Optimal Length-Constrained Segmentation and Subject-Adaptive Learning for Real-time Arrhythmia Detection

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Abstract—An algorithm of data segmentation with length constraints for each segment is presented and applied in the context of arrhythmia detection. The additivity property of the cost function for each segment yields the induction proof of the exact global optimal solution. The experiments were conducted on the MIT-BIH arrhythmia dataset with the heartbeat categories recommended by the ANSI/AAMI EC57:1998 standard. The heartbeat classification task is enhanced by an adaptive learning scheme. Incremental support vector machine is used to integrate a small number of expert-annotated samples specific to the subject into the existing classifier previously learned from the dataset. The proposed segmentation scheme obtains the sensitivity of 99.89% and the positive predictivity of 99.83%. The classification sensitivities of ventricular and supraventricular detection are significantly boosted from 85.9% and 83.5% (subject-unadaptive) to 97.7% and 93.2% (subject-adaptive), respectively. Similarly, predictivities increase from 94.8% to 99.3% (ventricular), to 97.7% and 93.2% (subject-adaptive), respectively. Similarly, predictivities increase from 94.8% to 99.3% (ventricular), to 97.7% and 93.2% (subject-adaptive), respectively.

Index Terms—Data segmentation, heartbeat classification, adaptive learning, arrhythmia detection.

I. INTRODUCTION

Correctly detecting heartbeat abnormalities is of great importance to provide promptly therapy and prevent life-threatening problems for patients with cardiac diseases. The detection of arrhythmias, or simply known as abnormal heart rhythms, is a crucial task in electrocardiogram (ECG) monitoring. Arrhythmias are presented in two major types. The first includes long-term rhythmic arrhythmias, i.e., bradyarrhythmias, tachyarrhythmias. The other is represented by transient morphological arrhythmias, i.e., ventricular ectopic beats (VEB), supraventricular ectopic beats (SVEB), as recommended by the Association for the Advancement of Medical Instrumentation (AAMI) [1]. This study focuses on the latter type and proposes a unified framework of ECG segmentation and classification between VEBs, SVEBs and non-VEBs, non-SVEBs.

Researchers have put their efforts to improve these following four major areas: preprocessing techniques (Bayesian [2], wavelet transform [3], [4], digital filters [5]–[7]), feature extraction methods (RR-intervals [8], [9], QRS complexes [10], ECG morphology [5], [6]), heartbeat segmentation algorithms (based on QRS complexes, R-peaks [11]–[14], or P-waves, T-waves [15], [16]), and learning algorithms (linear discriminant analysis (LDA) [5], [6], [17], [18], support vector machine (SVM) [19]–[21], artificial neural networks (ANN) [22], [23], reservoir computing with logistic regression (RC LR) [24]). Among those areas, this paper proposes methods on the segmentation and learning stages. For the other two, we select appropriate and inexpensive ECG preprocessing techniques and ECG features for the sake of real-time performance.

With regards to the segmentation problem, the methods mentioned in the literature are all based on the ECG morphology (i.e., the PQRST-wave features). One setback for these methods is that we must specify a specific ECG lead to process, since those mentioned morphologies are different among ECG leads. This paper aims to propose a general method not dependent on any special ECG feature but only the provided data itself, hence can be applicable to any ECG lead, or more generally, to any data type. One benefit of this approach is the boosted accuracy resulting from combination of the individual segmentation results from all possible ECG leads. The only information that can be exploited are the length constraints of each heartbeat segment (i.e., normal human resting heart rate varies between 0.6 and 1.0 seconds). We are inspired by the fact that normal heartbeats of a subject measured at a specific experimental setting share a similar pattern to a certain extent. We formulate that problem into an optimization problem with segment length constraints, then solve it using a novel dynamic programming algorithm. Our approach is developed from the method of curve fitting by line segments [25]. However the mentioned work did not impose length constraints on segments. Therefore it cannot be applicable to real-time ECG systems as the time needed for searching for the optimal solution far exceeds the allowable time for real-time processing.

