

ECG Segmentation in a Body Sensor Network Using Adaptive Hidden Markov Models

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ABSTRACT

In this paper, a novel approach for segmenting ECG signal in a body sensor network is presented. Hidden Markov Modeling (HMM) technique is employed. The parameter adaptation in traditional HMM methods is conservative and slow to respond to these beat interval changes. Since people's heart rates vary a lot, the corresponding characteristic waveform intervals and durations change with time as well. Moreover, for patients with cardiac diseases, such as arrhythmia, the heart beat interval may even change abruptly and irregularly. Therefore inadequate and slow parameter adaptation is largely responsible for the low positive predictivity rate (+P). To solve the problem, we introduce an active HMM parameter adaptation and ECG segmentation algorithm, which includes three parts: the pre-segmentation and classification, the HMM model training, and the detailed segmentation. Body sensor networks are used to pre-segment the raw ECG data by performing QRS detection. Then the R-R interval information that directly reflects the beat interval variation is extracted and used to classify the raw ECG data into several groups. One specific HMM is trained for each of the groups. Hence, instead of one single generic HMM, multiple individualized HMMs are set up. In the detailed segmentation, each HMM is only responsible for extracting the characteristic waveforms of the ECG signals with similar temporal features from the same group, so that the temporal parameter adaptation can be naturally achieved.

Categories and Subject Descriptors

I.5.4 [Pattern Recognition]: Applications – Signal Processing.

General Terms

Algorithms, Design, Experimentation.

Keywords

Body Sensor Networks (BSNs), ECG Segmentation, Hidden Markov Models (HMMs), parameter adaptation.

1. INTRODUCTION

Heart disease is the leading cause of mortality in the United States. It accounts for 30.4% deaths in the United States in 1999, which is ranked No. 1 [1]. Traditionally, exercise test and ambulatory ECG are two of the most widely accepted noninvasive procedures for identifying patients with probable heart disease [2]. Measurements of the width or duration of characteristic waveforms and analysis of their morphology variations in the ECG are used to define ectopic electrical activity in the heart, to detect myocardial damage, and to classify patients at risk of cardiac diseases [8]. However, these tests and ECG processing are usually performed in a lab environment and are under the supervision of specially trained physicians. This may cause so-called White Coat Syndrome (WCS), which may affect the accuracy of the test result due to mental stress effects. Moreover, since the test can only be performed occasionally due to the cost and schedule constraints, some important symptoms may be missed, which often lead to delayed diagnoses and even misdiagnoses.

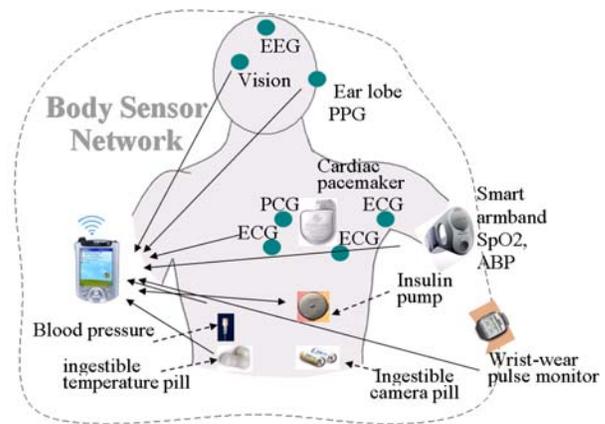


Figure 1. A body sensor network consisting of various biosensors

Recent significant progresses in wireless sensing/monitoring and wearable/implantable biosensors have enabled Body Sensor Networks (BSNs), a promising personal and ubiquitous healthcare candidate solution. Composed of various biosensors, such as electrocardiogram (ECG), phonocardiography (PCG), ambulatory blood pressure (ABP) and oxygen saturation (SpO2) sensors (as shown in Fig. 1), BSNs are capable of sensing,

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communicating and processing different physiological parameters and helping physicians to make critical clinical decisions. Benefitted from their miniature sized and biocompatible sensor nodes, BSNs can be deployed on the patient's body or even be implanted in the body, with their interference to the daily life of the users reduced to the minimum. Therefore, BSNs are ideal for collecting and monitoring ECG signals. Moreover, the context information provided by the body sensor network can improve the performance of many data processing algorithms, such as QRS detection [9].

