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Identity Recognition Based on the QRS Complex Dynamics of Electrocardiogram

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ABSTRACT Biometric identification based on electrocardiogram signals has attracted increasing attention. As the most dominant feature of the electrocardiogram signal, the QRS complex(i.e., the combination of ECG Q, R, and S waves) has been used for identification in some studies. This study aims to investigate the intra-individual stability of the QRS complex dynamics to assess its potential for human identification. The QRS complex dynamics are used as the unique feature to classify the QRS complex, which differs from the time/frequency domain features used in the literature. It is the fundamental feature of the QRS complex and contains the underlying information of the QRS complex. The dynamics of training QRS complexes are extracted and expressed as a constant radial basis function network by using deterministic learning. A set of estimators is constructed to represent the training QRS complexes using constant radial basis function networks. By comparing this set of estimators with the test QRS complex, a set of recognition errors is generated, and the average L_1 norms of the errors are taken as the similarity measure between the dynamics of the training QRS complexes and that of the test QRS complex. Therefore, the test QRS complex can be recognized according to the smallest error principle. The electrocardiogram is classified according to the vote of the test QRS complexes recognition results. A private database and PTB diagnostic ECG database are used to test the proposed method. Experimental results on the private database (PTB database) showed that the average identification accuracy was 96.12% (97.42%) for 5-fold cross-validation based on one-lead electrocardiogram and 99.50% (99.23%) for 2-fold cross-validation based on two-lead electrocardiogram, respectively. These show that the dynamics of the QRS complex are well-differentiated for different individuals.

INDEX TERMS Electrocardiogram, QRS complex, identity recognition, radial basis function networks, dynamics.

I. INTRODUCTION

In modern society, the application of identification in security systems is getting more and more attention. A combination lock is one of the most common and basic security systems. However, it has very limited security and can be easily cracked even with a variety of complex password policies (such as using a mix of numbers, letters, and special characters and changing passwords regularly) [1]. Security systems based on human biometrics (e.g., fingerprints, face, iris, hand geometry) and behavioral characteristics (e.g., gait, keystrokes, handwriting, voice) have been proposed to achieve higher security [2]. However, these features are either less reliable in terms of recognition accuracy (e.g., keystrokes, gait) or can be easily falsified (e.g., fingerprints can be copied through latex, voice can be recorded and played back on a recorder, irises can be faked with contact lenses printed with copied features, and faces can be artificially disguised) [3], [4]. As a result, researchers have been looking for new biometrics that are difficult to fake.

Electrocardiogram (ECG) is a graph of voltage versus time of the electrical activity of the heart using electrodes placed on the skin. It comprises three main components: P wave, QRS complex, and T wave. The QRS complex is the combination of Q, R, and S waves. Compared to other biological features such as face, fingerprints, gait, iris, palm print,

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sound, etc., ECG has proven to be the most promising biometric and stands out among most of the features that define biometric features [5], [6]. In recent years, ECG-based biometrics has attracted much attention from the scientific community, and a lot of studies have been conducted [7]–[14]. The comfort level for collecting ECG signals used for identity recognition has also evolved (e.g., using dry electrodes to collect ECG signals on the fingers, palm, or wrists) [15]–[17]. Moreover, preliminary progress has been made in several commercial applications [18], [19].

ECG-based identity recognition can go back to the pioneering works [20]–[22]. The main hypothesis of these studies is that the ECG signal contains enough information for a high-performance identification system [23]. ECG has the following characteristics that other biological features do not have: i) it is difficult to forge and can only be measured from living individuals [23], [24]; ii) it has good stability and reproducibility [20], [25], [26]; iii) it contains psychologically, physically, and clinically relevant information that may be valuable for some applications [23], [27] such as health monitoring, health evaluation, emotion recognition, etc.

In ECG-based identity recognition, the primary problem is to extract features that can realistically depict ECG signals. We can roughly divide the features used in the existing research into the following two categories: i) fiducial features that derived from characteristic points of ECG signals [20], [21], [24], [27], such as the temporal intervals and amplitude differences between these characteristic points (e.g., the RR interval); ii) non-fiducial features derived from segmented windows of ECG signals [28]–[30] without fiducial points (or only with the R peaks). Principal components, wavelet coefficients, and autocorrelation coefficients are some examples; iii) hybrid features that combine fiducial features with no-fiducial features to create the feature set [3], [31].

However, these static features do not adequately characterize ECG signals because ECG signals are inherently time-varying patterns with large morphological changes [32], [33]. From the perspective of pattern recognition, ECG-based identification is essentially a temporal pattern recognition problem. Existing classification methods developed for static patterns may not be the most suitable for ECG-based identification [33]. In [34], [35], it has been stated that time-varying pattern recognition methods should be fundamentally different from static pattern recognition methods. It is well known that the recognition of temporal patterns is one of the most difficult tasks in pattern recognition. Recently, a new algorithm, deterministic learning theory, has been proposed to deal with temporal patterns [35]–[37]. By using deterministic learning, the dynamics of temporal patterns can be accurately modeled and expressed in time-invariant form. This modeling result contains all the information about the temporal pattern. Therefore, it may be more suitable for recognizing those temporal patterns with large morphological changes (e.g., ECG, electroencephalogram) that are difficult to describe accurately with static features. Based on the time-invariant representation, Wang and Hill proposed a temporal pattern similarity measurement and a rapid recognition algorithm for temporal patterns in [37].

In this paper, we propose a new ECG-based method for identity recognition based on the QRS complex dynamics. The QRS complex usually appears as the center and most prominent part of the signal. It represents a single event, the depolarization of the left and right ventricles. Biometric identification based on the QRS complex can be advantageous because it provides the most relevant and unique information in the ECG signal, and it is the part of the ECG that is less sensitive to physical and emotional changes relative to other parts of the ECG signal [10], [38], [39]. Although the information on other parts of the ECG signal is missing, it also avoids negative effects on identity recognition performance due to the sensitivity of these parts to various noise disturbances. This may be more beneficial for identity recognition in cases where the ECG signal is subject to complex noise interference. This paper intends to conduct identity recognition research based on the QRS complex, which aims to investigate the intra-individual stability of the dynamics of the QRS complex to assess its potential for human identification.

Compared to existing ECG-based identity recognition studies, the proposed method has the following features: i) QRS complex dynamics is a holographic representation of QRS complex, and it can characterize various variations of the QRS complex more accurately; ii) the hard work in most of existing literature, finding suitable feature vectors for classification, is overcome by the proposed method; iii) the recognition of test QRS complexes not only needs not to extract any of its features (whether static features or dynamics) but also need not to directly compare the dynamics of the test and training QRS complexes by any form of numerical computation.

The rest of the paper is arranged as follows. Section II describes the proposed method. Section III describes the two databases used in this paper. Section IV shows the experimental results. Sections V and VI present the discussion and conclusions, respectively.

II. METHODS

A. DETERMINISTIC LEARNING

Deterministic learning theory [36] is a promising technology proposed for modeling and recognizing temporal patterns. It was developed mainly based on the theory and concepts of adaptive control, system identification, and radial basis function (RBF) networks. For a temporal pattern, which is defined as a periodic or recurrent trajectory generated by dynamic systems, the dynamics of the temporal pattern can be accurately modeled and stored as constant RBF networks, a time-invariant and spatially distributed manner [35], [37].