Another major difficulty imposed on heartbeat classification is the cardiac specificity of individual subjects. The trained classifier has no prior knowledge of the validation subject’s pattern, hence heavily affects the system’s accuracy. Previous studies also targeted this problem, i.e., adaptive LDA [6], [18], generalized regression neural networks [26], or switching Kalman filter [27]. For the real-time mode, however, one would consider several issues that have not been satisfactorily resolved in the mentioned studies, i.e., updating the classifier...
in a restricted amount of time, or discarding undesirable samples to avoid data accumulation. In this paper we propose a real-time subject-adaptive learning scheme using the incremental support vector machine algorithm [28].

In summary, our main contributions are:

- Propose a data segmentation algorithm with segment-length constraints. The exact global optimal solution is guaranteed by a dynamic program. The algorithm can perform in real-time, does not require the input number of segments, and is applicable to any ECG lead or any data type.

- Propose a real-time learning method to have the heartbeat classifier get adapted to a new subject. A small number of expert-annotated samples will enhance the existing SVM classifier using the Incremental SVM toolbox.

The rest of this paper is organized as follows: Section II presents the optimal segmentation method. The system’s framework including data preprocessing, dataset description, feature extraction and adaptive learning subsections are described in Section III. Section IV presents the experimental settings and performance assessment results. Finally the conclusions are given in Section V.

II. OPTIMAL LENGTH-CONRAINT DATA SEGMENTATION

The 1-D data signal of ordered individual data points \( d_i \) is denoted by \( d_{N_1:N_2} = \{d_i, N_1 \leq i \leq N_2\} \). We define a data segment \( s_i \) as any subset of \( d_{N_1:N_2} \) which has consecutive data points \( d_i \). A set of \( M \) non-overlapping contiguous segments constructing the data \( d_{N_1:N_2} \) is called a segmentation of \( d_{N_1:N_2} \), denoted as

\[
S = \left \{ s_i \right \}_{i=1}^M \bigcup s_i \cap i \neq i' s_i = \emptyset \right \}.
\]

The set of all possible segmentation \( S \) of \( d_{N_1:N_2} \) is denoted as \( S_{N_1:N_2} \). Given a full signal \( d \) of \( N \) points (i.e., \( d = d_{1:N} \)) and the length constraints on each data segment to be segmented (i.e., \( l_{\min} \leq |s_i| \leq l_{\max} \)), the segmentation problem of \( d \) can be formulated to the following constrained optimization problem

\[
\begin{align*}
\text{minimize} \quad & W(S) = \sum_{s_i \in S} ||r_{\mu}(s_i) - \mu||^2_2 \\
\text{subject to} \quad & l_{\min} \leq |s_i| \leq l_{\max},
\end{align*}
\]

where \( r_\mu(x) \) is the interpolated vector of \( x \) with length equaling to that of \( \mu \). Here \( |x| \) denotes the length of \( x \), \( ||x||^2_2 \) denotes the \( \ell_2 \)-norm of \( x \) in \( \mathbb{R}^N \), and \( \mu \) represents as the template model for \( s_i \) and only dependent on the change point locations. In this paper’s context, \( \mu \) is obtained by averaging the selected typical normal heartbeat samples from various learning subjects.

The number of all possible partitions \( S \) exponentially increases with respect to the number of data points \( N \), leading to the intractability of the optimization problem (2) when \( N \) is large. On a different perspective, we can consider \( W \) as the sum of \( M \) additive individual cost function \( F \) as

\[
W = \sum_{i=1}^{M} F(s_i),
\]

where \( F(x) = ||r_{\mu}(x) - \mu||^2_2 \). Using this denotation it is easily observed that the original objective function \( W \) in problem (2) possesses the property of additivity. By this important property, we are able to propose the dynamic programming method to find the exact global optimal of the problem (2) given the length constraints of each block.

**Lemma 1.** Given two disjoint segments \( A \) and \( B \), i.e., \( A \cap B = \emptyset \), then \( W(A \cup B) = W(A) + W(B) \).

