Hidden Semi-Markov Model-Based Heartbeat Detection Using Multimodal Data and Signal Quality Indices

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Abstract

The automatic detection of heartbeats within physiological signals collected from patients connected to bedside monitors is an important task as it allows the detection of pathological conditions. Heartbeat detection is traditionally performed using the ECG. However, all bedside monitors are prone to missing data, yet it is rare for any system to incorporate data from other cardiac signals, such as the arterial blood pressure (ABP) or photoplethysmogram waveforms. This paper discusses the development of an automatic heartbeat detector using multimodal data from bedside monitors for the Physionet/Computing in Cardiology Challenge 2014. The presented algorithm employs an extended hidden Markov model to identify beat locations from multimodal data. The model was extended to include F1-score based signal quality indices in order to identify noisy periods. Wavelet transform features from both the ECG and ABP signals were added to derive the probability of a beat being present at a given location. The overall score of the algorithm for the third phase of the Physionet Challenge 2014 was 83.47%. The algorithm was also evaluated and compared to the top ranked entries [1] on a sample of 5150 synchronous ECG and ABP records from the MGH/MF database [2]. The overall score in this case was 92.7%.

1. Introduction

Despite the existence of noisy and missing data in ICU signals, there are few approaches to intelligence data fusion or signal switching published in the literature. Li *et al.* [3] proposed a Kalman filter (KF) based approach for fusing heart rate (HR) derived from electrocardiogram (ECG), arterial blood pressure (ABP) or photoplethysmogram (PPG) waveforms, weighted by the KF innovation and objective signal quality indices (SQIs).

While KF-type approaches have shown to reliably detect trends, abrupt changes and artifacts from physiological signals with very little knowledge of the underlying model, machine learning techniques require large amounts of physiological data to train the model in detecting artifacts and important features efficiently [3]. Fortunately the existence of open-access databases, such as MIMIC II [4], provides a method of obtaining these data from clinical settings, such as the intensive care unit, and developing advanced machine learning techniques for robust heartbeat detection. This article proposes a novel hybrid probabilistic approach, inspired by this earlier work, based upon the use of SQIs and a hidden Markov model.

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2. Methods

2.1. Datasets

The training set consisted of 100, 10-minute long records of multiple, synchronous, physiological signals recorded from adult patients. Each record consists of the ECG signal, and a variety of other signals including the ABP, all sampled at 250 Hz. The heartbeat locations in the training set were manually annotated.

The test set consisted of an unseen set of similar signals, with a range of sampling frequencies (120-1000 Hz), from the 3-stage Physionet Challenge 2014. As the training set was found to be unrepresentative of the test set, the algorithm was also evaluated on 5150, 10-min long, synchronous, ECG and ABP records taken from the MGH/MF waveform database [2], all sampled at 360 Hz.

2.2. Feature Extraction and HR Estimation

The features extracted from both ECG and ABP signals are based on each signal's slope-sum functions. In order to suppress high frequency noise that might affect the ECG and ABP beat detection, we applied a low-pass filter to each signal. A second order recursive filter was used, whose difference equation, for a sampling frequency of 250 Hz, is given by $y_n = 2y_{n-1} - y_{n-2} + x_n - 2x_{n-5} + x_{n-10}$.

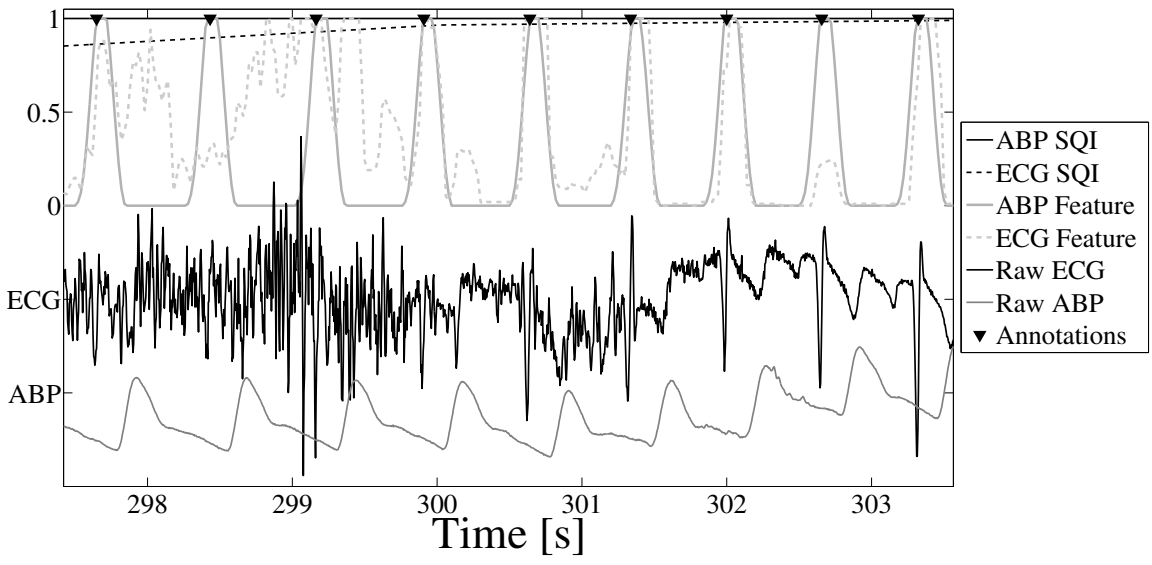

Figure 1. Features and SQIs derived from ECG and ABP signals (see Sections 2.2 & 2.3). The raw ECG and ABP signals are shown, as well as the locations of the heartbeat annotations.

