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Automated ECG Segmentation Using Piecewise Derivative Dynamic Time Warping

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***Abstract*—**Electrocardiogram (ECG) segmentation is necessary to help reduce the time consuming task of manually annotating ECG's. Several algorithms have been developed to segment the ECG automatically. We first review several of such methods, and then present a new single lead segmentation method based on Adaptive piecewise constant approximation (APCA) and Piecewise derivative dynamic time warping (PDDTW). The results are tested on the QT database. We compared our results to Laguna's two lead method. Our proposed approach has a comparable mean error, but yields a slightly higher standard deviation than Laguna's method.

***Keywords*—**Adaptive Piecewise Constant Approximation, Dynamic programming, ECG segmentation, Piecewise Derivative Dynamic Time Warping.

I. Introduction

AN electrocardiogram-abbreviated as EKG or ECG-measures the the electrical activity of the heart. The timing between the onset and offset of particular features of the ECG (referred to as an *interval*) is of great importance since it provides a measure of the state of the heart and can indicate the presence of certain cardiological conditions. Due to the time consuming nature of manually annotating the ECG by cardiologists, different automated methods have been proposed to overcome this problem. Here, we first give a brief review of some of these methods before describing our new approach based on Adaptive piecewise constant approxima-tion [1] and Piecewise derivative dynamic time warping (PDDTW) for ECG segmentation.

A very successful approach was first proposed by laguna et al. [2] which was based on second order band pass filtering the ECG and then differentiating it. In the end different waves would be detected based on their zero-crossings, and finding the nearest points exceeding empirical thresholds.

Segmentation of ECG based on Fourier transforms were implemented by Sahamabi [3] using the first four transforms .Murthy and Niranjan [4] used the DFT to segment the ECG. In [5] Vullings et al. proposed a method of ECG segmentation using Dynamic time warping , based on pre-filtering the signal and approximating the filtered signal with lines and using DTW for the final segmentation of the ECG. Different approaches to ECG segmentation have also been implemented using Hidden markov models by Clavier and Boucher [6]. In [7] Graja and Boucher use a multisclae hidden markov model applied to segment the ECG. Another method was proposed by Crouse et al. [8] using a combination of Wavelet and Hidden markov models. Recently, Hughes et al. [9] have proposed a segmentation method using Semi-Supervised Learning of Probabilistic Models which is based on the EM algorithm for maximum likelihood estimation, which can be used to learn probabilistic models from subjectively labeled data.

A problem with probabilistic models is the difficulty with HMMs is to determine suitable values for the different parameters: the initial state probabilities, the transition probabilities between states, and the output probabilities of the slope and the amplitude. Another significant limitation of the standard hidden Markov model is the manner in which it models state durations. Thus for a given ECG waveform the decoded state sequence may contain many more state transitions than are actually present in the signal. The resulting HMM state segmentation is then likely to be poor and the resulting QT and PR interval measurements unreliable. Although algorithms exist to overcome these limitations [10] but they are still sensitive to initial conditions and choosing the right probability density for the duration of each state.

This paper which is an extension of [5] will introduce a fast method based on Adaptive piecewise constant approximation method and Piecewise derivative dynamic time warping for automated ECG segmentation. The results will be evaluated

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on the QT database [11] and compared to Laguna's approach [2].

The remainder of the paper is organized as follows. Section II gives a brief review of the methods employed for segmenting the ECG signals. Section III presents the experiment results on performance comparison of our method and that of Laguna. Finally, section IV concludes the paper.

II. Method

The method consists of the following steps: first, we perform some pre-filtering to remove high frequency noise, and next we approximate the filtered signal by the Adaptive piecewise constant approximation method. Using a standard peak QRS detection algorithm from the literature, we divide the ECG signal into separate heartbeats. Finally, every heartbeat is compared using PDDTW with a set of P, QRS and T wave templates, and the best matches are selected for the detection of the fiducial points.