**Proof.** The proof implies in the additivity property of the objective function \( W \) as: \( W(A \cup B) = \sum_{s_i \in A \cup B} F(s_i) = \sum_{s_i \in A} F(s_i) + \sum_{s_i \in B} F(s_i) = W(A) + W(B) \).

**Theorem 1.** Let \( S^* = \{s^*_i, 1 \leq i \leq M^*\} \) denoted the global optimum solution of problem (2), and \( S^{*,m} = \{s_i|s_i \in S^*, 1 \leq i \leq m \leq M^*\} \) denoted the set of the first \( m \) segments of \( S^* \) that covers the first \( n \) points of the original signal (i.e., \( \bigcup s_i = d_{1:n} \)). Then \( S^{*,m} \) is the global optimal solution of the following optimization problem

\[
\begin{align*}
\text{minimize} \quad & W(S) = \sum_{s_i \in S} ||r_{\mu}(s_i) - \mu||^2_2 \\
\text{subject to} \quad & s_{\min} \leq |s_i| \leq l_{\max},
\end{align*}
\]

**Proof.** Suppose there exists an optimal solution of problem (4) other than \( S^{*,m} \), denoted as \( S^\prime \). This leads to \( W(S^\prime) < W(S^{*,m}) \). Since \( S^\prime \cup \emptyset \subset S_{1:N} \), and \( S^\prime \cup \emptyset \neq \emptyset \), \( S^\prime \cup \emptyset \) becomes the optimal solution of problem (2) rather than \( S^* \). This contradiction proves that \( S^\prime \) never exists, therefore \( S^{*,m} \) is the optimal solution of problem (4).

**Algorithm 1** Optimal Segmentation Algorithm

**Input:** 1-D data \( d_{1:N} \), segment constraints \( l_{\min}, l_{\max} \).

**Output:** Optimal segmentation \( S^* \).

1. **procedure** WarmUpPhase
2. \( i \leftarrow 2l_{\min} - 1 \)
3. **while** \( i < 2l_{\max} \) **do**
4. \( i \leftarrow i + 1 \)
5. \( W^*(i) = \min \left \{ F(d_{i:j}) + F(d_{j+1:i+1}) \right \}_{j=\min(l_{\min},i-l_{\min})}^{\max(l_{\min},i-l_{\min})} \)
6. **Save value of** \( j \) **where** \( W^*(i) \) **occurs**
7. **if** \( i \geq k_{\min} (k \geq 3 \text{ and possibly largest}) \) **then**
8. \( W^* = \min \{W^*(j) + F(d_{j+1:k})\}_{j=(k-1)l_{\min}}^{(k-1)l_{\min}} \)
9. \( i \leftarrow \min \{W^*(i), W^* \} \)
10. **end if**
11. **end while**
12. **return** \( a \)

**Theorem 2.** The Algorithm 1 (procedure WarmUpPhase) guarantees to find the exact optimal \( m \)-segment segmentation, \( S^{*,m} \), of \( n \) first data samples \( d_{1:n} \), for some \( n \in \{2l_{\min}, 2l_{\max} \} \).

**Proof.** We exploit Theorem 1 in the sense that we must initially search for the first two segments of the optimal solution, \( S^{*,2} \) (corresponding to the procedure WarmUpPhase). Taken the segment length constraints into account, we see
Algorithm 2 Optimal Segmentation Algorithm

Input: 1-D data $d_{1:N}$, segment constraints $l_{\text{min}}, l_{\text{max}}$.

Output: Optimal segmentation $S^*$.