where x_n is the input signal of the low-pass filter, and y_n is the filtered signal. The 3 dB cut-off frequency is about 16 Hz and the gain is 25 at 0 Hz. The phase shift is 20 ms. The slope-sum function was then determined to enhance the most significant slopes of the ECG and ABP pulses, highlighting the location of the peaks while suppressing the remainder of the waveforms.

For the ECG signal, the windowed and weighted slope-sum function at time i, z_i, is defined as follows:

$$z_i^{ECG} = \sum_{k=i-w}^{i} \Delta y_k^2, \;\; \Delta y_k = y_k - y_{k-1} \qquad (1)$$

where w is the length of the analyzing window (w =128 ms or 32 samples for the sampling frequency of 250 Hz), and y_k is the low pass filtered ECG signal as defined above.

For the ABP signal, the windowed and weighted slope-function is defined by:

$$z_i^{ABP} = \sum_{k=i-w}^{i} \Delta u_k^2, \;\; \Delta u_k = \begin{cases} \Delta y_k & \Delta y_k > 0 \\ 0 & \Delta y_k \leq 0 \end{cases} \qquad (2)$$

where w =128 ms, and y_k is the low pass filtered ABP signal as defined above. In order to account for the time difference between the ECG and ABP peaks (due to the pulse transit time), the first 40 ms of z^{ABP} were removed, and 10 samples (with the value of 0) were added to end of the signal.

Each feature vector (z^{ECG} and z^{ABP}) was then normalized using a non-overlapping window of 10 secs, and each window divided by that window's corresponding maximum value, so that the feature vectors are within the scale of $0, 1$ (as shown in Fig. 1). The feature vectors were down-sampled further to 50 Hz poly-phase anti-aliasing filter, in order to increase the speed of computation.

2.3. Signal Quality Index Estimation

In order to evaluate the quality of the waveforms considered for heart beat detection, a SQI for each signal was computed.

The SQI for the ECG signal was based on an algorithm that evaluates the matching of the beats detected by two independent ECG peak detector algorithms [5] (implementation based on [6][1]) and [7] (in which we consider a matching interval of 150 ms of a given beat). The F1-score was determined for each 10-second window (50% overlap). The segments of the signal in which the F1-score is 1 are used to determine the HR of the record: the inverse of the time difference between consecutive beats is determined; the median value is selected; and the average HR determined for all valid windows in the record (F1-score = 1) is determined as the overall HR for the record.

The SQI for the ABP signal was based on the identification of specific artifacts in the signal (SQI_{ABP1} and SQI_{ABP2}). For that, the baseline wander and high frequencies were first removed by a second order Butterworth filter with passband 0.5-10 Hz. Then, the segments of

[1]The submission code was a demo implementation in Matlab. More robust C code is available

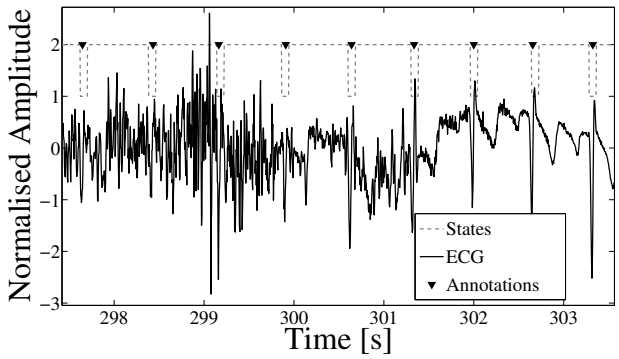

Figure 2. Example of a segmented noisy ECG (from Fig. 1), with the positions of the QRS annotations marked, along with the HsMM-labelled states. State 1 identifies the QRS complex, while the remainder of the heart cycle is labelled as state 2.

the signal that were "clipped" were identified (SQI_{ABP1}); i.e., the periods of saturation to a maximum or a minimum value were determined within each 10-second window (50% overlap). A hysteresis threshold (of 1 normalized unit) was defined to determine the smallest fluctuation that should be ignored. Such samples are defined to be "clipped". If the percentage of the window that is clipped was higher than 30%, the SQI value for that window would be set to 0 (1, otherwise). The second SQI was based on the inverse of the fourth moment (kurtosis) of the distribution of the signal segment (SQI_{ABP2}). The final SQI value for each window was determined as $SQI_{ABP1} \times SQI_{ABP2}$.

