

Ventricular Activity Residual Reduction in Remainder ECGs Based on Short-Term Autoregressive Model Interpolation

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Abstract

Considering the inability of existing methods to produce remainder ECGs free from QRS residuals, the present study puts forward a new method for ventricular (QRS) residual detection and reduction in remainder ECGs extracted for the analysis of atrial fibrillation (AF). Autoregressive interpolation (AR) is applied to reduce the amplitude of any QRS residual detected as not negligible by a newly-proposed index, considering the QRS interval as missing, and replacing its samples through interpolation. Performance has been evaluated on a dataset composed of 19 remainder ECGs with AF. Mean (\pm SD) spectral concentration improved from 56.7 ± 12.8 % of the original remainders to 58.1 ± 13.3 % of the interpolated ones, while mean (\pm SD) amplitude of original and processed QRS-T segments was 0.05 ± 0.03 mV. The proposed algorithm was found to improve the quality of the extracted AA remainders without attenuating their mean amplitudes inside the QRST segments.

1. Introduction

An appropriate way for studying atrial fibrillation (AF) is through the noninvasive analysis of the atrial activity (AA) signal extracted from the surface electrocardiogram (ECG) recorded during AF episodes [1].

There exist in the literature different families of methods to extract AA from an ECG, based on the direct estimation of the AA (e.g., [2–4]), or to cancel out ventricular activity through a direct suppression of the QRS-T complex (e.g., [5, 6]). However, up to now there is no method able to control the magnitude of the ventricular (QRS) residuals and to produce a remainder ECG completely free from them, so that QRS residuals can be several times larger than the surrounding AA waves. Although this shortcoming may be neglected when computing global measures from the AA signal, it must nonetheless be taken into account when performing detailed analysis, e.g., tracking variations in AF frequency [7] or characterizing the AA

waveform morphology [8] on a second-to-second basis. Then, there is a need to test the residual relevance, possibly avoiding visual inspection of the remainder ECG, and, if needed, replace them with samples which are better tuned to the surrounding AA waves.

The present study puts forward a new method for QRS residual detection and reduction in the remainder ECGs. The method is based on an autoregressive (AR) interpolation of the segments which contain not negligible QRS residuals, treating these segments as missing, to be replaced by model-based interpolation using surrounding samples.

2. Methods

2.1. Basic auto-regressive interpolation

QRS residuals can be treated as a sequence of missing samples. The objective is to make an optimal estimate of these missing samples, through AR interpolation based on surrounding samples [9]. Assuming the AA signal as reasonably stationary within two cardiac periods, that is about the temporal length of one QS segment (the unknown part of the signal, \mathbf{x}_{Uk}) surrounded by two SQ segments (the known part, \mathbf{x}_{K_n} , so that $\mathbf{x} = \mathbf{x}_{K_n} + \mathbf{x}_{Uk}$), a stationary AR formulation of the problem can be considered

$$x(m) = \sum_{k=1}^p a_k x(m-k) + e(m) \quad (1)$$

where $x(m)$ is the AR signal, a_k the model coefficients, p the model order, and $e(m)$ a zero mean excitation signal (supposed to be zero in the following). We can firstly obtain an estimate of the model coefficient vector \mathbf{a} from

$$\hat{\mathbf{a}} = (\mathbf{X}_{K_n}^T \mathbf{X}_{K_n})^{-1} (\mathbf{X}_{K_n}^T \mathbf{x}_{K_n}) \quad (2)$$

where \mathbf{X}_{K_n} contains all the $x(m-k)$ involved in the estimation of \mathbf{x}_{K_n} [9]. Then, the estimates of the model coefficients are used to interpolate the missing samples, leading to the estimate of the unknown data vector

$$\hat{\mathbf{x}}_{Uk} = -(\mathbf{A}_1^T \mathbf{A}_1)^{-1} (\mathbf{A}_1^T \mathbf{A}_2) \mathbf{x}_{K_n} \quad (3)$$

where \mathbf{A}_1 and \mathbf{A}_2 are coefficient matrices defined as in [9], in which each row is constructed arranging elements of $\hat{\mathbf{a}}$ so as to generate the predictor error $\mathbf{e} = \mathbf{A}_1 \mathbf{x}_{Uk} + \mathbf{A}_2 \mathbf{x}_{Kn}$.

