Block Projection Based Feature Extraction for Biometric Recognition with Multi-lead ECG

Shun-Chi Wu and Peng-Tzu Chen
Department of Engineering and System Science, National Tsing Hua University, Hsinchu, Taiwan, R.O.C.
Email: shunchi.wu@mx.nthu.edu.tw, libebc@hotmail.com.tw

***Abstract*—In order to reveal discriminant information from the multi-lead ECG to facilitate the ECG biometric recognition, two novel feature extraction algorithms are proposed in this paper. As opposed to the existing single-lead based techniques, the proposed algorithms which rely on the idea of block projection allow the features to be extracted without breaking the structure between the leads so that more information can be exploited for recognition. In addition, the algorithms require only one fiducial point (*i.e.*, R peaks) to be determined and are applicable to any multi-lead ECG regardless of its number of leads. Detailed experiments show that the proposed algorithms outperform the existing single-lead based approaches.**

***Index Terms*—biometric recognition, electrocardiogram (ECG), feature extraction, classification**

I. Introduction

Utilization of the electrocardiogram (ECG) for biometric recognition has being gaining much attention [1]-[9]. Being a biometric modality, the ECG possesses not just the desirable properties [10] such as universality and distinctiveness. Its inherent liveness-indicating nature is even more appealing since this property can further increase the difficulty in falsification [7], [8]. For the acquired biometric data to be applicable in a recognition task, a feature extraction step is needed. This step is essential since it reduces the effect of noise and also the redundant information in the data so that the following recognition process becomes computationally more manageable and leads to a higher recognition accuracy.

The two most widely discussed feature categories for ECG biometric recognition are: (1) fiducial (e.g., [1], [3], [6], [9]) and (2) nonfiducial features (e.g., [5]-[7], [11]). Fiducial features are constructed relying on the ECG wave minima, maxima, onsets and offsets, which are often referred to as the fiducial points. Once these points are determined, the temporal distances or amplitude differences between them can be calculated as the desired features. Nonfiducial features as the names imply are extracted without a need for or with a limited number of fiducial points (e.g., only with the peaks of the R waves or R peaks). Examples of the nonfiducial features include principal components (PCs) [5], [6], wavelet coefficients [11] and autocorrelation coefficients [6], [12]. One thing in common of the above features is that they are mostly extracted from the single-lead ECG [8].

The ECG is typically recorded with a multi-lead configuration to fully capture the spatiotemporal nature of the cardiac electrical activity. Each ECG lead picks one aspect of the nature, illustrating the "temporal" (or morphological) variations from one specific orientation in the space [13]. In addition, the recorded body surface potentials at different leads possess an *intrinsic structure* (or distribution) that is related to an individual's pericardium and torso surface geometries as well as the conductivity distribution in between [14]. Therefore, recognition simply relaying on the single-lead ECG can be suboptimal.

To exploit the temporal information used by the previous single-lead techniques meanwhile taking advantage of the structural information contained in the multi-lead ECG, two block projection based feature extractors are proposed. Inspired by the concept of a technique called Two-Dimensional Principal Component Analysis (2DPCA) [15], the proposed algorithms allow the features to be extracted without breaking the structure between the leads. As a result, the structural information among the leads can be preserved and the spatiotemporal information stored therein can be effectively explored for discerning the individuals. Lastly, the proposed algorithms require only the R peaks to be determined, which is also required by the most nonfiducial approaches mentioned above and are applicable to any multi-lead ECG regardless of its number of leads.

The remainder of the paper is outlined as follows. In the next section, some popular single-lead based algorithms for ECG feature extraction are reviewed. The proposed block projection based feature extractors are then presented in Section III. The results of some experiments are discussed in Sections IV. Finally, some conclusions are offered in Section V.

II. Existing Single-Lead Techniques

Several popular single-lead based feature extraction algorithms are briefly described in this section, especially those extracting features from the ECG of one cardiac cycle or, in other words, of a single heartbeat.

A. Fiducial Features

The construction of fiducial features requires several characteristic points on a heartbeat to be determined [1],

Manuscript received May 12, 2015; revised July 21, 2015

doi: 10.18178/ijpmbs.4.2.97-100

[3], [6]. As shown in Fig. 1, these include the standard medical labeled points like P, Q, R, S and T and four basal points: L', P', S' and T', which represent the onsets and offsets of the P and T waves, respectively. Given the R peak, P, Q, S and T can be found simply by searching for the local maxima and minima on the first and second halves of the heartbeat. As for the basal points, they can be located by tracking downward the P and T waves and finding the points having the minimum radii of curvature [5] as the targets. Once having these points, the morphological attributes such as the temporal distances, amplitude differences and angular displacements between these points can be calculated to form the desired feature set.

