AUTOMATIC ECG R-PEAK DETECTION ALGORITHM TOWARD COMPUTATIONAL ATRIAL FIBRILLATION DIAGNOSIS

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ABSTRACT

R peak detection is considered as a significant starting point in every automated ECG analysis. It is a crucial step to identify the rest of heartbeat peak cycle in the ECG data. A normal heartbeat cycle consists of 5 peaks including the P, Q, R, S and T wave. The highest amplitude signal among all peaks is the R peak. A huge number of studies have been carried out in this research domain using plenty of methods such as the wavelet technique, ranging from filtering and threshold methods, hidden Markov models, Pan Tompkins, neural networks, and so forth. Based on the track record, the performances of the existing methods are good, but each method has faced issues such as the lack of sensitivity in certain conditions of data. Furthermore, a good numbers of additional tools are currently used to assist in detecting the ECG peak. Too much reliance on these tools can actually restrict the possibilities of diagnosing ECG data from different angles. This paper proposes a simple algorithm for automatic detection of the R-peaks from a single-lead digital ECG data. The proposed approach consists of three stages: Identify (1) a positive value of group data from one patient`s 60 second ECG data, calculate (2) the average value in total of that group`s positive data point and lastly, compare (3) the total average value with the defined threshold and select the maximum value from it. The performance of the proposed algorithm was tested on 15 ECG data from MIT-BIH Normal Sinus, The result showed that the automatic R-peak detection accuracy is 100% with low computational complexity and low sensitivity to low frequency noises.

1. INTRODUCTION

The electrocardiogram (ECG) is a time series of signal recording of electrical activities of the heart myocardium during cardiac cycle. A recurrent process of depolarization and repolarization of the myocardium associated with the contraction of the atria and ventricles over each cardiac cycle create sequence of P, Q, R, S, and T wave in the ECG data. 12 lead system is used to catch an overall view of heart activities by placing electrodes on the body's surface where the total result will be represented in the ECG data record. A huge number of cardiac and critical diseases such as heart attack and preliminary signs of stroke can be identified through ECG. It is fundamental that almost all automated ECG analysis algorithm should detect the R-peak segment accurately as diagnoses of cardiac disorder, heart-rate variability analysis, biometric and even ECG coding system rely massively on the accuracy of the R-peak detector.

A number of methods for detecting R peaks such as digital filters, empirical mode decomposition (EMD) [1], mathematical morphology, wavelet transform [2], derivatives, geometrical matching [3], hybrid approach [4] and neural networks are available. Most of the methods include several stages like a preprocessing or feature extraction stage and a decision stage which in some cases consume high computational costs. The ECG data R-peak detection is more efficient in the sense that the duration is short (10 seconds duration) and the accuracy is at most 90% and above. Despite the high accuracy level, the ECG data often makes a lot of unexpected signal like noise after 10 second onwards. Due to that, many kinds of computer aided analysis techniques are introduced. There are different computer aided analysis techniques aiming at extracting these time series feature from digitized ECG data but none of them specifically focuses on extracting the exact data point from each ECG peak for any kind of analysis of cardiac rhythm which has been proposed for this paper.

In this paper a simple algorithm based on threshold has been proposed for automatic detection of R-peak value. The algorithm includes three stages as follows; (1) the Identification of a positive value of group data from one patient`s 60 second ECG data, (2) the calculation of the average value in total of that group`s positive data point and (3) the comparison of the total average value with the defined threshold and the selection of the maximum value from it. The proposed algorithm was tested on 15 ECG data from MIT-BIH Normal Sinus. The performance of the proposed algorithm yield with high accuracy but low computational complexity and cost. This paper will discuss in section 2, some related works towards this research area. Section 3 will introduce the feature extraction segment for this research. Section 4 will describe the details of the proposed algorithm. In section 5, the analysis of the experimental result will be discussed. In section 6, conclusion will be made with discussion on possible future works.

2. RELATED WORK

Deboleena et al. [5] have proposed an algorithm for automatic detection of R-peak from single lead digital ECG data by using squared double difference signal of the ECG data. In this proposed algorithm, the double difference approach is used to localize the QRS region so that it can identify the R peak region easily. In order to identify the R-peak segment accurately, this proposed method has been divided into three stages with about 99.8% of accuracy with low computational complexity to identify the R peak segment.

