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eigenPulse: Robust human identification from cardiovascular function

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ABSTRACT

This paper presents eigenPulse, a new method for human identification from cardiovascular function. Traditional biometric techniques, e.g. face and fingerprint, have used eigen analysis to exploit databases with tens of thousands of entries. One drawback of traditional biometrics is that the credentials, for example, fingerprints, can be forged making the systems less secure. Previous research [S.A. Israel, J.M. Irvine, A. Cheng, M.D. Wiederhold, B.K. Wiederhold, ECG to identify individuals, Pattern Recognition 38(1) (2005) 138–142] demonstrated the viability of using cardiovascular function for human identification. By nature, cardiovascular function is a measure of liveness and less susceptible to forgery. However, the classification techniques presented in earlier work performed poorly over non-standard electrocardiogram (ECG) traces, raising questions about the percentage of the population that can be enrolled. This paper combines the traditional biometrics' use of eigen analysis and previous analysis of cardiovascular function to yield a more robust approach. The eigenPulse processing had a near 100% enrollment rate, with a corresponding higher overall performance.

1. Introduction

Traditional methods of biometric authentication, such as face, fingerprint, and iris, provide accurate authentication across significantly large populations. One weakness of many biometric systems is that the features extracted from these biometric modalities can be counterfeited [2]. One avenue for addressing this limitation is to collect signals that verify the "liveness" of the individual. This paper presents a method for identification in which the verification of "liveness" is inherent to the biometric. We exploit cardiac function as measured by the electrocardiogram (ECG) to identify individuals.

ECG measures the change in the electrical potential of the heart over time. Because the signals originate at the heart, ECG describes a measure of liveness. The duration of a heartbeat varies with stress, anxiety, and even with time of day. However, the structure of the heartbeat contains only scalar differences with changes in stress. Israel et al. [1,5], Irvine et al. [3,4] and Biel et al. [6] showed the heartbeat structure to be unique to an individual. In each case, the extracted ECG attributes performed well for identifying individuals.

Initial ECG human identification experiments [1,4] indicate two important challenges. First, the small number of heartbeat features may not generalize well to large numbers of subjects (i.e. >1000 individuals).[1] Second, the approach relied on fiducial tributes, i.e. features obtained by identifying specific landmarks from the processed signal. The fiducial-based feature extraction was unable to enroll 30% of the collected population (10% due to irregular structure of the ECG trace and 20% due to noise, such as muscle flexure). A non-negligible portion of the population exhibits ECG traces that deviate from the ideal in predictable ways and additional condition handling would be needed to enroll and identify these individuals. To overcome these two deficiencies, another feature extraction technique is required.

This paper focuses on the application of principal components analysis (PCA) for feature extraction. The technique, which we call *eigenPulse*, uses an eigenvector decomposition of the normalized ECG signal. This approach addresses the two weaknesses identified above:

1. We are not limited to a small set of attributes; rather we use an orthonormal basis to represent the most significant features for distinguishing the ECG traces.
2. PCA features do not require fiducial extraction, which minimizes the exception handling problems and increases enrollment rate.

The remainder of this paper presents the processing required and results obtained using PCA-based ECG analysis. Section 2 reviews the previous literature associated with ECG data for biometric identification. Section 3 highlights the mathematical basis for eigen analysis as applied to identification. Section 4 describes the processing steps required to transform raw ECG traces into eigenPulse attributes. Section 5 provides the results, discussion, and comparison of these experiments to previous ECG recognition results.

[1] Face recognition databases are approaching 1000s of subjects and 100,000s of images [7].

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2. ECG as a biometric

Cardiac cells are electrically polarized. The change in the electrical current is a trigger for contracting the heart muscle. The atria and ventricles contract at different times to force blood flow in the correct direction. Heart rate is controlled by the heart's primary pacemaker called the sino-atrial (SA) node which is located in the right atrium (Fig. 1). The signal spreads outward from the SA node forcing the heart muscles to depolarize and contract (P wave). The signal is slowed at the atrio-ventricular (AV) node causing a time gap between the P and R complexes: a lag between atrial and ventricular compression. The R wave indicates ventricular contraction. The T wave occurs during ventricular repolarization. Atrial repolarization is less commonly observed in ECG traces and is labeled as a U wave.