B. Principal Components

Representing the data of the i^{th} heartbeat to be analyzed as $\mathbf{x}_i \in \mathbb{R}^{n\times 1}$, then features of the Principal Component Analysis (PCA) are extracted by [5]

$$\mathbf{c}_i = \Phi^T\left(\mathbf{x}_i - \bar{\mathbf{x}}\right) \tag{1}$$

with $\mathbf{c}_i \in \mathbb{R}^{d\times 1}$ being the PCA feature vector, and $\bar{\mathbf{x}} \in \mathbb{R}^{n\times 1}$ being the ensemble average of the N heartbeats selected for training: $\bar{\mathbf{x}} = \sum_{i=1}^{N}\mathbf{x}_i$. $\Phi \in \mathbb{R}^{n\times d}$ is a basis matrix of the so-called principal subspace with a dimensionality of d, which is normally found by taking the first d eigenvectors of the sample covariance matrix

$$\mathbf{G} = \frac{1}{N}\sum_{i=1}^{N}\left(\mathbf{x}_i - \bar{\mathbf{x}}\right)\left(\mathbf{x}_i - \bar{\mathbf{x}}\right)^T \in \mathbb{R}^{n\times n} \tag{2}$$

with the largest d eigenvalues. Typically, we have $d < n$.

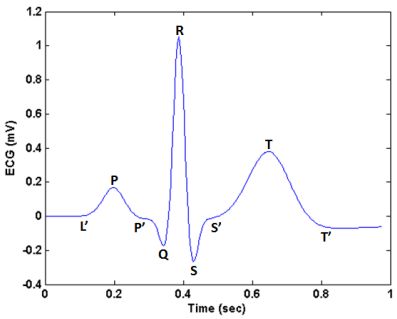

Figure 1. Typical fiducial points on a heartbeat.

III. Block Projection Based Feature Extraction

In this section, two block projection based feature extractors for the multi-lead ECG are presented. To begin with, we assume that the R peaks on one of the ECG leads (*e.g.*, lead I) have been detected, and the *multi-lead, time-aligned* ECG blocks around each detected R peaks have been isolated. Assuming m leads and n samples per block, the data corresponding to the i^{th} detected R peak will consist of an $m\times n$ matrix $\mathbf{X}_i$, which is hereafter referred to as a "beat bundle."

A. Temporal 2DPCA (t2DPCA)

Let $\mathbf{v}$ denote an n-dimensional column vector of unit length. The idea of feature extraction in t2DPAC is directly projecting the beat bundle $\mathbf{X}_i$ onto $\mathbf{v}$ via

$$\mathbf{y}_i = \mathbf{X}_i\mathbf{v} \tag{3}$$

to get the desired feature vector $\mathbf{y}_i \in \mathbb{R}^{m\times 1}$. The advantages of this approach are twofold. One is that the features are extracted without worrying about the determination of the fiducial points like PCA. The other is that data of all the leads are processed simultaneously while extracting the features so that the structural information among the leads is preserved. However, what vector $\mathbf{v}$ to be used so that the extracted features are most beneficial for recognition becomes crucial. One way to obtain the optimal vector of $\mathbf{v}$ is to search for a vector that maximizes the total scatter of the extracted features (*i.e.*, a measure of the discriminatory power of the features) [15]:

$$\begin{aligned}\hat{\mathbf{v}} &= \arg\max_{\mathbf{v}} J_t\left(\mathbf{v}\right) = \arg\max_{\mathbf{v}} \mathbf{v}^T\mathbf{G}_t\mathbf{v} \\ &\text{s.t. } \|\mathbf{v}\| = 1,\end{aligned} \tag{4}$$

where

$$J_t\left(\mathbf{v}\right) = tr\left[\frac{1}{N}\sum_{i=1}^{N}\left(\mathbf{y}_i - \bar{\mathbf{y}}\right)\left(\mathbf{y}_i - \bar{\mathbf{y}}\right)^T\right] \tag{5}$$

is the generalized total scatter criterion [15] with $\bar{\mathbf{y}}$ being the ensemble average of the extracted feature vectors from the N selected training beat bundles. Substitute (3) into (5), one can easily find that the second equality of (4) holds with

$$\mathbf{G}_t = \frac{1}{N}\sum_{i=1}^{N}\left(\mathbf{X}_i - \bar{\mathbf{X}}\right)^T\left(\mathbf{X}_i - \bar{\mathbf{X}}\right) \in \mathbb{R}^{n\times n} \tag{6}$$

being the temporal covariance matrix of the selected bundles and $\bar{\mathbf{X}}$ being their ensemble average.