2.2. Exclusion criterion for QRS residuals reduction

A criterion is needed for judging whether the QRS residuals are to be kept or replaced by interpolated samples. To this purpose, Alcaraz and Rieta proposed a specific criterion, named ventricular residue (VR) index [10], defined for the i -th QRS complex as

$$VR_i = \frac{1}{\frac{1}{Q} \sum_{q=1}^Q \hat{x}_{AA}^2} \sqrt{\sum_{k=r_i-H}^{r_i+H} \hat{x}_{AA}^2} \cdot \max_{k=r_i-H, \dots, r_i+H} (|\hat{x}_{AA}|) \quad (4)$$

where $2H + 1$ denotes the number of samples corresponding to the QRS interval (considered as 100 ms long), Q the samples of the AA involved, r_i the R peak occurrence time, and \hat{x}_{AA} an estimate of the AA. However, in order to improve performance of this index, we preprocessed the input of VR (the i -th QRS segment under analysis) with a high-pass filter with a cut-off frequency of 12 Hz. This cancels out part of the AF contribution from the calculus of VR . The output of the filter was then used to calculate VR . Finally, VR was normalized by the maximum of its absolute value ($VRN = \frac{VR}{\max(|VR|)}$).

2.3. Simulated AF signals

Simulated AF signals were obtained from 4 subjects affected by AF. The main advantage of taking an AA from real ECG recordings is in having a physiologically coherent representation of AF. All signals were acquired at a sampling rate of 1 KHz and recorded using a standard 12-lead system. Preprocessing was done by applying a zero-phase high pass filter with a -3 dB cut off frequency at 0.5 Hz to remove baseline wander (<1 Hz) [11]. As proposed in [3], atrial waves were simulated by isolating the AA from TQ intervals from lead V1 during AF episodes and carefully extrapolating it between those segments. However, we chose simply to connect all the extracted TQ segments from the same patient, instead of getting an interpolation of the QRS-T complex between them. A total of 21 10-s long simulated AF recordings were generated.

2.4. Simulated QRS residuals

In order to have an accepted model for roughly modeling the QRS residual shape, we adopted the one presented by Corino *et al.* in [12], with QRS residuals modeled by a modulated Gaussian function. The following setup of parameters was used

Parameter	Value
F_R	2 Hz
F_S	1000 Hz
σ_S	1
L	100 samples

Simulated QRS residuals were added at specific time locations to the simulated AF signals. We selected 5 real AF ECG R-peak event series from 5 patients affected by AF, so as to generate 105 simulated remainder ECGs. The advantage of taking real AF R-peak event locations is in the higher coherence with the patho-physiological RR series, and in the automatic avoiding of overlap in time. Performance of the method has been evaluated on simulated remainder ECGs in terms of normalized mean square error (NMSE), a measure that quantifies the difference with a particular signal and its estimate

$$NMSE = \frac{\sum_{i=1}^N (y(i) - \hat{y}(i))^2}{\sum_{i=1}^N y(i)^2} \quad (5)$$

where $y(i)$ denotes the reference signal, $\hat{y}(i)$ an estimate of it, and N its length.

2.4.1. Real AF ECGs

The method was evaluated on 19 remainder ECGs acquired from patients affected by AF. A continuous V1 lead remainder ECG was obtained exploiting a suitable blind source separation extracting approach [4]. Original ECGs have been acquired at a sampling rate of 1 KHz and recorded using a standard 12-lead system. Preprocessing was carried out as described in Section 2.3. None of the signals in this dataset was used to generate simulated AF signals. Performance of the method has been evaluated in terms of spectral concentration (SC) and signal amplitude. SC is a measure for the compactness of the spectrum around the AA central frequency (modal frequency in the 3-12 Hz interval) [3].