1: procedure MAINPHASE
2: $i \leftarrow 2l_{\text{max}} + 1$
3: while $i \leq N$ and $i - l_{\text{min}} > 2l_{\text{min}}$ do
4: \[ W^*(i) \leftarrow \min \{W^*(j) + F(d_{j+1:i})\}_{j=\max\{i-2l_{\text{min}},2l_{\text{min}}\}} \]
5: $i \leftarrow i + 1$
6: end while
7: return $a$

that the last index of the first segment, denoted as $\text{Idx}(s_1)$, lies somewhere between the interval $[l_{\text{min}}, l_{\text{min}} + \Delta b]$ (where $\Delta l = l_{\text{max}} - l_{\text{min}}$). $\text{Idx}(s_2)$ therefore falls in $[\text{Idx}(s_1) + l_{\text{min}}, \text{Idx}(s_1) + l_{\text{min}} + \Delta b]$. As a result $\text{Idx}(s_2)$ can take values from $[\min\{\text{Idx}(s_1)\} + l_{\text{min}}, \max\{\text{Idx}(s_1)\} + l_{\text{min}} + \Delta b] = [2l_{\text{min}}, 2l_{\text{max}}]$. The procedure WARMUPPHASE will find the exact value of $\text{Idx}(s_1)$ for each different value of $\text{Idx}(s_2)$. As explained, the search for all possible values of $\text{Idx}(s_2)$ must be conducted in the interval $[2l_{\text{min}}, 2l_{\text{max}}]$, as indexed by the iterative variable $i$ in Algorithm 1. For each given $i$, we search for the smallest segmentation cost value $W^*(i)$ which is the sum of the first two segments, $s_1 = d_{1:i}$ and $s_2 = d_{i+1:i}$. The second iterative variable $j$ indexes all possible values of $\text{Idx}(s_1)$. The smallest value $j$ can take is $\min\{l_{\text{min}}, i - l_{\text{max}}\}$ to not violate the length constraint of $s_2$, and the largest value of $j$ is $\max\{i - l_{\text{min}}, l_{\text{max}}\}$ to not violate the length constraint of $s_1$.

The above search for the optimal cost of the first two segments inevitably covers the possibilities of more than two segments in the search range. If $2l_{\text{max}} > kl_{\text{min}}$ (where $k \geq 3$), extra segmentation will occur as there can be $3, \ldots, k$ segments for the given iteration $i$. For $k = 3$, we need to select between the optimal two-segment cost, $W^*(i)$, and the optimal three-segment cost, $W^*$. The resulting optimal number of segments can be 2 or 3, and we denote this value as $m^*$. For $k > 3$, this recursive method always compare between the $m^*$-segment and the $(m^*+1)$-segment schemes. The algorithm 1 therefore obtains the exact optimal segmentation of $d_{1:n}$ for some $n \in [2l_{\text{min}}, 2l_{\text{max}}]$.

Theorem 3. The Algorithm 2 (procedure MAINPHASE) guarantees to find the exact optimal solution, $S^*$, of the input data $d_{1:N}$.

Proof. Suppose $S^{*,m^*}$ is obtained, then by Theorem 1 we can always obtain $S^{*,m^*+1}$ by conducting the search for the minimum value including $W(S^{*,m^*}) + F(d_{\text{Ind}(s_{m^*})+1:k})$, since $d_{\text{Ind}(s_{m^*})+1:k} = s_{m^*}$. Line 4 in Algorithm 2 performs this thorough search and guarantees that $s_{m^*}$ will be included in the search pool (which by definition will generate the optimal cost). Recall that $M^*$ is denoted as the number of segments in $S^*$. Algorithm 2 will successfully find $S^*$ when $i$ indexes the last sample ($d_N$), given that $S^{*,M^*-1}$ has already achieved. Similar process happens for $S^{*,M^*-2}$ (i.e., when $i = \text{Ind}(s_{M^*-1})$ we will achieve $S^{*,M^*-1}$, given that $S^{*,M^*-2}$ is obtained). Finally, by Theorem 2 we already have the optimal for the first $m$ segments, hence Theorem 3 holds.

The proposed constrained segmentation algorithm works in time $O(n\Delta b)$. Comparing to the other methods [25], [29] run in $O(n^2)$, our algorithm has the considerably lower complexity. The benefit of this point is discussed in more detail in Section IV.