Since the expression given by (4) represents a quadratic form, $\hat{\mathbf{v}}$ can be found as the eigenvector of $\mathbf{G}_t$ having the largest eigenvalue. In addition, for a low-dimensional representation to be effectively representing the original beat bundle, more than one such unit vectors may be required, which are often obtained by selecting the d eigenvectors of $\mathbf{G}_t$ with the largest d eigenvalues. Once the feature vector corresponding to each unit vector has been extracted, the complete feature vector $\mathbf{y}_i^{all}$ of $\mathbf{X}_i$ can be formed by stacking all them together:

$$\mathbf{y}_i^{all} = \left[\left(\mathbf{y}_i^1\right)^T \quad \cdots \quad \left(\mathbf{y}_i^d\right)^T\right]^T \tag{7}$$

where $\mathbf{y}_i^j = \mathbf{X}_i\mathbf{v}_j \in \mathbb{R}^{m\times 1}$ with $\mathbf{v}_j$ being the j^{th} determined unit vector. Notice that these d eigenvectors span a dominant subspace of the multi-lead ECG, to which most of the data variability is confined. Further looking into (6),

we can find that $\mathbf{G}_t$ is the sample covariance matrix of all the row vectors (*i.e.*, data of all the leads) of the selected bundles, and thus the variability of the multi-lead ECG is captured by $\mathbf{G}_t$ from a temporal (morphological) aspect. Hence, this approach is termed as the temporal 2DPCA (t2DPCA).

B. Spatial 2DPCA (s2DPCA)

Next, we reformulate the problem from the other aspect. Provided that a unit column vector $\mathbf{u} \in \mathbb{R}^{m\times 1}$ is available, but now the features are extracted by

$$\mathbf{z}_i = \mathbf{u}^T \mathbf{X}_i, \tag{8}$$

where $\mathbf{z}_i \in \mathbb{R}^{1\times n}$ is the s2DPCA feature vector of $\mathbf{X}_i$. Defining the total scatter of $\mathbf{z}_i$ as

$$J_s(\mathbf{u}) = tr\left[\frac{1}{N}\sum_{i=1}^{N}(\mathbf{z}_i - \bar{\mathbf{z}})^T(\mathbf{z}_i - \bar{\mathbf{z}})\right], \tag{9}$$

the optimal vector of $\mathbf{u}$ can then be determined similarly by searching for a vector that maximizes $J_s(\mathbf{u})$:

$$\hat{\mathbf{u}} = \arg\max_{\mathbf{u}} J_s(\mathbf{u}) = \arg\max_{\mathbf{u}} \mathbf{u}^T \mathbf{G}_s \mathbf{u} \quad \text{s.t. } \|\mathbf{u}\| = 1, \tag{10}$$

where

$$\mathbf{G}_s = \frac{1}{N}\sum_{i=1}^{N}(\mathbf{X}_i - \bar{\mathbf{X}})(\mathbf{X}_i - \bar{\mathbf{X}})^T \in \mathbb{R}^{m\times m} \tag{11}$$

can be obtained by substituting (8) into (9). As shown in (11), $\mathbf{G}_s$ represents a sample covariance matrix of all the column vectors of the selected bundles. Columns of a beat bundle are the projections of the "cardiac dominant vector" onto the *m*-lead coordinate system at each sampling time instants, revealing the travel directions of the electrical impulse throughout the heart [13]. Thus, $\mathbf{G}_s$ reflects the variability of multi-lead ECG from a spatial aspect. For this reason, we term this approach as the spatial 2DPCA (s2DPCA). The solution of (10) is the eigenvector of $\mathbf{G}_s$ with the largest eigenvalue as well. If more than one such unit vectors are utilized, the complete feature vector will be comprised of all the corresponding feature vectors like what is done in (7). Finally, with these unit vectors, a spatial dominant subspace of the multi-lead ECG can be uncovered.

IV. Experiments and Discussions

A. Dataset Descriptions and Preprocessing

Physikalisch Technische Bundesanstalt Database (PTB Database) [16] contains 549 records from 290 subjects. Each record provides 15 leads of the simultaneously measured ECG, including the standard 12-lead ECG together with the Frank-lead vectorcardiogram, sampled at 1000 Hz with 16-bit resolution over a range of ±16.384 mV. For performance evaluation, recordings of the lead-I, II and III from all the healthy subjects (52 in total) were utilized. Prior to the data segmentation and feature extraction, each ECG lead was subject to the baseline wander removal. Following the approach of [17], two median filters having window sizes of 200 ms and 600 ms, respectively, were used to extract the wander, and the resulted signal was then subtracted from the original ECG to get rid of the baseline wander. Finally, the heartbeats and beat bundles corresponding to each R peaks were cut with a fixed duration (determined empirically) of 240 ms and 420 ms before and after the R peaks, respectively.