2.4. Hidden Semi-Markov Models

HMMs are a statistical framework used to describe sequential data. They operate by making inferences about the likelihood of being in and transitioning between discrete hidden states. In this case, the HMM is first order while the observations are features derived from the ECG and ABP. The two states in this case are: 1) S_1: the QRS complex 2) S_2: the period from the S wave to the Q wave. The demarcation of these two states is illustrated in Fig. 2.

An HMM can be defined as a function of A, B and π, where A is the transmission matrix, governing the probability of transitioning between states, B is the emission or observation distribution, defining the probability of seeing an observation in each state, and π is the initial state probability distribution [8].

The utility of the HMM for heartbeat segmentation is finding the most likely state sequence, given a HMM, $\lambda = (A, B, \pi)$, and an observation sequence, $\mathbf{O}$. This is derived using a dynamic programming method called the Viterbi algorithm [8].

A HMM of this type does not incorporate information about the expected duration of each state. The state durations are governed only by the self-transition probabilities, resulting in an exponentially decaying probability of remaining in a state for longer than one time step. This is poorly suited for physiological signal analysis [8]. In order to improve the duration modelling, an extra parameter is introduced:

Let us define the new model as $\lambda = (A, B, \pi, p)$, where $p = \{p_i(d)\}$ is the explicitly defined probability of remaining in state i for duration d. This is then called a hidden semi-Markov model (HSMM) [9].

Therefore, a key component of the HSMM for heartbeat detection is an estimate of the amount of time expected to remain in each state. These durations were modelled as Gaussian distributions, following Schmidt *et al.* [10]. The parameters of the duration distribution for state one, D_{S_1}, were derived from [11] such that $D_{S_1} \sim \mathcal{N}\left(0.09, (0.034)^2\right)$.

The duration distribution for state two, the period from the S wave to the Q wave, can be modelled with knowledge of the mean and variance of the duration of each heart cycle, derived with knowledge of the HR: $D_{S_2} = D_{cycle} - D_{S_1}$, where D_{cycle} is the HR-derived duration of a cardiac cycle.

2.5. Model Training & Evaluation

The HMM parameters defined in Section 2.4 were derived from the training set. The QRS complexes within the training set signals were demarcated using the provided annotations and the mean QRS duration.

In the case of B, the emission or observation distribution, a Gaussian distribution, trained on the single feature from the ECG and ABP, was used for each of the ECG and ABP signals. The multiplication of the outputs from these two distributions allowed the fusion of the ECG and ABP signals in a probabilistic fashion.

Further, the signal quality of each signal was incorporated into the model by multiplying the output of the above Gaussian distributions with the signal quality scores, derived in Section 2.3. These scores, with a range of zero to one, can be interpreted as a probability of being good quality. This allows a greater weighting within the HMM to be applied to the signal with greater signal quality.

Evaluation of the method was performed on a hidden test set of recordings (see Section 2.1). Each detected heartbeat, labelled as the mid-point of each state 1 period, was correctly identified if it fell within 150 ms of the reference annotation. Entries were scored using bxb and $sumstats$ functions (components of the WFDB software package [1]), which processes the reference and test annotations (i.e., those generated by the participants entry) to obtain a sensitivity (SE) and positive predictive value

(PPV) for each test record, and calculate the average and gross SEs and PPVs using all records in the test set. The overall score results from averaging the average and gross SEs and PPVs.

3. Results

Table 1 shows the overall score of the three best entries, the sample QRS detector and the proposed algorithm, on both the challenge and the MGH/MH datasets. As the HSMM approach had an overall score of 99.84% in the provided training set, and a significantly lower score for the various phases hidden test sets, some of the features and filters were improved with the MGH/MH dataset, which provided more examples of signal artifacts.

Table 1. Overall score for 3 of the 4 top entries [1], the sample entry and the proposed HSMM entry, for the phase-III and the MGH/MF databases.

Entry	Overall Score (%)	
	Phase-III	MGH/MF
Joachim Behar	87.93	95.8
Teo Soo Kng	86.73	92.9
Thomas De Cooman	86.61	94.4
Sample entry	84.49	95.7
Proposed HSMM	83.47	92.7

4. Discussion

This paper introduced an extended HMM-based approach for the detection of heart beats in multimodal data, incorporating signal quality features.

As can be seen in Table 1, the proposed HSMM method did not outperform the sample Physionet Challenge entry. This is also the case for the entries ranked third and fourth, when evaluated in the MGH/MH dataset; only the first ranked entry remained consisted between datasets. It is thought that the main limitation of the HSMM approach is the constraint of the HSMM on near-periodic sequences, based on the Gaussian distributed duration distributions. While this works effectively for detecting beats in ECGs with near-regular beat intervals, beats in highly irregular signals, like those from an arrhythmic patient, would not be accurately detected. Indeed if the MGH/MH dataset contains more regular signals than the challenge dataset, this could explain the better performance of the sample entry (based only on the ECG signal), and the HSMM score only differing by 0.02% from the third ranking entry score. In addition, as QRS detection is vital for the SQI estimation, the use of more robust QRS detectors (which are available) are likely to lead to further (potentially significant) improvements. The HSMM approach could also be improved for highly irregular ECG signals by relaxing the duration constraints or trained on a set of recordings more representative of the test dataset.

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