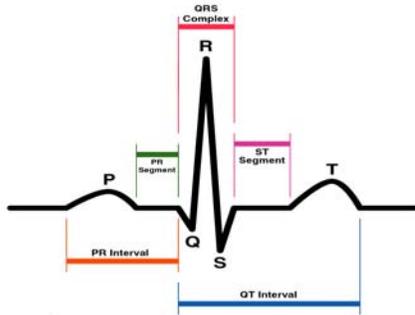


Figure 2. ECG and associated characteristic waveforms within one heartbeat.

Interpretations and annotations of ECG are extremely time consuming and usually made by experienced physicians. For long term ECGs, such as the 24x7 continuous records obtained from a BSN, it is almost impossible to manually scroll through all the records to locate interesting episodes. Therefore, automated ECG analysis systems have been intensely studied by many researchers [4-8]. As the basis of further analysis, the detection of the major characteristic waveforms in ECGs is one of the essential tasks in ECG analysis [4-8], in which the waveform boundaries (the onsets and ends of P, QRS, and T waves, as shown in Fig.2) are located. Once those characteristic waveforms are extracted, important clinical features, such as the QRS duration, the ST segment, and the QT interval can be obtained; cardiac beat classification and interesting episode definition can be made; clinical tests such as heart rate recovery (HRR) and ST segment depression analysis during exercise testing (ET) also depend on those features.

Hidden Markov Modeling (HMM) technique is employed in the ECG segmentation. Compared with methods purely based on heuristic rules [12-17], HMM methods have several advantages. Markov chain topology can preserve structural information of characteristic waveforms, and HMM model parameters can represent the statistical nature of the ECG signals [7]. As a probabilistic model, no thresholds used by the heuristic rules are needed any more. What's more, with HMM the ECG segmentation and feature classification can be achieved simultaneously.

ECG segmentation bears analogy to speech processing [6], in which HMMs have many successful applications. In both cases, a pattern recognizer that is insensitive to the temporal variation of the patterns and good segmentations of individual episode of interest in the training data are of great importance to achieve stable performance. In the field of ECG analysis, temporal

variations widely exist. Compared with speech processing, ECG signals to be processed are usually not segmented. Poor HMM temporal parameter adaptation will cause pattern misalignments in the unisolated ECG signals and become the major source of the ECG segmentation errors. Therefore, introducing adaptability to the HMM is crucial for the segmentation performance.

In the work of [4], HMM is adopted for cardiac arrhythmia analysis. Individual characteristic waveform within each beat, instead of R-R interval sequences, is modeled in order to perform arrhythmia analysis. Since heart rate varies a lot, the characteristic waveform intervals and duration change as well. The causes could be rate variations of the cardiac pacemaker, ectopic pacemaker sites, and abnormal propagation of pacing impulses through the specialized cardiac conduction system [4]. The cardiac rhythm of normal subjects also changes a lot during daily activities. Specially, for patients with heart diseases, such as cardiac arrhythmia, the change may be abrupt and unpredictable. In the ECG segmentation, those temporal variations could cause pattern misalignments that propagate for several beats, which seriously reduces the segmentation accuracy rate. The temporal HMM parameter adaptation is considered in [4], in which the model parameter is a combination of model parameters of the previous period and current estimates computed from the most recent 20 beats. To further improve the parameter adaptation performance, an isolated-beat Viterbi algorithm is also implemented. However those algorithms are quite conservative, hence slow to respond to the beat interval changes. Therefore inadequate and slow parameter adaptation is still the major cause for low positive predictivity (+P).

In order to make HMMs adapt promptly to the temporal variations and reduce the misalignment errors, a body sensor network based active HMM parameter adaptation and ECG segmentation algorithm is proposed in this work. Instead of a single generic model, multiple individualized HMMs are used to improve the temporal adaptability. MIT-BIH QT database and MIT-BIH Arrhythmia database are used to evaluate the algorithms.

