

Spatiotemporal QRST Cancellation Method Using Separate QRS and T-Waves Templates

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Abstract

The standard ECG remains the most common non-invasive tool for diagnosing and studying atrial fibrillation (AF). Due to the much higher amplitude of the electrical ventricular activity in the surface ECG, isolation of the atrial activity component is crucial to the analysis and characterization of AF. An average beat subtraction (ABS) based method is developed to perform this QRST cancellation. In contrast with standard methods, two sets of templates are created instead of one: one set for the QRS complexes and one for the T-waves. The QRS complexes are clustered according to their morphology; the T-waves, using both their preceding RR interval and their morphology. Next, spatial optimization (rotation and scaling) is applied to the QRS templates. ECG signals generated by a biophysical model are used to evaluate the performance of the proposed method in comparison with two other QRST cancellation methods. The proposed method decreases the averaged relative error by 19.7% and 29.0% in comparison with the standard ABS and the standard spatiotemporal method, respectively.

1. Introduction

Atrial fibrillation (AF) is the most common type of human cardiac arrhythmia. On the ECG, the AF signals are characterized by continuous, apparently disorganized, fibrillatory waves (F-waves). Due to the much higher amplitude of the electrical ventricular activity (VA) on the surface ECG, isolation of the atrial activity (AA) component is crucial for the study of AF. Some methods used to solve this problem are the average beat subtraction (ABS) based ones. These methods are built on the assumption that the atrial activity is uncoupled with ventricular activity. An average of the ventricular complexes (QRST complexes) is then used to subtract this ventricular activity. An interesting ABS based method is proposed by M. Stridh and L. Sörnmo in [1]. In their method, two major features are added to the basic ABS, F-wave reduction and spatiotem-

poral alignment. Before computing the ventricular templates, F-waves of each lead are estimated and subtracted to facilitate further processing. This estimation process is based on the replication of ECG segments with atrial activity only. A spatiotemporal alignment is applied to the ventricular templates to correct the variation in the electrical axis of the heart. Translation, amplitude scaling and rotation are the three different spatiotemporal operations performed.

In this paper, we propose a method that processes the QRS complexes and T-waves separately. It is also based on the ABS approach with spatiotemporal alignment. It comprises 4 main steps: (1) preprocessing, (2) QRS complex template selection with temporal alignment, (3) rotation and scaling on the QRS templates and (4) T-wave template selection with temporal alignment. The details of each of these steps are crucial to obtain good QRST cancellation results. The performance of our method is studied in its application to ECG signals generated by a biophysical model, as well as to clinical recordings. By using the model, realistic separate contributions of the atria and the ventricles were available. The performance of this method is compared to that of the standard ABS method and the standard spatiotemporal QRST cancellation method proposed in [1].

2. Methods

In the standard 12 lead ECG, only two of the first six leads (I, II, III, VR, VL and VF) are linearly independent. Therefore, the pertinent information was included in an N^{ECG} -by-8 matrix \mathbf{X} that contains N^{ECG} samples from eight leads: two limb leads (VR and VL) and six precordial leads (V1 to V6)

$$\mathbf{X} = [\text{VR} \ \text{VL} \ \text{V1} \ \dots \ \text{V6}]. \quad (1)$$

2.1. Preprocessing

Prior to the processing steps, the positions of artefacts were identified by visual inspection. These segments were

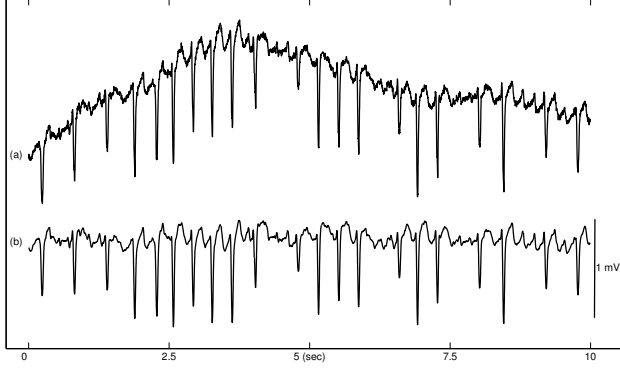


Figure 1. (a) Recorded 10 second ECG signal (V1). (b) Cleaned up version after preprocessing