B. Results and Discussions

Four feature extraction algorithms were implemented for performance comparison: (1) fiducial-based approach making use of 21 morphological attributes as specified in [6], which includes 15 temporal and 6 amplitude features, (2) PCA [5], [6], (3) temporal 2DPCA, and (4) spatial 2DPCA. The extracted features were classified using the k-Nearest Neighbors algorithm [18], and the Lead-I recordings were used in the single-lead based algorithms. The impact of various factors on the performance of the algorithms is presented below.

In the first example, the influence of the dimensionality of the principal subspace, *d*, on the recognition accuracy is investigated. Fig. 2 shows the mean recognition rates averaged over 10 trials with *d* being varied from 1 to 6.

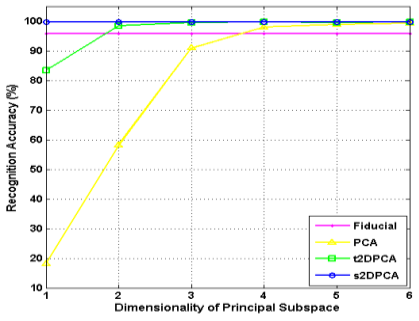

Figure 2. The influence of the dimensionality of principal subspace on the recognition accuracy.

For a given trial, 10 heartbeats/beat bundles from each subject were randomly selected for training, and another 10 were chosen for testing. The recognition rate of the fiducial-based approach is independent of the value of *d*, achieving a recognition rate of 95.69%. As the dimensionality increases, the recognition rates of the PCA/2DPCA based approaches increase as expected. The advantage of the multi-lead approaches over the single-lead based algorithms is also apparent, especially when the *d* is small.

In the next example, the influence of the sampling rate on the recognition accuracy is studied. Different sampling rates were achieved by downsampling the original recordings, ranging from 30 Hz to 1000 Hz. The numbers of *d* were set at 5 and 1 for temporal PCA algorithms (*i.e.*, PCA and t2DPCA) and s2DPCA, respectively. The results are depicted in Fig. 3. From Fig. 3, the recognition rates decrease as the sampling rate decreases. The degradation becomes apparent when the sampling rate is

less than 200 Hz. This is because a reduction in the sampling rate leads to a reduction in the number of time samples to represent a heartbeat/beat bundle, and differentiating them in a space with less dimensionality will become more difficult and thus more errors. However, 2DPCA based algorithms still maintain a better recognition rate due to its capability of well exploiting the information contained in the multi-lead recordings.

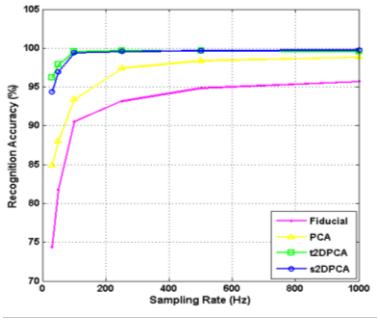

Figure 3. The influence of the sampling rate on the recognition accuracy.

V. Conclusions

This paper has presented two novel approaches to extract features from the multi-lead ECG for biometric recognition. The algorithms first uncover the dominant subspaces of the multi-lead ECG from temporal and spatial aspects. The feature extraction is then completed by projecting the beat bundles onto these subspaces. The algorithms require only the R peaks to be determined and are applicable to any multi-lead ECG regardless of its number of leads. Experiments demonstrate that the proposed algorithms yield features that lead to promising recognition results.

Acknowledgment

The authors would like to thank the financial support of the Ministry of Science and Technology of Taiwan, R.O.C. for the project under the contract No. MOST 103-2218-E-007-013.

References

[1] L. Biel, O. Pettersson, L. Philipson, and P. Wide, "ECG analysis: a new approach in human identification," *IEEE Trans. Instrum. Meas.*, vol. 50, pp. 808-812, Jun. 2001.

[2] T. W. Shen, W. J. Tompkins, and Y. H. Hu, "One-lead ECG for identity verification," in *Proc. Second Joint EMBS/BMES Conference*, vol. 1, pp. 62-63, Oct. 2002.

[3] S. A. Israel, J. M. Irvine, A. Cheng, M. D. Wiederhold, and B. K. Wiederhold, "ECG to identify individuals," *Pattern Recognition*, vol. 41, pp. 3427-3435, Jan. 2005.

