APPENDIX - II
A statistical approach for determination of time plane features from digitized ECG

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Abstract

This paper illustrates a method for time-plane feature extraction from digitized ECG sample using statistical approach. The algorithm detects the position and magnitude of the QRS complex, P and T wave for a single lead ECG dataset. The processing is broadly based on relative comparison of magnitude and slopes of ECG samples. Then the baseline modulation in the dataset is removed. The R-peak detection and baseline modulation is tested MIT-BIH arrhythmia database as well as 12-lead datasets in MIT-PTB database (PTDB) and available under Physionet. The overall accuracy obtained is more than 99%.

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1. Introduction

ECG, a graphic record represents the electric activation of the heart which takes place in a sequential order: One cardiac cycle in an ECG signal consists of the P-QRS-T waves. First the atria are depolarized (P-wave), then the ventricles the QRS complex, and finally the ventricles are re-polarized (T-wave). Each state can be associated with a heart activation time [3]. An experimental analysis on the database with various ECG shapes led us to model a beat by ten states: four iso-electric segments and two states per wave (Fig. 1):

state iso1: iso-electric line
state P1: first part of atrial activation
state P2: second part of atrial activation
state iso2: iso-electric line
state R1: first part of the ventricular activation
state R2: second part of ventricular activation
state iso3: iso-electric line
state T1: first part of the ventricular re-polarization
state T2: second part of the ventricular re-polarization
state iso4: iso-electric line

The clinical bandwidth used for recording the standard 12-lead ECG is 0.05–100 Hz. For monitoring applications, such as for intensive care patients and for ambulatory patients, the bandwidth is restricted to 0.3–50 Hz. QRS energy centered around 10 Hz, approximately in the range of 5–15 Hz range. P and T wave frequency is typically centered around 2.5–4.55 Hz. 2.5 s include 2–3 heart beats. 60–100 beats per minute constitute the standard heart rate. Heart rate slower than this leads to bradycardia and greater than this leads to tachycardia. ECG data is taken from 12 leads. Standard leads I, II and III are bipolar leads. aVR, aVL, aVF are unipolar extremity leads and are of low electric potential.

ECG signal is used for the analysis of different kind of heart diseases. Computerized automatic ECG measurement and analysis can be considered amongst the first application of computer in medicine. Computer assisted cardiac diagnosis is now an established area of research in biomedical engineering. For computer-aided analysis, at first, the analog ECG data need to be converted into a time sequenced digitized. This can be achieved by various methods, viz., scanning the paper ECG or using digitizers. ECG algorithms operate on these ECG data samples and can generate automatic outputs, including morphology, time-interval measurements, and rhythm analysis. Sometimes these outputs, accompanied by diagnostic statements can help a cardiologist to infer about cardiac condition of a patient [1–4].

Most of the clinically useful information in the ECG is found in the characteristic wave peaks and time durations of characteristic segments. ECG algorithms developed for different purpose employ computational techniques [5–10] for gradual elimination of insignificant portions of the ECG wave to reveal clinically significant portion. In most of the approaches, detection of R-peaks is the starting point. Once the R-peak positions are accurately determined in ECG dataset, tentative locations P, T-waves and ST
segment, etc., are found relative to the position of QRS, to reveal the complete cardiac period. In this sense, QRS detection provides the fundamental for almost all automated ECG analysis algorithms. Numerous QRS detection algorithms have been successfully implemented till date. Starting from simple derivative based methods, digital filters, ANN methods to wavelet based approaches have been used [11–15].

In support vector Machine (SVM) approach [16] the QRS detection rate obtained is 99.75%. Digital filtering based methods suffer from the disadvantage that QRS pass-band for different human are different and also overlaps with some artifact signals. To counteract this, adaptive matched filter was used that attempts to adjust it with changing signal shapes and noise levels [17]. A Neural-Network based adaptive matched filtering using hidden nonlinear model has shown better noise rejection [18]. Peak value extractor (PVE) is another approach where a morphological filter is followed by threshold based mapping operations to reveal the QRS peaks [11]. Owing to the high frequency content in QRS segment relative to other portions, Multiplication of Backward Difference (MOBD) algorithm, Okada algorithm, and Hamilton–Tompkins algorithm employ derivative and squared-difference approach to extract the QRS complexes [19].

In this paper a statistical approach is presented for extraction of time plane features from digitized ECG samples. The algorithm can operate on a single lead data at a time. First, all R-peaks in a 60 s database are accurately detected. Then baseline modulation in the dataset is corrected by an empirical formula. Finally, from the R-peaks other characteristic points in (Q, S, T, P) are detected by processing the relative magnitude and slopes comparison method. Finally, the time plane features of the lead are calculated by QRS width, QT, (QT), etc. are determined. The algorithm is tested with MIT-PTB database for normal and some abnormal datasets, leaving only Q, R, and S points. It is assumed that the minimum distance between two successive R-points can be 450 ms. A threshold criteria and slope comparison between samples is used to eliminate Q and S peaks, so that only R peaks are retained.

To ascertain the accuracy of R-peaks determination, interval between successive R-peaks is computed within a permissible band of 450–1300 ms. If difference between any two successive R-peak intervals exceeds 80 ms, it is concluded that the corresponding peak resembles either S or Qr or Qr. In such a case to determine the insignificant R-peak, some relaxation on R-slope threshold or direction criteria for slopes is allowed and the search for R-peak is reinitiated. If a valid R-peak search still fails, it is concluded that R-peak does not exist at all, or hidden with QS region. To find out the Q or S-peak (coincides), the direction criteria for slope is reversed and finally the Q (or S) peak is obtained.

(b) Baseline point detection and modulation correction:
Baseline of original ECG signal can be modulated by slow motion of the electrodes attached to the patient body and due to respiration of the patient during ECG procedure. Baseline modulation may lead to inaccurate determination of characteristics points like Q, S and also misinterpretation of ST segment. We consider that all the R-peaks may not be of equal height. So, baseline modulation correction is applied w.r.t. baseline points for the individual cycles. First, the baseline index points are accurately determined in the preceding TP segment for each R-peak in the dataset. Hence an array of such points is obtained. In case of baseline modulation, the focus of these points would be a curved line. The baseline modulation is corrected by vertically adjusting each sample depending on its position from a reference point for the R–R interval. The empirical formula used is given as:

\[
\text{Correction applied at point } i = \frac{x_i - b_{p_{i-1}} - b_{p_{i+1}}}{b_{p_{i+1}} - b_{p_{i-1}}} (y_{i+1} - y_{i-1})
\]

where \(x_i\) is the index of point \(i\); \(b_{p_{i-1}}\), \(b_{p_{i+1}}\), the two successive baseline point index (in ms); and \(y_{i+1}, y_{i-1}\) the ordinates (mV value) of baseline points

The baseline correction approach is shown in Fig. 2. After baseline correction a single baseline voltage is considered for the determination of characteristic points.

(c) Determination of P, Q, S, T points:
These points are determined for each cycle of the ECG dataset, starting from the R-peak in the corresponding cycle. First, the S-point is determined. From peak next 60 samples towards end of data array are sorted in ascending order in magnitude.
The minimum value corresponds to probable S-peak. Next, from this point, a slope threshold criteria-based search is applied to ±20 samples to find out the exact S-point. If the search fails, same procedure is applied for next higher value in the array and so on till the valid S-peak is found. For the case of insignificant S peak, as in case of qRs or Qr type waveform, the restriction on slope criteria is relaxed.

Next, the S-offset point is determined as follows. Starting from the S peak of the corresponding cycle, from the $S + 10$-point up to $S + 30$ point, for each point average slope of successive 15-points are calculated. The point with minimum average slope is taken as the valid S-offset point. The Q-point and the Q-offset point are determined in a similar approach starting from one R-Peak towards immediate preceding R-peak.

Region between two successive R peaks is divided into two halves. The T-peak is normally expected to be located in the left half, whereas the P-peak (of the following cardiac cycle) on the right half. A T-peak candidature is searched in the left region from S-offset point along the downside of the data (i.e. towards right side of the waveform) based on a slope and magnitude criteria. A sample having T-peak candidature should initially satisfy slope criteria. Towards upside (left) and downside (right) along 40 samples, a predefined slope criteria has to be matched. More than one sample may satisfy such criteria. Among them, the candidate with absolute maximum value of lead voltage w.r.t. baseline point is considered as the T-peak. For determining T onset point, starting from T wave peak upto next 90 points towards the beginning of the data array left side average slope is calculated for each data points. The point with minimum average slope is considered as T onset point. For determining T offset point, in a similar way starting from T wave peak upto next 90 points towards the end of the data array a search is done. The point among 40 points on right side with minimum slope is considered as T wave offset. A similar approach is followed in the right half of R–R interval for the determination of P wave and its constituent points. Fig. 4 illustrates the T and P wave constituent points’ determination along with their initiation search point.

After determination of all cardinal points, the following time-plane features are calculated:

- P wave width
- T wave width
- PR interval
- QRS width
- ST-segment width
- QT interval
- Corrected QT interval, $(QT)_{c} = \frac{QT}{\sqrt{RR}}$

3. Results and discussions

The ECG signal processing algorithm developed was accurately tested using normal and abnormal data in MIT-PTB database and MIT-BIH arrhythmia database under Physionet. Physionet [20] website is founded by National Institute of Biomedical Imaging and Bioengineering (NIBIB) and National Institute of General Medical Science (NIGMS), under US department of Human Health and Human Services. Physikalisch-Technische Bundesanstalt (PTB),
the National Institute of Germany, has provided a compilation of digitized ECGs for research, algorithmic benchmarking or teaching purposes to the users of Physionet. The ECGs are collected from healthy volunteers and patients with heart diseases. MIT-PTB database (PTBDB) provides digital recording of physiological signals and related data for use by the biomedical research community. It is an established benchmark for testing biomedical systems and algorithms. The MIT-BIH Arrhythmia Database (MITDB) [21] contains 48 half-hour excerpts of two-channel ambulatory ECG recordings (MLII and v5), with a recording rate of 360 samples per second and 11-bit resolution over a 10 mV range.

The first stage of ECG signal processing is accurate determination of R-peaks. First, R peaks are determined on 60 s dataset from MITDB database Figs. 6 and 7 show R peak detection and baseline correction for normal patients (PTBDB).
modulation correction result for PTB-DB for one normal and abnormal patient. The MIT-DB data files contain 360 samples in 1 s duration. That means, the sampling instants are uneven. Since the algorithm is developed for 1 ms sampling interval, it cannot be directly applied to MIT-DB data files. By interpolation method the intermediate data samples in MIT-DB data files are regenerated, and hence the modified data file has 60,000 samples in one minute, i.e., 1 ms sampling interval. So, the developed algorithm is now compatible with MIT-DB data files. Fig. 5 represents R-peak determination and baseline modulation using regenerated MIT-BIH arrhythmia database.

Next, 60 s data from PTB-DB database for 12 leads of different normal and abnormal patients are also tested. Quality figure of R-peak detection is given by R-peak sensitivity, given as:

\[ R_c = \frac{TP}{TP + FN} \]

where TP (True-Positive) stands for correctly found R-peaks and FN (False-Negative) for missed R-peaks.

Positive Predictivity is defined as

\[ P^+ = \frac{TP}{TP + FP} \]

where FP stands for the number of false positive misdetections.

Tables 1 and 2 show R-peak detection sensitivity for MITDB and PTB-DB, respectively. For MITDB 20 databases were tested. In case of PTBDB, 360 leads including normal and abnormal (Anterio, Anterio Septal, Anterio Lateral) were tested. The presented algorithm has achieved a good performance with a sensitivity of 99.96% and the predictivity of 99.95%. Since the PTB databases have different R-R intervals, a measure of correct feature extraction is represented by coefficient of variation, defined as

\[ \text{Coefficient of variation (Cv)} = \frac{\text{standard deviation} \sqrt{\bar{x}}}{\text{average} \bar{x}} \]

Table 3 shows the coefficient of standard deviation of variation of R-R interval calculated on 60 s database. Second, it is verified by making a relative comparison of algorithmically calculated R-wave peak time plane index points with manually observed time axis index values.

Next, using 60 s PTB-DB data files, time plane features for normal and abnormal patients is performed. This is shown in Figs. 8 and 9, where the individual characteristic points are shown by vertical coloured lines using a span of 4000 samples for visual clarity. Table 4 shows the relative comparison between algorithmically obtained mean and manually computed mean and coefficient of standard deviation of QRS width and QT interval, respectively, for lead I, II, while for other leads, the proposed algorithm yields equally good result. Considering all 12-leads of a standard ECG database, the average error obtained with 200 single lead MIT-PTBDB is 3.42%.

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**Table 1**

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<th>Patient_ID</th>
<th>Lead V5 (%)</th>
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<td>118</td>
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**Table 2**

<table>
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<th>Category</th>
<th>Lead I (%)</th>
<th>Lead III (%)</th>
<th>aVR (%)</th>
<th>VT4 (%)</th>
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<td>S0311 LRE</td>
<td>Normal</td>
<td>100</td>
<td>100</td>
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<tr>
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<tr>
<td>S0137 LRE</td>
<td>Anterio Septal</td>
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<tr>
<td>S0148 LRE</td>
<td>Inferio Lateral</td>
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**Table 3**

<table>
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<th>Patient_ID</th>
<th>Category</th>
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<th>Lead III</th>
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<td>0.720</td>
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<td>0.971</td>
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<td>Inferio Lateral</td>
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<td>0.719</td>
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Fig. 8. Detection of characteristic points in ECG waveform for normal patients.
Table 5 compares the QRS detection rates of the proposed work with some reported works. It is observed that our work yields equally good result with them.

4. Conclusion

A statistical approach for time-plane feature extraction for digitized ECG samples is described in this communication. The algorithm is validated with a 20 leads from MIT-BIH arrhythmia database (mit-db) and 360 leads from MIT-PTB diagnostic database (ptb-db). The algorithm detects the R-peaks accurately, and then determines other characteristics points w.r.t the R-peak for each cycle. Baseline modulation detection is done for accurate determination of characteristic points. The R-peak detection results show that the proposed method is equally good with other reported works. For time plane feature extraction, the proposed method can be considered fairly accurate.
5. Summary

Computer aided ECG signal analysis is one of the prime areas of research for the scientists for last few decades. This paper illustrates a method for time-plane feature extraction from digitized ECG sample using statistical approach. The algorithm detects the position and magnitude of the QRS complex, P and T wave for a single lead ECG dataset consisting of at least 60,000 samples. The processing is broadly based on relative comparison of magnitude and slopes of ECG samples for single lead data at a time. The R-peaks are gradually segregated from other samples by sorting the dataset based on some restrictions applied.

