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# Automated QRS Detection using Empirical Mode Decomposition and K-Means

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**Abstract:- This paper proposes an algorithm using Empirical Mode Decomposition (EMD) and k-means for the detection of QRS complexes present in the ECG signal. EMD is an innovative method for decomposing any time varying, nonlinear and non-stationerysignal into a set of intrinsic mode functions (IMF). This automated algorithm is applied to the filtered ECG signal for its decomposition into its intrinsic components and further its classification is done using k-means classifier. Dataset-3 of the CSE multi-lead measurement library is used for validating the performance of the algorithm. Detection rate of the proposed algorithm came out to be 99.42% with sensitivity (Se) and prediction (+P) rates being 99.39% and 99.93% respectively. The performance of this algorithm is quite satisfactory amongst many algorithms used for the automated detection of QRS complexes.**

***Keywords:-*** *Empirical Mode decomposition, K-means, ECG signal, QRS complex.*

## I. INTRODUCTION

Biosignals are defined as the electric, chemical or acoustic signals originated by a human body that conveys information which reflects the properties of the underlying biological system, thus helping in figuring out various pathologies. The most important category among them is the one originating from the electrical activity of the heart. Electrocardiogram (ECG or EKG) signals essentially depict the picture of heart's electrical activity over time captured via external electrodes placed at various places on the human body[2].

The advancement of ECG signal monitoring devices has proven to be quite beneficial tool for the detection of various life threatening arrhythmias in patients. ECG monitoring is the most widely used clinical cardic test extensively used at home, clinic and hospitals units such as intensive care environments, emergency rooms, ambulatory telemetry units, operating theatres etc. ECG monitoring has expanded from the single-lead to multi lead registration thus helping in the detection of complex arrhythmias, ST-segment/ischemia and in the identification of prolonged QT intervals.

The QRS complex forms a visuallyobvious and central part of the ECG signal (Fig. 1). This complex denotes the depolarization of the right and left ventricles of the human heart. The characteristic shape of the QRS complex forms the basis of the automated determination of the ischemic heart diseases. Its shape provides a fundamental reference for the classification algorithms implemented for the detection of cardiac diseases [7], [30]. Several studies are done to extract the QRS complex from the ECG signal.A conventional method of QRS detection is presented in [18], based on first and second order derivatives [17], digital filtering techniques [29], mathematical transformation [3], [5], Wavelet transform [14], time recursive prediction technique [1], hidden markov model [6], [19], Artificial Neural network [12], [22], [16], support vector machine [21], statistical methods [24], [25], [26], [29], Genetic algorithm [27], pattern recognition [24], fuzzy logic [7] [4], [23], etc. The various difficulties accompanying the ECG signal needed to be dealt withare low SNR, diversity of the QRS waveforms, artifacts and signal abnormalities. The detection of the accurate positions of the QRS complexes forms the basis of determination of other locations of other ECG components like ST segment, P and T waves etc.

N.E. Huang proposed a time-frequency domain signal processing method known as Empirical mode decomposition (EMD) [17]. It is a full self-adaptive, data-driven signal processing method thatdepicts signal features in both the time and frequency domain, and also decomposes them without assuming any basic function or using any pre-determined filter.A dataset consists of a finite set of categories present within them known as clusters. An unsupervised learning algorithm like Clustering aims to identify these clusters with the help of a similarity measure.A similarity measure is defined forsimilar type of data in a dataset and then this similar data in the dataset is grouped together to form clusters.K-means is one of the most widely studied clustering algorithmbecause of its simplicity and best-known squared error [28]. In the following sections an automated algorithm is proposed for the detection of the QRS complex in ECG signalwhich includes both Empirical Mode decomposition and k-means. EMD acts as feature selector by decomposing the ECG signal into its constituent signals and then k-means is used as a classifier to separate out the QRS complexes from non-QRS ones.