3. Results

3.1. Model order estimation

Model order estimation has been carried out exploiting the 105 simulated remainders free from QRS residuals, in order to evaluate the error introduced by the method and to guarantee an acceptable tradeoff between model distortion and model order value. The method was tested for different model order p ranging between 1 and 50. Results are visually presented in terms of NMSE in Fig. 1. A model order of 25 was chosen for subsequent analysis, since it gave an acceptably small mean NMSE of 5.72%, which did not reduce significantly for higher order values (5.34% for $p = 50$), so as to be in a stable position after the knee of the curve (around order 21).

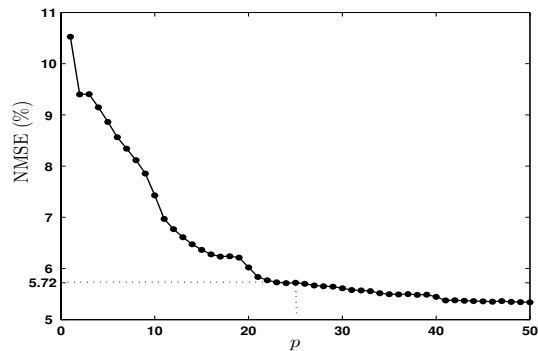


Figure 1. NMSE evolution vs. model order p , for the simulated remainder ECGs without presence of QRS residuals.

3.2. Exclusion criterion threshold estimation

Simulated QRS residuals were added to the simulated AF signals with different amplitude ratio (QRS amplitude over AF amplitude), ranging from 0.1 to 10 (100 realizations). All QRS segments were processed. Results are visually summarized in Fig. 2 which shows that the quality of the interpolation is not influenced by QRS residual importance (constant NMSE equals to 6.68% between the original AF remainder and the interpolated, independently on the amplitude ratio, dotted line). This is in line with the way AR model operates, giving an output which does not depend on the unknown segment that must be interpolated. QRS residual interpolation is unnecessary until the NMSE between the remainder ECGs and the original AF signals (solid line) is lower than the error introduced by the model (dotted line). The intersection is reached for an amplitude ratio of 1.6, related to a value of VRN equals to 0.4.

3.3. Real AF ECGs

For real remainder ECGs interpolation was applied only when VRN value for the QRS segment under analysis was greater than a certain threshold. Tested thresholds ranged from 0 to 1 (10 realizations). Fig. 3 shows the evolution of SC and of the percentages of interpolated QRS segments for different values of VRN . The lower VRN the higher the number of QRS segments processed by the method, and the better the SC of AF. Notice the plateau evolution of SC until VRN is lower than 0.3, and the sudden reduction of SC for higher values of VRN , suggesting 0.3 is a suitable threshold for this parameter. The proximity to the value found in Section 3.2 for simulated signals, confirms that a reasonable exclusion criterion thresh-

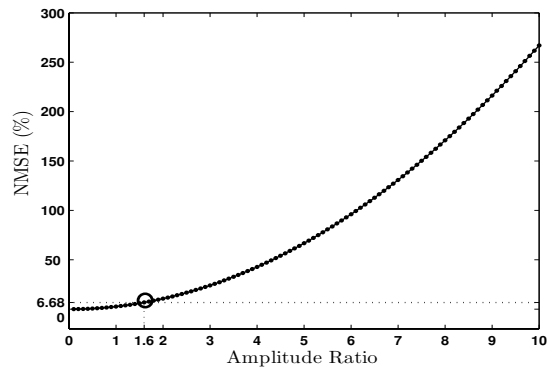


Figure 2. NMSE evolution vs. amplitude ratio, for the simulated remainder ECGs presenting QRS residuals. NMSE between the interpolated signals and the original AF signals (dotted line) and NMSE between the remainder ECGs and the original AF signals (solid line marked by dots) are shown.