Likewise, Sabarimalai Manikandan et al. [6] have proposed a new R-peak detector based on the new preprocessing technique and an automated peak-finding logic. Comparison has been made in terms of performance with Shannon energy envelope (SEE) estimator and has shown high accuracy performance of the proposed method by comparing with the comparison model. The level of sensitivity is at 99.8% by using MIT-BITH arrhythmia database as the main reference data for the experiment.

Indu Saini et al. [7] have proposed an algorithm by using an application of K-Nearest Neighbor (KNN) as a classifier for detecting QRS-Complex in ECG. Evaluation of the proposed algorithm was performed using CSE and MIT-BIH Arrhythmia database from Physionet.org. The levels of accuracy are above 90% and the results clearly establish the idea of using KNN algorithm for detecting this segment as reliable and good.

3. CHARACTERISTIC DOMAIN FEATURE FROM ECG

Presently, the R-peak and the QRS detection algorithm are classified as amplitude and derivative based, digital filter based, template matching technique based, non-linear transformation based and wavelet based. With the use of the proposed algorithm in detecting the R-peak segment, the threshold based R-peak detection based on the 3 stages is used when processes of identification rely on the threshold. Later, the process of collecting all of the R peak segment values in 60 seconds’ duration of cardiac cycle is applied. In this proposed method, all R peak values are collected in numerical form.

3.1 OVERVIEW OF CARDIAC RHYTHM

3.1.1 Normal Sinus Rhythm.

Normal sinus rhythm (NSR) is defined by its characteristic in the rhythm of a healthy human’s heart. Normal Sinus Rhythm originates from the sinus node. It normally has a consistent rate but differs in some cases depending on the autonomic input into the sinus node. Irregularity can occur in the sinus rate and is called “sinus arrhythmia”. A sinus rhythm can be classified into several conditions based on its pace, the faster rhythm is called sinus tachycardia, while the slower rate is called sinus bradycardia.

3.2 OVERVIEW OF DOMAIN PEAK FEATURE

3.2 R-PEAK SEGMENT

The R peak is the most visible peak of signal to detect the Normal Sinus rhythm. It is the center beat in each cardiac cycle. The example of this segment can be seen in figure 1 for Normal Sinus. R to R intervals for Normal Sinus Rhythm are very consistent with only small variations between beats. Contrastively, the R to R interval during Atrial Fibrillation has greater amplitude than P, Q, R, S, T interval variations [8].

Figure 1: Sample segment of R to R interval peak

4. METHODOLOGY

The proposed algorithm is based on the threshold based approach and operates on digitized ECG data from single lead. The digital ECG data from a single lead is read as a series of big array of the time instant. The method involves three different stages in order to achieve accurate detection of the R peaks.

The proposed algorithm is composed of the following stages:

- Stage 1: Identify a positive value of group of data from one patient`s 60 second ECG data.
- Stage 2: Calculate the average value in total of that group`s positive data point
- Stage 3: Compare the total average value with the defined threshold and select the maximum value from it.

5. EVALUATION

In this experiment, the MIT-BIH Normal Sinus Rhythm ECG database from Physionet [9] is considered in order to test the performance of the proposed algorithm. Each patient in this database is healthy cardiac cycle wise. The MIT-BIH Normal Sinus Rhythm database contains 8 hours of two channel ECG recordings with the resolution over 5mv range. PhysioNet is a free resource where it provides a lot of data related to biomedical research and development.

In this study, the entire 60 seconds ECG recording data relies on only one channel from two channels of ECG recording data to detect R-peak. An acceptable quality of the signal in the ECG record from the MIT-BIH Normal Sinus Rhythm found in this database are not only derived from sharp signal peak, tall P and T waves, uncertain negatives QRS complex, small QRS complex and wider QRS complex. It is also inclusive of some muscle noise, baseline drift, sudden changes in QRS amplitudes, sudden changes in QRS morphology and sometimes irregular heart rhythm. These are used for testing the proposed algorithm to detect R peak in 60 second duration. Measurement mechanism for detecting the quality of sensitivity of detecting R peak is defined as below.