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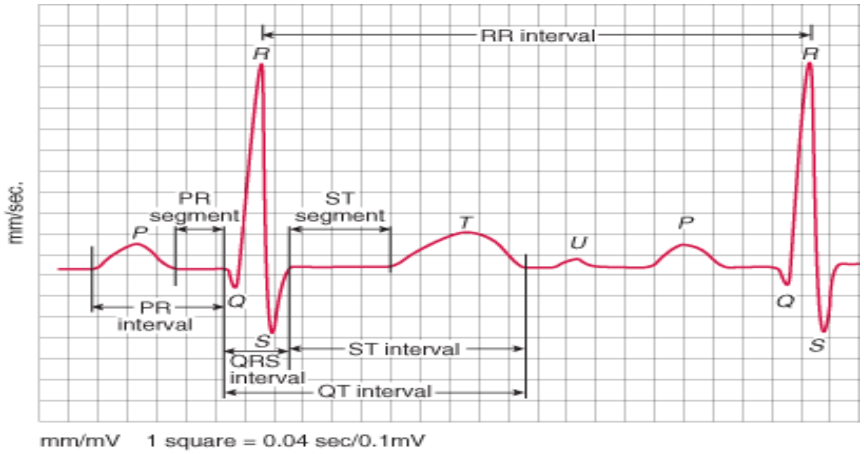


Fig. 1: ECG Signal representation

## II. ECG SIGNAL PREPROCESSING

The recoding of the ECG signal during strenuous or ambulatory conditions makes the signal corrupt by introducing various types of noises originating either from another physiological process of human body or acquired during their acquisition[15]. Biomedical signal processing is majorly concerned with the extraction of pure cardiological indices from the noise contaminated ECG signal. The noise corrupted ECG signal is passed through the 50 Hz noise removal digital filter designed by Furno and Tompkins [10]. Finite impulse response (FIR) notch filter proposed by Van Alste and Schilder [11]is applied to remove baseline wander with a notch at zero frequency (or dc) [17].

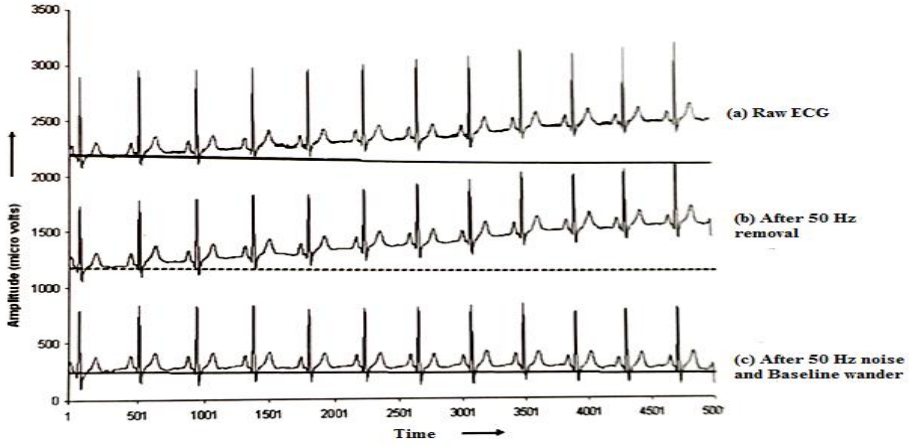


Fig. 2(a):Raw ECG Signal,(b) Filtered ECG signal after 50 Hz powerline removal,(c) ECG signal after 50 Hz noise removal and Baseline Wander

## III. EMPIRICAL MODE DECOMPOSITION

The Hilbert Huang Transformation (HHT) technique decomposes a time dependent data series into its individual characteristic oscillations.Hilbert Huang Transformation is a two stage process which involvesEmpirical Mode Decomposition (EMD) and Hilbert Spectral Analysis (HSA) techniques. N.E. Huang developed Empirical mode decomposition (EMD) [9], [20] technique.This is a time-frequency domain signal processing method, that deconstructs a time series signal into a set of mono component signals known as Intrinsic Mode functions (IMF). The Intrinsic Mode functions (IMFs) represent the oscillatory modes embedded in the signalthat satisfies two conditions:

- In the whole dataset, the number of extrema and the number of zero-crossings must be either equal or differ at most by one, and
- At any point, the mean value of the envelopes defined by the local maxima and local minima is zero.