This paper is organized as follows. In Section II, the background about the Hidden Markov Model is introduced. The body sensor network based ECG segmentation algorithm will be presented in section III. Simulation results are given in Section IV. Discussions and conclusions are given in Section V.

2. HIDDEN MARKOV MODELS (HMMS)

Hidden Markov Model (HMM) is a type of probabilistic signal model in which a discrete-time finite state homogeneous Markov chain is observed through a discrete-time memoryless invariant channel [10]. The system in a HMM is assumed to be a first order Markov process in this work, i.e., the probability that the system moves to a given state depends only on the state immediately preceding it. Unlike a regular Markov model, the states of a HMM are usually invisible and need to be estimated from a sequence of observations that are probabilistically related to the unknown states. Therefore, a HMM can be regarded as a bivariate parametric process: one is the underlying finite-state

homogeneous Markov chain that is unobservable (the hidden states); the other is a sequence of conditionally independent random variables emitted by the Markov chain (the observations).

HMM has been successfully applied in a variety of research fields and is well-known for their successful applications in temporal pattern recognition including speech processing, handwriting and gesture recognition, and DNA sequence identification. A HMM is characterized by a set of parameters which can be denoted by $\lambda = (A, B, \pi)$, where A is the state transition probability matrix, B is the observation symbol probability distribution, and π is the initial state distribution.

There are three fundamental problems in HMM designs that are identified in [6]: the evaluation of the probability of a sequence of observations given a specific HMM; the determination of a state sequence that best explains a sequence of observations given the model; and the adjustment of model parameters to maximize the probability of a given observation sequence. The first problem above is also called evaluation problem, and usually used for classification purposes. In the ECG analysis, multiple HMMs can be setup according to different training groups and by finding out the model giving the highest probability to certain observations, the ECG episodes can be grouped by the corresponding model, and then the classification can be inferred. The second problem, a.k.a. decoding problem, is used in ECG signal segmentation. If we associate each sample in an ECG sequence with a hidden state (P, QRS, or T wave), when the optimal state sequence is found using the Viterbi algorithm, the ECG segmentation is naturally accomplished. The third problem (learning problem) needs to be finished before the system models can be applied in the first and second problem.

One of the advantages of HMM is that computationally efficient algorithms to solve the three problems above are available. Forward-backward procedure, which is much more efficient than brute force calculation, can be used for the first problem. Viterbi algorithm is available to infer the optimal state sequence in the second problem. For the third problem, though there is no known analytical solution, Baum-Welch algorithm (expectation-modification) usually provides acceptable performance.

3. ALGORITHM DESCRIPTION AND DISCUSSIONS

3.1 Algorithm Overview

Our active HMM parameter adaptation and ECG segmentation algorithm includes three main parts: the pre-segmentation and classification, the HMM model training, and the detailed segmentation. Body sensor networks are used to collect ECG data and extract R-R interval information by performing QRS detection in the pre-segmentation. Based on the lengths of R-R intervals, pre-segmented raw ECG signals are classified into several (N) groups for the later HMM model training and detailed segmentation. HMM model training decides the proper parameters for the HMM models used in the detailed segmentation. Characteristic waveforms are finally obtained by the detailed segmentation. The mapping of ECG signal to HMM hidden states is done by associating each sample (voltage signal)

in the ECG with a hidden state representing a characteristic waveform (P, QRS, T, or isoelectric ISO). Therefore, once the hidden state sequence is identified, we'll have all the onsets, offsets, and duration information of any characteristic waveform, and the detailed segmentation is finished. The pre-segmentation and classification are heuristic, while the HMM model training and detailed segmentation base on probabilistic methods. We should point out that the pre-segmentation and classification process both the training and test data. HMM model training only needs the training data. The detailed segmentation only works on the test data.