ECG data are commonly collected by contact sensors at multiple positions around the heart [8]. The change in ECG electrode position provides different information because of their relative position to the heart's plane of zero potential. For nearly all individuals and all electrode locations, the ECG trace of a heartbeat produces three complexes (wave forms). The medical community [9] has defined the complexes by their peaks: P, R, and T (Fig. 2). The R–R interval, the time between two successive R peaks, indicates the duration of a heartbeat. Two other fiducials, Q and S, are also identified at the base of the R complex. Israel et al. [1] identified four additional fiducials at the base of the P and T complexes. These are noted with a prime (α') symbol (Fig. 2).

Although the ECG trace includes the same major components (P wave, QRS complex, and T wave) across individuals, the relative position, duration, and magnitude of these features vary by person (Fig. 3). These features provide the basis for identifying individuals from the ECG trace. Biel et al. [6] generated a large number of attributes from multi-lead ECG traces. The number of attributes exceeded the number of subjects. The data were collected within a single session. The extracted feature vectors were then transposed into the PCA space. Though they only missed 1 individual from 50, they did not address multi-session or multi-anxiety state normalization issues.

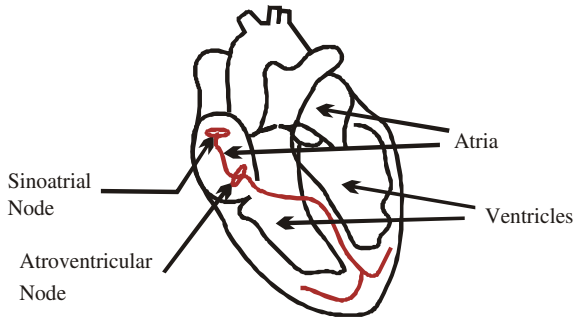

Fig. 1. The heart and its pacemakers: the sino-atrial node is the heart's primary pacemaker and the atrio-ventricular node forces the lag in the depolarization between the atrial and the ventricular contraction.

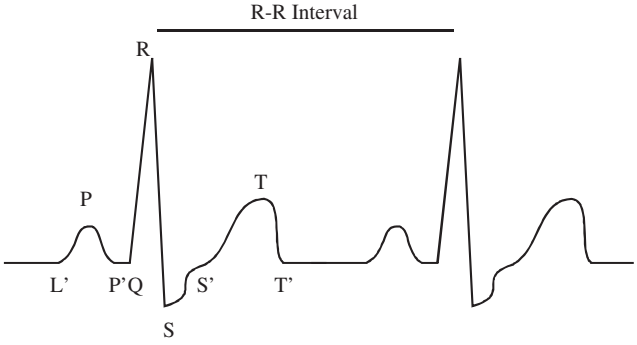

Fig. 2. Ideal ECG signal: this figure depicts two idealized heartbeats.

Israel et al. [1] developed attributes based upon temporal differences among the ECG fiducials from a single ECG lead (Fig. 4). The heartbeats were aligned iteratively using the highest cross correlation between the current heartbeat and the average heartbeat and stepping over time lags. After extraction, the temporal features were normalized by the length of the heartbeat. A total of 15 attributes were defined and stepwise discriminant analysis used Wilkes' λ to select the best features [10].

Discriminant analysis identified more than 95% of the individuals from the enrolled population of 29 individuals. In a later experiment that extracted only low-stress-state ECG data, a population of more than 100 subjects resulted in a degraded performance of 88% correctly identified individuals, indicating that the information content with a fiducial-based ECG system is not sufficient for large populations [5].

The experiments discussed above illustrate the problems with fiducial-based classification. Fiducials must be common to all signals. ECG traces that depart from the idealized shape are, in fact, fairly common in the general population. Anomalies can include multiple extrema (e.g. a double peak in the T wave) rather than a single peak in the various complexes, inversions of the P or T wave, and slope variations that require specific rules for handling these conditions (Fig. 5). Sensor noise also introduces uncertainly into the accurate extraction of the fiducials. Noise causes greater uncertainty into the computation of fiducial-based features and, in some cases, fiducial features cannot be calculated at all. The PCA approach overcomes this limitation.