A. Preprocessing

We first apply a moving average filter of order 5 to the signal. This filter removes high frequency noise like interspersions and muscle noise. Then, drift suppression is applied to the resulting signal. This is done by a high pass filter with a cut off frequency of 1Hz. Finally, a low pass Butterworth filter with a limiting frequency of 30 Hz is applied to the signal in order to suppress needless high-frequency information even more. Next, the APCA algorithm is used to adaptively represent the ECG signal.

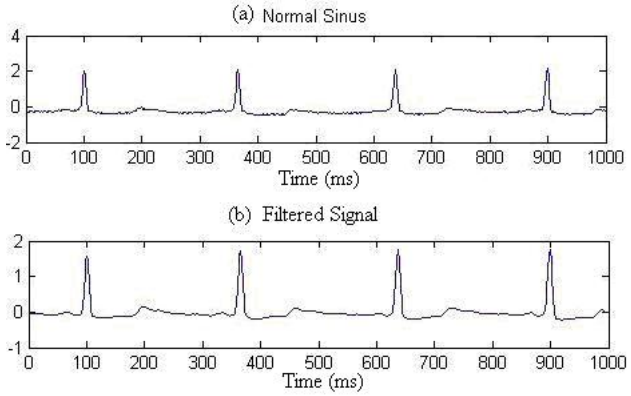

Fig. 1 Applying the appropriate preprocessing to a sample signal to remove unwanted noise.

The primary segmentation is done with the Pan and Thompson's QRS detector [12], which detects the position of the QRS complex in the ECG. Next, we select a region around the R-peak, 100 samples before and 200 sample after the R-peak, this ensures a heart beat to be confined to this region of 1.2 seconds with a sampling rate of 250Hz. Then this heartbeat is decomposed into three overlapping parts: a part before the QRS complex (ending one line before the R peak), a small region (150 samples wide) around the QRS, and a part after the QRS complex (starting one line after the QRS peak).

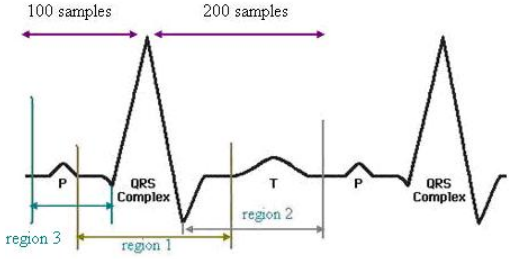

Fig. 2 Segmenting the adaptively approximated ECG signals.

B. Adaptive Piecewise Constant Approximation

Adaptive Piecewise Constant approximation (APCA) approximates each time series by a set of constant value segments of varying lengths such that their individual reconstruction errors are minimal. Given a time series $C = \{c_1, \ldots, c_n\}$, we need to be able to produce an APCA representation, which we will represent as:

$$C = \{\langle cv_1, cv_2 \rangle, \ldots, \langle cv_M, cr_M \rangle\}, \quad cr_o = 0 \tag{1}$$

Where cv_i are the mean value of data points in the i_{th} segment and cr_i the right endpoint of the i_{th} segment. The APCA approximation allows for segments of different size to minimize the approximation error.

The algorithm first takes the problem onto a wavelet domain compression problem, for which optimal solutions are already known, then converts it back to the ACPA representation and might even make some minor modifications. It uses the fact that the Haar wavelet transformation of a time series signal can be calculated in O (n), and that an optimal reconstruction of the signal for any level of compression can be obtained by sorting the coefficients in order of decreasing normalized magnitude, and then truncating the smaller coefficients. If the segments in the reconstructed signal have approximate mean values, they will be replaced by the exact mean values to get a valid APCA representation as described in Equation 1.

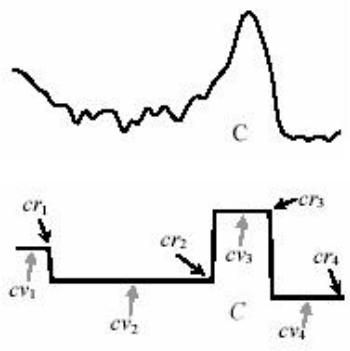

Fig. 3 A time series C and its APCA representation C, with $M = 4$ [1].

