PRONY RESIDUAL ANALYSIS FOR THE IDENTIFICATION OF CARDIAC ARRHYTHMIAS

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ABSTRACT

An investigation into the use of Prony modeling for the identification of *late potentials* (LPs) from *signal-averaged electrocardiograms* (SAECGs) is described. We develop a noninvasive method, based on the short-time Prony modeling algorithm, to extract a diagnostic feature, dubbed the *Prony residual marker* (PRM), from the SAECG waveform. The PRM is used as a marker for the presence of LPs and is thus used to predict the diagnostic outcome of invasive electrophysiologic study.

1. INTRODUCTION

Electrophysiologic study (EPS) is currently considered the most reliable indicator of heart attack risk. However, EPS testing is invasive, expensive, and is limited to large medical facilities with specialized personnel. Therefore, a noninvasive, low-cost diagnostic tool for identifying patients at risk of sudden cardiac death would represent a significant benefit. Many clinical reports confirm that the presence of late potentials (LPs) in normal sinus rhythm correlates strongly with the occurrence of cardiac arrhythmias such as *sustained monomorphic ventricular tachycardia* (SMVT) [1], a precursor to lethal ventricular fibrillation (VF).

LPs behave like low amplitude, fractionated potentials following, but in some cases appearing close to, or even overlapping the QRS complex in the ECG waveform. Haberl *et al.* [2] performed a *short-time Fourier transform* (STFT) analysis of multiple sequentially overlapping segments of QRS/ST waveforms in order to distinguish the LPs from the original signal and noise by differences in the frequency characteristics. However, STFT analysis is severely limited in resolving frequency components in the short data sets containing LPs. In this paper, we introduce a new approach, based on short-time Prony modeling, to obtain high resolution spectra from short SAECG segments so that we may accurately localize changes in the frequency and energy content of the signal, within and following the QRS complex. The proposed analysis procedure can be described in terms of a *pattern recognition* (PR) system. Our algorithm seeks to detect LPs, and the task of classification is performed using the detection results. We predict that SMVT will likely be inducible for a patient (i.e., EPS=+1) if we can detect LPs from the corresponding SAECGs. Likewise, we predict that a patient is SMVT not inducible (i.e., EPS=−1) if we cannot detect LPs.

This work was supported by the National Science Foundation under grant number MIP-9220769.

2. METHOD

2.1. Rationale

The technique employs a set of signal-averaged X, Y and Z lead ECG recordings. Our analysis is based on the assumption that the recorded signal can be described by a sum of three components: A component which can be modeled by a Prony series of order p, a fractionated component, and a component due to noise. Here, we assume that the Prony modeled component corresponds to *normal* ventricular depolarization, while the fractionated component, if present, to LPs. Such an assumption is appropriate since it is based on the claim that normal tissue response, such as ventricular depolarization, is *predictable* and can be predicted using a *linear prediction algorithm.* Subtracting the modeled depolarization from the original signal, we obtain the sum of the fractionated and noise components. According to the above assumption, this fractionated or residual signal thus corresponds to the *unpredictable* portion, which may be attributed to *abnormal* tissue response, such as LPs. Since the noise level is significantly lower for an SAECG than for a raw ECG [3], the residual signal can be viewed as primarily fractionated and therefore as a marker of LPs.

0-7803-2431-5/95 $4.00

2.2. Prony Modeling Analysis

Based on the fact that LPs occur in the region near the *end* of the QRS complex, a short-time Prony model can be fit to a series of overlapping windows comprising a region centered at the point corresponding to the end of the QRS complex [4, 5]. Denoting the ith segment of the sampled SAECGs corresponding to leads X, Y and Z as $x_i(n), y_i(n)$ and $z_i(n)$ respectively, we may write