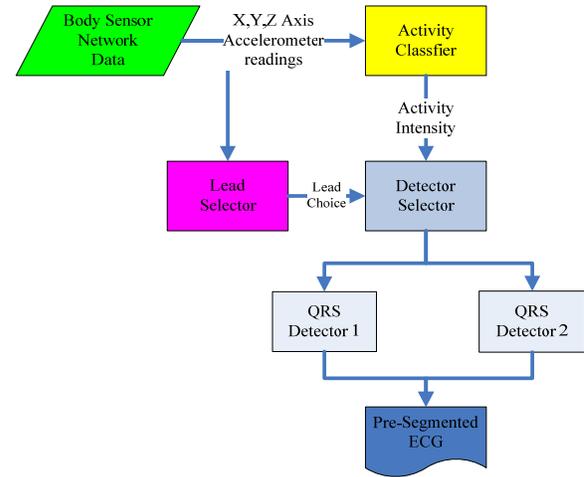


Figure 3. Block diagram of the QRS complex detection algorithm

3.2 The Pre-segmentation and Classification

In the pre-segmentation step, the QRS complex detection algorithm in our previous work [9] is employed to extract the R-R interval information. We choose QRS complex for the pre-segmentation is because it is the most significant characteristic waveform in the ECG, therefore easy to identify and relatively immune to potential noise interferences. The QRS complexes also mark the R-R intervals that directly reflect the beat variation. In [9], the QRS complex detection algorithm uses the context information provided by the body sensor network to improve the QRS detection performance by dynamically selecting the leads with best SNR and taking advantage of the best features of two complementary detection algorithms. The accelerometer data from the BSN can be used to classify the patients' daily activity and provide the context information. The classification results indicate both the type of the activities and their corresponding intensity, and the latter is directly related to the signal/noise ratio (SNR) of the ECG recordings. Activity intensity is first fed to lead selector to eliminate the leads with low SNR, and then is fed to a selector for selecting a proper QRS detector according to the noise level. The block diagram for the QRS complex detection algorithm is shown in Fig. 3.

The raw ECG data are then segmented based on the detected R peaks. The segmented ECG is further classified into several groups using a heuristic rule. The classification is based on the lengths of the R-R intervals to make sure the ECG data in each group have similar R-R intervals, hence temporal features.

Assuming that the maximum and minimum R-R interval is I_{MAX} and I_{MIN} , respectively, we can classify the pre-segmented ECG into N groups, with the R-R interval ranges:

$$[I_{MIN} + (k-1) \times D, I_{MIN} + k \times D] \quad (1 \leq k \leq N) \quad (1)$$

where $D = (I_{MAX} - I_{MIN})/N$.

The number N can be determined according to the variance of the ECG R-R intervals and the number of the training data. A bigger N could be chosen when the variance is large and the training data is adequate. A proper N can effectively reduce the temporal variations in each classified ECG group and also guarantee there are enough data in each group for the later HMM training. In this paper, N is usually chosen experimentally between 3 and 10. Fig. 4 is an illustration of the pre-segmentation and classification.

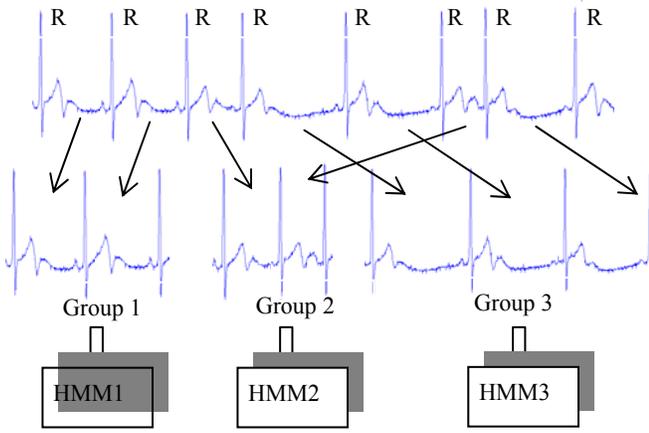


Figure 4. An illustration of the presegmentation and classification.

3.3 Training of the Hidden Markov Models

In this algorithm, one specific HMM is trained for each of the N groups, so N HMMs will be obtained. In the training process, each HMM adjusts its parameters to maximize the probability of the given observation, i.e. the ECG data with similar temporal features in that group. In this way, instead of one single generic HMM, multiple individualized HMMs are set up for the later detailed segmentation stage.