Consider a general nonlinear dynamic system of the following form:

$$\dot{u} = G(u; p), \quad u(t_0) = u_0 \tag{1}$$

where $G(u; p) = [g_1(u; p), \ldots, g_n(u; p)]^T$ is a continuous but unknown nonlinear function vector, $u = [u_1, \ldots, u_n]^T \in R^n$

is the system state, p is a vector of constant parameters, respectively.

To accurately model the unknown system dynamics $G(u; p)$ underlying a temporal pattern φ_ζ (i.e., a periodic or recurrent orbit), the following state estimator is constructed:

$$\dot{\hat{u}}_i = -d_i(\hat{u}_i - u_i) + \hat{W}_i^T S_i(u), \tag{2}$$

where $\hat{u}_i$ is system state of state estimator, u is the state of system (1), $d_i > 0$ is the design constant, and the RBF networks $\hat{W}_i^T S_i(u)$ for approximating $g_i(u; p)$, $\hat{W}_i = [w_{i1}, \ldots, w_{iN}]^T \in R^N$ and $S_i(u) = [s_{i1}(\| u - \xi_1 \|), \ldots, s_{iN}(\| u - \xi_N \|)]^T$, with $s_{ij}(\|u-\xi_j\|) = exp[\frac{-(u-\xi_j)^T(u-\xi_j)}{\eta^2}]$ being a Gaussian function, $\xi_j (j = 1, 2, \cdots, N)$ being distinct points in state space and η is the width of the receptive field.

From equations (1) and (2), the derivative of the state estimation error $\tilde{u}_i = \hat{u}_i - u_i$ satisfies the following equation:

$$\begin{aligned}\dot{\tilde{u}}_i &= -d_i\tilde{u}_i + \hat{W}_i^T S_i(u) - g_i(u; p) \\ &= -d_i\tilde{u}_i + \tilde{W}_i^T S_i(u) - e_i,\end{aligned} \tag{3}$$

where $\tilde{W}_i = \hat{W}_i - W_i^*$, W_i^* is the ideal constant weight vector, and $e_i = g_i(u; p) - W_i^{*T} S_i(u)$ is the ideal approximation error.

The weight estimate $\hat{W}_i$ is updated by the following Lyapunov-based learning law:

$$\dot{\hat{W}}_i = -\Gamma_i S_i(u)\tilde{u}_i - \sigma_i \Gamma_i \hat{W}_i, \tag{4}$$

where $\sigma_i > 0$ is a small constant parameter, $\Gamma_i = \Gamma_i^T > 0$.

It has been shown that for almost all temporal patterns the unknown dynamics within them can be accurately identified using deterministic learning [35]–[37] and expressed as follows:

$$\begin{aligned}g_i(\varphi_\zeta; p) &= \hat{W}_i^T S_i(\varphi_\zeta) + e_{\zeta i} \\ &= \bar{W}_i^T S_i(\varphi_\zeta) + e_{\zeta i1},\end{aligned} \tag{5}$$

where $\bar{W}_i = mean_{t\in[t_s,t_f]}\hat{W}_i(t)$, $mean$ is the arithmetic mean, $[t_s, t_f]$ is a short time after the weight is converged, $e_{\zeta i1} = O(e_{\zeta i}) = O(e_i)$ is the actual modeling error.

That is, the temporal pattern can be represented by a constant RBF network $\bar{W}_i^T S_i(\varphi_\zeta)$, which is a time-invariant neural network approximation of the system dynamics $g_i(\varphi_\zeta; p)$. Moreover, since information about the system dynamics is stored in many neurons, this representation $\bar{W}_i^T S_i(\varphi_\zeta)$ is also spatially distributed.

B. MECHANISM FOR IDENTITY RECOGNITION

1) PREPROCESSING

ECG is susceptible to various artifacts and noises during the measurement process, such as electromyography interference and power frequency interference. These noises will affect the accurate analysis and interpretation of ECG and then affect the recognition and classification performance of ECG. Therefore, the preprocessing of ECG signals is very important and necessary for related research on ECG identification and classification.

The filter for noise removal of raw ECG signals consists of the following steps [40]: 1) bandpass filter (5-15 Hz); 2) derivative filter to highlight the QRS complex; 3) Signal is squared; 4) Signal is averaged of noise (0.150 seconds length). More details and Matlab code for this filter can be found in [40].

To unify the statistical distribution of the QRS complexes and make them more comparable, the filtered ECGs are normalized to zero mean and unit variance by subtracting the mean and dividing by the standard deviation. This also facilitates the to unify the distribution of neurons in the RBF network.

2) MODELING OF QRS COMPLEX

As a comprehensive manifestation of cardiac electrical activity on the surface of the human body, the ECG signal is essentially a temporal pattern produced by the extremely complex high-dimensional continuous nonlinear dynamics system of cardiac electrical activity. We can express the dynamic system as follows:

$$\dot{e}(t) = f(e(t)) \tag{6}$$

where $e(t) = [e_1(t), \ldots, e_n(t)]^T$ is the system state and represents the ECG signal, n is the number of the leads, $f(e(t)) = [f_1(e(t)), \ldots, f_n(e(t))]^T$ is the system dynamics that represents the cardiac electrical activity, an unknown nonlinear function vector. It is clear that $e(t)$ is completely determined by system dynamics $f(e(t))$. The accurate identification of $f(e(t))$ will be important for studies related to ECG recognition and classification.

Construct the following dynamic model to identify the dynamics $f_i(e(t))(i = 1, 2, \cdots, n)$:

$$\dot{\hat{e}}_i(t) = -a_i(\hat{e}_i(t) - e_i(t)) + \hat{W}_i^T S_i(e(t)) \tag{7}$$

where $\hat{e}_i(t)$ is the estimation of $e_i(t)$ in the dynamic system (6), $0 < |a_i| < 1$ is a design constant, and the RBF networks $\hat{W}_i^T S_i(e(t))$ is used to approximate $f_i(e(t))$.

The weight estimate $\hat{W}_i$ is updated by the following update law:

$$\dot{\hat{W}}_i = \dot{\tilde{W}}_i = -\Gamma(S_i(e(t))\tilde{e}_i(t) + \sigma_i\hat{W}_i) \tag{8}$$

where $\Gamma_i = \Gamma_i^T > 0$, $\tilde{e}_i(t) = \hat{e}_i(t) - e_i(t)$, and $\sigma_i > 0$ is a small value.

Consider the system consisiting of the nonlinear dynamic system (6), the dynamic model (7), and the weight update law (8). It has been proven that for almost any temporal pattern, the unknown dynamics along the temporal pattern trajectory can be accurately modeled based on the deterministic learning [35]–[37]. Since the ECG signal $e_i(t)$ is quasi-periodic signal (a type of recurrent trajectory), the following conclusions can be drawn: (i) The state estimation error $\tilde{e}_i(t) = \hat{e}_i(t) - e_i(t)$ converges to zero; (ii) $f_i(e(t))$ can be represented as follows:

$$f_i(e(t)) = \bar{W}_i^T S_i(e(t)) + \epsilon_i, \tag{9}$$

where $\bar{W}_i = mean_{t\in[t_l,t_r]}\hat{W}_i$, *mean* is the arithmetic mean, $[t_l, t_r]$ is a short time after the weight estimate is converged, and ϵ_i is the approximation error that can be arbitrarily small.