$$\begin{aligned} x_i(n) &= \sum_{k=1}^{p} A_{Xik}\lambda_{ik}^n + f_{Xi}(n) + e_{Xi}(n) \\ &(\;= \hat{x}_i(n) + f_{Xi}(n) + e_{Xi}(n) \;), \\ y_i(n) &= \sum_{k=1}^{p} A_{Yik}\lambda_{ik}^n + f_{Yi}(n) + e_{Yi}(n) \\ &(\;= \hat{y}_i(n) + f_{Yi}(n) + e_{Yi}(n) \;), \\ z_i(n) &= \sum_{k=1}^{p} A_{Zik}\lambda_{ik}^n + f_{Zi}(n) + e_{Zi}(n) \\ &(\;= \hat{z}_i(n) + f_{Zi}(n) + e_{Zi}(n) \;), \\ & \quad n = 1, \ldots, L, \quad i = 1, \ldots, M, \end{aligned} \tag{1}$$

where $[f_{Xi}(n)\ f_{Yi}(n)\ f_{Zi}(n)]$ and $[e_{Xi}(n)\ e_{Yi}(n)\ e_{Zi}(n)]$ represent the associated fractionated and noise components, respectively. From Equations (1) we can see that the three leads are modeled using *common poles*, λ_{ik}, but *different amplitudes*, A_{Xik}, A_{Yik} and A_{Zik}. This is known as the *multi-snapshot* Prony model [7]. Here, the common poles can be viewed as the *fundamental modes* (or frequencies) of the heart beat segment and they should be unchanged from lead to lead over the same time interval. This permits processing of all three leads *coherently* and may provide an advantage over performing the analysis on each lead separately. In our experiments we have found that a Prony order of $p = 5$, a segment length of $L = 25$, and $M = 101$ overlapping windows gives good results. Note that the first 50 segments all begin at points inside the QRS complex, the 51st segment begins at the end point of the QRS complex, and the remaining 50 segments all begin at points outside the QRS complex.

To estimate the poles and amplitudes for the ith segment for each lead, first we compute the *linear prediction coefficients* (LPCs), $\{a_{ik}\}_{k=1}^{p}$, corresponding to the p poles, $\{\lambda_{ik}\}_{k=1}^{p}$, which are the roots of the algebraic equation [6]

$$1 + a_{i1}z^{-1} + a_{i2}z^{-2} + \cdots + a_{ip}z^{-p} = 0. \tag{2}$$

The coefficients are computed from the forward linear prediction equations

$$\mathbf{w_i} \approx -\mathbf{W_i}\mathbf{a_i}, \tag{3}$$

or

$$\begin{bmatrix} \mathbf{w_i} & \mathbf{W_i} \end{bmatrix} \begin{bmatrix} 1 \\ \mathbf{a_i} \end{bmatrix} \approx 0, \tag{4}$$

where

$$\mathbf{a_i} = [a_{i1} \ \cdots \ a_{ip}]^T, \tag{5}$$

$$\begin{aligned} \mathbf{w_i} = [&x_i(p) \ \cdots \ x_i(L-1)\ y_i(p) \ \cdots \\ &y_i(L-1)\ z_i(p) \ \cdots \ z_i(L-1)]^T, \end{aligned} \tag{6}$$

and

$$\mathbf{W_i} = \begin{bmatrix} x_i(p-1) & \cdots & x_i(0) \\ \vdots & \ddots & \vdots \\ x_i(L-2) & \cdots & x_i(L-p-1) \\ y_i(p-1) & \cdots & y_i(0) \\ \vdots & \ddots & \vdots \\ y_i(L-2) & \cdots & y_i(L-p-1) \\ z_i(p-1) & \cdots & z_i(0) \\ \vdots & \ddots & \vdots \\ z_i(L-2) & \cdots & z_i(L-p-1) \end{bmatrix}. \tag{7}$$

Note that if the data vector $\mathbf{w_i}$ and data matrix $\mathbf{W_i}$ contain significant noise, Equation (3) or (4) may produce inaccurate estimates of $\mathbf{a_i}$. Applying a *singular value decomposition* (SVD) truncation improves the estimates of $\mathbf{a_i}$ by reducing the effect due to the noise space [8, 9]. Here, An SVD of the matrix $[\mathbf{w_i}\ \mathbf{W_i}]$ is computed first. After the SVD truncation, a *low rank* approximation $[\hat{\mathbf{w}}_\mathbf{i}\ \hat{\mathbf{W}}_\mathbf{i}]$ is obtained which yields modified linear prediction equations

$$\begin{bmatrix} \hat{\mathbf{w}}_\mathbf{i} & \hat{\mathbf{W}}_\mathbf{i} \end{bmatrix} \begin{bmatrix} 1 \\ \mathbf{a_i} \end{bmatrix} \approx 0. \tag{8}$$