C. The PDDTW Algorithm

After the preprocessing, we now have a large set of adaptive approximations of heartbeats, each of them decomposed into three regions. Next, we have to select those points among the endpoints of these waveforms which are most likely the fiducial points we are looking for. This task is solved by the Piecewise derivative dynamic time warping (PDDTW) algorithm.

Piecewise Derivative Dynamic Time Warping (PDDTW), takes advantage of the fact that we can efficiently approximate most time series by a piecewise aggregate approximation [13] and use a derivative distance measure in order to reduce singularities and extracting higher level features [14]. In order to align two sequences Q and C, we first derive a reduced dimension of Q and C which we denote $\overline{Q_i}$ and $\overline{C_i}$ respectively. Then we construct an *N*-by-*M* matrix where the (i_{th}, j_{th}) element of the matrix contains the distance $d(\overline{Q_i}, \overline{C_i})$ between the two elements $\overline{Q_i}$ and $\overline{C_i}$.

Next similar to [14] we choose the distance measure $d(\overline{Q_i}, \overline{C_j})$ not Euclidean but rather the square of the difference of the estimated derivatives of $\overline{Q_i}$ and $\overline{C_i}$. We use the following estimate for simplicity and generality to computing derivatives.

$$D_x[Q] = \frac{(Q_i - Q_{i-1}) + ((Q_{i+1} - Q_{i-1})/2)}{2} \quad (2)$$

In order to obtain such a matching, this path can be found very efficiently using dynamic programming to evaluate the following recurrence which defines the cumulative distance $\gamma(i,j)$ as the distance $d(i,j)$ found in the current cell and the minimum of the cumulative distances of the adjacent elements:

$$\gamma(i,j) = d(\overline{Q_i}, \overline{C_i}) + \min\{\gamma(i-1, j-1), \gamma(i-1, j), \gamma(i, j-1)\} \quad (3)$$

The warping path which minimizes the warping cost becomes :

$$PDDTW(\overline{Q}, \overline{C}) = \min\left\{ \sqrt{\sum_{k=1}^{K} w_k} \Big/ \sqrt{c} \right\} \quad (4)$$

Where the compression ratio c is the ratio of the length of the original time series to the length of its Piece wise aggregate approximation. Because the length of the warping path is measured in the same units as DTW we have:

$$PDDTW(Q, C) \cong DTW(Q, C) \quad (5)$$

The time complexity for a PDDTW is O(*NM*), where *M* = *m*/*c* and *N*= *n*/*c*. The time complexity for the original DTW algorithm is O(*nm*). So the speedup obtained by PDDTW should be O(*nm*)/O(*MN*) which is O(*c*2).

Once we have found the minimal path connecting the two waveforms. Similar to [5] we look for the lines in the reference period which are indicators of fiducial points and take the corresponding line of the new period. This label along with the time stamp is then copied to file. Fig. 4 shows how a sample signal is aligned and segmented using the described approach.

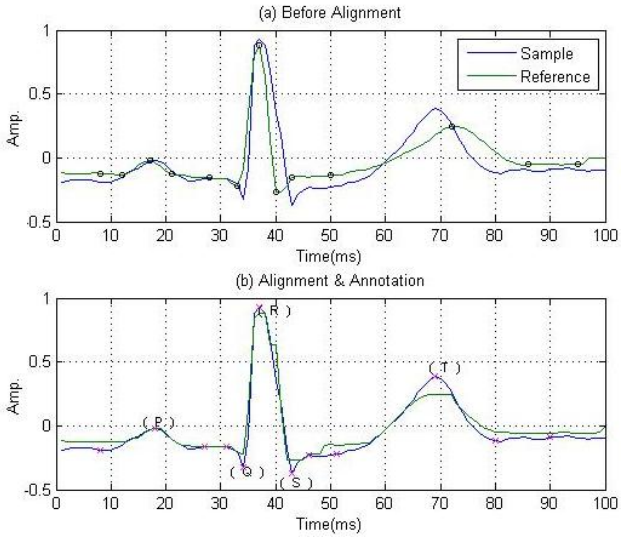

Fig. 4 Segmenting the new incoming beat by the reference beat. The two beats are aligned according to the DTW matrix to each other.