In this way, we have achieved an accurate modeling of ECG dynamics, which is represented in the form of a constant RBF network $\bar{W}_i$, a time-invariant form. Since it stores the basic information in neurons distributed along the state trajectory of ECG, the representation is also spatially distributed. Thus, this expression contains both state information and dynamic information of ECG. On this basis, we can extract the QRS complex dynamics according to the start and end points of the QRS complex in the ECG signal.

Since there have been many studies on the extraction of QRS complexes, here we extract QRS complexes directly based on the position of the *R*-peak, which is detected by using Pan-Tompkins algorithm proposed in [41]. To ensure that all QRS complexes have the same length, we extract QRS complexes empirically by choosing a window of -160 *ms* to 340 *ms* around the *R*-peak. As the sampling frequency is 500 HZ, each extracted QRS complex contains 251 samples. Denote the start and end points of the QRS complex as k_Q and k_S, respectively. Then, the QRS complex can be represented as $e(t)|_{t=k_Q}^{t=k_S}$. For simplicity, denote $e(t)|_{t=k_Q}^{t=k_S}$ as e_{qrs} in the following text. Then, we can represent the dynamics of the QRS complex as follows:

$$f(e(t))|_{t=k_Q}^{t=k_S} \approx \bar{W}^T S(e_{qrs}) \tag{10}$$

Figures 1 and 2 show the modeling results of one-lead (lead I) QRS complexes and two-lead (leads V2 and V3) QRS complexes for 4 subjects, respectively. In these figures, different colored lines are the modeling results of different QRS complexes, which are extracted from a 20-second ECG without selection. We can see that: i) the QRS complexes dynamics of the same subject are very similar in morphology; ii) the QRS complexes dynamics of different subjects differ greatly from each other. These show that the QRS complex dynamics can distinguish individuals.

Remark 1: The subscript of the QRS complexes modeling results of different leads is consistent with their order in standard 12-lead ECG. Figure 1 shows the modeling results of QRS complexes extracted from lead I, which is the first lead in the standard 12-lead ECG, so the y-axis is $\bar{W}_1^T\ S_1(e_{qrs})$. Figure 2 shows the modeling results of QRS complexes extracted from leads V2 and V3, which are the eighth and ninth leads in the standard 12-lead ECG respectively, so the x-axis is $\bar{W}_8^T\ S_8(e_{qrs})$ corresponding to lead V2, and the y-axis is $\bar{W}_9^T\ S_9(e_{qrs})$ corresponding to lead V3.

3) MECHANISM FOR SUBJECT IDENTITY RECOGNITION

Based on the modeling of the QRS complexes dynamics of the ECG signals in the training set, for an ECG signal to be recognized, first extract its QRS complexes (i.e., test QRS complexes), and then build a set of state estimators based on the modeling results of the training QRS complexes:

$$\dot{\hat{e}}_{qrs}^k = -B(\hat{e}_{qrs}^k - e_{qrs}) + \bar{W}^{k^T} S(e_{qrs}) \tag{11}$$

where $\hat{e}_{qrs}^k$ is the system state, e_{qrs} is the test QRS complex state, $B = diag\{b_1, \ldots, b_n\}$ is a diagonal matrix, $b_i > 0$ $(i = 1, \ldots, n)$ is the design constant, and $\bar{W}^{k^T}$ is constant neural network weights of the k-th training QRS complex modeling result. Then we can obtain the following error system corresponding to the dynamic model (11) and the test QRS complex:

$$\dot{\tilde{e}}_{qrs}^k = -B\tilde{e}_{qrs}^k + \bar{W}^{k^T} S(e_{qrs}) - f(e_{qrs}) \tag{12}$$

where $\tilde{e}_{qrs}^k$ is the tracking error between the k-th training QRS complex and the test QRS complex. According to the dynamic pattern recognition theory proposed in [37], the state tracking error $\tilde{e}_{qrs}^k$ is approximately proportional to the dynamics difference between the test and the training QRS complexes. Thus, the state tracking error can be used as a measure of the similarity between the test and the training QRS complexes. The test QRS complex can be classified according to the principle of minimum errors. Each test QRS complex classification result is a vote for the candidate subject of the test ECG signal classification, which is elected by a majority of votes (i.e., the candidate with the most votes is the test ECG classification result). For example, if a test ECG signal contains 20 QRS complexes, of which 10, 6, and 4 QRS complexes are classified in the category of subjects A, B, and C, respectively, then this test ECG signal is classified in the category of subject A.

Through the above description, we can summarize the proposed method for identity recognition as the following steps:

Step 1: Extract the dynamic features of the training QRS complexes and store it with the corresponding identity labels to build an identity pattern library;
Step 2: Extract the QRS complexes of the test ECG signal;
Step 3: Construct a set of state estimators based on the training QRS complexes modeling results as (11), where the RBF networks input is the test QRS complex's state;
Step 4: A set of state errors can be obtained according to the error system as (12), compute the average L_1 norm of the state estimation error;
Step 5: Classify the test QRS complex according to the principle of the minimum error;
Step 6: Vote according to the classification results of all test QRS complexes to achieve the classification of the test ECG, i.e., identity recognition;

Figure 3 illustrates the general flowchart of the proposed method.

The performance of the proposed method was evaluated by the classification accuracy of the QRS complex, the Macro-F1 score of the QRS complex classification, and the identification accuracy of ECG. The classification accuracy of the QRS complex is defined as

$$Acc_Q = N_Q/N_{te} \times 100\%$$

where N_Q and N_{te} are the number of correctly classified test QRS complexes and the total number of test QRS