III. FRAMEWORK

A. ECG Preprocessing

Various ECG denoising methods had been proposed depending intrinsically on the final objective of each study. Studies focusing on ECG feature extraction or segmentation require a more sophisticated preprocessing technique (i.e., multiadaptive bioradonic wavelet transform [4], adaptive neural network [30], extended Kalman filter [7]) as one would preserve the signal morphology. A specific ECG lead must be specified for morphology. A specific ECG lead must be specified for each study. Studies focusing on ECG feature extraction or segmentation require a more sophisticated preprocessing technique (i.e., multiadaptive bioradonic wavelet transform [4], adaptive neural network [30], extended Kalman filter [7]) as one would preserve the signal morphology. A specific ECG lead must be specified for each study. Studies focusing on ECG feature extraction or segmentation require a more sophisticated preprocessing technique (i.e., multiadaptive bioradonic wavelet transform [4], adaptive neural network [30], extended Kalman filter [7]) as one would preserve the signal morphology. A specific ECG lead must be specified for each study.
notch finite-impulse response filter [31] to suppress power line interference and muscle contraction noise.

B. Heartbeat Categories

The experiments were conducted on the Massachusetts Institute of Technology and Beth Israel Hospital arrhythmia database (MITBIH) [32], consisting of 109492 labeled heartbeats from 46 patients. Recommended by the ANSI/AAMI EC57:1998 standard [1], fifteen beat types of this database are grouped into 5 classes: normal beat (N), ventricular ectopic beat (V), supraventricular ectopic beat (S), fusion of normal and ventricular (F), and unknown (Q), as presented in Table I.

Two classification schemes are to be conducted: scheme A for class V (or VEB) against non-VEB, and scheme B for class S (or SVEB) against non-SVEB. The learning and validation set configuration is described in Section IV-A.

<table>
<thead>
<tr>
<th>AAMI Class</th>
<th>MITBIH Annotation</th>
<th>Total beats</th>
<th>Validation beats</th>
<th>Scheme A SVM class</th>
<th>Scheme B SVM class</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>N, L, R, e, j</td>
<td>90126</td>
<td>44259</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>V</td>
<td>V, E, !</td>
<td>7235</td>
<td>3221</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>S</td>
<td>A, a, J, S, x</td>
<td>2779</td>
<td>1837</td>
<td>-</td>
<td>1</td>
</tr>
<tr>
<td>F</td>
<td>F</td>
<td>803</td>
<td>388</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Q</td>
<td>f, Q, /</td>
<td>15</td>
<td>?</td>
<td>-1</td>
<td>-1</td>
</tr>
</tbody>
</table>

C. Feature Extraction

There were numerous studies proposing different schemes to extract ECG features from segmented data [5], [6], [8]–[10], [17], [21]. Assigning all points of a segmented heartbeat, even after down-sampling, causes detrimental effects to the classification process for several reasons. One of them is the high dimensionality of feature vectors which decreases the real-time adaptive learning process. Another drawback would be the redundancy of trivial information, since only special morphology features substantially determine the class of a heartbeat. Moreover there are hidden essential features related to the segments’ neighborhood (i.e., abrupt inconsistencies in successive beats), or to the frequency domain [17], [21].

In this study, we select a combined set of features with the aim to avoid those mentioned problems, as shown in Table II. The set includes 29 features of RR-interval and interpolated ECG morphology [5], 7 features of discrete wavelet transform coefficients [17], and 36 features obtained from 3 different dimension-reduction techniques [21]. The selected features form a 59-dimension feature vector for each heartbeat. It should be noted that although the segmentation decisions are combined on multiple separate ECG leads (see Section IV-B), the selected features only require lead A of MITBIH. This will generate significantly lower dimension feature vectors for our real-time performance.