The classic Baum-Welch (forward-backward) algorithm is used to perform the training. By analyzing the characteristic waveform amplitude histograms of annotated ECGs, the output functions can be selected to be multidimensional (d -dimensional) Gaussian probability density functions, specified by two parameters, the mean vector $\underline{\mu}_i$ and the covariance matrix $\overline{\Omega}_i$.

$$b_j(\underline{x}) = \frac{1}{\sqrt{(2\pi)^d |\overline{\Omega}_j|}} \exp\left[-\frac{1}{2}(\underline{x} - \underline{\mu}_j)^T \overline{\Omega}_j^{-1} (\underline{x} - \underline{\mu}_j)\right], \quad (1 \leq j \leq n) \quad (2)$$

Multiple random initializations are performed to avoid local maximums. The number of hidden states is also chosen carefully to avoid the over-fitting problem. The maximum

likelihood reestimation formulas (3-5) are similar to the formulas for discrete outputs [5]:

$$\overline{a}_{ij} = \frac{\sum_{k=1}^{T-1} \alpha_{k,i} a_{ij} b_j(x_{k+1}) \beta_{k+1,j}}{\sum_{k=1}^{T-1} \alpha_{k,i} \beta_{k,i}}, \quad (1 \leq i \leq n, 1 \leq j \leq n) \quad (3)$$

$$\overline{\mu}_i = \frac{\sum_{k=1}^T \alpha_{k,i} \beta_{k,i} x_k}{\sum_{k=1}^T \alpha_{k,i} \beta_{k,i}}, \quad (1 \leq i \leq n) \quad (4)$$

$$\overline{\Omega}_i = \frac{\sum_{k=1}^T \alpha_{k,i} \beta_{k,i} (x_k - \overline{\mu}_i)(x_k - \overline{\mu}_i)^T}{\sum_{k=1}^T \alpha_{k,i} \beta_{k,i}}, \quad (1 \leq i \leq n) \quad (5)$$

where $\alpha_{k,i}$ and $\beta_{k,i}$ are the forward and backward variables, respectively, which can be constructed inductively. a_{ij} is from the state transition probability matrix A .

3.4 Detailed Segmentation

Once the HMMs had been trained, the system is ready for the detailed segmentation, which aims to extract characteristic waveforms. Before the detailed segmentation, the test ECG data need to be pre-segmented and classified using the algorithm in the previous section. The classification rules are similar to the rules used on the training data. The only difference is that when the minimum R-R interval in the test data is less I_{MIN} or greater than I_{MAX} , they are classified to the groups with the range $[I_{MIN}, I_{MIN} + T]$ and $[I_{MAX} - T, I_{MAX}]$, respectively.

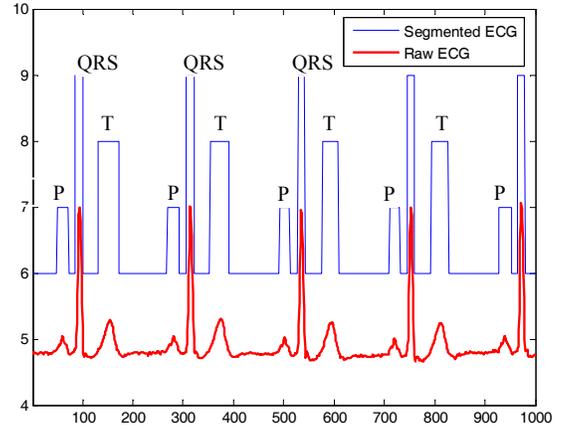


Figure 5. Detailed segmentation results: the onset and offset of P-wave, QRS complex and T wave are detected.

Each HMM is only responsible for segmenting the test ECG episodes with matched temporal features, so that the temporal HMM parameter adaptation can be naturally achieved and misalignments that cause reduced positive predictivity rate (+P)

can be avoided. Compared with the conservative temporal adaptation algorithm in the work of [4], this active parameter adaptation scheme is much faster, especially in the case of abrupt R-R interval changes because of the pre-segmentation and classification. Each sample in an ECG sequence is associated with a hidden state (P, QRS, or T wave). Viterbi algorithm [6] is used to infer the optimal state sequence for ECG in each of the test groups.