A systematic way to extract the characteristic time scale from intrinsic oscillatory mode is designated as sifting process. The repeated application of the sifting process in EMD separates out the oscillatory modes present in the signal in ascending manner of their frequencies i.e. fastest oscillatory modes are extracted first followed by the next fastest and so on. This sifting process is repeated until the signal is broken down into simple oscillatory components known as Intrinsic Mode Functions (IMF). This procedure is repeated on all subsequent residuals and terminates on fulfillment of any one of the following predetermined conditions [3] i.e.

- The component or residual becomes lesser than the predetermined value or
- Till the residual becomes a monotonic function from which no further IMFs could be extracted.

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## IV. EMPIRICAL MODE DECOMPOSITION (EMD) ALGORITHM

Empirical mode decomposition of signal (X(t))

- ***Initialize*** $r_0(t) = X(t)$ *and set* $j = 1$
- ***Repeat*** *(Extraction of* $j^{th}$ *IMF by sifting process)*
  - **Initialize** i = 1; $h_{i-1}(t) = r_{j-1}(t)$
  - Locate **maxima** and **minima** of $h_{i-1}(t)$. $(max_{i-1}(t), min_{i-1}(t)) = find\_extreme\ (h_{i-1}(t))$
  - Pass a cubic spline through maxima to form upper envelope $up\_envelope_{i-1}(t) = cubic\_spline\ (h_{i-1}(t), max_{i-1}(t))$
  - Similarly, pass a cubic spline through minima to form lower envelope $low\_envelope_{i-1}(t) = cubic\_spline\ (h_{i-1}(t), min_{i-1}(t))$
  - Find the mean of upper and lower envelope i.e.

$$\boldsymbol{m_{i-1}(t) = \frac{[up\_envelope_{i-1}(t) + low\_envelope_{i-1}(t)]}{2}}$$

  - The detail after subtraction of mean given as $\mathbf{h_i(t) = h_{i-1}(t) - m_{i-1}(t)}$
  - if stopping condition is satisfied by $h_i(t)$ then it is designated as the IMF as $\mathbf{IMF_j(t) = h_i(t)}$

    else

    Goto step 2 (b) with i = i+1
- Once an IMF is found the residual is calculated as $r_j(t) = r_{j-1}(t) - IMF_j(t)$
- if $r_j(t)$ is monotonic i.e it is a constant, a trend or has no more than three extrema then end EMD else goto 2(a) with j=j+1.

(At the end of the algorithm $r_j(t)$ obtained is the final residue of X(t)).

## V. K-MEANS CLUSTERING ALGORITHM

Cluster Analysis is based on the concept of dividing the objects or data into groups/clusters of objects having similar properties. Thus the objects within the cluster are similar to each other than in other clusters. It aims at extracting the valuable information hidden in the data and further analyzing it.It also attempts to abstract the prototypes or the representative objects from individual objects in the same cluster.

K-means is the most popular and simplest method of cluster analysis in metric space. This method aims at partitioning*n* observations into *k* clusters where each observation belongs to the cluster with the nearest mean. k is provided as an input parameter and this algorithm clusters observations into k groups. The algorithm starts by initializing k cluster centroids at random.k-means is an iterative procedure whichiteratively reassigns all the points to their nearest centroids and recomputed centroids of the newly assembled groups until the convergence of the criteria function i.e. square-error[10]. The various procedural steps are explained below as:

- **Step 1:**Initialize K cluster centers $Z_1(1)$, $Z_2(1)$, ……, $Z_K(1)$ arbitrarily. These are usually selected as the first K samples of the given samples set X and $Z_{l+1}(1) \neq Z_l(1)$, for l=1, 2… K-1.
- **Step 2:** At the $m^{th}$iterative step, distribute the samples X among K cluster domain, using the following relation.

$$X \in S_j(m) \text{ if } \|X - Z_j(m)\| < \|X - Z_i(m)\| \quad (4.1)$$

For all i = 1, 2… K; j = 1, 2… K-1; $i \neq j$,

Where$S_j(m)$ denotes the set of samples whose cluster center is $Z_j(m)$.