3. PCA features for identification

The ECG trace is not a random event. It is cyclic with regularly occurring P, R, and T waves (Fig. 2). If this common cyclic pattern is removed from an individual's datastream, the remaining information describes the individual's uniqueness or difference to the population norm. The fiducial features only capture information about relative position of features within the normalized heartbeat. Because the eigenvectors form an orthonormal basis for the feature space, the expression of normalized heartbeats using this decomposition provides a complete characterization. Any normalized heartbeat can be approximated as a linear combination of a subset of the eigenvectors.

For eigen analysis, the entire heartbeat trace is presented to the system. This yields attributes that are always defined, even for atypical ECG traces discussed above. The PCA approach insures that individuals can be enrolled without retraining. This approach has proved successful in face recognition, which has exploited eigenspace analysis for human identification [11–17]. The remainder of this paper applies eigenspace analysis to ECG traces for human identification.

3.1. Preprocessing the ECG trace

These experiments compare the performance of the eigenspace attributes and classifier to previous experiments performed using fiducial-based attributes and discriminant functions. To these ends, we tested the relationship between the number of attributes and performance. Attribute reduction was performed by normalizing each heartbeat to fixed lengths of 250, 100, 50, 25, and 10 samples from the original 12-bit-1000 Hz data.

The raw data were Fourier bandpass filtered [18] to eliminate electrical, thermal, and A/D noise sources (Fig. 6). Then, the individual heartbeats were aligned by the peak of their R wave [5,19–21]. Alignment was performed by computing the autocorrelation