At first, R-peaks in the dataset are determined. For this, samples are sorted in descending order of magnitude and then grouped in ascending order of position (indices). The local maxima of each group are determined based on some slope and magnitude comparison restriction. Hence the neighbouring members of an R-peak are eliminated to get the R-peaks. To ascertain the accuracy of R-peaks determined, successive R-peak differences are computed. The algorithm also can detect a rS or Qr or QS in the dataset.

Baseline modulation correction is necessary for accurate determination of characteristic points in the ECG wave. The baseline modification is removed by using an empirical formula, and the data points between two successive baseline points are proportionally shifted in vertical direction. This process is carried to the entire dataset to get all the baseline points in a horizontal line.

From the each R-peak, S, S-offset, Q, Q-offset, T, T-onset, and T-offset points are determined for each cardiac cycles. For S-peak determination, from R peak next 60 samples towards end of data array are sorted in ascending order in magnitude. The minimum value corresponds to probable S-peak. Next, from this point, a slope threshold criteria-based search is applied to ±20 samples to find out the exact S-point. If the search fails, same procedure is applied for next higher value in the array and so on till the valid S-peak is found. Starting from S-peak, S-offset point is found by detecting the minimum average slope point for next ±20 samples. The Q-peak, and then Q-offset is found by a similar approach from R-peak towards left side of database. The T-point is determined by a two step process: the first one being a slope threshold based criteria to find out all candidates, followed by determining the absolute maximum value w.r.t baseline point from S-offset within the first half of two equal regions between two successive R-peaks. Similarly the P-peak is found in the right half of the same zone. The onset and offset points of T (and P) peaks are calculated by determining the points of minimum average absolute average on either side of T (and P) peaks within predefined span of the dataset.

The R-peak detection and baseline modulation is tested MIT-BIH arrhythmia database (mit-db) as well as 12-lead datasets in MITPDB database (ptb-db) and available under Physionet. Cardiac point detection algorithm is tested with 360 normal and abnormal PTDB databases. The overall accuracy obtained is more than 99% which is acceptable as compared to other standard methods.

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References

An approach to determine the amplitude features from ECG records

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Abstract: In this work, an electrocardiogram feature extraction algorithm is developed by analysing ECG signal in time domain. At first all R peaks are determined using amplitude and slope based criteria. Base line modulation was removed from ECG signal by making the midpoint of successive R to R regions to lie on the same horizontal line and thereby adjusting the values of all intermediate points proportionately. With respect to detected QRS peak positions, other wave peaks are determined based on slope and then amplitude based search in the respective searching zone. P, Q, R, S and T wave peak positions, their onset and offset points and their heights w.r.t. the baseline are calculated. The algorithm is validated with mit-db and ptb-db ECG data files over a number of class of abnormalities, and achieved an average variance and percentage error of 0.0020 and 1.88% for wave peak height computation.

Keywords: ECG; QRS detection; amplitude features; physionet; ptb-db; mit-db; baseline; onset; offset.

Reference to this paper should be made as follows: Chatterjee, H.K., Gupta, R. and Mitra, M. (2013) ‘An approach to determine the amplitude features from ECG records’, Int. J. Biomedical Engineering and Technology, Vol. 12, No. 2, pp.130–146.

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1 Introduction

Analysis of Electrocardiogram (ECG) signals is an important task in diagnosis and detection of cardiac anomalies. One cardiac cycle in an ECG signal consists of the P-QRS-T waves, as shown in Figure 1. Most of the clinically useful information in the ECG is found in the widths and amplitudes of characteristic wave peaks, and time interval and slope between some characteristics points. Amplitude features are height and polarities of different component wave peaks (P, Q, R, S, T) of ECG signal, QRS vector amplitude and phase. As per the significance of amplitude features are concerned, Q wave amplitude greater than one third QRS amplitude (R + S) or greater than one fourth of R wave indicate presence of infarction. In Myocardial Infarction (MI) sharply pointed symmetrical T wave are found. Unusually tall T waves are found in MI, ischemia without infarction, hyperkalemia, CVAs and sometimes in psychotic patients. Increased amplitude of P wave (more than 3 mm in height) gives rise to atrial hypertrophy, A-V valvular disease, hypertension, cor-pulmonale and congenital heart disease. Peaking of P wave corresponds to Right atrial strain. Absence of P waves indicates A-V nodal rhythms and S-A Block. Elevated S-T segment, tall and wide T waves and increased R wave amplitude in affected lead positions are found in hyperacute phase of MI. In Fully evolved phase of MI, Deep and wide Q wave or QS wave, elevated and coved S-T segment and inverted arrowhead T wave are found.

Figure 1 One cycle of ECG signal showing different amplitude features (see online version for colours)
Most of the published literature have tried to find out the temporal location of significant ECG wave peaks, but does not give clear indication about actual features, which are clinically significant for the purpose of diagnosis of heart diseases. Many algorithms are computationally intensive. Some literatures have used FIR or IIR filters to reduce noise, but it may deform the original ECG signal. The inclusion of a High Pass Filter (HPF) may reduce the baseline modulation of ECG signal, but may result into wrong interpretation of ST segment analysis. In the present literature above mentioned problems are addressed. Clinically significant amplitude features of ECG component wave peaks are determined, with a simpler approach and good detection rate. Baseline modulation is minimised, without using conventional filters, so that the original ECG signal does not get deformed.

2 Literature review

Most of the published algorithms start with detection of ECG QRS of the ECG beats, which is taken as the reference point to find other wave peaks. ‘Amplitude and first Derivative’, ‘first and second derivative’ and ‘filter’ based QRS detection methods are described by Morizet-Mahoudeaux et al. (1981), Fraden and Neumann (1980), Gustafson (1977), Balda (1977), Ahlstrom and Tompkins (1983) and Engelse and Zeelenberg (1979), respectively. Morizet-Mahoudeaux et al. (1981) and Fraden and Neumann (1980) calculated an amplitude threshold as a fraction of the largest positive valued element of ECG data array \( x(n) \) and calculated the first derivative array \( y(n) \) using difference equation 

\[
y(n) = x(n+1) - x(n-1).
\]

Morizet-Mahoudeaux et al. (1981) proposed that a QRS candidate occurs when three consecutive points in \( y(n) \) exceed a positive slope threshold and within the next 100 ms two consecutive points exceed the negative (descending slope) threshold. All data points in the ECG between the onset of the rising slope and before the end of the descending slope must meet or exceed the amplitude threshold. Fraden and Neumann (1980) at first rectified and clipped \( x(n) \) w.r.t. an amplitude threshold, then \( y(n) \) was formed, and concluded the occurrence of QRS when a point in \( y(n) \) exceeds the fixed constant threshold. Gustafson (1977) formed \( y(n) \) using same difference equation and suggested that a point can be classified as a QRS candidate if four consecutive derivative values exceeds a threshold and two consecutive sample points have positive slope amplitude products. Balda (1977) scanned the scaled and summed first and second derivative array until a point exceed a fixed threshold and at least six points, out of next consecutive eight points also exceeds the threshold for detection of QRS candidate. Ahlstrom and Tompkins (1983) also have used similar approach based on first and second derivative, but with different difference equations. They calculated a primary and secondary threshold as a percentage of summed first and second derivative arrays. A point is classified as a QRS candidate, if it exceeds primary threshold and six consecutive points exceed secondary threshold. According to Engelse and Zeelenberg (1979), the differentiated, filtered (62.5 Hz notch), ECG data \( \tilde{x}(n) \) is passed through a digital low-pass filter (LPF), with difference equation 

\[
y'(n) = \tilde{x}(n) + 4\tilde{x}(n-1) + 6\tilde{x}(n-2) + 4\tilde{x}(n-3) + \tilde{x}(n-4).
\]

Two thresholds are used, equal in magnitude but opposite in polarity. The output of the LPF is scanned until a point with amplitude greater than the positive threshold is reached. This point is the onset of a 160 ms search region. The number of alternate threshold crossings is used to classify the initial crossing as either a baseline shift, a QRS candidate. Hamilton and Tompkins
(1986) described a real time QRS detection consisting of five stages (LPF, HPF, differentiation, squaring and time averaging of the signal). Real-time analysis of Ventricular Late Potentials using wavelets and FFT spectrum is addressed by Sivakumar et al. (2011), with simultaneous processing and recording of the next beat, for increasing speed of processing. In the work of Mukhopadhyay et al. (2012) after doing Hilbert transform on first derivative of the ECG signal, samples having amplitude within a certain threshold, if undergo slope reversals are identified as R-peaks. Q, S, QRS onset and offset points are also detected properly. Novel FECG Blind Source Extraction (BSE) algorithm based on Blind Source Separation (BSS) in noise is presented by Wang et al. (2012). Automatic ischemic beats classification has been addressed by Murugan and Radhakrishnan (2012) using Genetic-based Least Square Support Vector Machine (GLSSVM). In this paper, the Genetic Algorithm (GA) and fuzzy logic is combined with Principal Component Analysis (PCA) and Independent Component Analysis (ICA) (FGPCA and FGICA) to improve their performance. The results demonstrated that the GLSSVM with FGICA achieved greater accuracy higher than the other automated diagnostic systems. In the work of Lindecrantz and Lilza (1988), in a similar approach to matched filtering but instead of computing the cross correlation between the template and the signal, the algorithm searches for the minimum of the Average Magnitude Cross Difference (AMCD), and thus avoiding multiplications to make the algorithm computationally inexpensive.

Use of Simultaneous Perturbation Stochastic Approximation (SPSA) method in ECG Analysis is described (Gerencsér et al., 2002). Analysis of beat to beat variability of frequency contents in the electrocardiogram using two dimensional Fourier transforms has been discussed (Spiegl et al., 1998). Murthy and Durga Prasad (1992) described a pole-zero method of ECG analysis. Application of adaptive signal processing for determining the limits of P- and T-waves in an ECG have been discussed (Olivas et al., 1998). Sameni et al. (2008) described multichannel electrocardiogram decomposition using periodic component analysis. For gradual elimination of insignificant portions of the ECG wave to reveal clinically significant portion, a mathematical morphology based QRS detection technique is illustrated (Trahanias, 1993). Poli et al. (1995) illustrated an optimum linear and nonlinear QRS Detector’s design. Starting from simple derivative based methods, digital filters, Artificial Neural Network based methods to wavelet based approach of ECG signal processing and characteristics points determination have been addressed (Li et al., 1995; Suzuki, 1995; Martinez et al., 2004; Legarreta et al., 2005; Arzevo et al., 2008; Ghaffari et al., 2008). In Support Vector machine (SVM) approach (Mehta and Lingayat, 2009) the QRS detection rate obtained is 99.75%. Digital filtering based methods suffer from the disadvantage that QRS pass-band for different human are different and also overlaps with some artefact signals. To counteract this, adaptive matched filter was used that attempts to adjust it with changing signal shapes and noise levels (Hamilton and Tompkins, 1988). A Neural-Network based adaptive matched filtering using hidden nonlinear model has shown better noise rejection (Xue et al., 1992). Mehta and Lingayat (2008) detected QRS complexes are removed from the ECG signal by replacing them by a based line, for detection of T-waves, in next stage. The slope is used as an important criterion because slope of the signal is much more in the T-wave region than in the region of P-wave. The SVM is trained on a set of training data covering wide variety of ECG signals with different morphologies of T waves picked from (Common Standard of Electrocardiograph) CSE ECG database. After testing, a train of 1’s is obtained at the output of SVM, when the window traverses through the T
wave region and –1 for the remaining region. The train of 1’s is picked and using their
duration, average pulse duration of 1’s is evaluated. Those trains of 1’s, whose duration
turns out to be more than the average pulse duration are detected as T waves. At third
stage for the detection of P-wave, The T-waves are removed from the ECG signal, by
replacing them with a baseline. And similar procedure tried for P-wave detection.

In this paper, the objective is to determine the wave peaks and hence compute
amplitude features from pre-recorded ECG data, primarily based on statistical
comparison of a group of samples in regard to their relative magnitude and slope. In the
present work, only baseline modulation is minimised by an empirical method, without
using any filter after the R peaks are determined. The features determined in this paper
are P-, Q-, R-, S- and T-wave peak positions, their amplitudes with respect to the onset
and offset points of the corresponding wave peaks. The algorithms presented in this
section are applied directly on single lead digitised ECG signal sampled at 1 kHz
frequency. The algorithm is divided into a number of segments, each of which is
designated to extract certain features of the ECG signal. First, the peak of the QRS
complex with its high dominated amplitude in the signal is detected. Then Q- and
S-waves are detected, to detect a complete QRS. P- and T-waves are found next with
their respective onsets and offsets. The following amplitude features are determined
using the following formula:

\[
R\text{-wave height} = R \text{ peak amplitude} - R \text{ peak baseline amplitude}, \text{ where } R \text{ peak baseline amplitude} = (Q\text{-wave onset value} + S \text{ peak offset value})/2
\]

\[
Q\text{-wave height} = Q \text{ peak amplitude} - Q\text{-wave onset amplitude}
\]

\[
S\text{-wave height} = S \text{ peak amplitude} - S\text{-wave offset amplitude}
\]

\[
T\text{-wave height} = T \text{ peak amplitude} - T \text{ peak baseline amplitude}, \text{ where } T \text{ peak baseline amplitude} = (T\text{-wave onset value} + T\text{-wave offset value})/2
\]

\[
P\text{-wave height} = P \text{ peak amplitude} - P \text{ peak baseline amplitude}, \text{ where } P \text{ peak baseline amplitude} = (P \text{ peak onset value} + P \text{ peak offset value})/2
\]

3 Materials and methods

The feature extraction is performed in the following sequence. All the R peaks in the
entire dataset are determined at first since these are taken as reference points to detect the
other wave components in the respective cycle in a window based search of appropriate
width. Therewith, the baseline modulation in the ECG dataset is removed so as to use a
single baseline voltage for the entire dataset for detection of Q and S peaks. Finally, the
wave peaks and respective onset and offset points are detected.