- **Step 3:** From the results of step 2, compute the new cluster centers $Z_j(m+1)$, j=1,2,…..,K, such that the sum of the squared distances from all points in $S_j(m)$ to the new cluster is minimized. In other words, $Z_j(m+1)$ is computed so that the performance index,

$$J_j = \sum_{X \in S_j(m)} ||X - Z_j(m+1)||^2$$

for all j = 1,2,… K. (4.2)
is minimized.
where, $J_j$ = Performance index.
$Z_j$ (m+1) = sample mean of $S_j(m)$.
$Z_j$ (m+1) minimizes this performance index Therefore, the new cluster center is given by,

$$Z_j(m+1) = \frac{1}{N_j} \sum_{X \in S_j(m)} X$$

for all j = 1 ,2,… K. (4.3)
where, $N_j$ is the number of samples in $S_j(m)$. The name "k-means" is derived from the manner in which clusters are sequentially updated.
**Step 4:** If $Z_j(m+1) = Z_j(m)$ for j = 1 ,2,.. K, the algorithm has converged and the procedure is terminated. Else go to step 2.

## VI. QRS DETECTION PROCESS AND ITS CLASSIFICATION INTO QRS AND NON-QRS REGIONS

The performance of the proposed algorithm is evaluated by takingstandard CSE dataset 3 containing the ECG signal of 125 patients [12]. The procedural steps adopted are described here along with the block diagram as shown in Fig.3. The aim of this step is to obtain the feature signal from the ECG signal which basically highlights the QRS region from non QRS ones. Since the QRS regions are higher frequency regions so they are separated first followed by lower frequency constituents of the ECG signal.Initially the data is in raw form due to the presence of noise and needs to be filtered and fine-tuned for further analysis. The filtering of the ECG signal includes baseline wander removal and 50 Hz noise removal. The resulting filtered signal is presented to the Empirical Mode decomposition algorithm described in section IV. This is a recursive algorithm which aims to decompose the ECG signal into its intrinsic modes known as Intrinsic Mode Functions (IMFs) with the help of a process called '*sifting process*'. This process of decomposition continues until the residual signal becomes monotonic. Since the extracted IMFs consist of the constituent of the original signal in

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ascending order of frequency so the averaging operation for first three IMFs will be sufficient for determination of QRS regions. This signal is converted into its absolute form and passed through moving average window thereby forming the upper envelope of the feature signal. Thus, finally the processed signal is presented to the K-means algorithm which acts as a classifier and classifies the signal into 2 classes i.e. class-1 with label '1' representing QRS regions and class-2 with label '0' representingnon-QRS regions. Due to peaky P or T waves there might exists a spike of one's pulse trains misinterpreted as the QRS complex region. These false positives are discarded by average pulse width criterion i.e. the pulses below one fourth of the average width of the pulses are discarded while rest remains intact in their positions. The procedural steps of the overall process are depicted below:

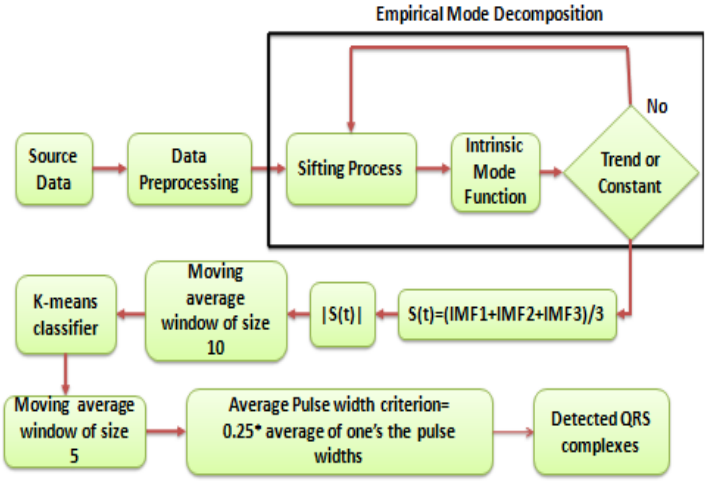


Fig. 3: Block Diagram for QRS Detection

- **Step 1:** A raw ECG signal of the patient is acquired and shown in Fig. 4(a) of a certain record of CSE ECG database.
- **Step 2:** This raw ECG signal is filtered to remove the baseline wander and power line interference. Fig. 4(b) shows the filtered ECG signal.
- **Step 3:** Empirical Mode Decomposition (EMD) algorithm is applied to the filtered ECG signal which decomposes it into a collection of Intrinsic Mode Functions (IMFs) in descending order of their frequencies.
- **Step 4:** The first three IMFs being the higher frequency components are summed up. Since the QRS complexes are the higher frequency components so the summation of the first three IMFs gives us enough details about the QRS complexes.
- **Step 5:** Step 1 to 4 are repeated for each of the 12 leads.
- **Step 6:** The feature signal containing the prominent parts of QRS complexes in each of 12 leads are averaged to obtain one signal containing the information of QRS and non-QRS regions. This signal is further normalized as shown in Fig. 4(c).
- **Step 7:** This normalized signal is converted into its absolute form wherein all the negative values are converted into their equivalent positive values above the reference line. It is shown in Fig. 4(d).
- **Step 8:** The signal is further passed through the moving average window of duration ten seconds wherein in each window the mean of the samples within it is taken. This forms the upper envelope of the absolute signal as shown in Fig. 4(e).
- **Step 9:** K-means is applied to the signal obtained in the previous step where the value of K is set as 2. So the input signal is divided into two clusters representing QRS and non-QRS regions. The QRS cluster is assigned a value '1' and non-QRS is assigned as '0' as shown in Fig. 4(f).
- **Step 10:** Further, the resulting signal have peaks in close proximity of the QRS pulses. These spikes are combined with the QRS pulses so that exact width of the QRS complex could be obtained. This is done by running a moving window through the signal and taking the mean value of the samples within it. The signal is then thresholded at an appropriate level so that the signal above the threshold is one and is zero otherwise. Thus the result is a signal containing pulses of zeros and ones representing the positions of non-QRS regions and QRS complexes respectively.
- **Step 11:** Sometimes, there appear certain spikes due to peaky P and T waves**.** These are removed by average pulse width criterion. The continuous trains of all 1's are picked and using their duration average pulse duration of 1's is evaluated. Those trains whose duration comes out to be greater than the average pulse duration are retained and rests are discarded. Final signal representing the position of QRS complexes is shown in Fig. 4(g).

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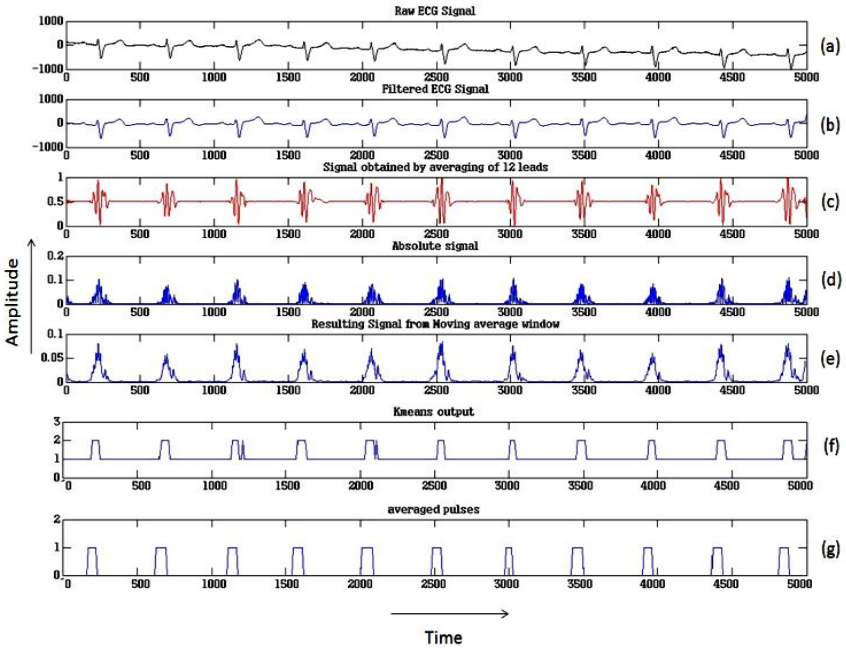