4. EXPERIMENTAL TESTING AND SIMULATION

The MIT-BIH QT database and MIT-BIH Arrhythmia database are used to evaluate the algorithms. QT database is chosen because it provides expert annotated characteristic waveforms, including P wave, QRS-complex, T and U waves [18]. It also cross-links several records from other Physionet Bank [19] databases, including MIT-BIH Arrhythmia database and ST-T database, etc. The arrhythmia database is chosen to show the adaptability of the presented algorithm with the presence of intensive temporal changes. QT database contains 105 two-channel records. Each record is 15 min and sampled at 250 Hz. Each record has manual characteristic waveforms annotation for at least 30 beats by two experts. Only the annotations from the first expert are considered since the second one is not complete. 750 annotated beats are selected to perform the evaluation. One third (250 beats) is used as training data, the others (500 beats) are used as test data. The onsets and offsets of P wave, QRS complex, and T wave are detected.

Table 1. Algorithm 1 & 2 performance comparison (N=7, $\Sigma=0.0637$)

	P wave	QRS	T Wave
SE1 (%)	95.85	99.49	98.86
+P1 (%)	93.79	96.11	94.80
SE2 (%)	96.18	99.89	99.06
+P2 (%)	98.64	99.46	99.32

Table 2. Algorithm 1 & 2 performance comparison (N=7, $\Sigma=0.0911$)

	P wave	QRS	T Wave
SE1 (%)	96.23	99.35	98.54
+P1 (%)	92.11	95.27	93.88
SE2 (%)	96.21	99.80	98.87
+P2 (%)	98.45	99.37	98.92

Two widely accepted statistical benchmarks, the sensitivity (SE) and positive predictivity (+P), are adopted to evaluate the performance of the algorithms proposed in the previous sections:

$$SE = \frac{TP}{TP + FN} \quad (6)$$

$$+P = \frac{TP}{TP + FP} \quad (7)$$

where TP is the number of true positives (correct detections), FN is the number of false negatives (missed detections), and FP (false detections) is the number of false positives. True positive means that there is a characteristic waveform matching (within 150 msec) between the annotations made by experts and those generated by the algorithm under test. Otherwise, a false negative (missed detection) or a false positive (extra detection) is recorded.

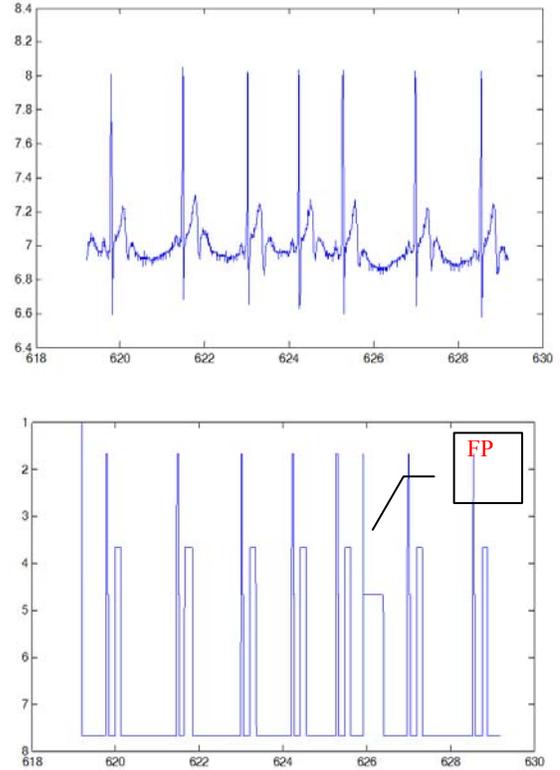


Figure 6. False positive detection caused by temporal variations.

An episode of detailed segmentation result is shown in the Fig. 5. The performance for individual characteristic waveforms detection is shown in table I and II. The variance of the R-R intervals is 0.0637 in Table I, and 0.0911 in Table II. Algorithm 1 uses one single generic HMM for the segmentation. Algorithm 2 is the one presented in this paper. N is set to 7 for algorithm 2, i.e. the test data are pre-segmented and classified into 7 groups during the comparison.