The *total least squares* (TLS) solution for the LPC vector $\mathbf{a_i}$ can be found as [9]

$$\mathbf{a_i} = -\hat{\mathbf{W}}_\mathbf{i}^{\dagger}\hat{\mathbf{w}}_\mathbf{i} = -(\hat{\mathbf{W}}_\mathbf{i}^H\hat{\mathbf{W}}_\mathbf{i})^{-1}\hat{\mathbf{W}}_\mathbf{i}^H\hat{\mathbf{w}}_\mathbf{i}, \tag{9}$$

where $\dagger$ denotes the *pseudoinverse* and superscript H denotes *Hermitian transpose*. Thus, the p poles can be computed simply by finding the roots of Equation (2). Rewriting Equations (1) compactly and assuming the noise and fractionated components are very small, we have the approximation

$$\mathbf{u_i} \approx \mathbf{\Lambda}\mathbf{A_i}, \tag{10}$$

where

$$\mathbf{u_i} = \begin{bmatrix} x_i(0) & y_i(0) & z_i(0) \\ x_i(1) & y_i(1) & z_i(1) \\ \vdots & \vdots & \vdots \\ x_i(L-1) & y_i(L-1) & z_i(L-1) \end{bmatrix}, \tag{11}$$

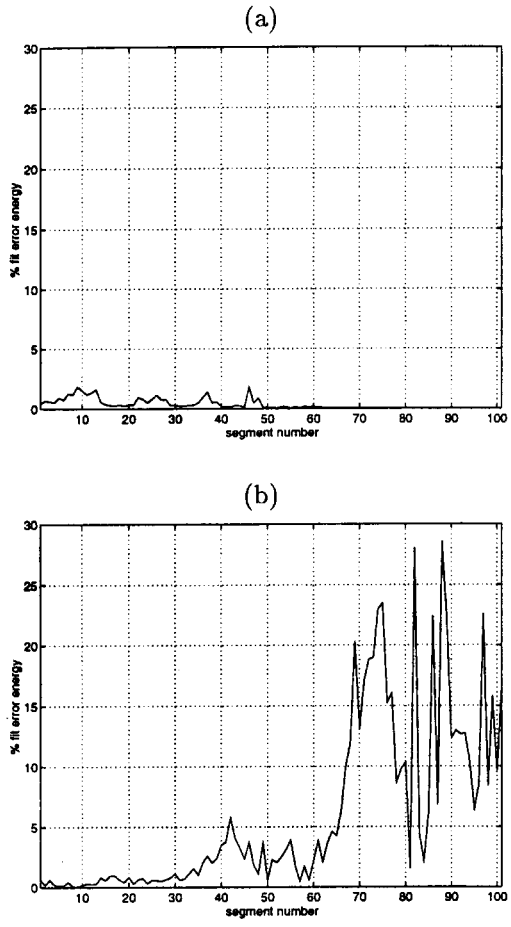

Figure 1: Average percent fit error energy for three SAECG leads. (a): A negative EPS patient (no LPs detected) (b): A positive EPS patient (LPs detected)

$$\mathbf{\Lambda} = \begin{bmatrix} 1 & \cdots & 1 \\ \lambda_1 & \cdots & \lambda_p \\ \vdots & & \vdots \\ \lambda_1^{L-1} & \cdots & \lambda_p^{L-1} \end{bmatrix}, \tag{12}$$

and

$$\mathbf{A_i} = \begin{bmatrix} A_{Xi1} & A_{Yi1} & A_{Zi1} \\ A_{Xi2} & A_{Yi2} & A_{Zi2} \\ \vdots & \vdots & \vdots \\ A_{Xip} & A_{Yip} & A_{Zip} \end{bmatrix}. \tag{13}$$