D. Choosing the Appropriate Reference Heartbeat

Before aligning the heartbeats we need a reference heart-beat. Due to the high variability between different heartbeats, it would acquire a very large database in order to capture all range of possibilities. Instead, similar to [5] we selected a small set of QRS(8), P waves (5), and T waves (10) to reflect the variations in the ECG, which combined generate 400 possible heartbeats.

The main difference between this approach and equation (3) is the addition of an extra layer:

$$\gamma(i,j) = d(\overline{Q_i}, \overline{C_i}) + \min\{\gamma(i-1, j-1, k), \gamma(i-1, j, k), \gamma(i, j-1, k)\} \quad (6)$$

where *k* represent the layer (from one to the number of waves, which is 5, 8, and 10, respectively). In the overlapping we select the previous distance over all previous layers.

In the case where we don't have a waveform but instead we have noise, sometimes a match is made between a reference wave and the noise. To diminish this we set a threshold of 7 samples as the minimum distance between a P or T top and its onset or offset. If this is not the case, annotations of the wave will not be considered.

Another approach in order to find adequate QRST reference heartbeats would be to take some of the ECG signals in the QT database, and perform QRST clustering to obtain suitable reference beats. This would be done as follows:

Suppose N is the number of created clusters and n_k is the number of beats assigned to cluster k (*i.e.* C_k):

1) Assign the centroid of the first cluster to the first QRS vector, set N to 1 and n_1 to 1.
2) Compare the next input signal vector (X) to all created clusters and find the nearest cluster C_k according to a minimum distance measure
$$d_{\min} = \min(d_f(C_i, X)) = d_f(C_k, X) \quad , i \in [1, N]$$
3) Update centroid of cluster k, $C_k = (C_k n_k + X)/(n_k + 1)$ if the distance (d_{min}) is less than a specified threshold, increment n_k and go to the second step. Else, If the minimum distance is larger than the threshold, create a new cluster and increment the number of created classes N and go to the second step.

It should be noted that we do not have any restrictions on distance functions, i.e., any distance function is possible. Here for demonstration we used the Euclidean distance measure to find the suitable templates.

$$d_f(x_1, x_2) = \min\left(\sqrt{\sum_{i=B+k}^{A+k} (x_1(j, B, A) - x_2(j+k, B, A))^2}\right)$$

where k indicates the shift between two vectors for alignment and B and A are the start and endpoints of the QRS complex, respectively.

So the input vectors x_1 and x_2 are first modified by removing the dc-component and normalizing their energy. For example for x_1:

$$x(j) = \frac{x(j) - \frac{1}{A-B+1}\sum_{k=B}^{A} x(k)}{\sqrt{\sum_{t=B}^{A} (x(t) - \frac{1}{A-B+1}\sum_{k=B}^{A} x(k))^2}}$$

where $j = 0, \ldots, L$. Here L is the length of the QRS feature vectors.

Next, the distance is measured between different beats in order to perform clustering. So at the end of this algorithm we will have different clusters (i.e. different reference heartbeats), at our disposal. Fig. 5 shows sample QRS templates extracted using the above approach. Then is up to the user how many reference beat he or she sees appropriate for the task in hand.

It also should be stated that one may as well perform QRST morphological clustering of the channel by the l_1 norm distance or the l_1 norm normalized by the l_2 norm with wiggling and vertical shifting to find the reference heartbeats. In order to further improve the quality of the extracted reference beats, one would classify beats to normal or abnormal. Because although normal beats recorded from a patient are usually not exactly the same as the normal beats of another patient, but as its almost the case, normal beats remain morphologically very similar to one another during the long-run. Also, the variety of beats in normal classes is significantly lower than that of all classes associated with abnormal beats. This would indeed increase the size of the reference beat database and consequently the search size. So there would be a trade-off between accuracy and run-time.