D. Adaptive Learning using Incremental Support Vector Machine

Various learning algorithms for heartbeat classification were suggested with promising results as mentioned in the literature. In our study SVM [33] is employed as the baseline method for the exploitation of the incremental SVM (ISVM) toolbox [28]. ISVM is an analytical method which can integrate a small portion of newly-classified samples into the existing SVM solution without re-training all the sample pool from scratch. That is done by analytically adding each new sample at a time to the solution while retaining the Karush-Kuhn-Tucker conditions on all previously learned data. ISVM is therefore tailored with our original purpose to tackle the ECG subject-adapting problem and efficient in the real-time context. Furthermore ISVM can also unlearn samples from the solution which is essential for the real-time speed adjustment in this study. We will briefly summarize both SVM and ISVM as black boxes (i.e., with just inputs and outputs without regards to the internal structure) for notational convenience.

The learning dataset $\mathcal{T} = \{\bar{x}_i, \bar{y}_i\}_{i=1}^{N_T}$ consisting of $N_T$ labeled samples from various subjects, is given for the learning stage. In our context, each sample $\bar{x}_i$ corresponds to one 59-dimensional heartbeat segment, and $\bar{y}_i$ is the corresponding label taken the value of 1 or −1. SVM learns from these samples and builds a classifier denoted (in dual form) by $(\alpha_T, b_T)$, or in other words

$$ (\alpha_T, b_T) = \text{SVM}(\mathcal{T}). \tag{5} $$

Then, a set $\mathcal{L} = \{x_i, \bar{y}_i\}_{i=1}^{N_L}$ with $N_L$ manually-annotated labels $\bar{y}_i$ (where $N_L \ll N_T$), is used construct the subject-specific classifier based on $(\alpha_T, b_T)$. ISVM only deals with $N_L$ new samples to construct $(\alpha_{T\cup\mathcal{L}}, b_{T\cup\mathcal{L}})$, the SVM solution of the combined set $\mathcal{T} \cup \mathcal{L}$, as

$$ (\alpha_{T\cup\mathcal{L}}, b_{T\cup\mathcal{L}}) = \text{SVM}(\mathcal{T} \cup \mathcal{L}) = \text{ISVM}^+(\alpha_T, b_T, \mathcal{L}). \tag{6} $$

ISVM is also able to unlearn a set $\mathcal{T}^-$ (where $\mathcal{T}^- \subset \mathcal{T}$) from $\mathcal{T}$ as

$$ (\alpha_{T\setminus\mathcal{T}^-}, b_{T\setminus\mathcal{T}^-}) = \text{SVM}(\mathcal{T} \setminus \mathcal{T}^-) = \text{ISVM}^-(\alpha_T, b_T, \mathcal{T}^-). \tag{7} $$

The class decision of any new unclassified sample $x_i$ classified by any trained set $\mathcal{D}$ is given by

$$ y_i = f(x_i, \alpha_D, b_D) = \text{sign}\left(\sum_{\alpha_{j}, y_{j} \in \mathcal{D}} \alpha_{j} y_{j} x_{j}^{T} x_{i} + b_{D}\right). \tag{8} $$

Table II: List of ECG Features for Classification Stage.

<table>
<thead>
<tr>
<th>Study</th>
<th>Feature Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>[5]</td>
<td>RR-intervals (4 features)</td>
</tr>
<tr>
<td></td>
<td>Heartbeat intervals A (3 features),</td>
</tr>
<tr>
<td></td>
<td>Morphology IA (9 features)</td>
</tr>
<tr>
<td>[17]</td>
<td>Discrete Wavelet Transform (7 features)</td>
</tr>
<tr>
<td></td>
<td>(as derived from Section II.C.3.a in [17])</td>
</tr>
<tr>
<td>[21]</td>
<td>Principle Component Analysis (12 features)</td>
</tr>
<tr>
<td></td>
<td>Linear Discriminant Analysis (12 features)</td>
</tr>
<tr>
<td></td>
<td>Independent Component Analysis (12 features)</td>
</tr>
</tbody>
</table>
The algorithm for ISVM batch learning is summarized in Algorithm 3. In the validation stage, the first 100 expert-labeled beats are used as ISVM reinforced set $\mathcal{L}$ for each subject. Then after each $k_1$ classified beats, the last $k_2$ ones are fed into ISVM again with $k_2$ arbitrary samples of $\mathcal{T}$ discarded from the learning pool. This is referred to as batch learning. For the sake of real-time performance $k_1 = 200$ and $k_2 = 100$ are chosen. The classification accuracy is calculated based on the label of every individual beat of the whole real-time process. The real-time mechanism is simulated by a virtual data pumping model built by MATLAB Simulink.