3.1 R-peak detection

R peak detection is performed in following steps:

1 For determination of R-wave peaks, entire dataset is scanned with an amplitude
based search and then slope criteria are imposed. At first a single lead ECG dataset is
sorted in descending order of magnitude. First 4% samples empirically selected, are
chosen from sorted dataset to form a new dataset, which may possibly include all
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R-wave peak along with some neighbours and some T-wave peaks also. Q and S peak gets discarded from the dataset, at the first screening of the dataset, as they are obviously being negative.

2 Derived dataset is rearranged in ascending order of their index.

3 The derived new dataset is then regrouped into a number of blocks in the ascending order of indexes, such that successive data points within a block differs from previous sample by not more than 20 points (empirically selected). If index difference exceeds 20 later sample is assumed to lie on next QRS zone (i.e. in the next group).

4 Maxima selection is done in each group (probable R-wave peak candidate).

5 Around each such maximum, ±450 ms searching window is formed.

6 From each of such window formed, maximum slope (average of both sides) point is determined. Average absolute slope is computed by taking a ±20 ms window around each point in the searching window. The point having maximum slope in the said ±450 ms region, eliminates the presence of tall T- or P-wave peaks in that region, extracting R-wave peaks only in that region. If \( m_i \) represent magnitude of \( i \)-th sample, then Average absolute slope (Slp\(_{\text{avg}}^{\pm20} \)) of \( i \)-th sample (in ±20 ms window) is computed as:

\[
\text{Slp}_{\text{avg}}^{\pm20} = \frac{\left( (m_i - m_{i-20}) + (m_i - m_{i+20}) \right)}{2}
\]

A data block centred on a T peak may get eliminated by ±450 point search around maximum value point in the respective block. As it will try to detect just previously detected R wave peak. This is because although in most of the cases, T- and P-wave amplitude is much less than R-wave peak, but in some situations T-waves, may even be larger than R-waves, but obviously having smaller slope than R-waves.

7 Next, R slope threshold criteria is imposed to eliminate T and P peaks. 20 point slope on both side (left and right) \((m_i - m_{i-20})\) and \((m_i - m_{i+20})\), respectively of the concerned R-wave peak must be greater than R-wave slope threshold value (R\(_{\text{slpth}}\)). The R-wave slope threshold value is empirically determined from a number of ECG leads from physionet database (see http://www.physionet.org).

8 It is checked whether rS or Qr (insignificant R-wave) or QS (negative R-wave) exists. If the R-wave peak intervals do not remain within a span of 450–1300 ms or if the difference between successive R peak intervals exceeds 80 ms, it is concluded that concerned dataset does not contain dominant R-wave peak, but contain rS or Qr or QS type peak. In such a case to determine less dominant R-wave peak, some relaxation on R slope threshold or direction criteria for slope is allowed, and search for R-wave peak is reinitiated. In that case it is checked whether either side 20 point slope around the concerned R-wave peak is greater than R-wave slope threshold value (R\(_{\text{slpth}}\)). And the respective other side 5 point slope also should exceed \((R_{\text{slpth}})/5\). If a valid R peak search still fails, it is concluded that concerned dataset contain QS type peak. In such a case to determine coincided Q and S peak, direction criteria for slope is now reversed, and by using the same approach entire dataset is scanned a new way by sorting it in ascending order of magnitude and QS peak is determined.
3.2 Baseline modulation correction

Due to slow motion of electrodes attached to the patient body or respiration of the patient during recording, ECG signal baseline can get modulated, which may lead to misdetections of characteristics feature of different waveforms. Baseline modulation is eliminated from the ECG dataset using following steps:

1. Selection of provisional baseline points as midpoint of R-R intervals. So a dataset with \( x \) number of detected R peaks will have \( (x - 1) \) provisional baseline points.

2. Adjusting the magnitude of all sample values proportionately between two successive provisional baseline points, such as to keep baseline points to lie on the same horizontal line.

To eliminate baseline modulation effect, a baseline point is empirically chosen to exist at the middle of R-R interval. For each R-R segment in the dataset, each point is shifted by an amount which is proportional to the interval between the point and previous baseline point. As according to Figure 2, point A corresponds to the provisional baseline point of \( p \)-th cardiac cycle having time plane index value \( i \) and magnitude \( m_A \). Point B corresponds to the provisional baseline point of \( (p + 1) \)-th cycle and have the coordinate \( (i + n, m_B) \). If no base line modulation is present in the signal, then point A and B are supposed to be in the same horizontal line, i.e. must have same magnitude. Hence to minimise baseline modulation effect, magnitude of any point C \( (i+k, m_C) \) in between A and B needs to be adjusted by an amount \( H \). \( H \) is defined as in equation (7). For all successive R peak locations identified, successive R-R intervals are determined. If \( R_1, R_2, R_3, \ldots \) represent successive R peak locations, then \( \Delta R_1, \Delta R_2, \ldots \) represent successive R-R intervals, where \( \Delta R_i \) is calculated as in equation (8). If \( R-R_{avg} \) represents average R-R intervals, then for each \( \Delta R_i \) following condition is checked in equation (9):

\[
H = (m_A - m_B) \times \frac{k}{n} \quad (7)
\]

\[
\Delta R_i = R_{i+1} - R_i \quad (8)
\]

\[
\left| R - R_{avg} - \Delta R_i \right| < 150 \text{ ms} \quad (9)
\]

Figure 2 Baseline modulation corrections (see online version for colours)
If for any $AR$, the condition is violated then after baseline correction R peaks are again determined from the derived dataset. This is because before baseline modulation correction, some R peaks may have been missed during initial amplitude based screening of the entire dataset.

### 3.3 Fiducial point detection

It is assumed that Q- and S-wave have the same slope as that of R-wave. For determining S-wave peak, following steps are performed:

1. The region between an R peak and next 30 samples (empirically determined) is sorted in ascending order of sample values to generate array $y_i$.

2. If both side 20 point slope around the minimum value point of array $y_i$ satisfies R slope threshold value, considered to be S peak. Both side 20 point slopes must be negative going towards the concerned S peak. If $m_i$ represent magnitude of $i$-th sample, then condition $(m_{i + 20} - m_i) > R_{sph}$ and $(m_{i - 20} - m_i) > R_{sph}$ is checked for minimum value point, where $i$ is the point to be considered as S-wave peak.

3. If the minimum point does not satisfy the criteria, then next higher value in that region is searched. Because some ST segment may have downward slope, and any point in the ST segmented can be wrongly interpreted as S-wave peak.

4. If still the search fails, then it is concluded to be the case of insignificant S-wave. In such case some relaxation on slope criteria is imposed, to detect insignificant S-wave. Relaxation means at least R-wave side slope around the concerned wave peak must exceed R slope threshold value. That means condition $(m_{i - 20} - m_i) > R_{sph}$ is checked only.

For determining S-wave offset following steps are used:

1. For all points in the region between $i_S + 10$ to $i_S + 30$ ($i_S$ represent index of a S peak), successive 20 point absolute average slope is calculated. That means for all point $i$ in the region $|m_{i + 20} - m_i|$ is calculated.

2. The point with the minimum slope is considered S offset point.

3. The provisionally selected point must also satisfy a slope threshold criteria (i.e. $(m_{i} - m_{i - 20}) > R_{sph}$, if $i$ be the concerned S offset point) towards the S peak in case of significant S-wave.

Similarly for determining Q-wave peak, the minimum value point in the interval between last detected R peak and previous 30 samples are chosen. If both side 20 point slopes around the point satisfies R slope threshold value, is considered to be Q peak. Both side 20 point slopes must be negative going towards the concerned Q peak. If $i$ be the concerned point and $m_i$ represent magnitude of $i$-th sample, then condition $(m_{i + 20} - m_i) > R_{sph}$ and $(m_{i - 20} - m_i) > R_{sph}$ is checked for minimum value point. If the minimum point does not satisfy the criteria, then next higher value in that region is searched for. If still the search fails, it can be the case of insignificant Q-wave. In such case some relaxation on slope criteria is imposed, to detect insignificant Q-wave. For determining such insignificant Q-wave, only R-wave side slope around the concerned point (i) is checked to exceed R slope threshold value. That means condition $(m_{i + 20} - m_i) > R_{sph}$ is checked only.
If $i_Q$ represent index of a Q peak then for determining Q-wave offset, for all points in the region between $i_Q - 10$ to $i_Q - 30$, last (previous) 20 point absolute average slope (i.e. towards the beginning of the data array) is calculated. That means for all points $i$ in the region, \[ |m_{i-20} - m_i| \] is calculated. The point with the minimum slope is considered Q-wave offset point. The point must also satisfy a slope threshold criteria (i.e. $m_i - m_{i+20} > R_{\text{slope}}$, if $i$ be the concerned Q offset point) towards the Q peak (towards the end of the data array) in case of significant Q-wave.

An ECG cycle can be considered to be consisting of a QRS region and a non QRS region. Non QRS region exists within R-R interval between the S offset point and subsequent Q-wave onset point. T- and P-wave lie in the left half and right portion of the non QRS region respectively as shown in Figure 3. T and P-wave can be positive or negative. For determining T-wave peak a search is made on the left half portion of the non QRS region.

Figure 3  Non QRS region where T, P peak exists

T peak detection is performed in the following steps:

1. For all points in the left half portion of non QRS region, both side (left and right) 40 point slopes are determined.
2. The points satisfying a slope threshold criteria mentioned below are selected. To satisfy slope threshold criteria, the point $i$ is checked so that it satisfies following two conditions.

\[
\text{Cond1:} \quad |m_i - m_{i+40}| > TP_{\text{syst}} \quad \text{and} \quad |m_i - m_{i-40}| > TP_{\text{sys}}
\]  

(10)

That means both side absolute slope exceeds a threshold value.

\[
\text{Cond2:} \quad (m_i - m_{i+40}) > 0 \quad \text{and} \quad (m_i - m_{i-40}) > 0
\]  

(11)

or

\[
(m_i - m_{i+40}) < 0 \quad \text{and} \quad (m_i - m_{i-40}) < 0
\]  

(12)

That means both side slope is either positive going or negative going towards the peak.
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where TP_{th} is empirically determined T- and P-wave 40 point slope threshold value.

3. Amongst the selected sample points, which already satisfied the conditions mentioned in step 2 of T peak detection, the point having maximum absolute height with respect to current local baseline is considered as T-wave peak.

If \( i_T \) be an already detected T-wave peak point, then for determining T-wave onset, following steps are used:

1. For all points \( i \) in the region between \( i_T - 10 \) to \( i_T - 90 \), last (past) 20 point absolute average slope \(|m_i - m_{i-20}|\) and forward 40 point slope magnitude \(|m_i - m_{i+40}|\) (i.e. from that point on towards the T peak) is calculated, as shown in Figure 4.

2. The sample points are sorted in ascending order of last (past) 20 point absolute average slope.

3. The point with the minimum last 20 point slope, is checked, so that its forward 40 point slope magnitude \(|m_i - m_{i+40}|\) exceeds T- or P-wave slope threshold value (TP_{slpt}).

4. If the criteria are satisfied, it is considered as T onset point.

5. If the criteria is not satisfied, then the point with next higher value of last 20 point slope is checked and so on.

Figure 4  T-onset point determination (see online version for colours)

Similarly for determining T-wave offset point a searching is made in the region from \( i_T + 10 \) to \( i_T + 90 \). The point having minimum next 20 point slope and backward slope magnitude from that point on towards the T peak, exceeds a threshold value, and is considered T offset point.

For determination of P-wave peak a similar type of search (as for determining T-wave peak) is made on the right half portion of the non QRS region. For determination of P-wave onset and offset point also a similar type of searching (as for determining T-wave onset and offset point) is made in the region \( i_P - 10 \) to \( i_P - 90 \) and \( i_P + 10 \) to \( i_P + 90 \), respectively where \( i_P \) corresponds to an already determined P-wave peak index position.
4 Testing and results

The developed algorithm is validated with normal and abnormal data in MIT-PTB (ptb-db) database and MIT-BIH (mit-db) arrhythmia database under Physionet (see http://www.physionet.org). The QRS detection algorithm is tested with arbitrarily chosen 20 leads from mit-db data files, each containing 30 minute data and 360 leads from ptb-db dataset each containing 60 second data. ECG component wave amplitude feature extraction is validated with a total of 360 lead data using normal and abnormal patients obtained from ptb-db database. 40 leads are arbitrarily taken from normal patient and rest are taken from a diversity of Myocardial Infarction (MI) patients which include anterio, inferio, anterio lateral, inferio lateral, inferio posterio lateral and anterio septal categories. Ptb-db data files contain 12 lead ECG data for each patient-record number combination and millivolt level of ECG signal sampled at 1 kHz. Mit-db data files contain single lead data for a number of patients at 360 Hz sampling. But our algorithm is developed for 1 ms sampling interval. Hence to make the algorithm compatible with the mit-db data files, they are up sampled to 1 kHz sampling rate using interpolation method.

At first R-peaks are determined accurately for each of the 60 second dataset. Figures 5(a) and (b) shows R peak detection correctness and baseline modulation correction result for two single lead mit-db data files. Secondly it is verified by making a relative comparison of algorithmically calculated R-wave peak time plane index points with manually observed time axis index values.

![Figure 5](image.png)

Then different fiducial points corresponding to different characteristic wave peak points and their respective onset and offset points are determined. Figures 6 (a–c) illustrate the accurate detection of all characteristic points, which are shown by separate coloured dots.

Sensitivity ($S_e$) and positive predictivity ($P^+$) of R peak detection algorithm is defined as:

$$S_e = \frac{TP}{TP + FN}$$

(13)
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\[ P_+ = \frac{TP}{TP + FP} \]  

where TP is the number of true positive detections, FN stands for the number of false negative detections, and FP stands for the number of false positive misdetections. Table 1 shows sensitivity values for some of the mit-db data files. Table 2 also compares the QRS detection rates by different reported works. The presented algorithm has achieved a good performance with the sensitivity of 99.96% and the predictivity of 99.95%.