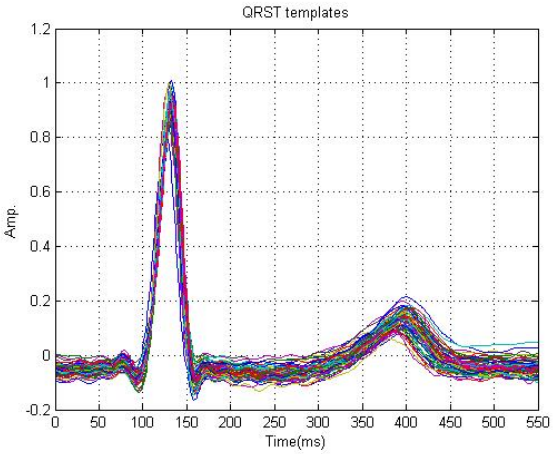

Fig. 5 Extracted QRST reference beats from 10 ECC signals from the database.

III. Results

The proposed approach for ECG segmentation was tested using the second ECG leads from the QT database. This database is a mixed database with a sampling frequency of 250 *Hz*, which consists of 105 excerpts (each 15 minutes long) taken from other ECG databases, where, 15 from MIT-BIH Arrhythmia Database, 6 from the MIT-BIH ST Change Database, 13 from the MIT-BIH Supraventricular Arrhythmia Database, 10 from the MIT-BIH Normal Sinus Rhythm Database, 33 from the European ST-T Database, 24 from "sudden death" patients from BIH, and 4 records from the MIT-BIH Long-Term ECG Database. The method was entirely implemented in MATLAB on a Pentium IV, 2.4 MHz processor.

One set of annotations were produced for each record.The results are shown in Table 1.

TABLE I
Evaluation Results

	Our Method			Laguna's Method		
	Beats	Me	SD	Beats	Me	SD
P_{on}	1821	7.23 *	17.79	2596	10.26	14.08
P	1834	3.21	13.47	2626	-0.48	10.96
P_{end}	1834	2.43	15.01	2627	-5.73	13.57
QRS_{on}	2710	-5.22	3.60 *	3130	-9.32	4.41
R	2710	-9.56	6.34	3130	-9.32	4.41
QRS_{end}	2710	-2.13 *	11.24	3130	-3.64	10.74
T_{on}	410	-11.62	28.6 *	1241	-16	29.82
T	2246	-4.76	29.86	2932	23.26	28.26
T_{end}	2246	6.72	33.46	2996	18.68	29.79

Comparing the automatic waveform The last three columns are reproduced from [2] .Mean and Standard deviation are in milliseconds

The performance of our method was based on calculating the mean error (me) and the standard deviation of this error (SD) [15]. The mean error determines how close is the detector's criterion to the experts'. The standard deviation shows the stability with which the detection criterion has been implemented.

IV. Conclusion

In this paper, a new algorithm based on Piecewise derivative dynamic time warping has been developed for the automated segmentation of ECG signals. We have verified and validated our method for automatic ECG segmentation using beats from 95 different records. By taking advantage of dimension reduction techniques such as Piecewise aggregate approximation and Adaptive piecewise constant approximation we significantly speed up our algorithm both in the preprocesing and segmentation stage .

The results show that the mean error from our method is comparable to Laguna's, sometimes even better, yet the standard deviation is a little bit higher. As the segmentation was solely on the second lead, we cannot measure the positive predictivity of the method.

We conclude that for single-lead wave boundaries detection, our proposed method is robust enough to give measures comparable to those given by experts. We could further expand this method to two leads, in which for each record to sets of annotation file would be created. First, we would analyze annotations from one channel, and when evaluation results in a record were disappointing with this channel's annotations, results in the other channel would be studied .

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