old should be set between 0.3 and 0.4. Mean (\pm SD) SC improved from $56.7 \pm 12.8\%$ of the original remainders to $58.1 \pm 13.3\%$ of the interpolated ones. Mean (\pm SD) amplitude of QRST segments of V1 was 0.23 ± 0.16 mV, compared to 0.05 ± 0.03 mV of the original remainder ECGs and to 0.05 ± 0.03 mV of the interpolated remainder ECGs (in line with the amplitude of TQ segments of original remainders equals to 0.05 ± 0.03 mV). The spectral content improved by interpolation (Δ SC of ≈ 2 between interpolation of all QRS segments ($VRN = 0$) and no interpolation ($VRN = 1$)), with no attenuation of the mean amplitudes inside the QRS-T segments. Fig. 4 shows an example of interpolation on a remainder ECG presenting evident QRS residuals.

4. Discussion and conclusions

All methods which attempt to obtain a remainder ECG completely free from ventricular activity suffer from the inability to cancel out completely QRS-T complexes, so that more or less significant QRS residuals can be still present in the remainder ECG. This work introduced a new method for getting rid of the QRS residuals within a remainder ECG, independently on the way remainders have been obtained. Although the presence of QRS residuals do not prevent from analyzing AA, they still constrain more detailed analysis of AF, as, e.g., when analyzing the AA spectral content [7] or characterizing the AA waveform morphology [8] on a second-to-second scale. In these cases, even a small improvement in the spectral content of the remainder signal might produce better results for the signal window under analysis. This is in line with the slight

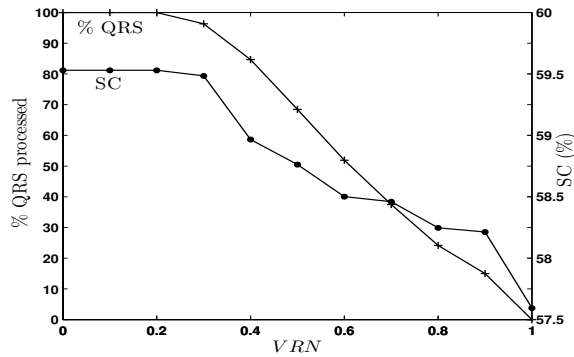


Figure 3. SC (solid line marked by dots) and percentage of processed QRS segments (solid line marked by crosses) evolutions vs. VRN index, for the real remainder ECG dataset. Mean SC value for the original remainders is 57.44%.

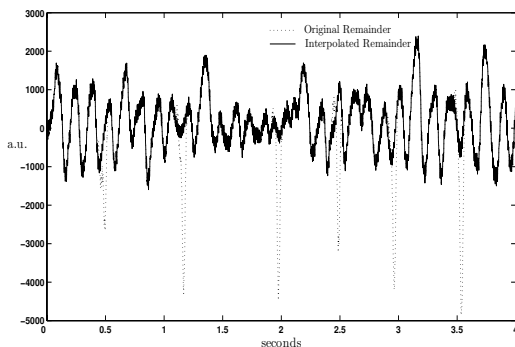


Figure 4. Real 4-s remainder ECG (dotted line) characterized by evident QRS residuals and its interpolated version (solid line), using $VRN = 0.3$; a.u., arbitrary units.

improvement in the SC obtained for the real AF dataset, suggesting that the overall features of the remainders have not been changed significantly by the interpolation, but they may have improved locally. Moreover, the agreement between simulated and real datasets in the identification of a threshold for the new QRS residual evaluation index VRN , makes it reliable. In conclusion, the proposed algorithm improves the spectral quality of the extracted AA remainders without attenuating their mean amplitudes inside the QRS-T segments.

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