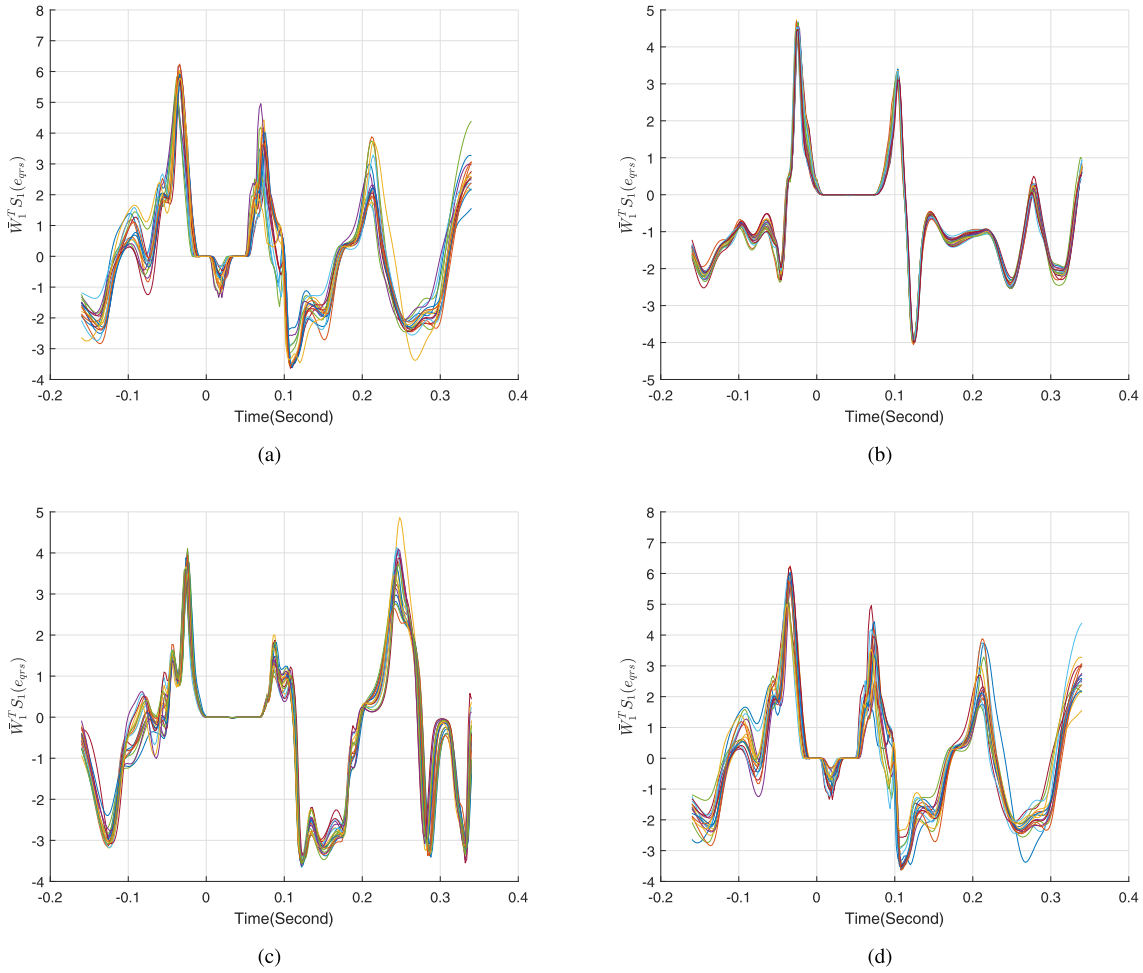

FIGURE 1. The modeling results of QRS complexes extracted from lead I of 4 subjects. Different colored lines are the modeling results of different QRS complexes, which are extracted from a 20-second ECG without selection.

complexes, respectively. The identification accuracy of test ECG signals is defined as

$$Acc_E = N_E/N_{tE} \times 100\%$$

where N_E and N_{tE} are the number of correctly classified test ECG signals and the total number of test ECG signals, respectively. The Macro-F1 score is calculated by averaging the F1 scores for each individual category:

$$F1 = 2 \times \frac{precision \times recall}{precision + recall}$$

$$precision = \frac{TP}{TP + FP}$$

$$recall = \frac{TP}{TP + FN}$$

where TP, FP, and FN are the number of the true positive set, the false positive set, and the false negative set, respectively.

Remark 2: In practice, the number of training QRS complexes in the pattern library depends on the number of subjects to be identified. The recognition of test QRS complexes not only needs not to extract any of its features but also need not to directly compare the dynamics of the test and training QRS complexes by any form of numerical computation. It reduces the amount of computation to a greater extent. The rapid increase in computing power (e.g., GPU parallel computing, cloud computing) also guarantees the real-time nature of the proposed method. In addition, considering that ECG signals may change with age, regular updates to the ECG in the pattern library may be necessary. In future work, we will conduct further research on the application of the proposed method.

III. DATABASES

We believe that the difference in ECG signals of the healthy subjects in the same age group is much smaller than that of the subjects with various heart diseases in the different age groups. The identity recognition of healthy people in the same age group can better demonstrate the effectiveness of the proposed method. Two ECG databases of healthy subjects are used to evaluate the proposed method. The first database is a private database called the GGH database, which contains ECGs from 94 healthy subjects. The second database is a subset of the PTB diagnostic ECG database, which contains ECGs from 52 healthy subjects.

The GGH database was collected from a local hospital (General Hospital of Southern Theatre Command). The ethics committee approved the study, and the subjects were informed and gave verbal consent to our study but not to

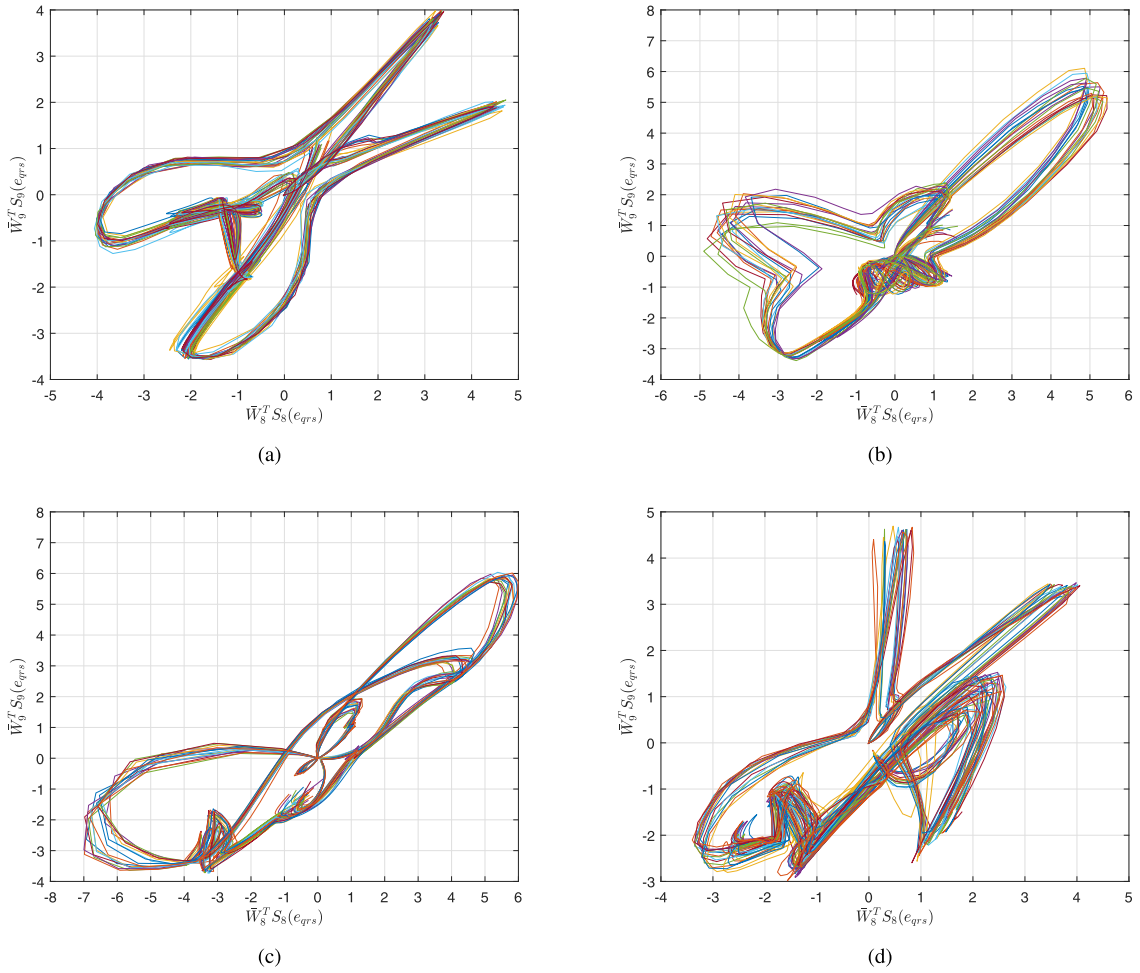

FIGURE 2. The modeling results of QRS complexes extracted from leads V2 and V3 of 4 subjects. Different colored lines are the modeling results of different QRS complexes, which are extracted from a 20-second ECG without selection.