IV. EXPERIMENTAL RESULTS AND DISCUSSION

A. Dataset Configuration

The MITBIH is divided into the learning and validation sets (namely DS1 and DS2 respectively) as in [5]. Ten subjects who possess the highest percentages of abnormal beats in DS1 (as named in MITBIH: 106, 116, 119, 201, 203, 207, 208, 209, 215, 223) are designated for the learning stage (hereinafter referred to as learning subjects). All subjects in DS2 are validated and hereinafter referred to as validation subjects.

Only 500 random beats from both classes in DS1 for each classification scheme are selected for the initial SVM classifier construction. The reason for this setting is that there will be a maximum of $N_T = 500$ samples/class × 2 classes = 1000 training samples. Our benchmarking result, as shown in Fig. 3, points out that it took approximately 2 seconds to integrate $N_L = 100$ samples into the 1000-sample pool. For the real-time requirements, in these 2 seconds there will be approximately 2-3 beats pending for classification after the ISVM updating process. This is the threshold of our system’s processing capacity.

B. Segmentation Performance Assessment

The separate segmenting results from two leads are combined if a lead A segment has above 80% of their data points in common with a lead B segment within the same time frame, or vice versa. In that case both segments from two leads are designated as a successfully-detected segment. Two standard
measures to evaluate the segmentation stage are the sensitivity (Se) and the positive predictivity (+P), calculated by

\[ Se = \frac{T^+}{T^+ + F^-}, \quad (9) \]

\[ +P = \frac{T^+}{T^+ + F^+}, \quad (10) \]

where \( T^+, F^-, \) and \( F^+ \) are the number of correctly segmented heartbeats (true positive), actual heartbeats that are not detected (false positive), and segmented heartbeats that do not correspond to any actual heartbeat (false positive) respectively. The result of our proposed segmentation method and the related studies is shown in Table III(a). As presented there, our segmentation method can provide multi-lead processing and the result is competitive to the state-of-the-arts.

C. Classification Performance Assessment

With regards to the performance assessment of the classification stage, the three most important measures are the sensitivity (Se), positive predictivity (+P), and accuracy (Acc) of ventricular detection (scheme A) and supraventricular detection (scheme B), calculated by

\[ Se = \frac{\text{number of class 1 samples correctly classified}}{\text{number of class 1 samples classified}}, \quad (11) \]

\[ +P = \frac{\text{number of class 1 samples correctly classified}}{\text{number of samples classified into class 1}}, \quad (12) \]

\[ Acc = \frac{\text{number of samples correctly classified}}{\text{number of samples classified}}, \quad (13) \]

with the class labeling strategy as shown in Table I. The measures in Eq.(11), Eq.(12) and Eq.(13) are interpreted in a simple way and identical to the same measures used in most related studies. The beat-by-beat confusion matrix result and the comparison with typical selected researches are presented in Table IV and Table III(b) respectively. Thanks to ISVM fortification there are more 382 VEB beats (from 2766 to 3148) and 178 SVEB beats (from 1534 to 1712) successfully detected. As compared to the previous studies we obtained a promising result in all three assessment measures.

V. Conclusion

We consider the ECG segmentation process as a global optimization problem rather than the local detection problem of specific heartbeat features. With the proposed dynamic programming algorithm written to solve this problem, the achievement of the optimal solution is guaranteed. This method also offers a wide range of real-time applications for other data types alongside ECG.

With regards to the classification stage, we are able to establish the subject-adapting capability by use of the ISVM
toolbox. As a result significant boosts in sensitivity, predictivity and accuracy of ventricular and supraventricular detection are obtained. The overall performance assessment when combining both the proposed segmentation and classification methods is highly competitive to the previous studies.

REFERENCES


