Genetic algorithm with Gaussian function for optimal P-wave morphology in electrocardiography for atrial fibrillation patients☆

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ABSTRACT

Atrial fibrillation (AF), which is a rapid-irregular heartbeat and shows abnormal heart rhythm of the supraventricular tachycardia class, has proved to increase the risks of heart failure, dementia, and stroke. To detection AF, P-wave morphology in electrocardiography (ECG) is suggested to be a strong indicator. To make computerized detection possible, most approaches decompose the ensemble of signals into a finite set of features and establish the relation between symptoms and values of features. Therefore, the disease can be asserted solely by the values of the decomposed features. For early diagnosis of AF, this study develops a hybrid Taguchi-genetic algorithm (HTGA) that facilitates Gaussian decomposition in ECG signals, because P-wave morphology can be well approximated by a family of Gaussian functions. The HTGA optimizes features with minimized performance index of the normalized root mean square error. With accurate decomposition in characterizing parameter values of P-wave morphology, the performance of disease classification improves by using appropriate feature set. Our experiments indicate that the proposed HTGA with Gaussian function obtains a better fit to the actual P-wave compared to the conventional nonlinear least-squares approaches.

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1. Introduction

Because it enables low-cost and noninvasive analysis of heart function, surface electrocardiography (ECG) is the conventional method for diagnosis of cardiac diseases [1]. Arterial fibrillation (AF) is the strongest risk factor for ischemic stroke, which always causes disability and has a high socioeconomic burden and national healthcare burden [2–4]. Many stroke prevention medications (e.g., new oral anticoagulants) and treatments (e.g., left atrial appendage occluder implantation) have been introduced in recent years. However, early detection of AF is a continuing challenge in the healthcare systems of many countries [5]. Recent studies suggest that AF is provoked and maintained by electrophysiological conditions [6]. Some researchers have proposed methods of extracting morphological features of a P-wave and using the features to improve

accuracy in identifying at-risk patients [7–12]. For example, the nonlinear least-squares approach (NLSA) presented in Martinez et al. [12] models the P-wave as a Gaussian function. However, no studies have investigated whether an evolutionary optimization algorithm with a single Gaussian function can be used to model a P-wave.

Of the evolutionary optimization algorithms proposed so far, the hybrid Taguchi-genetic algorithm (HTGA) has proven to be among the most effective techniques for solving complex optimization problems in varying domains [13–17]. Therefore, the objectives of this study were (a) to develop an HTGA with a single Gaussian function to model a P-wave and (b) to find the optimal feature solution for P-wave morphology by minimizing the normalized root-mean-square error (NRMSE) performance index.

This paper is organized as follows. Section 2 describes the use of HTGA to solve the optimal feature solution for P-wave morphology. To evaluate the efficiency and effectiveness of the proposed HTGA, Section 3 compares the performance of the HTGA and NLSA method developed by Martinez et al. [12]. Finally, Section 4 concludes the study.

2. Materials and methods

This study was approved by the Institutional Review Board of National Yang-Ming University Hospital (NYMUH No. 2017A016). The subjects were six patients treated for paroxysmal AF at National Yang-Ming University Hospital, Yilan, Taiwan. In all patients, diagnosis of AF was supported by documented results for ECG or for 24 h Holter monitoring.

All patients were admitted for AF ablation. All patients had normal sinus rhythm before ECG sampling. Before the procedure, all ECG data were recorded in the electrophysiology study room with a LABSYSTEM^TM PRO EP Recording System (Boston Scientific). Before the ablation procedure (before blood vessel cannulation), the stable sinus rhythm interval was selected and analyzed. A 12-lead ECG recording machine was used to acquire ECG data at a 1000 Hz sampling rate. Only lead II was used to acquire ECG data because it obtains the highest P-wave amplitude and because previous works have recommended its use for evaluating P-wave morphology [18].

For lead II, the sampling data $y(n)$ for the P-wave ($n = n_b, n_{b+1}, \ldots, n_e$, where n_b and n_e are the beginning and end of the P-wave, respectively) were obtained with the ECG recording machine. Thus, the measured ECG data were used to obtain the P-wave, which was defined as

$$w(i) = [y(n_b), y(n_{b+1}), \ldots, y(n_e)] \ (i = 1, \ 2, \ldots, \ L), \tag{1}$$

where L is a total length of the P-wave samples.

The morphology of a P-wave was quantified by a Gaussian function defined as

$$\hat{w}(i) = Ae^{-((i-C)/W)^2} \ (i = 1, \ 2, \ldots, \ L), \tag{2}$$

where features *A, W,* and *C* represent its amplitude, width, and time position, respectively.

The P-wave alteration was quantified by computing the NRMSE (performance index *J*) between $w(i)$ and $\hat{w}(i)$ as

$$J = \frac{\sqrt{\frac{\sum_{i=1}^{L} \left(w(i) - \hat{w}(i)\right)^2}{L}}}{w_{\max} - w_{\min}}, \tag{3}$$

where $w_{\min}$ and $w_{\max}$ are the minimum and maximum values for the ECG data $w(i)$ ($i = 1, \ 2, \ldots, \ L$), respectively.

Eq. (3) shows that the NRMSE actually depends on the feature set {*A, C, W*}. Therefore,

$$J = f(A, \ C, \ W). \tag{4}$$

Eq. (4) is an optimization problem which can be expressed as

$$\text{minimum } J = f(A, \ C, \ W). \tag{5}$$

The HTGA can then be used to solve the optimization problem in Eq. (5). The details of the HTGA are given in Tsai et al. [19].

3. Results and discussion

The feature set {*A, C, W*} was used to compare the proposed HTGA with the NLSA presented in Martinez et al. [12]. The HTGA was performed with a population size of 100, a crossover rate of 0.8, a mutation rate of 0.1, and a generation count of 100. The HTGA method was performed with $\underline{A} \leq A \leq \bar{A}$, $\underline{C} \leq C \leq \bar{C}$, $\underline{W} \leq W \leq \bar{W}$, in which $\underline{A} = \underline{C} = \underline{W} = 0$ and $\bar{A} = \bar{C} = \bar{W} = 600$. For the six patients, Table 1 shows the optimal features *A, C,* and *W* of a Gaussian function for the P-wave and the NMRSE. In patient 1, for example, these values were $A = 367.95$, $C = 96.05$, $W = 146.40$, and $J = 0.0995$. Fig. 1 shows the convergence results obtained for the NRMSE when HTGA was used for the P-wave of six patients. In patient 1, for example, the generation count stabilizes at approximately 50.

Fig. 2 shows the original P-wave data and the Gaussian function for the P-wave for the six patients. Table 2 compares the Gaussian function obtained by HTGA and NLSA for the P-wave in the six patients. For the six patients, the NRMSE values obtained by HTGA (0.0995, 0.1067, 0.0788, 0.1364, 0.0541 and 0.1162) were superior to those obtained by NLSA (0.1015, 0.1085, 0.0796, 0.1373, 0.0563 and 0.1266). In terms of NRMSE, the HTGA method also outperformed the NLSA method developed by Martinez et al. [12].