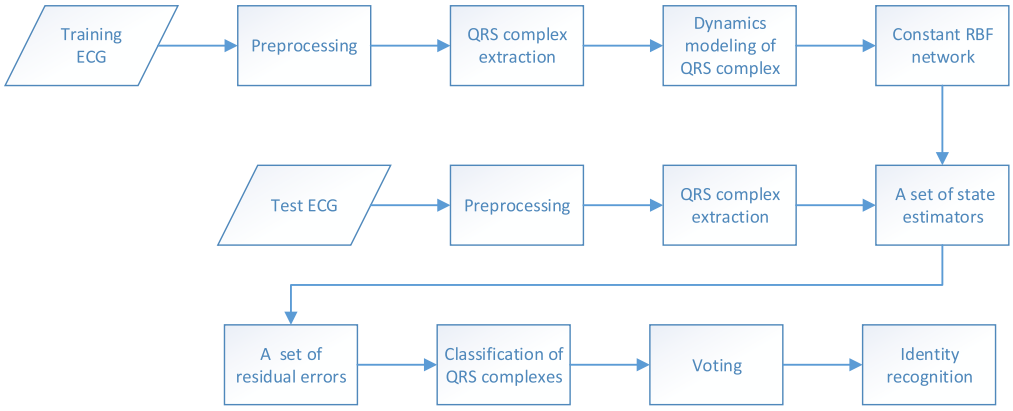

FIGURE 3. The flow diagram of the proposed method.

our disclosure of the data. The inclusion criteria are as follows: aged 18-45 years old, physical and clinical examination report with normal findings; no history of cardiovascular disease or any other disease. A total of 94 subjects were enrolled with informed consent, and two 12-lead ECGs of 20 seconds in length were collected from each subject. The two ECGs for each subject were measured at two different sessions of the same day, with a two-hour interval. The subjects remained supine for 20 seconds before the data collection. That is, the GGH database contains 188 20-second standard 12-lead ECG records. The equipment used to measure ECG records is an ECG sampling module named AIKD812-256 (Changsha Aikang Electronics Company, Ltd., Changsha, China), with a sampling rate of 500HZ and a resolution of 12-bit.

The PTB Diagnostic ECG Database is a public database and has been used by many studies on biometric recognition

TABLE 1. The experimental results based on one-lead ECG. N_Q and N_E are the number of correctly classified test QRS complexes and correctly identified test ECG signals, respectively. Acc_Q and Acc_E are the classification accuracy of the test QRS complexes and identification accuracy of the test ECG signals, respectively.

Lead	GGH database					PTB database				
	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E
I	1465	78.76%	0.8818	88	93.62%	829	80.96%	0.8948	50	96.15%
	1462	79.16%	0.8837	88	93.62%	823	80.69%	0.8931	49	94.23%
II	1652	88.82%	0.9408	90	95.74%	914	89.26%	0.9433	51	98.08%
	1648	89.23%	0.9431	90	95.74%	910	89.22%	0.9430	51	98.08%
III	1662	89.35%	0.9438	90	95.74%	904	88.28%	0.9378	51	98.08%
	1660	89.88%	0.9467	90	95.74%	915	89.71%	0.9458	52	100.00%
avR	1513	81.34%	0.8971	88	93.62%	830	81.05%	0.8953	50	96.15%
	1508	81.65%	0.8990	88	93.62%	828	81.18%	0.8961	50	96.15%
avL	1448	77.85%	0.8755	87	92.55%	825	80.57%	0.8924	50	96.15%
	1443	78.13%	0.8772	88	93.62%	826	80.98%	0.8949	50	96.15%
avF	1635	87.90%	0.9356	90	95.74%	897	87.60%	0.9339	51	98.08%
	1627	88.09%	0.9367	90	95.74%	900	88.24%	0.9375	51	98.08%
V1	1663	89.41%	0.9441	91	96.81%	910	88.87%	0.9411	51	98.08%
	1660	89.88%	0.9467	90	95.74%	914	89.61%	0.9452	52	100.00%
V2	1654	88.92%	0.9414	90	95.74%	905	88.38%	0.9383	52	100.00%
	1650	89.33%	0.9436	91	96.81%	909	89.12%	0.9425	52	100.00%
V3	1596	85.81%	0.9236	89	94.68%	889	86.82%	0.9295	51	98.08%
	1590	86.09%	0.9253	89	94.68%	878	86.08%	0.9252	51	98.08%
V4	1481	79.62%	0.8865	89	94.68%	820	80.08%	0.8894	50	96.15%
	1477	79.97%	0.8887	89	94.68%	815	79.90%	0.8883	50	96.15%
V5	1515	81.45%	0.8978	88	93.62%	831	81.15%	0.8959	50	96.15%
	1507	81.59%	0.8986	88	93.62%	833	81.67%	0.8991	50	96.15%
V6	1411	75.86%	0.8627	87	92.55%	794	77.54%	0.8735	49	94.23%
	1405	76.07%	0.8641	87	92.55%	789	77.35%	0.8723	49	94.23%
Average	1555.5	83.92%	0.9118	89.0	94.64%	862.0	84.34%	0.9145	50.5	97.20%

methods based on ECG signals. It contains 549 recordings from 290 subjects (52 healthy subjects and 238 patients) with different time durations of around 2 minutes. Each ECG recording consists of standard 12-lead ECG signals and three Frank leads ECG signals. For comparison with other methods, we selected the ECG signals of the 52 healthy subjects, which are commonly used in other studies. 14 of these 52 healthy subjects had more than two ECG recordings, while the others had only one ECG recording. For these 14 healthy subjects, we selected two of the ECG recordings, each lasting 20 seconds. For healthy subjects with only one ECG recording, we intercepted two ECG signals of 20 seconds' length from this ECG recording. That is, the subset of the PTB database contains 104 ECG signals from 52 healthy subjects, each of whom had two ECG signals of 20 seconds duration. For the sake of simplicity, we will refer to this subset of the PTB database as the PTB-H database in the following context.

Remark 3: The GGH database cannot be fully disclosed, both because it is not authorized by the subject and because of the sensitivity of the subject's identity. Interested researchers can contact us for access to this database.