Therefore, the amplitudes can be found simply using a least squares solution as

$$\mathbf{A_i} = \mathbf{\Lambda}^{\dagger}\mathbf{u_i} = (\mathbf{\Lambda}^H\mathbf{\Lambda})^{-1}\mathbf{\Lambda}^H\mathbf{u_i}. \tag{14}$$

2.3. Example

Figure 1 shows the three-lead average percent fit error energies[1] for all 101 segments for two typical patients. Figure 1(a) shows a patient with EPS=−1 (SMVT not inducible) and Figure 1(b) shows one with EPS=+1 (SMVT inducible), respectively. From Figure 1(a), we can see that the average percent fit error energies are less than 5% for all segments, which implies that there may be no LPs in the fit region. Such a finding is consistent with the corresponding EPS result, and we can conclude in this case that low fit error does correspond to SMVT not inducible. As for Figure 1(b), we see that the average percent fit error energies are significantly larger for many of the segments. This suggests the presence of LPs in the later part of the fit region.

2.4. Pattern Classification

Choosing the mean value of the average percent fit error energies as a feature, the classification task can then be performed simply using this single feature y, referred to as a *Prony residual marker* (PRM). Choosing a threshold T, we can formulate a decision rule:

If $y \geq T$, => SMVT inducible;
if $y < T$, => SMVT not inducible.

3. RESULTS

We have tested the short-time Prony modeling algorithm on a database consisting of 41 patients (21 negatives and 20 positives) who underwent EPS in the electrophysiology laboratory at the Ohio State University Hospital. The results are shown in Table 1. The overall classification accuracy exceeded 85%. Further,

Table 1: Results of the short-time Prony residual analysis (optimum threshold for PRM = 1.7%)

	Detection (%)
not SMVT induced (EPS = −1)	19/21 = 90.5%
SMVT induced (EPS = +1)	16/20 = 80.0%
overall classification accuracy	35/41 = 85.4%

we compared the performance obtained from our PRM approach and that obtained by applying the standard time domain criteria developed by Gomes *et al.* [10]. We found that the PRM approach has a higher classification accuracy and more general applicability than the standard time domain criteria. This is because the

[1] Here, we define the % fit error energy for the ith segment as $100 \times \frac{\|l_i(n)-\hat{l}_i(n)\|^2}{\|l_i(n)\|^2}$, where $l = x, y, z$.

time domain criteria cannot be applied to ECGs with *prolonged* standard QRS duration (i.e., $\geq$ 120 ms). Additionally, adopting different model orders (p) and segment lengths (L) produced only small changes from the results shown in Table 1 and the overall classification accuracy remained above 80% for all choices of p and L evaluated.

4. DISCUSSION

From Table 1, we note that there are four *false negative* (FN) patients (EPS=+1, negative PRM). We may speculate that this false detection is possibly a result of the *signal averaging* process. Generally we know that the noise level can be reduced by the square root of the number of ECGs after signal averaging if the noise is *independently* and *identically distributed* (iid) [3, 5]. However, signal averaging may also cause *reduction* of LP level since LPs are known to behave as low-amplitude fractionated components, and are not completely constant from cycle to cycle. Thus, the PRM values may be very small for some positive-EPS cases. In addition, it is also very difficult to distinguish LPs from noise if both of them are highly *dependent* on each other [5] and this may be associated with a small PRM value.

Overall our results indicate that the PRM can provide an accurate, noninvasive identification of patients at risk of arrhythmic events. By facilitating the detection of low amplitude fractionated behavior masked by systolic depolarization of healthy myocardium, we are able to predict inducibility of SMVT with higher classification accuracy and wider applicability than is possible by standard time domain criteria.

ACKNOWLEDGMENT

The authors would like to thank Dr. S. Nelson and Dr. B. Jaffe, of the Division of Cardiology at the Ohio State University, for providing the database and medical interpretation. Also, we thank Prof. L. Potter, of the Electrical Engineering Department at the Ohio State University, for many useful discussions concerning this research.

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