set to zero. After this first operation, a derivative-based method for QRST detection was applied [2]. The total root-mean-squared (RMS) signal was used to evaluate the QRST locations. This total RMS signal is

$$r(t) = \sqrt{\frac{1}{8} \sum_{l=1}^8 x_l(t)^2}, \quad t = 1 \dots N^{\text{ECG}} \quad (2)$$

where $x_l(t)$ is sample t of the l^{th} column of \mathbf{X} . This total RMS signal combines the information of all leads in one signal. In this signal, the timing of Q-wave starting points, R-wave peaks, J-points and T-wave peaks were identified. Each R-wave peak timing was identified as the middle point between the closest samples on either side 3 dB below the maximum value of the RMS curve. Each J-point timing was identified as the local minimum between the R-wave peak and the subsequent T-wave peak. Next, a baseline correction was applied by means of a cubic spline interpolation anchored on the onset points of ventricular depolarization as identified in the RMS curve. The QRST detection and the baseline correction were recursively applied to the new N^{ECG} -by-8 ECG matrix, \mathbf{Y} , until no changes in the timing of the fiducial points were observed. A low pass finite impulse response filter (moving averaged window of 20 ms) was also employed to smooth the ECG signals. Figure 1 shows the results of the entire preprocessing applied to a clinical signal.

2.2. Cancellation method based on ABS using separate QRS and T templates

The i^{th} cardiac cycle in the ECG was represented by an $N_i^{Q \rightarrow Q}$ -by-8 matrix \mathbf{F}_i that contained the samples between the i^{th} and the subsequent QRS starting points. In AF, the ventricular and atrial activity are assumed to be uncoupled [3]. In this paper, the QRS complexes (depolarization) and T-waves (repolarization) were treated separately.

2.2.1. QRS complex templates with temporal alignment

The QRS complexes were clustered using their morphologies. The i^{th} QRS complex was defined by an $N_i^{Q \rightarrow J}$ -by-8 matrix \mathbf{A}_i that contains the samples between the i^{th} QRS starting point and the subsequent J-point. The comparison of morphologies between two QRS matrices \mathbf{A}_i and \mathbf{A}_j was performed as follows: first, the normalized cross-correlation between the corresponding columns (leads) of the two matrices was computed. Then, the matrices were considered similar if all normalized cross-correlation values were above a given threshold (θ).

The iterative clustering procedure was defined by the following steps, where complexes were treated in their order of occurrence in the recording:

1. First QRS complex \mathbf{A}_1 was placed in the first cluster Ω_1 ;
2. If any, all the complexes similar to \mathbf{A}_1 (as defined above) were placed in Ω_1 ;
3. First unclassified QRS complex \mathbf{A}_i was placed in a new cluster Ω_k ;
4. If any, all the complexes similar to \mathbf{A}_i were placed in Ω_k ;
5. Steps 3 and 4 were repeated until all QRS complexes were classified in a cluster set $\{\Omega_k\}$.

Next, cluster template \mathbf{T}_k was defined as the sample-wise average of the QRS complexes composing cluster Ω_k . The QRS complexes had variable lengths. First, the QRS complexes were aligned with respect to their R-wave peaks. The subsequent averaging at each time index was carried out only on the QRS complexes for which a sample was available at that time index. If a time index was taking place on only one QRS complex, the average was set to zero. Finally, each QRS template \mathbf{T}_k was temporally aligned with all the QRS complexes of class k by their R-wave peak.