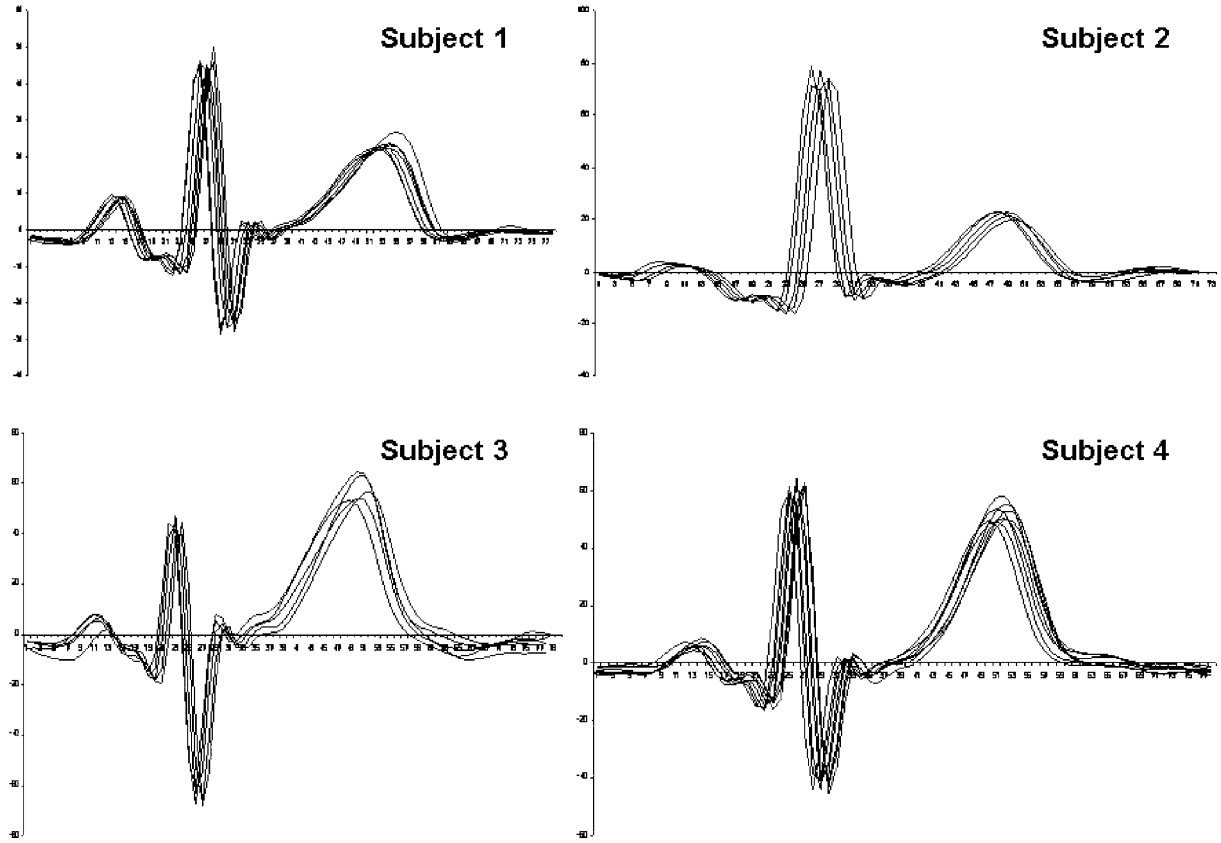

Fig. 3. Heartbeats from four subjects. ECG traces from four subjects have been segmented into individual heartbeats. Note the differences in relative size and shape of the P wave, the QRS complex, and the T wave.

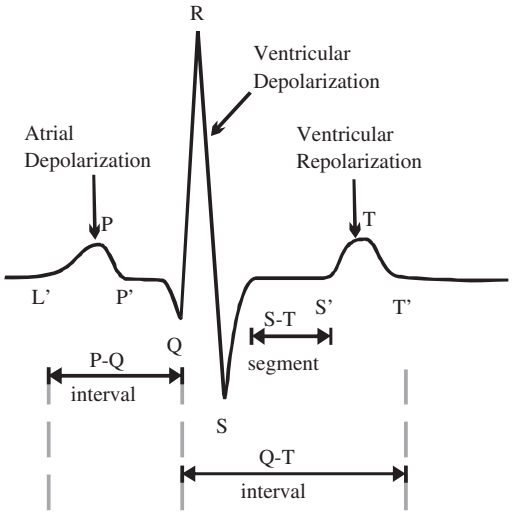

Fig. 4. Idealized ECG trace showing the fiducial points.

function of the ECG datastream and using that function to segment the heartbeats.

3.2. PCA attributes and classifiers

The development of the features set begins with the filtering and segmentation described above. Then, the electrical potential values were normalized to [0,1]. After segmentation, the training data are normalized and the covariance matrix is calculated (Fig. 7). The eigenvectors from the covariance matrix form the basis representation of both the gallery and probe signals (Fig. 8).

To make these ideas precise, let $\{X_t\}$ denote the sequence of raw ECG observations indexed by time t. The filtering process transforms this to the new series $\{Y_t\}$. Segmentation requires identifying the individual heartbeats that comprise the filtered series $\{Y_t\}$. Autocorrelation analysis indicates the periodicity of the series and facilitates rapid identification of the individual R peaks. We denote the segmented heartbeats by $\{W^h_{t,i}\}$ where h denotes the hth subject, i refers to the ith heartbeat, and t is the time index within a single heartbeat.

For a given heartbeat, t ranges from 1 to T_i, which can vary from heartbeat to heartbeat and subject to subject. The normalization process first re-samples $\{W^h_{t,i}\}$ to yield a vector of fixed length (Fig. 7). The chosen heartbeat sample width (resolution) was synchronized to the aligned full resolution heartbeats. The nearest sample was selected for the chosen temporal resolution. All lower resolution selections were registered to the original 1000 Hz data; i.e., the 1000 Hz heartbeat data were mapped to 250 samples per heartbeat, then 100 samples per heartbeat, etc. The final step is to normalize the heartbeats to have a minimum value of zero and a maximum value of 1. We denote the normalized heartbeat by $\{Z^h_{t,i}\}$ where

$$Z^h_{t,i} = [U^h_{t,i} - \min(U^h_{t,i})]/[\max(U^h_{t,i}) - \min(U^h_{t,i})]$$

and $\{U^h_{t,i}\}$ is the re-sampling of $\{W^h_{t,i}\}$ to the desired temporal resolution.

The $\{Z^h_{t,i}\}$ form a vector of length K, where $K = 10$, 25, 50, 100, or 250, depending on the level of down-sampling. We compute the