Fig. 4: Results depicted at each step of the algorithm. (a) Raw ECG Signal of Patient MO1_001; Lead V6. (b) Filtered ECG Signal. (c) Signal obtained by taking average of feature signal of each lead and then normalizing it. (d) Normalized signal is converted to the absolute signal. (e) Signal passed through moving average window of size 10 i.e. Mean of the absolute signal taken at an interval of ten samples. (f) K-means output signal. (g) Final positions of QRS complexes after passing the signal through moving average window of size 5 and average pulse width criterion.

## VII. RESULTS

Twelve lead simultaneously recorded ECG picked fromCSE (Common Standards for Quantitative Electrocardiography) ECG datset-3 has been used as a testing database to evaluate the performance of the proposed algorithm. This dataset consists of number of pathologies of various records recorded for the duration of 10 sec and sampled at 500 Hz thereby giving 5000 samples in each lead. The QRS detection is done in two folds wherein firstly the feature signal is obtained with Empirical Mode Decomposition followed by its classification using k-means algorithm. True Positive detection is when the QRS complexes are correctly identified by the automated algorithm. A false positive is defined as an error in data reporting when the algorithm falsely indictes presence of a QRS complex, when actually it is not present. A false negative is defined as an error when a test result improperly indicates no presence of a QRS complex, when actually it is present.

Sensitivity and predictivity are the two parameters on the basis of which the performance of the algorithm is evaluated. Sensitivity (Se) refers to the ability of the algorithm to correctly identify the QRS complexes in the ECG signal. Positive predictivity (+P)is defined as the ratio of true positives to the sum of true positives (TP) and false positives (FP). The predictivity indicates the accuracy of the identification of QRS complexes in ECG signals.

$$\mathrm{Se} = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}}$$

$$+\mathrm{P} = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FP}}$$

The proposed algorithm is able to detect the QRS complexes of 125 records in simultaneously recorded ECG signal with a detection rate of 99.42%. The performance parameters i.e. Se and +P are 99.39% and 99.93% respectively. The percentage of false positive (FP) is 0.06% and false negative is 0.61%.

- **Case I:** Fig. 5 shows the QRS detection for patient no. M01_110 of CSE ECG database. Though the QRS complexes appears to be of very small amplitudes as compared to P or T waves yet the detection is not too difficult here just because of the variations of QRS complexes w.r.t time is relatively higher as compared to P or T-waves. Further, the majority of leads except lead I has clearly distinct frequency range of the QRS complex as compared to P or T waves hence the detection of all 16 QRS complexes is obtained accurately with 100% detection rate.
- **Case II:**QRS detection for patient M01_053 is shown in Fig.6. The effectiveness of the algorithm is revealed in this case wherein cent percent detection rate is obtained. The detection is not affected by the problems like prominent P waves with their amplitudes comparable with the QRS complexes like in Leads I, II, III, aVR, aVL, aVF and baseline wander in leads III and aVR.

The proposed algorithm in combination with Empirical Mode decomposition and k-means is able to recognize the positions of QRS complexes accurately to an appreciable level reflecting the effectiveness of the algorithm and assisting in diagnosis of cardiac diseases.