Sensitivity = True Positive / (True Positive + False Negative)

Where,

True Positive = actual R peaks correctly detected as peaks;

False Negative = actual peaks not detected as peak

Table 1 tabulates some test result for healthy patients known as Normal Sinus rhythm and also shows the detection sensitivity for one lead. All 15 data are tested with the proposed algorithm and some false negative results have been identified as shown below.

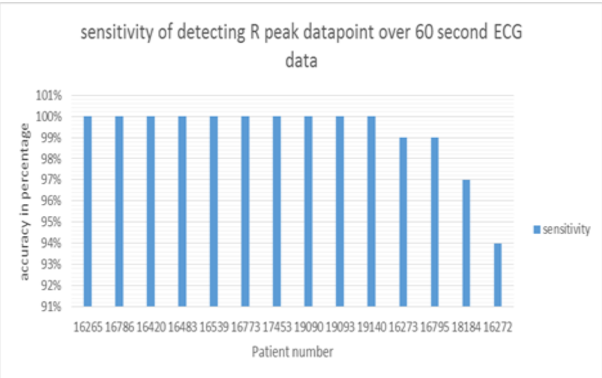

Figure 2: Sensitivity of detecting R peak value over 15 patient data

Patient number	False negative	False positive	Sensitivity
16265	0	0	100%
16786	0	0	100%
16420	0	0	100%
16483	0	0	100%
16539	0	0	100%
16773	0	0	100%
17453	0	0	100%
19090	0	0	100%
19093	0	0	100%
19140	0	0	100%
16273	1	0	99%
16795	1	0	99%
18184	3	0	97%
16272	3	0	94%

Table 1: Test result for Normal Sinus Rhythm patient

The overall detection sensitivity is above 90%. The detection effect of false peaks is almost minor. The algorithm shows the performance for data affected with low frequency noises as small.

In the MIT-BIH Normal Sinus Rhythm database, the ECG records number 16273, 16795, 18184 and 16272 contain high-level of noise and artifact compared to the other ECG record. It also consists of abrupt changes and severe baseline drift. For this ECG recording, the number of false negative detection is more compared to the false positive which is none. The ECG records number 16273, 16795, 18184 and 16272 contain sudden changes in QRS morphology. This sudden changes make the QRS amplitude heading too positive millivolt value for a certain period of time for several PQRST cycle before returning back to isolated line which is unusual for normal cardiac rhythm. For a normal healthy cardiac rhythm cycle; in every peak formation, every peak will always make a return to isolated line before it forms another peak. However, false negative for several data has occurred. Sudden changes are consistently created before returning to normal rhythm which has led to errors in detecting the R-peak by using this proposed algorithm. This unexpected signal may be due to external factors like environment or human behavior during data recording. One of the most important parts in data analysis and peak detection in ECG data that affect the accuracy of analysis is how the ECG data recording procedure has been conducted. By applying proper ECG data recording procedure, a proper analysis with high accuracy can be achieved.

However, the proposed algorithm has led to a significant progress in detecting the R-peak under time-varying QRS complex morphology cycle and has succeeded in identifying many different kinds of noises and artifacts without relying too much on the ECG filtering technique in identifying the R-peak. The effectiveness of the proposed method has been proven as a positive move in light of a number of false negatives and false positive as shown in table 1.

CONCLUSION

In this paper, an effective three stage methodology has been discussed for the automated detection of R-peaks in an ECG signal. The proposed method is based on three stages; (1) Identify a positive value of group data from one patient`s 60 second ECG data, (2) calculate the average value in total of that group`s positive data point and lastly, (3) compare the total average value with the defined threshold and select the maximum value from it. Amplitude threshold and prior knowledge of the past detected R-peaks are not needed for this proposed method in order to get a better accuracy in detecting the R-peaks. The performance is measured through several mechanisms such as number of false positives, true positives and false negatives for each record by using a standard MIT-BIH Normal Sinus Rhythm with 15 ECG records of 1 minute's data. The detection results obtained are presented and discussed. The method's average detection accuracy is 90% above. Despite all the series of noises and artifacts contained in the ECG signals of the database, the proposed method has achieved a much higher detection rates. In the near future, another several peaks are needed to identify future analysis on detecting cardiac disorder. This value can be considered as a new alternative in diagnosing cardiac disorder from different angles.

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