2.2.2. Cancellation of QRS complexes

A spatial optimization similar to the one presented in [1] was applied to the QRS templates to compensate the variation in the electrical axis, in tissue conductivity and heart position. This spatial optimization was performed iteratively for each QRS complex \mathbf{A}_i belonging to cluster Ω_k by applying to templates \mathbf{T}_k the transform defined by the product of rotation matrix \mathbf{Q}_i and diagonal matrix \mathbf{D}_i where index i refers to the the complex \mathbf{A}_i ,

$$\tilde{\mathbf{T}}_i = \mathbf{T}_k \mathbf{Q}_i \mathbf{D}_i. \quad (3)$$

Matrix \mathbf{Q}_i and matrix \mathbf{D}_i were chosen to minimize the squared Frobenius norm, Δ_i , of the difference between the

QRS complex \mathbf{A}_i and the modified template $\tilde{\mathbf{T}}_i$. Initially, $\mathbf{Q}_i = \mathbf{I}$, then the c^{th} diagonal entry in \mathbf{D}_i was updated using

$$D_i(c) = \frac{(\mathbf{T}_k]_c^T [\mathbf{A}_i \mathbf{Q}_i^T]_c}{[\mathbf{T}_k]_c^T [\mathbf{T}_k]_c} \quad (4)$$

where $[\]_c$ is the c^{th} column of the matrix. After this, a new estimate of \mathbf{Q}_i was evaluated with

$$\mathbf{Q}_i = \mathbf{U}\mathbf{V}^T, \quad (5)$$

where \mathbf{U} and \mathbf{V} were the two orthonormal matrices of the singular value decomposition of $\mathbf{D}_i^T \mathbf{T}_k^T \mathbf{A}_i$, see *Procrustes problem* [4]. After each step, Δ_i was evaluated. This iteration stopped when Δ_i started to increase or remained unchanged. The final estimate of atrial activity inside the complex \mathbf{A}_i was taken to be the difference $\mathbf{A}_i - \tilde{\mathbf{T}}_i$.

2.2.3. Cancellation of T-waves

T-wave template selection employed additional electrophysiological information: action potential duration is influenced by the preceding diastolic interval [5]. Thus, the morphology of the ventricular depolarization (T-wave) depends also on the preceding diastolic interval. Based on this observation, each T-wave was clustered using both its preceding RR interval and its morphology. The i^{th} T-wave was defined by an $N_i^{J \rightarrow Q}$ -by-8 matrix \mathbf{B}_i that contained the samples between the i^{th} J-point and the subsequent QRS starting point. A histogram of the preceding RR intervals with evenly spaced bins was computed. Each non-empty bin defined a T-wave cluster. Then, the same morphological clustering as for the QRS templates was applied in order to further subdivide each cluster if needed. Finally, a template was built for each cluster.

In order to perform T-wave cancellation, each T-wave template was temporally aligned with all corresponding T-waves based on the location of their apexes. No spatial optimization was applied to these templates. The final estimate of the atrial activity inside the T-wave \mathbf{B}_i was taken to be the difference $\mathbf{B}_i - \mathbf{T}_z$, with \mathbf{T}_z the template corresponding to \mathbf{B}_i . As in the preprocessing step, the finite impulse response filter was also applied after the cancellation to smooth the difference of levels between each QRS complex and its corresponding T-wave.

2.2.4. Validation

A biophysical computer model of the atria was used to obtain a realistic atrial electrical activity on the torso [6]. The AF signals that were generated in the 12-lead ECG were added to a clinical 4-minute standard 12-lead ECG of an AF paroxysmal patient (78 years old) in sinus rhythm in which the P-waves were removed. The clinical ECG was selected to represent the ventricular activity in AF as

closely as possible. The relative error between the true and the estimated AA was used to evaluate the performance of our method compared to the standard ones.

3. Results

Figures 2 and 3 show the different steps in our approach from synthetic AF ECG signal creation to the estimated AA signal. The threshold θ for QRS clustering was set to 0.98 which led to 25 clusters for 287 QRS complexes. The bin width and the threshold θ used for the T-waves were respectively set to 30 ms and 0.8, which led to 22 clusters for 287 T-waves. Our method was compared to two other methods: the standard ABS method (method 2) and the standard spatiotemporal QRST cancellation method (method 3) proposed by [1]. Using the synthetic AF ECG signals, the relative error between true and estimated AA was evaluated on each lead (see Table 1). Figure 4 shows a estimated AA on lead V1 obtained on a real ECG signal. The same parameters as mentioned above were used. This example demonstrates that even premature beats can be removed efficiently if all processing steps are performed appropriately.