Table 1  R-point detection sensitivity table for MIT-BIH arrhythmia data

<table>
<thead>
<tr>
<th>Patient-ID</th>
<th>Lead</th>
<th>( S_+ (%) )</th>
<th>( P_+ (%) )</th>
<th>Patient-ID</th>
<th>Lead</th>
<th>( S_+ (%) )</th>
<th>( P_+ (%) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>100</td>
<td>II</td>
<td>100</td>
<td>100</td>
<td>112</td>
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<td>V5</td>
<td>100</td>
<td>100</td>
<td>114</td>
<td>V5</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>103</td>
<td>II</td>
<td>100</td>
<td>100</td>
<td>117</td>
<td>II</td>
<td>100</td>
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<td>104</td>
<td>V5</td>
<td>100</td>
<td>100</td>
<td>118</td>
<td>II</td>
<td>100</td>
<td>100</td>
</tr>
</tbody>
</table>
Table 2  R-peak detection performance on mit-db data

<table>
<thead>
<tr>
<th>QRS detector</th>
<th>Annotations</th>
<th>TP</th>
<th>FP</th>
<th>FN</th>
<th>Sn (%)</th>
<th>P+ (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Presented work</td>
<td>50038</td>
<td>50013</td>
<td>25</td>
<td>20</td>
<td>99.96</td>
<td>99.95</td>
</tr>
<tr>
<td>Ghaffari et al. (2008)</td>
<td>110159</td>
<td>109837</td>
<td>322</td>
<td>120</td>
<td>99.91</td>
<td>99.72</td>
</tr>
<tr>
<td>Legarreta et al. (2005)</td>
<td>58523</td>
<td>58346</td>
<td>186</td>
<td>177</td>
<td>99.7</td>
<td>99.68</td>
</tr>
<tr>
<td>Li et al. (1995)</td>
<td>104182</td>
<td>104070</td>
<td>65</td>
<td>112</td>
<td>99.89</td>
<td>99.94</td>
</tr>
</tbody>
</table>

Table 3  Q-wave height (in mV)

<table>
<thead>
<tr>
<th>Patient ID and record No. in physionet</th>
<th>Lead II</th>
<th>Lead V2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Algo mean</td>
<td>Variance</td>
</tr>
<tr>
<td>P042/S037LRE (Anterio Septal)</td>
<td>0.084</td>
<td>0.0008</td>
</tr>
<tr>
<td>P030/S003LRE (Anterio Septal)</td>
<td>0.2312</td>
<td>0.0007</td>
</tr>
<tr>
<td>P155/S030LRE (Normal)</td>
<td>0.0792</td>
<td>0.0007</td>
</tr>
<tr>
<td>P003/S001LRE (Inferior Posterio Lateral)</td>
<td>0.3585</td>
<td>0.0012</td>
</tr>
<tr>
<td>P014/S004LRE (Anterio)</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 4  S-wave height (in mV)

<table>
<thead>
<tr>
<th>Patient ID and record No. in physionet</th>
<th>Lead I</th>
<th>Lead III</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Algo mean</td>
<td>Variance</td>
</tr>
<tr>
<td>P004/S002AARE (Anterio Septal)</td>
<td>0.9836</td>
<td>0.0005</td>
</tr>
<tr>
<td>P008/S003LRF (Inferio)</td>
<td>0.0752</td>
<td>0.0002</td>
</tr>
<tr>
<td>P011/S003LRE (Inferio)</td>
<td>0.3247</td>
<td>0.0003</td>
</tr>
<tr>
<td>P014/S004LRE (Anterio)</td>
<td>0.2029</td>
<td>0.0002</td>
</tr>
<tr>
<td>P045/S014LRE (Inferio lateral)</td>
<td>0.2275</td>
<td>0.0028</td>
</tr>
</tbody>
</table>

The detection of wave peak heights w.r.t. detected onset and offset point of the respective wave peaks are shown in Figure 6. Tables 3–6 respectively shows the relative comparison between algorithmically obtained mean and measured mean, percentage error and variance of Q, S, T and P-wave amplitude. Variance and percentage error is defined as in equations (15) and (16), where $d_i$, $d_j$,... are successive difference in amplitude w.r.t. mean.

\[
\text{Variance} = \frac{\left( d_1^2 + d_2^2 + \ldots + d_n^2 \right)}{(n-1)}
\] (15)
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\[
\text{\% error} = \frac{(\text{actual mean} - \text{measured mean})}{\text{actual mean}} \tag{16}
\]

Table 5  T-wave height (in mV)

<table>
<thead>
<tr>
<th>Patient ID and record No. in physionet</th>
<th>Lead I</th>
<th>Lead III</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Algo mean</td>
<td>Variance</td>
</tr>
<tr>
<td>P004/S0020ARE (Anterior Septal)</td>
<td>0.1846</td>
<td>0.0002</td>
</tr>
<tr>
<td>P005/S0021ARE (Anterior)</td>
<td>0.1257</td>
<td>0.0010</td>
</tr>
<tr>
<td>P014/S0046LRE (Anterior)</td>
<td>0.1573</td>
<td>0.0002</td>
</tr>
<tr>
<td>P024/S0083LRE (Anterior Septal)</td>
<td>0.2090</td>
<td>0.0003</td>
</tr>
<tr>
<td>P024/S0084LRE (Anterior Septal)</td>
<td>0.2090</td>
<td>0.0003</td>
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</table>

Table 6  P-wave height (in mV)

<table>
<thead>
<tr>
<th>Patient ID and record No. in physionet</th>
<th>Lead I</th>
<th>Lead III</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Algo mean</td>
<td>Variance</td>
</tr>
<tr>
<td>P010/S0042LRE (Anterior)</td>
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</tr>
<tr>
<td>P015/S0047LRE (Inferior Lateral)</td>
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<td>0.0001</td>
</tr>
<tr>
<td>P016/S0052LRE (Inferior Lateral)</td>
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<td>0.0001</td>
</tr>
<tr>
<td>P027/S0089LRE (Anterior Lateral)</td>
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<td>0.0002</td>
</tr>
<tr>
<td>P105/S0303LRE (Normal)</td>
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<td>0.0001</td>
</tr>
<tr>
<td>P105/S0303LRE (Normal)</td>
<td>0.1128</td>
<td>0.0001</td>
</tr>
</tbody>
</table>

5 Discussion and conclusions

A statistical approach for amplitude feature extraction from digitised ECG samples using mit-db and ptb-db database is described. Empirically determined parameters are at first chosen arbitrarily, and are tested with 120 different leads. Average computational time for each single lead ECG data consisting of 60,000 samples (60 second data) is found to be around 5 second over 100 records using a personal computer with 1.66 GHz Intel
Atom processor and 1 GB RAM. No denoising has been performed on data. Baseline modulation is minimised from ECG dataset. The algorithm is directly applied on noisy samples to check its robustness. The algorithm works fairly well in noisy data. However when noise level is very high, the algorithm fails. Proposed technique is purely offline, hence can be applied to Halter records or offline records.

In future a strong rule base can be formed, in terms of different features of ECG signal, for distinguishing different type of myocardial infarction, or other diseases from normal patients. The study can be extended for calculation of average QRS vector magnitude and phase, considering all the 12 leads of a patient. Considering the orientation of the leads in frontal plane and in horizontal plane separately, phase and magnitude of two separate QRS vector can be determined. This may reveal an important phenomenon, to be useful in distinguishing different kinds of cardiac abnormalities, at least to differentiate between normal and abnormal characteristics. A modified version of the algorithm can be used for real time ECG feature extraction, by an embedded system.

In this paper, using an offline processing algorithm, R peaks are gradually segregated from other samples by sorting the dataset based on some restrictions applied. But this approach can not be applied for real time processing of ECG signal, by an embedded system. Because for real time processing, an algorithm, while processing a particular ECG sample, can access the past history of last few samples, which can be buffered into a memory element. In such situation a slope based searching can be initiated, and during a training period characteristics of wave peaks can be determined, which can be used for further detection of that type of peaks. The baseline modulation removal algorithm discussed in the literature, is also an offline process, where the algorithm is runned after having entire ECG dataset of a particular lead. Hence in real-time processing for removing baseline modulation effect from ECG signal, above mentioned algorithm cannot be applied. An FIR or IIR based approach can be suitable for that purpose.

References


An approach to determine the amplitude features from ECG records


An online ECG QRS Detection Technique

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Abstract— A simple technique, based on measuring the amplitude-span and slope of QRS in Electrocardiograph (ECG) data is described in this paper. Detection of QRS is done in two phases, viz., training and detection. At first, the dataset is searched by sliding a window of 96 ms width, from which an amplitude and slope threshold criteria is learned. From these criteria a QRS template is defined in terms of some signatures. In the detection phase, a QRS is located by matching a QRS template in a sliding 96 ms window. MATLAB simulation, using proposed technique with ECG data from Physionet yields over 98% accuracy. The algorithm is implemented on a standalone embedded system using 8851 microcontroller, which processes 10-12 beats stored in the external on-board RAM. The technique is suitable for online computation of heart rate.

Index Terms— ECG, QRS, Embedded system.

I. INTRODUCTION

An Electrocardiogram (ECG) represents small electrical potential generated by heart muscles. A typical ECG wave includes repeated sequences of P, QRS and T waves associated with each beat, which represent polarization of the atria and the ventricles in a sequential manner. The clinical bandwidth used for recording the standard 12-lead ECG is 0.05-100 Hz. QRS energy is centered on 15 Hz. 60 to 100 bits per minute constitute standard heart rate. Heart rate slower than this leads to Bradycardia and greater than this leads to Tachycardia. Till date, many computer based algorithms are available for automated analysis of ECG samples for assisted diagnosis. QRS complex, representing the ventricular depolarization of the heart, is the most prominent segment of the ECG wave. Many of the ECG analysis algorithms use QRS finding as their starting point due to its characteristic shape. Heart rate variability is another important parameter that can be directly analyzed from prolonged QRS recording.

QRS detection is a challenge not only due to variability of the QRS wave shape but also influence of different artifacts. Over the last few decades, many methods have been prescribed for QRS identification. Most of the QRS detectors use a pre-processor to enhance the QRS complex and suppressing the other waves of ECG. This is followed by a decision rule that identifies and often characterizes the QRS. Early approaches for QRS detection used simple derivative based methods and digital filters. Since a typical QRS wave frequency range is between 10-25 Hz, a simple digital filter with cut-off frequencies at extrema of the interval would attenuate other wave components and some artifacts. This band pass operation is implemented in combination of a low-pass and high pass filters, each operation being carried out separately, while some other use the high pass only [1]-[2].

The filtered signal is compared with a threshold for QRS detection. Digital differentiation based methods exploit the fact that QRS wave is having the maximum slope change in the samples. Most of the real time QRS detectors use a differentiator at initial stage of processing. A DSP based differentiator followed by squaring method is reported [3]. Differentiation and an adaptive threshold can be used on the differentiated signal to identify the QRS regions [4]. Digital differentiation technique followed by a Support Vector Machine (SVM) classifier to identify the QRS achieved 99.75% accuracy [5]. Pan and Tompkins reported a processor based real-time QRS identification mechanism which used digital analysis of slope, amplitude and width of QRS complexes after pre-processing [6]. Later, it was modified by introducing an adaptive threshold [7]. A comparative study on different first derivative based QRS detection approaches is reported [8]. Algorithms involving advanced computational techniques for QRS detection use Hilbert Transform, Neural Networks, Wavelets, and Hidden Markov Models [9]-[13]. In real time acquisition applications, one or two ECG leads are used. Microcomputer based systems are now increasingly being used for QRS detection in ambulation appliances [14]-[15], Holters and bedside monitors in intensive care units (ICU). In one such application [16], self adaptive threshold based QRS detection is described. In another application [17], a combination of differential threshold and amplitude detection is used for localization of QRS regions quickly. A morphological operator based peak value extractor is used for QRS detection [18]. Some other approaches include zero crossing counts and syntactic methods [19]-[20]. In recent years there has been considerable use of embedded systems for ECG denoising [21] and QRS detection [22]-[23]. In [22] a decision rule to analyze quadratic ‘spline’ wavelet coefficients to detect the QRS is described. In [23] a QRS detection algorithm is described which calculates the threshold of the next peak detection cycles from the median of eight previously detected peaks. Adaptive lifting scheme, an advanced wavelet tool is used for QRS detection in [24]. The method shows lower execution time compared to DSP platform with TMS320VC5509A, both run in simulation platform. The evaluation criteria used in the QRS detection algorithm are Sensitivity (Se) and Positive Predictivity (P+), defined as:

\[
Se = \frac{TP}{TP + FN}
\]

(1)
A typical ECG beat comprises of some equipotential segments connected by wave peaks, among which QRS is with highest slope and normally, the tallest. The QRS morphology varies among different age groups, communities and subcontinents. The proposed QRS detection technique exploits the following QRS signatures, viz., (i) the amplitude span, which is R to S (or Q) height remains almost constant throughout a particular lead data and (ii) QRS region is having the maximum slope, (actually, inter-sample difference), (iii) the width of QRS segment is nominally 96 ms, within which, Q (or S) to R distance is maximum 60 ms. Hence, to implement a technique which relies only such signatures essentially require training with data before the actual QRS detection is performed. In the proposed algorithm, two such signatures were extracted in the training period from the acquired (and buffered) data, typically from 8-10 beats. These signatures were used to define a QRS template, which was then used for exact localization of the QRS peaks in the entire data. Thus the entire operation can be divided into two parts, viz., training period and detection period.

During the training period, a sliding window of 96 ms width was moved by 20 ms in steps through the entire dataset to capture these two signatures. The objective was to capture a QRS zone which could be defined using the following parameters. The sliding shift 20 ms (empirically determined) was taken to ensure capture of QR or QS peaks in a single window.