[4] G. Wübbeler, M. Stavridis, D. K. R. D. Bousseljot, and C. Elster, "Verification of humans using the electrocardiogram," *Pattern Recognition*, vol. 28, pp. 1172-1175, Jul. 2007.

[5] J. M. Irvine, S. A. Israel, W. T. Scruggs, and W. J. Worek, "eigenPulse: Robust human identification from cardiovascular function," *Pattern Recognition*, vol. 41, pp. 3427-3435, Nov. 2008.

[6] Y. Wang, F. Agrafioti, D. Hatzinakos, and K. N. Plataniotis, "Analysis of human electrocardiogram for biometric recognition," *Eurasip J. Advances in Signal Processing*, vol. 2008, no. 1, p. 11, 2008.

[7] S. Z. Fatemian, S. Edward, S. R. Rogers, and D. Hatzinakos, "A new ECG feature extraction for biometric recognition," *in Proc. International Conference on Digital Signal Processing*, pp. 1-6, Jul. 2009.

[8] I. Odinaka, P. H. Lai, A. D. Kaplan, J. A. O'Sullivan, E. J. Sirevaag, and J. W. Sirevaag, "ECG biometric recognition: a comparative analysis," *IEEE Trans. Inf. Forensics Security*, vol. 7, pp. 1812-1824, Aug. 2012.

[9] Y. N. Singh and S. K. Singh, "Evaluation of electrocardiogram for biometric authentication," *J. Information Security*, vol. 3, pp. 39-48, Jan. 2012.

[10] A. K. Jain, A. Ross, and S. Prabhakar, "An introduction to biometric recognition," *IEEE Trans. Circuits Syst. Video Technol.*, vol. 14, pp.4-20, Jan. 2004.

[11] A. D. C. Chan, M. M. Hamdy, A. Badre, and V. Badee, "Wavelet distance measure for person identification using electrocardiograms," *IEEE Trans. Instrum. Meas.*, vol. 57, pp. 248-253, Feb. 2008.

[12] F. Agrafioti, E. S. Rogers, and D. Hatzinakos, "Fusion of ECG sources for human identification," in *Proc. Int. Symposium on Communications, Control and Signal Processing*, pp. 1542-1547, Mar. 2008.

[13] L. Sörnmo and P. Laguna, *Bioelectrical Signal Processing in Cardiac and Neurological Applications*, Academic Press, 2006.

[14] A. van Oosterom, "The use of the spatial covariance in computing pericardial potentials," *IEEE Trans. Biomed. Eng.*, vol. 46, pp. 778-787, Jul. 1999.

[15] J. Yang, D. Zhang, A. F. Frangi, and J. Y. Yang, "Two-dimensional PCA: A new approach to appearance-based face representation and recognition," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 26, pp. 131-137, Jan. 2004.

[16] A. L. Goldberger, L. A. N. Amaral, L. Glass, J. M. Hausdorff, P. C. H. Ivanov, R. G. Mark, *et al*., "Physiobank, physiotoolkit, and physionet: Components of a new research resource for complex physiologic signals," *Circulation*, vol. 101, pp. 215-220, Jun. 2000.

[17] D. Widjaja, C. Varon, A. C. Dorado, J. A. K. Suykens, and S. V. Huffel, "Application of kernel principal component analysis for single lead-ECG-derived respiration," *IEEE Trans. Biomed. Eng.*, vol. 59, pp. 1169-1176, Apr. 2012.

[18] R. O. Duda, P. E. Hart, and D. G. Stork, *Pattern Classification*, 2nd ed. Wiley-Interscience, New York, 2001.

Shun-Chi Wu received the B.S. and the M.S. degrees in engineering and system science from National Tsing Hua University, Hsinchu, Taiwan, in 2000 and 2002, respectively, and the Ph.D. degree in electrical engineering and computer science from University of California, Irvine, California, in 2012.

From 2003 to 2007, he was a research assistant at National Space Organization, Hsinchu, Taiwan. In 2013, he was employed at IMEC, Taiwan Co., of Hsinchu, Taiwan, where he was involved in the design of algorithms and architectures for several wearable devices. He is currently an assistant professor of engineering and system science at National Tsing Hua University. His research interests include biomedical signal processing, pattern recognition, source localization/reconstruction, and brain connectivity analysis. He is also a member of the IEEE.

Peng-Tzu Chen received the B.S. degree in engineering and system science from National Tsing Hua University, Hsinchu, Taiwan in 2015. She is currently working toward the M.S. degree in National Tsing Hua University, Hsinchu, Taiwan. Her research interests include pattern recognition and machine learning.