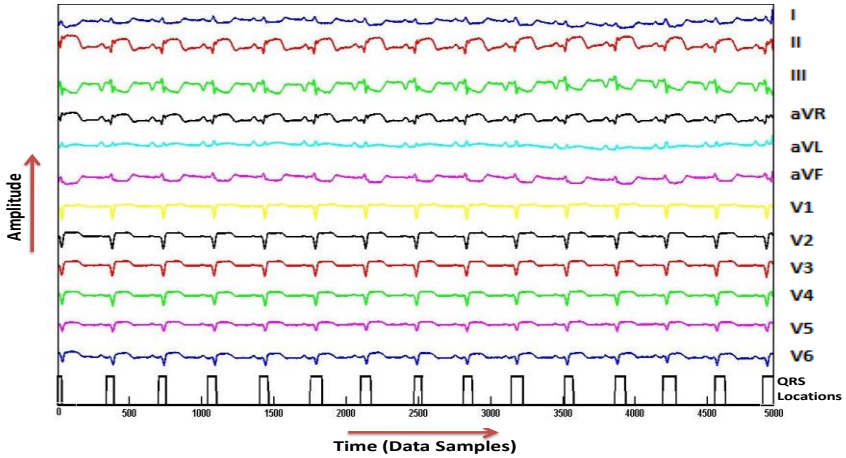


Fig. 5: QRS Detection of record M01_110 of CSE ECG Database

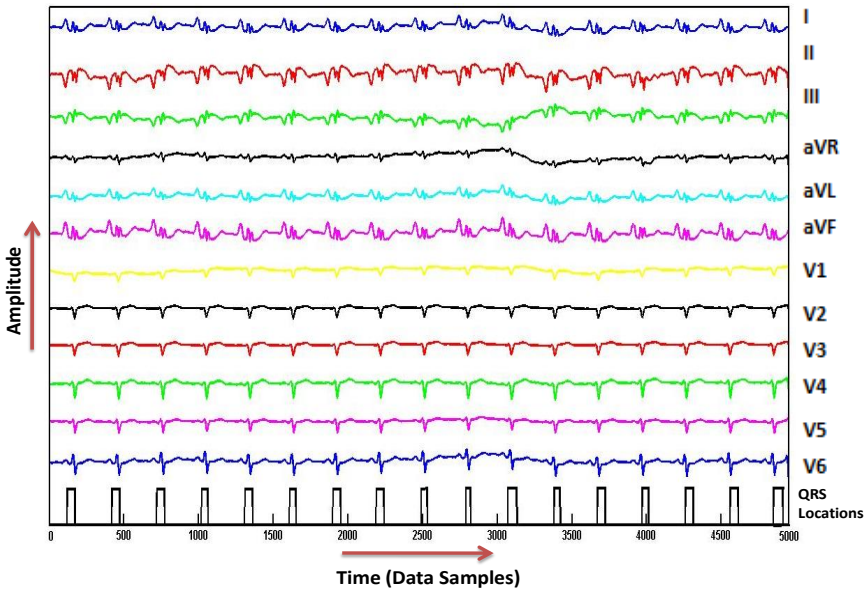


Fig. 6: QRS Detection of Record M01_053 of CSE ECG Database

## VIII. CONCLUSION

The QRS complex is the most prominent region of the ECG signal. Its identificationhelps the medical practitioners for diagnosing and curing heart diseases.An automated algorithm comprising of two fold QRS detection method is proposed in this paper. This algorithm employs Empirical mode decomposition on ECG signals to obtain intrinsic mode functions known as feature signals followed by k-means classifier. The proposed algorithm's results are quite efficient, reliable and encouraging. Thus, ECG has been established as a fast and reliable tool for deciphering the current status of the heart and is widely used in prognosis and diagnosis of various cardiovascular diseases and abnormalities.

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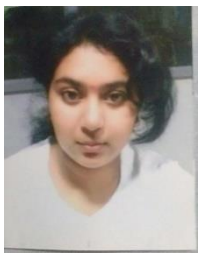

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