The (i) Maximum amplitude span;
(ii) Maximum positive slope averaged over 8 points, The slope at a sample i was computed as:
\[
slp(i) = x(i+1) - x(i) \quad (3)
\]
To minimize the high frequency noise, 8-point average slope was used and calculated as,
\[
slp(i) = \frac{\sum_{j=(i+1)}(i+8) - x(i)}{8} \quad (4)
\]

Since non-QRS regions of the ECG wave used to be more flat and with lower amplitude span (except for tall T waves) and threshold, the sliding window had been used to continuously compute the amplitude span and average slope to store the tallest and sharpest QRS. To minimize high frequency spike at sample i, an empirically determined threshold was used as,
\[
x(i) - x(i-1) \leq \text{threshold} \quad (5)
\]

In the training period each sample was checked for validation using equation (5) and were discarded in case if violation. Hence at the end of training period, the following parameters were obtained.

\[
\text{(ampl)max} = \text{max. amplitude span in 96 ms window} \quad (6)
\]
\[
\text{(slp)max} = \text{max. 8-point average slope} \quad (7)
\]

The following rules for the detection of probable QRS neighbourhood are formulated as: (a) Amplitude span in moving 96 ms window should exceed 80% of maximum amplitude span computed over the entire dataset. This was named as ‘amplitude threshold criteria’ (ATC) and the value could be denoted by \(
\text{ampl}_{\text{th}} \quad (8)
\)
(b) Average (8-point) slope should exceed 80% of maximum slope computed over the dataset. This was named as ‘slope threshold criteria’ (STC) and the value could be denoted by \(\text{slp}_{\text{th}} \quad (9)\)

In the detection period, a new search was initiated in a 96 ms window with a sliding step of 20 ms to get a match of ATC. If for a particular window in the detection phase, ATC was found to be satisfied, a probable QRS neighborhood was assumed. Figure 1 shows different types QRS templates with respective amplitude span match with a moving 96 ms window (shown in green dashed line). It is also imperative that to meet with the ATC criteria, this window must contain either R or Q or S peak as its local maxima or minima. However, tall T peak for some abnormal ECG record may also meet the ATC. Now, at this position of the window, at first, any of the R or Q or S peak is to be determined by a slope reversal search initiated from the local maxima or minima. This is shown in Figure 2.
age slope), at 20 samples upside and 18 samples downside w.r.t \( p_{\text{max}} \) and \( p_{\text{min}} \) was calculated. Computed values could be denoted as:

\[
slp_{r_{20}}: 20 \text{ sample downside average slope w.r.t } p_{\text{max}} \\
slp_{r_{18}}: 18 \text{ sample upside average slope } \text{w.r.t } p_{\text{max}} \\
slp_{q_{20}}: 20 \text{ sample downside average slope w.r.t. } p_{\text{min}} \\
slp_{q_{18}}: 18 \text{ sample upside average slope w.r.t } p_{\text{min}}
\]

Now, two conditions may arise as follows:

- **Condition 1:** \( slp_{r_{20}} > 0 \) and \( slp_{r_{18}} < 0 \); (10)
- **Condition 2:** \( slp_{q_{20}} < 0 \) and \( slp_{q_{18}} > 0 \); (11)

Both conditions (1) and (2) may also get simultaneously satisfied. But it does not ensure a location of R-peak, since a positive or negative T-peak may also satisfy conditions (1) and (2). To ascertain the position of QRS, STC criteria were used in the following way: For condition (1) [or (2)] being satisfied, a new window of 96 ms was formed around \( p_{\text{max}} \) (or \( p_{\text{min}} \)), keeping that at the midpoint. From the starting point of the new window formed, for each sample (say index n) 8-point average slope was computed at n and \((n+25)\) index positions, with an objective to locate the position of upside and downside of positive R-wave.

The following conditions are tested:

- **Condition 3:** \( (slp)_n \geq (slp)_p \) (12)
- **Condition 4:** \( (slp)_n+25 < 0 \) (13)

where, \((slp)_n\) is slope at nth index etc.

Condition 3, actually being the STC, was used to reject out any falsely detected probable T-peak, because QRS complex used to be sharper than the T wave. If condition (3) was satisfied, then condition (4) was searched to find a positive R peak.

In case conditions (3) and (4) are found to be satisfied, existence of a positive R peak was concluded. It was also verified by a slope direction reversal within next 70 ms along the array, confirming occurrence of an S peak. The correct position of R-peak was determined by finding the local maximum within next 50 samples from sample n. For QS peaks (i.e., no positive R peak), condition (3) has to be satisfied only, not the condition (4). In that case, it has to be concluded that a positive R-peak does not exist and search for QS peak has to be initiated. The local minimum within the current window (of 96 ms width) has to be taken as the QS peak.

Once the R-peak (or QS peak) was determined, the next QRS search was initiated at 400 samples upside the data array, based on the assumption that the minimum R-R interval is 400 ms. For ECG data with tall T peaks, equation (10) and (11) may get initially satisfied, but condition (3) will not match within 96 ms window. Hence, in that case the next search have to be initiated from 200 samples upside the data array.

Due to noise problem one of more R-peak may have been missed, resulted into erroneous R-R interval calculation. In such a case the average R-R interval was computed as follows: If the following represent detected R-peak indexes:

\[516, 1510, 2517, 4516, 5517, 6517, 8512, 9517, 12517, 16512\ldots\]

Then at first, all the R-peak indexes were taken in an array. All the R-R intervals were computed and a new array was generated using following formula:

\[r_{ri} = r_{ri+1} - i\] for \( i = 1 \) to \( n-1 \), where \( n \) being the number of peaks determined.

From this array the minimum value, say \( r_{ri} \) was taken, and compared with other elements of this array to determine missed R peaks. If \( r_{ri} \) exceeds \( r_{rm} \) by 80, occurrence of some missed R-peak was concluded. The corresponding positions of R were discarded and only the valid R-R intervals were taken for calculation of average R-R interval. The algorithm was implemented with a standalone embedded system based on 8051 MCU. The system was tested with single lead synthetic ECG data, each consisting of 10000 samples. The digitized samples at 8 bit resolution were generated in a desktop PC and were delivered through the serial port for serial storage in an on-board RAM. Then standalone system performed the QRS detection task on these pre-stored data.

### III. Testing and Results

The algorithm was initially validated with MATLAB using synthetic ECG data from Physionet [25]. Physionet offers digital recordings of different physiological signals and related data for use of biomedical research. PTB Diagnostic ECG database (ptb-db) is available in Physionet under Physionet.
TABLE I. SENSITIVITY AND POSITIVE PREDICTIVITY WITH PTB-DB (IN PERCENTAGE)

<table>
<thead>
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<th>Patient file ID from Physiogear</th>
<th>ID N</th>
<th>Lead I</th>
<th>Lead II</th>
<th>Lead aVR</th>
<th>Lead aVF</th>
<th>Lead V1</th>
<th>Lead V3</th>
<th>Lead V5</th>
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<tr>
<td>P001 '0010 loc (Inf Lat)</td>
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</table>


Since the developed algorithm was applicable for ECG records at 1 kHz, an interpolation technique was used to up-sample the mit-db data to a 1 kHz sampling level. 50000 samples from a single lead are used for validation of the algorithm. Table 2 shows the Sensitivity (S) and Positive Predictivity (P+) figures for mit-db data. An average sensitivity of 94% and predictivity of 100% was obtained with 20 different records. Figure 5(d) represent R-peak detection using a single lead of arrhythmia data under mit-db, containing 50000 samples in MATLAB. The detected R-peaks are indicated by red vertical lines. As evident from the plots shown in Figure 5, the algorithm is immune from baseline modulation, if any, in the ECG data. Testing of the algorithm in embedded system platform was achieved in two stages.

A. Normalization and delivery of ECG data to the standalone system

A separate application software was developed which, at first digitized the single lead millivolt level ECG samples as obtained from Physiogear database, with 8 bit resolution and have saved in a text file. The second function was to deliver these quantized samples to the embedded system through the serial port, using an event driven programming technique. A typical serial port session [26] involving data output through the serial port involves the following steps:

i) Fixation of initial communication settings like baud rate, number data bits, parity and stop bit etc

ii) From computer memory, data bytes are to be sent to the output buffer of the USART (of the serial port) by using commands in MATLAB.

iii) The USART have to transmit continuously the data bytes to the external device using the TxD line, which is connected to the RxD pin of the MCU.

iv) An 'OutputEmpty' event is generated when the output buffer goes empty, triggering the corresponding event described by 'BytesAvailableFcn' and 'OutputEmptyFcn'. The calling function loads the next block of data to the USART for delivery to the external device.

The steps (ii) to (iv) were repeated till all the ECG data were delivered to the standalone embedded system. A GUI based front end was provided to perform the entire operation, i.e., choosing the ptb-file and lead for quantization, and then delivering the serial data to the standalone system. After all samples have been delivered, the software have to wait for the QRS locations to be sent back from the standalone embedded system to the PC using serial port for automatic storage in a text file.

B. QRS Detection from digitized samples

The standalone embedded system was consisted of an 8051 microcontroller, on-board RAM and MAX-232 level converter as the principal components. Figure 3 shows block diagram of the testing hardware. At first, 10000 samples were stored in the temporary RAM.

Figure 3. Block diagram of the developed system
The data set was searched and each detected R-peak index was stored in two consecutive locations of the 128 byte internal RAM of the MCU. The stored indexes were delivered back to the PC using RS-232 communication. The R-peak indices were captured in a separate data file for verification with the actual R-peaks of the corresponding lead data. A snap shot of test layout of the system with detection of R-peaks indicated by the alteration of a signal between two different logic levels has been represented in Figure 4.

### CONCLUSIONS

A QRS detection technique based on amplitude span and slope signature of QRS has been described. One advantage of the proposed algorithm is that it required the processing of a few samples at a time, hence utilizing minimum internal resources of processor. The method has shown fairly good results with noisy samples. Thus, no preprocessing of data was required. For online applications involving large amount of data (70-100 beats), a trade-off can be done between computational time and accuracy of detection. Here, training period can be confined to 10 beats, so as to reduce the overall computational time and ‘latency’ of detection. However, training with more data would increase the accuracy. The simplicity of the algorithm provides its suitability to implement it in a low level microcontroller like 8051. In its present form the developed system accepts 8 bit digitized ECG data from serial port. However, it can be modified to interface directly with a standard ECG lead system with amplifier module to directly acquire ‘live’ ECG from human patients. The standalone system can be used in a primary healthcare unit for heart rate computation of patients during initial check up. The existing system can be upgraded to a real-time QRS detector using a modification of the algorithm by using a 96 sample first-in-first-out stack. The first 2000 incoming data samples (expected to contain at least one QRS region) can be used for learning phase and the next incoming samples can be treated as detection phase. Additionally, this modified technique would not require an external RAM.

### ACKNOWLEDGMENT

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### REFERENCES


Real-time detection of electrocardiogram wave features using template matching and implementation in FPGA

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Abstract: Electrocardiogram (ECG) can provide valuable clinical information on cardiac functions. This paper illustrates an algorithm for real-time detection of wave peaks and their features from single lead ECG data. At first, the ECG data was filtered for power line interference and high frequency noise. Then, a set of slope and polarity-based rule bases were generated from the first 6000 samples, which define templates of R-peak, P- and T-wave detection from the following beats. The algorithm was implemented on Xilinx Spartan III Field Programmable Gate Array (FPGA). For testing of the algorithm, ECG data was quantised at 8-bit resolution and delivered to the FPGA using synchronous transfer mechanism using parallel port of computer. Xilinx implementation results provided 97.58%, 98.4% and 97.78% detection sensitivity for P-, R- and T-waves, respectively. Different wave features (height, polarity and duration) were detected with an average error rate of 9.3%. The detected wave signatures were clinically validated by medical expert.

Keywords: electrocardiogram; peak detection; template matching; FPGA.


Biographical notes: H.K. Chatterjee is currently Assistant Professor and Head in ECE Department, Camellia School of Engineering & Technology, Kolkata, India. He has done MTech from Bengal Engineering and Science University, Howrah, India, and currently pursuing PhD from Department of Applied Physics, University of Calcutta. His research interests include ECG signal processing and FPGA or microcontroller-based embedded systems. He has five publications in international journals and conferences.
1 Introduction

Electrocardiogram (ECG) represents spatio-temporal average of small electrical pulses generated on heart and their propagation along the specialised conducting fibres on heart muscles. It is characterised by a time-variant cyclic occurrence of patterns which are denoted as P-wave, QRS complex and T-waves. One typical ECG beat (cycle) and its clinically significant features are indicated in Figure 1. In clinical settings, ECG data is collected from 12 leads, positioned in different predefined positions of human body. Visual inspection of prolonged ECG records is a tedious job for cardiologists and may often lead to misinterpretations. Manual interpretation of ECG signal also suffers from inter-observer variability. This is the reason why computerised feature extraction of the ECG signal can support physicians in their diagnosis for early detection of cardiac troubles.

Figure 1 One ECG cycle with clinical significant features (see online version for colours)

1.1 Computerised ECG feature extraction

Pre-processing of the ECG signal for noise elimination and enhancement of the wave features can improve the accuracy in feature recognition. QRS being the sharp and prominent feature of an ECG wave, its detection is the starting point of analysing ECG
signal in many of the published literatures. QRS positions are often indicated by R-peak index (QS for negative QRS). Some popular approaches used for the purpose of detection of R-peak include derivative based approach (Friesen et al., 1990), artificial neural network based approach (Hu et al., 1993), transform domain (Wavelet Transform, Hilbert Transform) approach (Di-Virgilio et al., 1995; Xu and Liu, 2005; Benitez et al., 2000), matched filter based approach (Ruha et al., 1997; Lindecrantz and Lilja, 1988) and many other.

Real-time analysis of ventricular late potentials using wavelets and FFT spectrum is addressed by Sivakumar et al. (2011), with simultaneous processing and recording of the next beat, for increasing speed of processing. A Hilbert transform on first derivative of the ECG signal with thresholding was used for R-peak detection (Mukhopadhyay et al., 2012). Q, S, QRS onset and offset points are also detected properly. Wang et al. (2012) presented a Novel Fetal ECG Blind Source Extraction (BSE) algorithm based on Blind Source Separation (BSS) in the presence of noise.