Figure 2. (a) Original 10-second ECG signal on V1. (b) Real VA on V1 from a 78 years old patient in sinus rhythm (c) Sum of the AA and VA on V1. (d) Baseline correction on V1 (e) Total RMS signal after baseline correction. (f) Estimated AA with the proposed method. (Boxed-in segments are shown magnified in Figure 3)

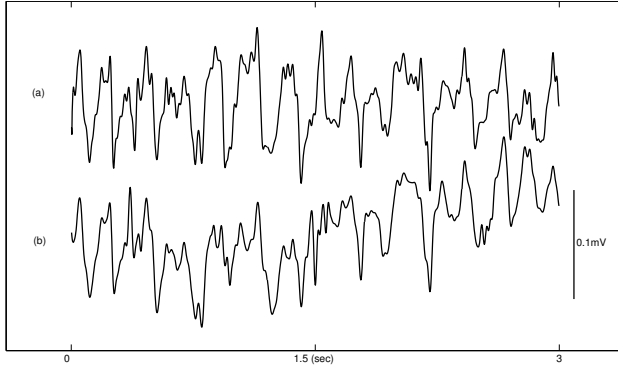


Figure 3. (a) The synthetic AA signal of the 3-second dashed rectangle indicated in Figure 2 a. (b) Corresponding estimated AA signal (the dashed rectangle of Figure 2 f), relative error between the signals : 1.02).

4. Discussion and conclusions

A major part of the residual error (Figure 3) may be attributed to an imperfect baseline correction. Compared to other methods, our method produces better results for each lead of the synthetic signals. The average relative error is diminished by 19.7% and 29.0% in comparison with the standard ABS and the standard spatiotemporal method, respectively. We attribute this to the flexibility and the precision induced by the separate QRS complex and T-wave cancellations. Clustering of the QRS complexes alone improves the spatial optimization of QRS cancellation. Also, it is beneficial not to perform spatial optimization of T-wave cancellation, due to the smaller difference in amplitude between T-waves and atrial activity.

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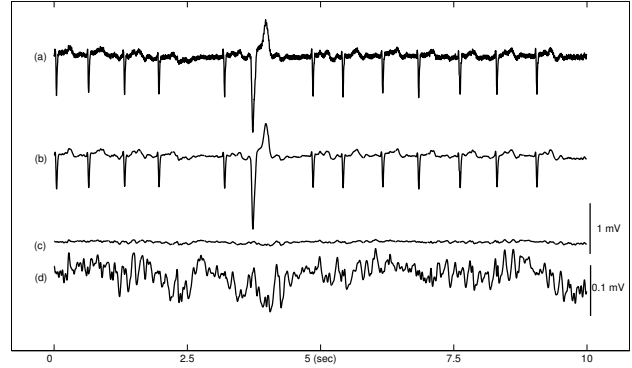


Figure 4. (a) Raw 10-second real V1 lead signal. (b) V1 signal after preprocessing. (c) Results of the proposed method on V1. (d) Results in (c) amplified by factor of 10.

| | Our method | Method 2 | Method 3 |
|----------------|-------------|----------|----------|
| Vr | 1.55 | 2.04 | 2.24 |
| V1 | 1.39 | 1.75 | 1.87 |
| V1 | 0.87 | 0.94 | 1.05 |
| V2 | 0.98 | 1.44 | 1.52 |
| V3 | 0.82 | 0.94 | 1.03 |
| V4 | 0.84 | 0.92 | 1.01 |
| V5 | 0.88 | 0.90 | 0.97 |
| V6 | 1.08 | 1.16 | 1.19 |
| Average | 1.05 | 1.26 | 1.36 |

Table 1. Relative errors on all significant leads. Our method is compared to the standard ABS (method 2) and the spatiotemporal QRST cancellation method (method 3) proposed by [1].

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