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

H.K. Chatterjee, R. Gupta, M. Mitra

Department of Electronics and Communication Engineering, Camellia Institute of Technology, Kolkata 700129, Calcutta, India
Department of Applied Physics, University of Calcutta, 92, APC Road, Kolkata 700009, Calcutta, India

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 (PTBDB) 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 (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 2.5–4.5 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 approached 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 extractor (PVE) is another approach where a morphological filter is followed by threshold based mapping operations to reveal the QRS pass-band for different human are different and also overlaps with some artifact signals.

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 R5 or Qr or QS. 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.

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, (QTc), etc. are determined. The algorithm is tested with MIT-P TB database for normal and some abnormal database. The results obtained confirm the accuracy of the proposed method at par with reported works.

2. Materials and methods

The entire method can be divided into some steps. The starting point of any ECG signal processing algorithm is determination of the R-peaks in the entire dataset. This is based on a magnitude and slope comparison criteria imposed between the data samples. This yields the indices of all the R-peaks in the data. For ascertaining the accuracy, successive R-peak intervals are computed. After that, the baseline modulation (if any) is compensated by an empirical formula. The maximum duration of the segments such as QRS, ST, QT etc. are known. So, w.r.t R-peak positions, other characteristic points like P-onset, P, P-offset, Q, Q-offset, S, S-offset, T, T-onset, and T-offset are determined using upside and downside search from R-peak along the ECG data array (Fig. 3). Hence the following time-plane features are computed: QRS-width, ST-segment width, QT-width, and corrected QT-width.

The brief outlines of the steps are described as follows:

(a) R-peaks determination: First, the entire dataset is sorted for descending order of magnitude and first 2200 samples are taken from total 60 s data-points. This possibly includes all R-peaks and some neighbours w.r.t certain peaks, assuming that the lead signal dataset contains baseline modulation. This derived dataset then is re-grouped into some blocks in ascending order of indices, based on certain restrictions on difference between successive data points. The selection of maxima within such a block eliminates the nearest neighbour’s candidature for being considered as R-peak. From each of these maxima, left and right approach for 450 ms is done in the original dataset for computing the average absolute slope for each data points. For each maximum, these data points are sorted in descending order of absolute slope. The average slope is calculated by taking a $\pm 20$ ms window across each data point. This eliminates the T and P points in the individual 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 R5 or Qr or QS. 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 characteristic 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 locus 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:

$$\text{Correction applied at point } \dot{t}_{i} = \frac{x_{i} - blp_{n}}{blp_{n+1} - blp_{n}} \left( y_{n+1} - y_{n} \right)$$

where $x_{i}$ is the index of point $i$; $blp_{n+1}$, $blp_{n}$ the two successive baseline point index (in ms); and $y_{n+1}$, $y_{n}$ 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 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. 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 up to 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 up to 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, \((QT)_{c} = \frac{(QT)}{\text{Sqrt}(R/C0)}\).

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] con-
tains 48 half-hour excerpts of two-channel ambulatory ECG record-
ings (ML II 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 determina-
tion 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

determination.
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:

\[ R_e = \frac{TP}{TP + FN}, \]

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

Coefficient of variation \( CV = \frac{\text{standard deviation}}{\text{average}} \)

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.

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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%.
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.

### Table 4

Time-plane features.

<table>
<thead>
<tr>
<th>Patient ID in physionet</th>
<th>Category of data</th>
<th>Lead I</th>
<th>Lead III</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Algo mean</td>
<td>Coefficient of standard deviation</td>
</tr>
<tr>
<td>(a) QRS width (in ms)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S0301lre</td>
<td>Normal</td>
<td>109.4</td>
<td>5.72</td>
</tr>
<tr>
<td>S0308lre</td>
<td>Normal</td>
<td>105.1</td>
<td>8.49</td>
</tr>
<tr>
<td>S0311lre</td>
<td>Normal</td>
<td>96</td>
<td>8.05</td>
</tr>
<tr>
<td>S0287lre</td>
<td>Normal</td>
<td>98.5</td>
<td>13.13</td>
</tr>
<tr>
<td>S0299lre</td>
<td>Normal</td>
<td>107.5</td>
<td>9.99</td>
</tr>
<tr>
<td>S0083lre</td>
<td>Anterio Septal</td>
<td>106.7</td>
<td>3.83</td>
</tr>
<tr>
<td>S0091lre</td>
<td>Anterio Septal</td>
<td>121.1</td>
<td>11.79</td>
</tr>
<tr>
<td>S0148lre</td>
<td>Inferio Lateral</td>
<td>115.7</td>
<td>16.16</td>
</tr>
<tr>
<td>S0061lre</td>
<td>Anterio</td>
<td>114.8</td>
<td>8.14</td>
</tr>
<tr>
<td>(b) QT width (in ms)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S0301lre</td>
<td>Normal</td>
<td>399.1</td>
<td>2.39</td>
</tr>
<tr>
<td>S0308lre</td>
<td>Normal</td>
<td>411.4</td>
<td>4.94</td>
</tr>
<tr>
<td>S0311lre</td>
<td>Normal</td>
<td>390.88</td>
<td>3.46</td>
</tr>
<tr>
<td>S0287lre</td>
<td>Normal</td>
<td>432.7</td>
<td>6.07</td>
</tr>
<tr>
<td>S0299lre</td>
<td>Normal</td>
<td>389.2</td>
<td>4.13</td>
</tr>
<tr>
<td>S0083lre</td>
<td>Anterio Septal</td>
<td>391.8</td>
<td>3.45</td>
</tr>
<tr>
<td>S0091lre</td>
<td>Anterio Septal</td>
<td>408.7</td>
<td>4.14</td>
</tr>
<tr>
<td>S0148lre</td>
<td>Inferio Lateral</td>
<td>397.9</td>
<td>3.53</td>
</tr>
<tr>
<td>S0061lre</td>
<td>Anterio</td>
<td>447.1</td>
<td>2.84</td>
</tr>
</tbody>
</table>

Table 5

QRs detection performance on MIT-BIH arrhythmia database.

<table>
<thead>
<tr>
<th>QRS detector</th>
<th>Annotations</th>
<th>TP</th>
<th>FP</th>
<th>FN</th>
<th>Se (%)</th>
<th>P+ (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Presented work</td>
<td><strong>100,110</strong></td>
<td>100,108</td>
<td>0</td>
<td>2</td>
<td>99.988</td>
<td>100</td>
</tr>
<tr>
<td>Ghaffari et al. [22]</td>
<td>110,159</td>
<td>109,837</td>
<td>322</td>
<td>120</td>
<td>99.91</td>
<td>99.72</td>
</tr>
<tr>
<td>Addison et al.</td>
<td>58,523</td>
<td>58,346</td>
<td>186</td>
<td>177</td>
<td>99.7</td>
<td>99.68</td>
</tr>
<tr>
<td>Li et al.</td>
<td>104,182</td>
<td>104,070</td>
<td>65</td>
<td>112</td>
<td>99.89</td>
<td>99.94</td>
</tr>
<tr>
<td>Martinez et al.</td>
<td>109,428</td>
<td>109,208</td>
<td>153</td>
<td>220</td>
<td>99.80</td>
<td>99.86</td>
</tr>
</tbody>
</table>

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 maximum 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 Qt 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 entire 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 candidatures, 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 my determining the points of minimum average absolute 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 MIT-PTB database (ptb-db) and available under Physionet. Cardinal point detection algorithm is tested with 360 normal and abnormal PTBDB. The overall accuracy obtained is more than 99% which is acceptable as compared to other standard methods.

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References