A multi-lead ECG delineation using spatially projected leads from wavelet transform loops is addressed by Almeida et al. (2009). Vaneghi et al. (2012) analysed six ECG feature extraction methods, namely, Autoregressive (AR), Wavelet Transform (WT), Eigenvector, Fast Fourier Transform (FFT), Linear Prediction (LP), and Independent Component Analysis (ICA), and finally concluded the superiority of Eigenvector method over the others. Mazomenos et al. (2013) extracted ECG fiducial points by analysing modulus-maxima on the DWT (Discrete Wavelet Transform) coefficients, with the Haar function being the mother wavelet. Finally the initial findings are complemented with a refinement stage, based on the time-domain morphological properties of the ECG, which diminishes the decreased temporal resolution of the DWT.

Sikkandar et al. (2013) decomposed ECG signal into so-called Intrinsic Mode Functions (IMFs) using Empirical Mode Decomposition (EMD) algorithm, as the key feature of HHT (Hilbert-Huang Transform), to analyses cardiac abnormalities. CWT (Continuous Wavelet Transform) and finally a thresholding technique based complete ECG delineation have been addressed by Londhe et al. (2012). A support vector machine based QRS detection approach has been described by Saini et al. (2012).

1.2 Background: ECG analysis using embedded systems

With the advent of low power, miniature VLSI technology, portable standalone systems are increasingly being utilised in biomedical measurements (BP measurement, blood glucose, SpO₂, heart rate etc.), ICU (intensive care unit) instrumentation (bed side monitoring) and remote healthcare applications. Over the last decade researchers have used Field Programmable Gate Array (FPGA) for biomedical signal analysis and health monitoring application, mainly due to its parallel operation capability. These include noise reduction (Kasetwar and Gulhane, 2013; Li and Wang, 2010; Ramos et al., 2007), QRS detection (Shukla and Macchiarulo, 2008; leong et al., 2008a; leong et al., 2008b; Li et al., 2010; Zemva and Cvikl, 2007; Kurakula et al., 2011), signal analysis (Timothy et al., 2014; Homaeinezhad et al., 2014; Karimipour and Homaeinezhad, 2014; Chouhan and Mehta, 2008), and monitoring (Ravinder et al., 2013; Alemzadeh et al., 2011). For QRS detection, most of the researchers have used mitdb data base from Physionet, which is an established benchmark for testing biomedical signal analysis algorithms. Shukla and Macchiarulo (2008) implemented FPGA implementation of widely popular Pan-Tompkins algorithm (Hamilton and Tompkins, 1986), using a threshold calculated on last
8 detected R-peaks. With 200 Hz re-sampled data under Physionet, 93% correct detection was achieved using 30 min data records on Xilinx Spartan xc3s500. QRS detection using morphological filtering followed by quadratic spline wavelet transforms and modulus maxima pair recognition is reported by Ieong et al. (2008a). Adaptive Lifting Scheme (ALS), a derivative of wavelet transform, was implemented by Li et al. (2010) in Xilinx Virtex Pro II as well as in DSP (TI’s TMS320VC5509A), with 99.681% detection accuracy in both. However, the implementation took 15% less time in FPGA. Another wavelet-based approach for the first derivative of the ECG is reported by Ieong et al. (2008b).

There are few studies available in the literature on FPGA-based beat-to-beat wave extraction. Reliable detection of P- and T-wave are more difficult than QRS complex for several reasons such as their low amplitudes, susceptibility to noise, amplitude and morphological variability and even, possible overlapping of the P-wave with the QRS complex. A model-based approach to delineate P-QRS-T-wave is reported by Timothy et al. (2014). Here, the major waves and in-between equipotential segments were modelled as continuous waveforms defined in a piecewise-defined function using Markov-Chain Monte Carlo approach. ‘Template matching’ is one of the techniques adopted by researchers for complete beat detection in ECG cycles. Homaeinezhad et al. (2014) extracted morphology-based templates for detection of P- and T-waves in the non-QRS region (or R–R interval). For these, clustering of ECG data in the R–R interval was done to extract the desired templates. In another approach (Karimipour and Homaeinezhad, 2014), a correlation analysis was performed between the training generated template and probable candidates of P- and T-waves in the R–R interval. In the training phase, all the waves were detected and their characteristics were determined by clustering and ensemble averaging in the corresponding cluster. The parallelism operation of the training and testing phase added the capability of self-tuning of the algorithm for continuous operation. However, there are very limited studies on complete amplitude and feature detection implemented in FPGA platform. Chouhan and Mehta (2008) addressed a threshold-based detection of P- and T-wave in ECG using new feature signal.

The motivation of this work was to develop an algorithm for ECG feature extraction which can be implemented using reduced memory allocation in FPGA system. The ECG features were extracted from very few cycles of ECG. An FPGA-based-R-peak detection was addressed by us (Chatterjee et al., 2011). In the present work, the other wave peaks and fiducial points were assessed in the R–R region using minimum number of templates. The algorithm is divided into two phases of operation. During a training period (phase), a reference slope and polarity characteristics (template) were extracted for the concerned wave peaks. In the detection phase, template or signatures were matched with group of incoming ECG samples. The developed algorithm was tested with normal and abnormal ECG data from mit-db and ptb-db database under ‘www.physionet.org’. The proposed algorithm yielded comparable results with other reported works.

2 Materials and methods

The algorithm stages were divided into three stages namely, noise removal, template generation from first 6–7 beats and feature detection. Amongst these, filtering operation was continuously performed. For real-time operations, the FPGA maintained a first-in
first-out (FIFO) stack of 200 last samples at any point of time. To simulate the real-time computing environment, a PC-based digital ECG simulator was developed to deliver digitised (8 bit) ECG samples at 1 kHz sampling frequency ($f_s$) to the FPGA board. The detailed diagram of the developed system is described in testing and results Section 3, in accordance with Figures 9–11. A concise logic flow diagram of the ECG feature extraction algorithm is given Figure 2.

2.1 Filter implementation

For the removal of power line interference, two comb filters were designed. One comb filter (comb1) was designed to remove 50–60 Hz noise and their entire odd harmonics. Another comb filter (comb2) was designed to remove 100–120 Hz noise and their entire odd harmonics. Actually, comb filters were designed from a 4th-order IIR Butterworth LPF (basic LPF) with a cut-off frequency of 350 Hz ($f_s = 1$ kHz). Two comb filters were followed by a 4th-order IIR Butterworth low-pass filter (final LPF) with a 50 Hz cut-off frequency, so as to remove other high frequency noises.

The transfer function $H(z)$ of basic LPF, comb1, comb2 and final LPF were expressed by equation (1). Frequency response of basic LPF, comb1, comb2 and final LPF is expressed in Figure 3 (a–d), respectively. Around 70 last samples were used from the FIFO stack to get the filtered data.

$$H(z)_{\text{basic LPF}} = \frac{0.275 + 1.102z^{-1} + 1.653z^{-2} + 1.102z^{-3} + 0.275z^{-4}}{1 + 1.570z^{-1} + 1.276z^{-2} + 0.484z^{-3} + 0.076z^{-4} + 0.275z^{-5}}$$

$$H(z)_{\text{comb1}} = \frac{0.275 + 1.102z^{-1} + 1.653z^{-2} + 1.102z^{-3} + 0.275z^{-4}}{1 + 1.570z^{-2} + 1.276z^{-3} + 0.484z^{-4} + 0.076z^{-5} + 0.275z^{-6}}$$

$$H(z)_{\text{comb2}} = \frac{0.275 + 1.102z^{-1} + 1.653z^{-2} + 1.102z^{-3} + 0.275z^{-4}}{1 + 1.570z^{-3} + 1.276z^{-4} + 0.484z^{-5} + 0.076z^{-6} + 0.275z^{-7}}$$

$$H(z)_{\text{final LPF}} = \frac{0.275 + 1.102z^{-1} + 1.653z^{-2} + 1.102z^{-3} + 0.275z^{-4}}{1 + 1.570z^{-3} + 1.276z^{-4} + 0.484z^{-5} + 0.076z^{-6} + 0.275z^{-7}}$$

(1)
Figure 3  Frequency response of (a) basic LPF, (b) comb1, (c) comb2 and (d) final LPF (see online version for colours)
2.2 Algorithm for detection of ECG wave peaks

2.2.1 R-peak detection

In the presented R-peak detection technique, slope or first-order difference was used as the principal feature to characterise R-wave. R-, T- and P-peak can be positive (upright) or negative (inverted) as shown in Figure 4. Q- and S-peak is always negative. If positive R-peak exists in the concerned ECG signal, it can be significant (qRs) or insignificant (qr or rS). In case of significant (positive) R-wave, both side (left and right in terms of wave morphology) slopes are well dominated. Insignificant (positive) R wave is associated with either of Q- or S-wave, but not with both. For insignificant (positive) R-wave, either of the two side slopes is dominated. In case of negative R-peak, coincided Q- and S-wave gives rise to negative R-peak (QS-wave). Hence, in the training period of R-peak detection, it needs to be identified that whether positive or negative R-peak exists. Presence of Qr or rS peak is also determined.

![Illustration of various QRS morphology for R-wave detection and the organisation of FIFO stack](image)

R-peak characterisation and detection used only last 40 samples (empirically determined) of FIFO data structure, as shown in Figure 4. If $m_i$ represents current ECG sample magnitude, $m_{i-20}$ and $m_{i-40}$ represent magnitude of 20th sample and 40th sample before the current sample, respectively; and $(i-20)$th sample is considered as current sample of reference. Slopes were computed as:

Left side (upside) slope $s_{lp, 20} = m_{i-20} - m_{i-40}$,

Right side (downside) slope $s_{lp, 20} = m_{i-20} - m_i$.  

(2)
With each incoming samples ($i$-th) to the FPGA module, both side slopes were computed continuously in two separate groups.

It was assumed that at least one R-peak is encountered in 1400 ms. R-peak detection initiated after 110 (70 for filtering followed by 40 sample stack) ms. A total of 1510 (1400 + 110) ms period was used to estimate the slope and characteristics of R-wave, to generate a slope and polarity-based reference template. This period was considered as the training period for the detection of R-wave.

**Training phase: template generation during 111–1510 samples**

In the first group (gr1), only those samples were considered for which a positive peak occurs around $i$–20th sample and both side slopes are positive going towards ($i$–20)th sample, satisfying condition 1 as given in equation (3). Similarly, only those samples were considered in the second group (gr2) for which a negative peaking occurs around ($i$–20)th sample, satisfying condition 2, as given in equation (4).

$$\text{Condition 1 (gr2): } s_{lp_{20+}} > 0 \text{ and } s_{lp_{20-}} > 0$$

$$\text{and } m_{-20} = \text{Max}\{m_{-21}, \ldots, m_{-23}\}$$

$$\text{Condition 2 (gr2): } s_{lp_{20-}} < 0 \text{ and } s_{lp_{20+}} < 0$$

$$\text{and } m_{-20} = \text{Min}\{m_{-21}, \ldots, m_{-23}\}$$

gr1 and gr2 maintained and continuously updated a maximum sum of left- and right-side 20 sample slopes, denoted as $\max \sum s_{lp_{i-20}}$ and $\max \sum s_{lp_{i+20}}$, respectively. This extracted most prominent positive and negative peak characteristics in the training period. gr1 and gr2 also maintained corresponding left- and right-side 20 sample slope abbreviated as $s_{lp_{20+}}^{\text{left}}$, $s_{lp_{20-}}^{\text{left}}$, $s_{lp_{20+}}^{\text{right}}$, and $s_{lp_{20-}}^{\text{right}}$, respectively, where the sum of both side slopes are maximum. On capturing $i$-th sample, if it was found that ($i$–20)th sample belongs to gr1, then $\max \sum s_{lp_{i-20}}$, $s_{lp_{20+}}^{\text{left}}$, $s_{lp_{20-}}^{\text{left}}$ and $s_{lp_{20+}}^{\text{right}}$, $s_{lp_{20-}}^{\text{right}}$ were maintained as in way equation (5).

$$\text{if } \left| s_{lp_{20+}} \right| > \max s_{lp_{i-20}}, \text{ then } \max s_{lp_{i-20}} = \max \left( s_{lp_{20+}}, s_{lp_{20-}} \right),$$

$$s_{lp_{20+}}^{\text{left}} = s_{lp_{20+}}, \quad s_{lp_{20-}}^{\text{right}} = s_{lp_{20-}}$$

Parameters of gr2 are also determined in a similar way according to equation (6).

$$\text{if } \left| s_{lp_{20-}} \right| > \max s_{lp_{i-20}}, \text{ then } \max s_{lp_{i-20}} = \max \left( s_{lp_{20+}}, s_{lp_{20-}} \right),$$

$$s_{lp_{20-}}^{\text{left}} = s_{lp_{20-}}, \quad s_{lp_{20+}}^{\text{right}} = s_{lp_{20+}}$$

After processing 1510 samples gr1 and gr2 have the parameters $\{\max \sum s_{lp_{i-20}}, s_{lp_{20+}}^{\text{left}}, s_{lp_{20-}}^{\text{left}}, s_{lp_{20+}}^{\text{right}}, s_{lp_{20-}}^{\text{right}}\}$ and $\{\max \sum s_{lp_{i-20}}, s_{lp_{20+}}^{\text{left}}, s_{lp_{20-}}^{\text{left}}, s_{lp_{20+}}^{\text{right}}, s_{lp_{20-}}^{\text{right}}\}$ respectively. In case of insignificant positive R-wave, one side slope is much less than other side slope as shown in Figure 4. If one side slope is too less than another side slope, then only the occurrence of negative R-peak was concluded. Even in the presence of deep Q- or S-wave, presence of positive R-peak was tried to get detected. ECG signal can contain either significant R-wave (qRs)
or insignificant R-wave (Qr or rS) or QS type peak. Hence, at 1510 sample, to discriminate between these three types of peaks following criteria are applied as given below:

\[
\begin{align*}
\text{if } 0.1 \times s_{\text{lpV}}^{qRs} > s_{\text{lpV}}^{gr2} \text{ or } 0.1 \times s_{\text{lpV}}^{rS} > s_{\text{lpV}}^{gr1} & \\
\Rightarrow \text{QS peak, negative R peak, gr.2 dominant} \\
\text{else if } 0.4 \times s_{\text{lpV}}^{qRs} > s_{\text{lpV}}^{gr1} \text{ or } 0.4 \times s_{\text{lpV}}^{rS} > s_{\text{lpV}}^{gr2} & \\
\Rightarrow \text{Qr or rS, positive R peak, gr.1 dominant} \\
\text{otherwise qRs peak, positive R peak gr.1 dominant}
\end{align*}
\]

(7)

If QS peak exists, gr2 was considered dominant, otherwise gr1 was considered dominant. Both side R slope threshold value (\(R_{\text{lpV}}^{gr1}\) and \(R_{\text{lpV}}^{gr2}\)) was calculated, which is 75% of the left and right side 20-sample slope, respectively, of the dominant group.