IV. RESULTS

A. EXPERIMENTS BASED ON ONE-LEAD ECG

To reduce the bias in the selection of training and testing sets for QRS complexes classification, the k-fold cross-validation method is used in the study. The average accuracy of classification is used as a benchmark for comparison. To facilitate direct comparison with relevant studies, we conducted the same experiments based on the PTB-H and GGH databases, respectively.

As each subject has two 12-lead ECG records in the GGH database and PTB-H database, we first use the 2-fold cross-validation method to test the proposed method. In the experiments based on the GGH database (PTB-H database), the 188 (104) ECG records are divided into two subsets, each subset containing 94 (52) ECG records from 94 (52) subjects, one for each subject.

TABLE 2. The experimental results of 5-fold cross-validation experiments on lead I. N_Q and N_E are the number of correctly classified test QRS complexes and correctly identified test ECG signals, respectively. Acc_Q and Acc_E are the classification accuracy of the test QRS complexes and identification accuracy of the test ECG signals, respectively.

Fold	GGH database					PTB database				
	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E
Fold 1	626	93.43%	0.9660	179	95.21%	380	93.83%	0.9682	100	96.15%
Fold 2	635	94.78%	0.9732	181	96.28%	388	95.80%	0.9785	102	98.08%
Fold 3	632	94.33%	0.9708	180	95.74%	379	93.58%	0.9668	99	95.19%
Fold 4	644	96.12%	0.9802	183	97.34%	389	96.05%	0.9799	103	99.04%
Fold 5	621	92.69%	0.9621	178	94.68%	382	94.32%	0.9708	102	98.08%
Average	631.6	94.27%	0.9705	180.2	95.85%	383.6	94.72%	0.9728	101.2	97.31%

TABLE 3. The average accuracy of the 5-fold cross-validation experiments on one-lead ECG. Acc_Q and Acc_E are the classification accuracy of the test QRS complexes and the identification accuracy of the test ECG signals, respectively.

Lead	GGH database			PTB database		
	Acc_Q	Macro-F1 score	Acc_E	Acc_Q	Macro-F1 score	Acc_E
I	94.27%	0.9705	95.85%	94.72%	0.9729	97.31%
II	96.08%	0.9891	95.96%	95.46%	0.9768	97.50%
III	96.49%	0.9934	97.34%	95.85%	0.9788	98.46%
avR	95.20%	0.9801	96.28%	95.51%	0.9770	97.88%
avL	94.90%	0.9770	96.06%	95.16%	0.9752	97.69%
avF	95.09%	0.9790	96.27%	95.36%	0.9762	97.88%
V1	96.60%	0.9945	97.34%	96.35%	0.9814	98.08%
V2	96.19%	0.9903	95.43%	96.05%	0.9799	97.12%
V3	96.41%	0.9925	96.27%	96.25%	0.9809	97.31%
V4	94.49%	0.9728	95.96%	94.77%	0.9731	96.92%
V5	95.31%	0.9812	95.47%	95.56%	0.9773	96.54%
V6	93.79%	0.9656	95.21%	94.42%	0.9713	96.35%
Average	95.41%	0.9822	96.12%	95.46%	0.9767	97.42%

The results of the 2-fold cross-validation experiments are shown in Table 1. We can see that in the experiments based on the GGH database (PTB-H database): the classification accuracy of QRS complexes is between 75.86% and 89.88% (between 77.35% and 89.71%), and the average accuracy is 83.92% (84.34%); the Macro-F1 score is between 0.8627 and 0.9467 (between 0.8723 and 0.9458), and the average Macro-F1 score is 0.9118 (0.9145); the identification accuracy of test ECG (i.e., identity recognition) is between 92.55% and 96.81% (between 94.23% and 100%), and the average accuracy is 94.64% (97.20%). The highest classification accuracy of QRS complexes and identification accuracy of test ECG are the experiments on lead V1 and lead III, and the lowest accuracy is the experiment on lead V6.

We further test the generalization ability of the proposed method on one-lead ECG using a 5-fold cross-validation method. To be precise, in each fold experiment, 20% of the QRS complexes of each ECG signal are selected as the test pattern, and the rest is used as the training pattern. That is, 20% of each original ECG record is used as a test pattern, and the test sets for the GGH database and the PTB-H database comprised 188 and 104 processed ECG records, respectively.

The results of the 5-fold cross-validation experiments on lead I are shown in Table 2 as an example. For the experiments based on the GGH database (PTB-H database): the classification accuracy of the QRS complex is between 92.69% and 96.12% (between 93.58% and 96.05%), and the average accuracy is 94.27% (94.72%); the Macro-F1 score is between 0.8627 and 0.9467 (between 0.8723 and 0.9458), and the average Macro-F1 score is 0.9118 (0.9145); the classification accuracy of test ECG is between 94.68% and 97.34% (between 95.19% and 99.04%), the average accuracy is 95.85% (97.31%), respectively. The average accuracies of the 5-fold cross-validation experiments on the 12 leads are shown in Table 2.

In the 5-fold cross-validation experiments, the best classification performance was obtained based on lead III and lead V1, and the worst classification performance was obtained based on lead V6. These are the same as the 2-fold cross-validation experiments. However, since the number of training QRS complexes is 4 times that of the test

TABLE 4. Experimental results of group A. N_Q and N_E are the number of correctly classified test QRS complexes and correctly identified test ECG signals, respectively. Acc_Q and Acc_E are the classification accuracy of the test QRS complexes and identification accuracy of the test ECG signals, respectively.

Lead	GGH database					PTB database				
	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E
I and II	1669	89.74%	0.9459	93	98.94%	909	88.77%	0.9405	51	98.08%
	1667	90.28%	0.9489	93	98.94%	921	90.29%	0.9490	51	98.08%
I and III	1745	93.84%	0.9682	94	100.00%	966	94.34%	0.9709	52	100.00%
	1744	94.44%	0.9714	94	100.00%	965	94.61%	0.9723	52	100.00%
I and aVR	1637	88.04%	0.9364	93	98.94%	907	88.57%	0.9394	51	98.08%
	1632	88.36%	0.9382	93	98.94%	911	89.31%	0.9435	52	100.00%
I and aVL	1837	98.78%	0.9939	94	100.00%	1009	98.54%	0.9926	52	100.00%
	1829	99.05%	0.9952	94	100.00%	1011	99.12%	0.9956	52	100.00%
I and aVF	1685	90.60%	0.9507	93	98.94%	928	90.63%	0.9508	51	98.08%
	1681	91.03%	0.9530	94	100.00%	935	91.67%	0.9565	52	100.00%
II and III	1609	86.50%	0.9276	92	97.87%	889	86.82%	0.9295	50	96.15%
	1602	86.72%	0.9289	92	97.87%	903	88.53%	0.9392	51	98.08%
II and aVR	1584	85.14%	0.9197	92	97.87%	888	86.72%	0.9289	50	96.15%
	1581	85.57%	0.9222	92	97.87%	891	87.35%	0.9325	50	96.15%
II and aVL	1701	91.45%	0.9553	93	98.94%	933	91.11%	0.9535	51	98.08%
	1699	91.99%	0.9583	93	98.94%	939	92.06%	0.9587	52	100.00%
II and aVF	1542	82.92%	0.9066	91	96.81%	865	84.47%	0.9158	50	96.15%
	1546	83.68%	0.9111	91	96.81%	857	84.02%	0.9132	50	96.15%
III and aVR	1618	87.01%	0.9305	93	98.94%	901	87.99%	0.9361	51	98.08%
	1611	87.23%	0.9318	93	98.94%	897	87.94%	0.9358	51	98.08%
III and aVL	1676	90.08%	0.9478	94	100.00%	928	90.63%	0.9508	51	98.08%
	1672	90.51%	0.9502	94	100.00%	929	91.08%	0.9533	52	100.00%
III and aVF	1571	84.45%	0.9157	92	97.87%	887	86.62%	0.9283	51	98.08%
	1572	85.10%	0.9195	92	97.87%	879	86.18%	0.9258	51	98.08%
aVR and aVL	1764	94.86%	0.9736	94	100.00%	954	93.16%	0.9646	52	100.00%
	1758	95.18%	0.9753	94	100.00%	961	94.22%	0.9702	52	100.00%
aVR and aVF	1590	85.48%	0.9217	92	97.87%	889	86.82%	0.9295	50	96.15%
	1588	85.97%	0.9246	92	97.87%	881	86.37%	0.9269	50	96.15%
aVL and aVF	1695	91.11%	0.9535	93	98.94%	934	91.21%	0.9540	52	100.00%
	1692	91.60%	0.9562	93	98.94%	931	91.27%	0.9544	52	100.00%
Average	1659.9	89.56%	0.9444	92.9	98.94%	919.9	90.01%	0.9471	51.2	98.40%

