the data. Generally RVM classifier is designed as a binary classification. The aim of RVM classifier is to find the posterior probability of membership for any one of two classes.

The advantages of RVM classifier over SVM are listed below:

- RVM classifier requires smaller amounts of relevance vector than the SVM.
- The testing time is less than SVM classifier.
- The design complexity and cost is lower for RVM when compared to SVM.

For data modeling using RVM algorithm for a set x input we will suppose that output will be approximated as follows:

$$y = w^T \Phi(x) \quad (4)$$

Where $w = (w_1, w_2, ..., w_n)^T$ is the matrix of weights, $\Phi(x) = (\phi_1(x), \phi_2(x), ...\phi_N(x))^T$ is a set of basic functions. If between x, y a linear relation exists basic relation could be used $\Phi(x)$. For computing w vector we will suppose that t_i is indication of exact model y_i. In this case, we have:

$$t_i = y_i + \varepsilon_i \quad (5)$$

Where are assumed to be independent samples from a Gaussian noise process with zero mean and variance σ^2, Looking at N training points simultaneously, the vector t represents all the individual training points and the $M \times N$ design matrix Φ is constructed such that the it row represents the vector $\Phi(x)$ we have:

$$p(t \mid x_i, w, \sigma^2) = \prod_{i=1}^{N} N(w^T \Phi(x_i), \sigma^2) \quad (6)$$

To learn the relationship between x, y with definition, a probability distribution growth of the weights w will be presented as follows:

$$p(w \mid \alpha_i) \sim N(0, \alpha_i^{-1}) \quad (7)$$

Where, we have used α_i to describe the inverse variance (i.e. precision) of each w_i. We are trying to find α , w and σ^2which maximize this posterior probability. We can decompose the posterior:

$$p(w, \alpha, \sigma^2 | t) = p(w \mid t, \alpha, \sigma^2) p(\alpha, \sigma^2 | t)$$

Substituting β^{-1} for σ^2:

$$p(w \mid t, \alpha, \beta) \sim N(m, \Sigma)$$
$$\sum = (A + B + \Phi^T \Phi)^{-1} \quad (8)$$
$$m = \beta \sum \Phi t$$
$$A = diag(\alpha)$$

Where, m is mean and $\sum$ is variance. For evaluation of $\sum$, m we should find α, β parameters to maximize the first part of equation. After finding the α, β parameters we will find parameter of $\sum$, m and we will repeat values of α, β to get the time of cooperation values [12, 13].

To use support vector machine, first we arrange the 4 characters of healthy and disorder signals on the matrix through which each row represents the healthy and illness data and columns represent 4 characters of healthy and disorder signals. Then, features of Matrix obtained on index matrix with demotion of m*n will be definite in a way that this matrix will be used as classification matrix. In the presented index, matrix for support vector machine, the numbers of 1 and -1 are used. That number 1 indicates healthy signals and -1 indicates illness signals. The created index matrix for support vector machine is as follow:

$$A=[1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ -1\ \ -1$$
$$-1\ \ -1\ \ -1\ \ -1\ \ -1\ \ -1\ \ -1\ \ -1\ \ -1\ ]^T$$

In the nonlinear approaches, the selection of core function is important. In this research the correlation function of RBF is used and in case of use of Gaussian correlation function selection and adjustment of stable correlation function, Margin software is necessary. In case of use of relation vector machine we act as the same of SVM with this difference that we use number 1 and 0 for health signals and unhealthy signals. The target matrix for relational vector machine is as follow:

$$A=[1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1$$
$$0\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0\ ]^T$$

Correlation function selection and adjustment of stable correlation function for relational vector machine is necessary. After the creation of character matrix, definition of target matrix and determination of initials, the last value of constant correlation function and value constant Margin software used in the support vector machine 19-22 are selected. The outcome matrix stage test SVM is as follow:

$$B=[1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ 1\ \ -1$$
$$1\ \ 1\ \ 1\ \ -1\ \ -1\ \ -1\ \ -1\ \ -1\ \ -1\ \ -1\ ]^T$$

As it is presented in 13 the first samples are healthy. Only one of them is ill and from 10 samples 3 illness samples are diagnosed as healthy signal. At the time of using relational vector machine the last value of constant correlation functions 1/950 of constant correlation function. The default network will be selected. Outcome of RVM algorithm will be in the shape of matrix B:

$$B=[0.7117\ \ 0.7484\ \ 0.7477\ \ 0.7477$$
$$0.7472\ \ 0.7365\ \ 0.7484\ \ 0.7468\ \ 0.7469$$
$$0.7165\ \ 0.7466\ \ 0.7484\ \ 0.7484\ \ 0.0001$$
$$0.6746\ \ 0.1491\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0\ \ 0]^T$$

As it has been shown, the outcome Algorithm of RVM is estimated. It is due to the target matrix definition through which number 1 indicates healthy signals and 0 indicates illness signals. In the outcome matrix B the samples that include value of 0.7 and higher than 0.7 are seen as healthy signals and the samples that include values under 0.7 are considered as illness signals. Considering this, approximations to the conclusion at RVM algorithm output all signals to correct diagnosing.

8- Conclusion

In this study for diagnosis of cardiac hypertrophy, an algorithm is displayed. In this algorithm for hypertrophy diagnosis time and frequency character of signals such as skewness, kurtosis, R peak height and cumulants are extracted. After extraction of characters and with use of SVM and RVM classifiers, this result is archived that the algorithm RVM has a higher accuracy than SVM.

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