As shown in Table I and II, algorithm 1 has lower +P rate than algorithm 2. Multiple individualized HMMs perform better than one single generic HMM. As discussed before, the slow temporal parameter adaptation in HMM is largely responsible for a low positive predictivity (+P) due to an excessive number of false positive (FP) beat detections. This problem is further illustrated in the Fig. 6. (The ECG record is from MIT-BIH arrhythmia database.) When the R-R interval changes abruptly, a false positive (FP) detection is observed.

With the pre-segmentation and classification, false positive detections can be effectively reduced because the temporal variation in the test ECG data is suppressed by dividing ECG with huge R-R interval difference into different groups. As shown in the Fig. 7, the false positive detection caused by the temporal variation is eliminated using the proposed algorithm.

A larger temporal variation (indicated by the variance of the R-R intervals) makes the +P performance in algorithm 1 worse because more misalignments will happen, while it doesn't hurt algorithm 2 much because most of the temporal variation is compensated by the process of pre-segmentation and classification.

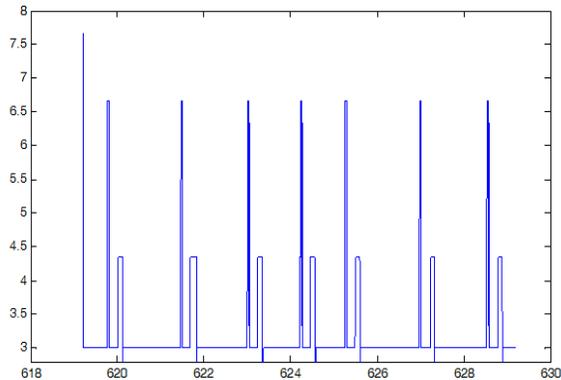


Figure 7. False positive detection removed by proposed algorithms (raw ECG is the same as in Fig.5).

Intuitively, the larger the N is the better performance the algorithm 2 will have. However, we should notice that HMM can achieve temporal adaptability to certain degree through the learning process of its parameters. Moreover, increasing N will decrease the number of samples available for the HMM learning in each classified group. Therefore, N must be chosen properly according to the variance of R-R intervals. The relation between +P and the number N for P-wave detection when R-R interval variance is 0.0911 is shown in Fig. 8. When N = 1, algorithm 1 is used. +P increases rapidly when N increase from 1 to 5, then reaches the maximum when N is around 7. Further increasing N will not improve the +P anymore. If N is too large to provide enough data for the HMM training in each group, +P may even decrease.

5. CONCLUSIONS AND FUTURE WORK

A novel body sensor network based ECG segmentation algorithm has been developed. Hidden Markov Model is employed to perform the segmentation. The HMM temporal adaptability is improved by introducing the pre-segmentation and classification procedure. Body sensor networks are used to collect and pre-segment the raw ECG data by performing QRS detection. Then the R-R interval information that directly reflects the beat variation is extracted and used to classify the raw ECG data into several groups. One specific HMM is trained for each of the groups. Therefore, instead of one single generic HMM, multiple individualized HMMs are set up. Each HMM is only responsible for extracting the characteristic waveforms of the ECG signals with similar temporal features, so that the temporal parameter adaptation is naturally achieved. The

experiment results show that the proposed algorithm can effectively improve the positive predictivity (+P) rate if a proper N is selected.

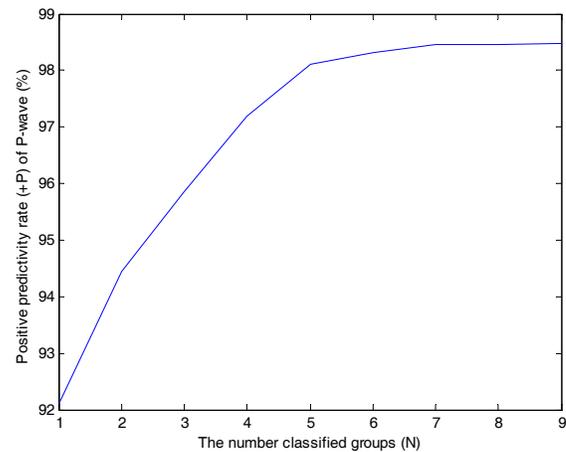


Figure 8. False positive detection removed by proposed algorithms (raw ECG is the same as in Fig.5).

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