QRS complexes, the difference in classification performance based on different leads is smaller than that of the 2-fold cross-validation experiments.

B. EXPERIMENTS BASED ON TWO-LEAD ECG

In this subsection, we will test the proposed method on two-lead ECG. Since no standard indicates which lead combination is optimal, we will conduct two sets of experiments: experiment group A and experiment group B. In the experiment group A, the two leads ECG is selected from lead I, lead II, lead III, lead aVR, lead aVL, and lead aVF, a total of 15 two-lead combinations. In the experiment group B, the two leads ECG is selected from lead V1, lead V2, lead V3, lead V4, lead V5, and lead V6, also a total of 15 two-lead combinations.

Similar to experiments based on one-lead ECG, 2-fold cross-validation experiments are conducted on each two-lead combination, where one ECG record of each subject is still used as the training pattern, and another ECG record is used as the test pattern. The results of the experiment group A and experiment group A are shown in Table 4 and Table 5, respectively.

From the experiment results, we can see that the classification performance on two-lead ECG is improved compared with one-lead ECG. For the GGH database, in the 2-fold cross-validation experiments of experiment group A

TABLE 5. The experimental results of experiment group B. N_Q and N_E are the number of correctly classified test QRS complexes and correctly identified test ECG signals, respectively. Acc_Q and Acc_E are the classification accuracy of the test QRS complexes and identification accuracy of the test ECG signals, respectively.

Combination of Leads	GGH database					PTB database				
	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E	N_Q	Acc_Q	Macro-F1 score	N_E	Acc_E
V1 and V2	1712	92.04%	0.9586	93	98.94%	935	91.31%	0.9546	51	98.08%
	1705	92.31%	0.9600	93	98.94%	942	92.35%	0.9602	52	100.00%
V1 and V3	1807	97.15%	0.9855	94	100.00%	978	95.51%	0.9770	52	100.00%
	1797	97.29%	0.9863	94	100.00%	971	95.20%	0.9754	52	100.00%
V1 and V4	1765	94.89%	0.9738	94	100.00%	970	94.73%	0.9729	52	100.00%
	1757	95.13%	0.9750	94	100.00%	965	94.61%	0.9763	52	100.00%
V1 and V5	1722	92.58%	0.9615	94	100.00%	944	92.19%	0.9594	52	100.00%
	1716	92.91%	0.9632	94	100.00%	947	92.84%	0.9629	52	100.00%
V1 and V6	1713	92.10%	0.9589	94	100.00%	950	92.77%	0.9625	52	100.00%
	1708	92.47%	0.9609	94	100.00%	949	93.04%	0.9639	52	100.00%
V2 and V3	1835	98.66%	0.9933	94	100.00%	1001	97.75%	0.9886	52	100.00%
	1832	99.19%	0.9959	94	100.00%	1004	98.43%	0.9921	52	100.00%
V2 and V4	1730	93.01%	0.9638	94	100.00%	970	94.73%	0.9729	52	100.00%
	1722	93.23%	0.9650	94	100.00%	964	94.51%	0.9718	52	100.00%
V2 and V5	1741	93.60%	0.9669	94	100.00%	972	94.92%	0.9739	52	100.00%
	1733	93.83%	0.9682	94	100.00%	966	94.71%	0.9728	52	100.00%
V2 and V6	1813	97.47%	0.9872	94	100.00%	998	97.46%	0.9871	52	100.00%
	1809	97.94%	0.9896	94	100.00%	1000	98.04%	0.9901	52	100.00%
V3 and V4	1741	93.60%	0.9669	94	100.00%	954	93.16%	0.9646	52	100.00%
	1737	94.04%	0.9693	94	100.00%	953	93.43%	0.9660	52	100.00%
V3 and V5	1784	95.91%	0.9791	94	100.00%	967	94.43%	0.9714	52	100.00%
	1781	96.43%	0.9818	94	100.00%	973	95.39%	0.9764	52	100.00%
V3 and V6	1821	97.90%	0.9894	94	100.00%	999	97.56%	0.9876	52	100.00%
	1814	98.21%	0.9910	94	100.00%	1005	98.53%	0.9926	52	100.00%
V4 and V5	1568	84.30%	0.9148	92	97.87%	909	88.77%	0.9405	50	96.15%
	1560	84.46%	0.9158	92	97.87%	901	88.33%	0.9380	50	96.15%
V4 and V6	1692	90.97%	0.9527	93	98.94%	922	90.04%	0.9476	51	98.08%
	1684	91.17%	0.9582	93	98.94%	918	90.00%	0.9474	51	98.08%
V5 and V6	1538	82.69%	0.9052	91	96.81%	864	84.38%	0.9153	50	96.15%
	1534	83.05%	0.9074	91	96.81%	855	83.82%	0.9120	49	94.23%
Average	1729.0	93.29%	0.9648	93.5	99.50%	955	93.43%	0.9658	51.6	99.23%

(experiment group B), the classification accuracy of QRS complexes is between 82.92% and 99.05% (between 82.69% and 99.19%), and the average accuracy is 89.56% (93.29%), the Macro-F1 score is between 0.9066 and 0.9952 (between 0.9052 and 0.9959), and the average Macro-F1 score is 0.9444 (0.9648), the classification accuracy of test ECG (i.e., identity recognition) is between 96.81% and 100% (between 96.81% and 100%), and the average accuracy is 98.94% (99.50%). For the PTB-H database, in the 2-fold cross-validation experiments of experiment group A (experiment group B): the classification accuracy of QRS complexes is between 84.02% and 99.12% (between 83.82% and 98.53%), and the average accuracy is 90.01% (93.43%); the Macro-F1 score is between 0.9132 and 0.9956 (between 0.9120 and 0.9926), and the average Macro-F1 score is 0.9471 (0.9658); the classification accuracy of test ECG is between 96.15% and 100% (between 94.23% and 100%), and the average accuracy is 98.40% (99.23%).