If gr1 was found to be dominant, R-peaks were detected; otherwise QS peak search was initiated in the detection phase. Hence during this training period

\[
\begin{align*}
\text{if } + R : & \\
\text{Condition (1)} & & \text{Condition (2)} \\
\Rightarrow & & \\
\text{otherwise, } & & \\
\text{Condition (1)} & & \text{Condition (2)}
\end{align*}
\]

(8)

QRS template was defined in terms of both side 20 sample slope threshold value and polarity of the wave peak. The presence of qRs, Qr, rS or QS peak was indicated by flag bits. The simplified logic flow diagram of R-peak characterisation and detection is given in Figure 5.

**Figure 5** Logic flow diagram of R-peak characterisation and detection

Detection phase: template matching after 1510 samples

The polarities and slope signatures of the R-peak as determined in the training period were used for detection of R-peak from 1501th sample. Each sample captured after first 1510 samples, were checked for one of the following conditions.

\[
\begin{align*}
\text{if peak type } & = qRs: \ |s_{\text{lpV}}^{qRs}| > R_{\text{lpV}}^{gr2} \text{ and } |s_{\text{lpV}}^{qRs}| > R_{\text{lpV}}^{gr1} \text{ and Condition 1} \\
\text{if peak type } & = Qr \text{ or rS: } \left(|s_{\text{lpV}}^{Qr}| > R_{\text{lpV}}^{gr1} \text{ or } |s_{\text{lpV}}^{rS}| > R_{\text{lpV}}^{gr2}\right) \text{ and Condition 1} \\
\text{if peak type } & = QS: \ |s_{\text{lpV}}^{QS}| > R_{\text{lpV}}^{gr2} \text{ and } |s_{\text{lpV}}^{QS}| > R_{\text{lpV}}^{gr1} \text{ and Condition 2}
\end{align*}
\]

(9)
That means for QS or qRs type peak, absolute value (magnitude) of both side 20 sample slopes were greater than respective R-wave slope thresholds. And for Qr or rS type peak, the dominant side (as learned in training period) slope magnitude is greater than respective R slope threshold.

On satisfying the condition \((i-20)\)th sample was detected as R-peak. It is also checked that last detected R-peak (previous R-peak) should be 400 samples apart from the time plane index of \((i-20)\)th sample.

A ‘sample_count’ variable was used to keep track of number of sample currently being processed, which holds absolute time plane index of current sample. After detection of an R-peak, ‘sample_count’-20 was considered as last detected R-peak index (LastR). R–R interval \((t_{RR})\) is calculated after detecting two R-peaks. It is expected that within 1500–3500 samples, at least two R-peaks were determined.

2.2.2 Q- and S-peak detection

If qRs or rS type peak was detected in R-peak finding training period, then only, S-peak occurrences with respect to already determined R-peak locations were searched. It is assumed that after the characterisation of R-peak, within next another 1500 ms, at least one R-peak will occur. For S-peak detection the following conditions are checked:

\[
\begin{align*}
(a) \ s\text{lp}_{20\_20} &< 0 \text{ and } (b) \ |s\text{lp}_{20\_20}| > R_{wave}^{\text{lower}} \text{ and } (c) \ (\text{LastR} + 10) \\
< (\text{sample\_count} - 20) &< (\text{LastR} + 50) \\
\text{and } (d) \ (i - 20)\text{ th sample value must have lowest} \\
\text{value within that region}
\end{align*}
\]

Principle of S- and Q-peak detection is illustrated in Figure 6. Since Q- and S-peaks are obvious negative peak and slope is nearly the same as the R-peak, no separate training phase is required for them. Condition (10 c) defines the searching window for detection of S-wave. In criteria (10 a) and (10 b), only left-hand side, that means R-wave side slope, is considered for satisfying certain conditions, but T-wave side slope is not considered. This is because of insignificant type S-wave, only the left hand side (upside) or the R-wave side slope is prominent. Right-hand side (downside) or T-wave side slope is less prominent or last for very small duration.

Figure 6  S- and Q-peak detection (see online version for colours)
Q-peak detection was performed, only for ‘significant positive R’ or ‘Qr’ type QRS complex. Similarly for determining a Q-wave peak, the following conditions are checked:

(a) \( slp_{20} < 0 \) and (b) \( |slp_{20}| > R_{max}^{\text{up}} \) and (c) \((\text{LastR} + 340) < (\text{sample_count} - 20)\) and (d) \( (i - 20)\)th sample value must have lowest value within that region

lies the R slope threshold criteria (i.e. \(|slp_{20}| > R_{max}^{\text{up}}\)), then it was checked that if 20 samples before the current sample have the minimum value in the region. If the criteria are satisfied, then 20 samples before the current sample (i.e. \((i - 20)\)th sample) were chosen as Q-peak. If at least one R-peak is determined by the algorithm then for determining all subsequent Q-peaks, search is initiated for those samples which are at least 340 samples after the last detected R-peak.

### 2.2.3 T- and P-wave peaks detection

Since T- and P-waves occur in the non-QRS region of two successive beats, i.e. between S-offset of the current beat and Q-onset of the following beat, their detection were also performed in two phases (i.e. separate template generation and detection) in the mid-RR zones with respect to last detected R-peak and S-peak. T- and P-wave detection is shown in Figure 7. T- and P-wave signatures were extracted during a training period of 6000 samples. After determination of R-wave characterisation using first 1510 samples, another 3000 samples are used for estimating R–R interval, which was used to estimate probable location of T- and P-waves. During another next 1500 samples (i.e. from 4500 to 6000 samples) T- and P-peak characterisations (slope and polarity based) were determined.

**Figure 7** T-peak detection (see online version for colours)

Since T- and P-waves are normally flatter and wider than QRS complexes, hence slope characterisation was done with 100 sample window (50 on each side), while keeping the midpoint \((i-50)\) as current sample of reference in the following way:

Left side (upside) slope \( slp_{i-50} = m_{i-35} - m_{i-100} \)

Right side (downside) slope \( slp_{i+50} = m_{i+35} - m_{i} \)

\[ (12) \]
Real-time detection of electrocardiogram wave features

T- and P-wave characteristics extraction during a training period of 4500–6000 samples

R-, T- or P-peak can be positive or negative as shown in Figures 4 and 8. Hence, T- and P-wave characterisation extraction was performed in a similar manner as that described for R-peak. The P-waves follow the T-wave (of the preceding beat) in the R–R interval and hence their detection was initiated in the post T regions in the current R–R interval. To determine T-wave (or P-wave) signatures following conditions were checked for each (i–50)th sample.

\[ \text{Condition 1: } slp_{p_t} > 0 \text{ and } slp_{p_r} > 0 \text{ and } m_{r-5} = \text{Max}\{m_{r-4}, \ldots, m_{r-5}\} \]

or \[ \text{Condition 2: } slp_{p_t} < 0 \text{ and } slp_{p_r} < 0 \text{ and } m_{r-5} = \text{Min}\{m_{r-4}, \ldots, m_{r-5}\} \]

(13)

The respective searching zones are as follows:

- \((\text{Last } R + 80) < (\text{sample count } - 50) < (\text{Last } R + 0.5 \times t R R - 10)\)
  - defines T wave searching zone

- \((\text{Last } R + 0.5 \times t R R + 10) < (\text{sample count } - 50) < (\text{Last } R + t R R - 80)\)
  - defines P wave searching zone

For detecting T-peaks, amongst those (i–50)th samples that satisfy above given criteria, maximum sum of both side slopes (\(|slp_{p_t}| + |slp_{p_r}|\)) were calculated in two separate groups. Groups were formed based on whether both side slopes are positive or negative going towards (i–50)th sample. In a similar manner as that of R-peak, at the end of training period both groups were having with their parameter values \(\{\text{max } slp_{p_t}, slp_{p_t}^{\text{ave}}, slp_{p_r}^{\text{ave}}\} \) for group1 and \(\{\text{max } slp_{p_r}, slp_{p_r}^{\text{ave}}, slp_{p_r}^{\text{ave}}\} \) for group2) using equations (14) and (15).

\[
\text{For gr. 1: } \text{if } (|slp_{p_t}| + |slp_{p_r}|) > \text{max } \sum slp_{p_t}, \text{ then } \sum slp_{p_t} = (|slp_{p_t}| + |slp_{p_r}|), \text{ slp}_{p_t}^{\text{ave}}
\]

\[
= |slp_{p_t}|, \text{ slp}_{p_t}^{\text{ave}} = |slp_{p_r}|
\]

(14)

\[
\text{For gr. 2: } \text{if } (|slp_{p_t}| + |slp_{p_r}|) > \text{max } \sum slp_{p_r}, \text{ then } \sum slp_{p_r} = (|slp_{p_t}| + |slp_{p_r}|), \text{ slp}_{p_r}^{\text{ave}}
\]

\[
= |slp_{p_r}|, \text{ slp}_{p_r}^{\text{ave}} = |slp_{p_t}|
\]

(15)

At the end of the training period, the group having higher \(\text{max } \sum slp_{p_t}\) was considered dominant, and determines the polarity of T-wave according to equation (15).

\[
\text{if } \sum slp_{p_t} > \sum slp_{p_r} \Rightarrow \text{Positive } T \text{ peak, gr. 1 dominant}
\]

\[
\text{if } \sum slp_{p_r} < \sum slp_{p_t} \Rightarrow \text{Negative } T \text{ peak, gr. 2 dominant}
\]

(16)

Left and right side T-wave slope threshold value \(T_{p_t}^{\text{ave}}\) and \(T_{p_r}^{\text{ave}}\) were denoted as \(0.75 \times slp_{p_t}^{\text{ave}}\) and \(0.75 \times slp_{p_r}^{\text{ave}}\) (empirically determined), respectively, which were calculated from the dominant group.
T- and P-waves detection phase

After 6000 samples, for each successive captured samples, corresponding \((i-50)\)th sample was considered as \(T\), if it satisfied the following criteria.

\[
\begin{align*}
\text{if peak type= Positive: } & \left| s_{P_{50}} \right| > T_{50}^{\text{Thr}} \quad \text{and} \quad \left| s_{P_{150}} \right| > T_{150}^{\text{Thr}} \quad \text{and Condition 1} \\
\text{if peak type= Negative: } & \left| s_{P_{50}} \right| < T_{50}^{\text{Thr}} \quad \text{and} \quad \left| s_{P_{150}} \right| < T_{150}^{\text{Thr}} \quad \text{and Condition 2}
\end{align*}
\]

(17)

Similar logic was followed for the characterisation and detection of the P-waves.

Wave peak duration (QRS duration, T- and P-wave durations) were calculated with respect to detected onset and offset points of respective wave peaks. In consultation with cardiologists, considering widest T-wave, it was assumed that maximum duration of an ECG component wave can be maximally 300 ms. Onset point search of a peak was initiated just after detection of the peak. Starting from that particular peak point, a backward search (i.e. towards earlier sample values) was initiated until the value of an ECG sample remained within 0.8% tolerance of last baseline magnitude. If within previous 150 samples, no such onset point detected, some relaxation on percentage of tolerance was applied in a recursive manner, until a valid onset point detected. For determining T-wave onset, search is initiated from \((i-50)\)th to \((i-200)\)th sample, while capturing \(i\)-th sample, if a T-peak was found at \((i-50)\)th sample. Offset point detection of a particular peak was initiated 150 samples after the peak occurrence. Here, a forward search was initiated from peak point towards next successive 150 samples. T-wave offset search was initiated from \((i-150)\)th sample to \(i\)-th sample, on capturing \(i\)-th sample, if a T-wave is already detected for \((i-150)\)th sample.

2.3 Baseline detection for wave peak height detection

Since ECG records may contain baseline wander, individual wave peak heights were determined by comparing wave peak temporal location magnitude with respect to the baseline of the current beat. Local baseline magnitudes were determined in three different methods and results were compared to select the best one in terms of memory utilisation and accuracy. In first method, average magnitude value of consecutive 30-sample value calculated at the midpoint of last two detected R-peaks was considered as baseline magnitude. In second approach, index having minimum 30 sample absolute slope value around the 2/3rd and 1/3rd division line of R–R interval was considered as baseline voltage. In third approach, the index with most frequently occurring quantisation level in between two successive R–R peaks was assumed as baseline magnitude.

3 Testing and results

The developed real-time ECG wave peak feature detection algorithm was tested using pre-recorded normal and abnormal ECG data in PTB diagnostic ECG database (ptb-db) and MIT-BIH arrhythmia database (mit-db) under Physionet, up-sampled at 1 kHz frequency.
3.1 Filtering performance measure in simulation platform

To test the filter performance, power line noise and high frequency noise (above 200 Hz) were added to the ECG samples and the following performance parameters were estimated: Signal-to-Noise Ratio improvement (SNR imp), Percentage of Noise Reduction (PNR), Mean Square Error (MSE), percentage root mean square difference (PRD) and Noise Reduction Factor (NRF), given as:

\[
\text{SNR imp [db]} = 10 \times \log \left( \frac{\sum s^2(i)}{\sum s_i^2(i)} \right) / \left( \frac{\sum [\hat{s}(i) - s(i)]^2}{\sum s_i^2(i)} \right)
\]

\[
\text{PNR} = \frac{\left(10 \times \log \left( \sum (\hat{s}(i))^2 \right) \right) - \left(10 \times \log \left( \sum s_i^2 \right) \right)}{\left(10 \times \log \left( \sum s_i^2 \right) \right)} \times 100
\]

\[
\text{MSE} = \frac{1}{N} \sum [s(i) - \hat{s}(i)]^2
\]

\[
\text{PRD} = \frac{\sum [s(i) - \hat{s}(i)]^2}{\sum s_i^2(i)}
\]

\[
\text{NRF} = \frac{\sum [\hat{s}(i) - s(i)]^2}{\sum [\hat{s}(i) - s(i)]^2}
\]

Here, \( s \) and \( \hat{s} \) represent clean and denoised samples, respectively. The noise performance parameters were calculated over a window size consisting of \( N \) number of samples. Here, window size (\( N \)) is considered to be of 1500 samples.