Remark 4: Due to the high average classification accuracy of 98.94% (99.5%) for the two-lead ECG in the 2-fold cross-validation experiments, no other multi-fold cross-validation experiments will be performed here.

V. DISCUSSION

In the paper, we propose a novel method for identity recognition via the QRS dynamics of ECG. The QRS

TABLE 6. Summary of the key features of different studies. NS: Number of subjects. NL: Number of leads.

Reference	Year	Database and NS	NL	Features	Technique	Accuracy
Jung et al. [47]	2017	ptbdb, 50		AC, DCT	NN, SVM, LDA	99.40%
Pal et al. [48]	2018	ptbdb, 100	1	Interval, amplitude, angle, and area fiducial fetures	PCA, KPCA, EDIST	97.10%
Labai et al. [10]	2019	ptbdb, 52	3		1D CNN, softmax, HDIST	100.00%
Zhang et al. [43]	2019	ptbdb, 234	1		CNN, NNC, SVM	99.5%(SVM) 98.7%(NNC)
Hanilcci et al. [49]	2019	ptbdb, 42	1	AC, DCT, cepstral features	MFCC, 2D CNN	90.48%
Alotaiby et al. [50]	2019	ptbdb, 200	1	CSP features	CSP, SVM	98.93% (lead V3) 95.15% (lead I)
Proposed		ptbdb, 52	1	dynamics	DL	AA: 97.20% (2F)
						AA: 97.42% (5F)
			2			AA: 98.40% (GA)
						AA: 99.23% (GB)
		Private, 94	1	dynamics	DL	AA: 94.64% (2F)
						AA: 96.12% (5F)
			2			AA: 98.94% (GA)
						AA: 99.50% (GB)

Abbreviations of features and techniques
DL: Deterministic learning; AC: Autocorrelation coefficients; DCT: Discrete cosine transform; EDIST: Euclidean distance; HDIST: Hamming distance; DC: Discrimination coefficient; KPCA: Kernel principal components analysis; CNN: Convolutional neural network; NNC: Nearest neighbor classifier; CSP: common spatial pattern; MFCC: Mel-frequency cepstral coefficients.
Others
AA: average accuracy; 2F: 2-fold cross-validation experiments; 5F: 2-fold cross-validation experiments; GA: experiment group A; GB: experiment group B;

complexes are first classified, and then the test ECG is classified according to the voting of the QRS classification result. Thus, the focus of the proposed method is the classification of the QRS complex. Most of the existing methods use the time-domain features or frequency-domain features, which can not describe subtle changes and hidden complexities in QRS [42], for classifying the QRS complexes. QRS dynamics is used as a unique feature for QRS classification. Since the dynamics contain complete information on the QRS complex, it also includes the subtle changes of the QRS complex. It would be more suitable for the QRS classification, especially for the classification of QRS with wide variations in morphology. It is the main feature of the proposed method. Experimental results show that the proposed method has good classification performance for different leads ECG.

Table 6 summarizes the state-of-the-art in ECG-based identity recognition methods using PTB databases and provides a direct comparison with the proposed method. It can be seen that the identity recognition accuracy of the proposed method is comparable to or even better than some of the existing methods. In [10], [43], the convolutional neural network was used for identity recognition and obtained satisfactory results. Nevertheless, it requires a large amount of data to train the model as there are a lot of neuron weights need to be adjusted. While, in this paper, the RBF networks used in extracting the dynamics of one-lead and two-lead QRS complexes were only 201 and 1600 neurons, respectively, far fewer than the number of neurons in convolutional neural networks. In addition, the trained model may not be suitable for other databases.

In summary, it can be seen from Table 6: 1) QRS complex dynamics is used as a unique feature for identity recognition in the proposed method, avoids the feature selection which is a hard task that needs various techniques [44]; 2) the proposed method has comparable performance to other state-of-the-art methods for identity recognition; 3) the good performance of the proposed method based on 12 one-lead ECG and 30 two-lead ECG shows that the proposed method has good generalization for different leads of 12-lead ECG.

Finally, it is important to note that while ECG-based identification has come a long way, it is still far from practical application. In our opinion, there are still several open questions in ECG-based identity recognition as follows: 1) The morphology of ECG signals is influenced by physical and emotional state, various heart diseases, diet or drug use, and other factors. Therefore, it is necessary to evaluate the impact of various factors on the ECG biometric. 2) The morphology of ECG signals can also change with lifestyle, age, etc., causing a decrease in identification performance. More attention should be paid to the impact of cross-sessions

on ECG biometrics. 3) Real-time measurement of ECG signals from mobile devices will be the inevitable trend, but the quality of ECG signals will be low due to the unstable external environment. How to extract sufficiently discriminating features from this-low quality ECG signal will be a research direction. 4) ECG signals contain private information about the subject's health, and how to effectively protect the subject's privacy is also a worthwhile research direction.

Remark 5: Compared to our previous works [32] and [45], the approach of this paper has the following advantages and improvements: (1) The method reduces the requirement for the number and location of ECG lead. The VX, VY, and VZ leads were used in [32], and the 12-lead ECG signal was used in [45], while the single-lead or double-lead ECG signal selected arbitrarily from the standard 12-lead ECG signal was used in this paper, making this method more applicable; (2) The method reduces the amount of computation. Both [32] and [45] performed identity recognition based on the entire ECG signal, whereas in this paper, identity recognition based only on the QRS complex of the ECG signal was performed; (3) Most importantly, good recognition accuracy is obtained on each lead, indicating that the method has good generalization capabilities. Moreover, the present study is also different from another study [46]. In this paper, we classify QRS complexes according to identity tags, while in [46], we classify QRS complexes according to heartbeat type, which essentially belongs to the research area of arrhythmia detection.

VI. CONCLUSION

In this paper, we propose a new method for identity recognition via QRS complexes dynamics. The QRS complex extracted from training ECG is accurately modeled by using deterministic learning. The modeling results and corresponding identity labels are stored as a pattern library. For QRS complex classification, a set of state estimator is constructed by using the modeling results, and then a set of errors can be obtained. The test QRS complex is classified according to the principle of minimum error. Finally, the classification of the test ECG, i.e., identity recognition, is achieved according to the voting of all test QRS complexes classification results. Experimental results show the effectiveness and feasibility of the method for identity recognition.

The results of the present study are based on ECG recordings obtained under calm conditions, where heart rate changes of the signal measurement process can be expected to be minimal. However, in practice, individuals are not usually in a normal resting state. In future work, we will investigate the robustness of the proposed method to changes in ECG morphology caused by subjects in different physical and emotional states. Furthermore, given the simplicity and comfort of practical applications, it may be more acceptable to collect ECGs in an off-the-person manner in practice. Therefore, we will also conduct further studies based on the off-the-person ECG database, such as the CYBHi database [51] and the UofTDB database [52].

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