The parameters were calculated in the presence of 60 Hz noise and its harmonics and also in the presence of white noise. The performance is pictorially indicated in Figure 8a and 8b, respectively. For determining SNR improvement, clean ECG signal was contaminated with known simulated noise (\( n \)). Finally de-noised signal (\( \hat{s} \) ) was obtained. Residual noise was calculated as (\( s - \hat{s} \)). Maximum amplitude of simulated noise was chosen to be 50% of maximum amplitude of clean ECG signal. Performance parameters were calculated over 50 single lead ECG data. Performance parameters values obtained over some of ptb-db leads are indicated in Table 1. Average SNR improvement factor was found to be 29 db and 19 db, respectively, for 60 Hz noise (and its harmonics) and white noise, respectively. Owing to the effect of filtering, the wave peaks are getting time shifted (slightly) with respect to original signal. Hence, for calculating the noise performance parameters, exactly the same time span window frame was not considered for \( s \) and \( \hat{s} \), but a time shifted version of \( \hat{s} \) is considered, where MSE is becoming minimum.

3.2 Development of digital ECG simulator

For real-time ECG wave feature measurement in FPGA, a personal computer (PC) based digital ECG simulator was developed, as shown in detailed block diagram of the system (Figure 9). Digitised ECG samples at 8-bit resolution were delivered from a PC parallel data port at 1 ms interval to the FPGA board, using parallel bus using a synchronous data transfer scheme illustrated by Chatterjee et al. (2011).
Figure 8  Performance of de-noising algorithm in the presence of simulated noise (a) 60 Hz noise and (b) white noise (see online version for colours)

Table 1  The noise removal performance parameter values

<table>
<thead>
<tr>
<th>Patient ID, record no. in physionet</th>
<th>Lead</th>
<th>SNR&lt;sub&gt;imp&lt;/sub&gt; (in db)</th>
<th>%PNR</th>
<th>MSE</th>
<th>PRD</th>
<th>NRF</th>
<th>SNR&lt;sub&gt;imp&lt;/sub&gt;</th>
<th>%PNR</th>
<th>MSE</th>
<th>PRD</th>
<th>NRF</th>
</tr>
</thead>
<tbody>
<tr>
<td>P172/S0471_RE V2</td>
<td>28.51</td>
<td>0</td>
<td>2.12</td>
<td>0.0086</td>
<td>26.65</td>
<td>20.78</td>
<td>0</td>
<td>2.12</td>
<td>0.0086</td>
<td>10.94</td>
<td></td>
</tr>
<tr>
<td>P182/S0499_RE V2</td>
<td>26.93</td>
<td>0.0017</td>
<td>3.62</td>
<td>0.0115</td>
<td>22.21</td>
<td>18.75</td>
<td>0.0017</td>
<td>3.6213</td>
<td>0.0115</td>
<td>8.66</td>
<td></td>
</tr>
<tr>
<td>121/S0336LRE V4</td>
<td>31.19</td>
<td>0.0002</td>
<td>1.45</td>
<td>0.0072</td>
<td>36.28</td>
<td>22.73</td>
<td>0.0002</td>
<td>1.4483</td>
<td>0.0072</td>
<td>13.69</td>
<td></td>
</tr>
<tr>
<td>P006/S0526_RE II</td>
<td>26.90</td>
<td>0.0003</td>
<td>2.71</td>
<td>0.0109</td>
<td>22.12</td>
<td>19.61</td>
<td>0.0003</td>
<td>2.7129</td>
<td>0.0109</td>
<td>9.56</td>
<td></td>
</tr>
<tr>
<td>046/S0377LRE V6</td>
<td>29.21</td>
<td>0.0061</td>
<td>1.13</td>
<td>0.028</td>
<td>28.85</td>
<td>23.89</td>
<td>0.0061</td>
<td>1.1268</td>
<td>0.028</td>
<td>15.64</td>
<td></td>
</tr>
</tbody>
</table>
Two control signals are ‘start capture’ and ‘trigger pulse train’. A ‘start capture’ signal was used for handshaking. Successive ECG data sample delivery and reception between ECG simulator and FPGA was synchronised with respect to rising and falling edge of each individual pulses of ‘trigger pulse train’, as shown in Figure 10. Figure 11 shows the interfaces of design module.

3.3 Testing in Xilinx ISE 8.2i simulation environment

At first the algorithm was simulated using Xilinx ISE 8.2i. For simulating the developed algorithm two VHDL modules were designed. One module was named as ‘test bench module’, it was simulateable module. Another module named as ‘FPGA design module’, it was FPGA synthesisable or implementable module, where the algorithm was
implemented. The ‘test bench module’ simulates the behaviour of PC and the rest of SDK (Software Development Kit) board other than FPGA kit. An instance of ‘FPGA design module’ was created within the test bench module to simulate its performance. The filtered ECG data as obtained from Xilinx simulation were stored in a separate file and are plotted in MATLAB as shown in Figure 12.

**Figure 11** Interfaces of the designed module along with assigned pins of Xilinx Spartan XC3s2000fg900-4

**Figure 12** (a) and (b) filtered output obtained in Xilinx simulation on ptb-db ECG data records (see online version for colours)
The ‘design module’, on detection of a Q-, R-, S-, T- or P-waves peak, complemented the logic levels of five output signals denoted by Q10, R10, S10, T10 or P10, respectively, as shown in Figure 9. Figure 13a and 13b shows the timing diagram of Q10, R10, S10, T10 and P10 signals, obtained with Xilinx ISE 8.2i simulation, for V6 lead of ptb-db ECG data set record number s0072lre and s0143lre, respectively. The Figure 13 also shows last detected Q-, R-, S-, T- and P-wave peak index positions, on detection of successive wave peaks, in decimal notation with latency of 20 ms for R-peak and 50 ms for T- and P-wave peaks.
3.4 Implementation in Xilinx Spartan III

Finally, the algorithm (‘FPGA design module’) was implemented in the Xilinx Spartan XC3s2000fg900-4 FPGA. Q10, R10, S10, T10 and P10 binary signals were captured through status port and serial port of PC, as shown in Figure 9. The five binary signals were scaled to 50, 255, 100, 200, 150 values, respectively, before storing them to five separate files. The simultaneous plot of scaled Q10, R10, S10, T10, P10 and quantised ECG signal, as shown in Figure 14a and 14b, indicate the wave peak detection correctness. Figure 14a and 14b shows Xilinx implemented wave peak detection results for V5 lead of ptb-db ECG data file record number s0064lre and s0072lre, respectively.

Figure 14 (a) and (b) Xilinx implemented wave peak detection with V5 lead of ptb-db record no. (a) s0064lre (b) s0072lre (see online version for colours)
In the peak detection algorithms, the evaluation criteria are sensitivity ($S_r$) and positive predictivity ($P^+$), defined as:

$$S_r = \frac{TP}{TP + FN} \quad P^+ = \frac{TP}{TP + FP}$$

(19)

where TP (true-positive) stands for correctly found wave peaks. False positive (FP) is an extra beat not present in data, but detected by device. False negative (FN) is a missed beat present in ECG but not detected by the algorithm.

A total of 180 single lead data, each containing 60,000 samples were tested, with an average $S_r$ and $P^+$ of 98.4% and 98.17%, respectively, for R-peak detection. Table 2 represents some of the sensitivity and predictivity values for R-peak detection on single lead ECG using mit-db data with Xilinx implementation. An average $S_r$ and $P^+$ of 97.58% and 96.84% for P-wave detection, and 97.78% and 98.04% for T-wave detection are obtained, respectively. Table 3 shows some test results for P- and T-wave detection with ptb-db data. Table 4 represents a comparison of %FN, %FP and %+P obtained in Xilinx implementation of the of P- and T-wave detection in the presented algorithm with another reported work. Although the referenced reported works have used another ECG database, still the table shows an appreciable detection rate for current implementation. Table 5 shows the comparison of algorithmically measured relative duration and height values of P- and T-waves with actual values (manually interpreted). Relative duration and height were measured with respect to determined average R–R interval and total amplitude span of QRS wave, respectively.

Table 2 
Sensitivity and predictivity figures for R-peak detection using mit-db data (with Xilinx implementation) (with 15,000 samples)

<table>
<thead>
<tr>
<th>P-ID Lead</th>
<th>%Re</th>
<th>%P+</th>
<th>P-ID Lead</th>
<th>%Re</th>
<th>%P+</th>
<th>P-ID Lead</th>
<th>%Re</th>
<th>%P+</th>
</tr>
</thead>
<tbody>
<tr>
<td>100 V5</td>
<td>100</td>
<td>100</td>
<td>104 V2</td>
<td>100</td>
<td>100</td>
<td>108 V1</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>102 V2</td>
<td>100</td>
<td>100</td>
<td>106 V1</td>
<td>100</td>
<td>100</td>
<td>109 V1</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>103 V2</td>
<td>100</td>
<td>100</td>
<td>107 V1</td>
<td>100</td>
<td>100</td>
<td>112 V1</td>
<td>100</td>
<td>100</td>
</tr>
</tbody>
</table>

Table 3 
Sensitivity and predictivity figures for P- and T-peak detection using ptb-db data (with Xilinx implementation) (with 15,000 samples)

<table>
<thead>
<tr>
<th>Patient-ID and record number in Physionet</th>
<th>Lead I</th>
<th>Lead II</th>
<th>aVr</th>
<th>V2</th>
<th>V3</th>
</tr>
</thead>
<tbody>
<tr>
<td>%Re</td>
<td>%P+</td>
<td>%Re</td>
<td>%P+</td>
<td>%Re</td>
<td>%P+</td>
</tr>
<tr>
<td>-----</td>
<td>-----</td>
<td>-----</td>
<td>-----</td>
<td>-----</td>
<td>-----</td>
</tr>
<tr>
<td>P172/S0304LRE(N)</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>P182/S0308LRE(N)</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>P121/S0311LRE(N)</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>P006/S0022LRE(MI)</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>P046/S0168LRE(MI)</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>P003/S0017LRE(MI)</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>85</td>
</tr>
</tbody>
</table>

Table 4 
Comparison of %FN, %FP and %+P obtained in Xilinx implementation of the of P- and T-wave detection in the presented algorithm with another reported work.

Table 5 
Comparison of algorithmically measured relative duration and height values of P- and T-waves with actual values (manually interpreted). Relative duration and height were measured with respect to determined average R–R interval and total amplitude span of QRS wave, respectively.
4 Discussion

To reduce the device utilisation, an external memory can be interfaced the FPGA module for implementing FIFO data structure. In that situation, the algorithm can be implemented with an FPGA module with low device density.

The implementation of the proposed algorithm in FPGA device had a latency of 20 ms (which is 20 sampling interval) for Q, R and S-peak and 50 ms for T and P peak plus few nanoseconds (for actual implementation of the algorithm by the programmable hardware). A hardware design described in the work of Shukla et al. (2008) on the FPGA took 4 min and 43 sec for analysis of 30 min record for detection of R-wave only. In
comparison with that the presented FPGA implementation has much less latency. Table 6 summarises the resource utilisation within FPGA device Xilinx Spartan XC 3s2000fg900-4 for the said implementation of the algorithm. As per resource utilisation, design described in the work of Shukla et al. (2008), consumes 76% resource of Xilinx Spartan xc3s400 for R-wave peak detection only, which is much higher than present implementation. If Q-, R-, S-, T- and P-wave peak detection algorithm (excluding height, duration detection and LCD interface) of the present implementation is mapped to architecture of Xilinx xc3s400, it consumes only 50% resources.

Table 6  
Device utilisation summary using Xilinx Spartan III XC 3s2000fg900-4

<table>
<thead>
<tr>
<th>Elements</th>
<th>Used</th>
<th>Available</th>
<th>% Use</th>
<th>Elements</th>
<th>Used</th>
<th>Available</th>
<th>% Use</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of Slices</td>
<td>15,459</td>
<td>20,480</td>
<td>75%</td>
<td>No. of bonded IOBs</td>
<td>30</td>
<td>565</td>
<td>5%</td>
</tr>
<tr>
<td>No. of Slice Flip Flops</td>
<td>4845</td>
<td>40,960</td>
<td>11%</td>
<td>No. of MULT18X18</td>
<td>3</td>
<td>40</td>
<td>7%</td>
</tr>
<tr>
<td>No. of 4 input LUTs</td>
<td>29,389</td>
<td>40,960</td>
<td>71%</td>
<td>No. of GCLKs</td>
<td>3</td>
<td>8</td>
<td>37%</td>
</tr>
</tbody>
</table>

In the present work, only a few cycles of ECG data has been handled only to establish the proof-of-concept. However, in real-time implementation for continuous ECG analysis, to handle the inter-beat variability of wave templates; an updation of the feature with each incoming beat will make the system truly adaptive in nature. However, this may demand higher version of the FPGA.

For more accurate detection of clinical features, more efficient rule base needs to be described. For accurate detection of weak wave peaks, ECG signals needs to be digitised with higher bit resolution. In that situation for generating ECG signals with 16-bit resolution, using PC parallel port, 16-bit word (representing sample) can be delivered to microcontroller or FPGA board by sending two sequential bytes.

In future a strong rule base can be formed in terms of different features of ECG signal, for distinguishing different type of myocardial infarction, or other diseases from normal patients.

5 Conclusion

This paper describes an approach for real-time detection of electrocardiogram wave time plane features using FPGA-based system. For clinical validation, the feature extraction results were shown to a cardiologist, who confirmed that the proposed algorithm could properly detect wave peaks in the ECG data. In the current implementation, only normal and a few MI variant data has been used with the respective lead, yielding a fairly accurate result. However, for clinical application, multilead acquisition and parallel processing of lead signals can be implemented.

References


Real-time detection of electrocardiogram wave features