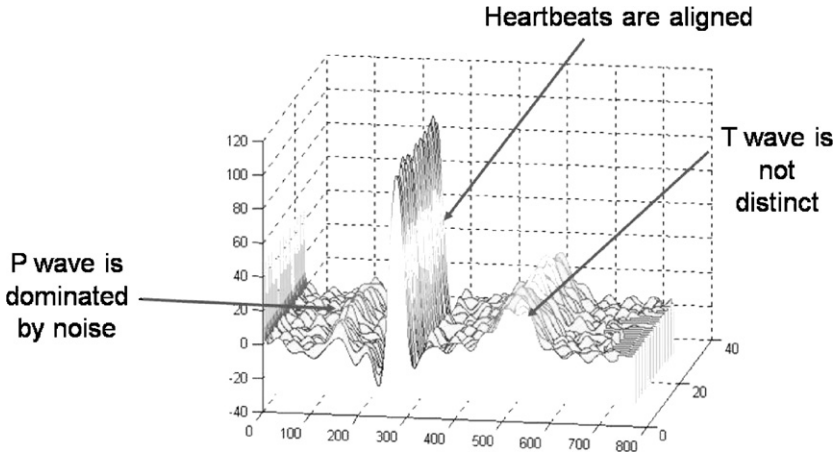

Fig. 5. Aligned heartbeats from a single subject with a noisy P wave and an ambiguous T wave.

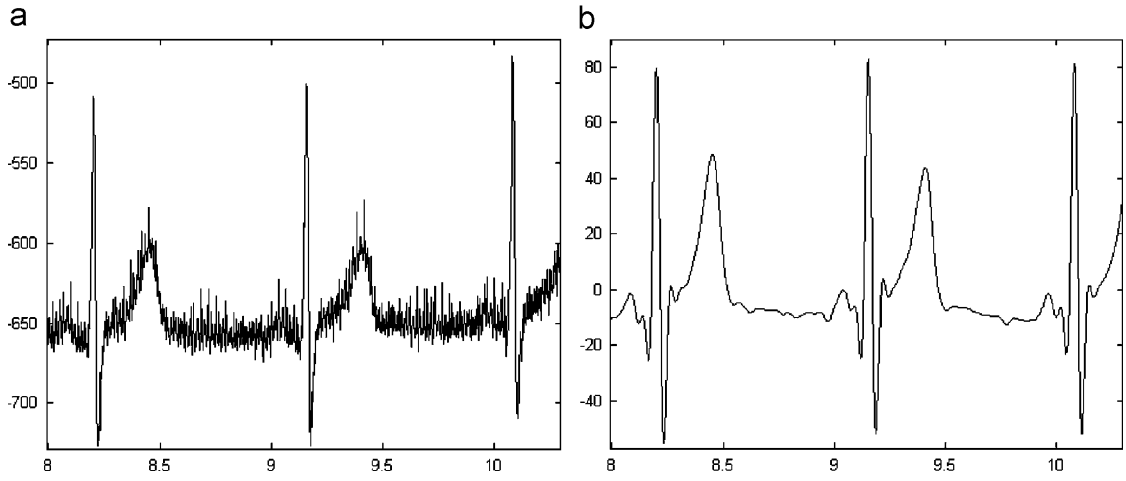

Fig. 6. (a) Raw and (b) filtered ECG data.

covariance matrix $\mathbf{\Sigma}$ for $\{Z_{t,i}^h\}$ and calculate the eigenvalues $\{\lambda_j\}$ and corresponding eigenvectors $\{V_j\}$ of $\mathbf{\Sigma}$, where $j = 1, \ldots, K$. The dominant features are contained in the eigenvectors corresponding to the largest eigenvalues (Fig. 9). Note that the average heartbeat departs from the "idealized" heartbeat due to the variation in the relative positions of the R and T peaks. The first several eigenvectors capture the relative placement of these features (Fig. 10a). When the standard heartbeats $\{Z_{t,i}^h\}$ are projected into the subspace spanned by the dominant eigenvectors, the separability among the subjects is evident (Fig. 10b). Note that heartbeats from each subject tend to cluster, although there are some discontinuities in the clusters. In addition, a few heartbeats fall into ambiguous regions, as is the case for a few heartbeats from Subject D which fall in the cluster associated with Subject C.

As is common in many instances, the same data were employed for *training* (deriving the eigenspace representation) and the *gallery* set (the set of individuals against which new datastreams are compared for identification). Let $\mathbf{Z}^h$ denote the vector representation of the down-sampled, normalized heartbeat for the hth subject and let $\overline{Z}$ denote the mean heartbeat. Then

$$C_j^h = \boldsymbol{V}_j[\boldsymbol{Z}^h - \overline{\boldsymbol{Z}}]$$

where V_j is the eigenvector corresponding to the jth eigenvalue. The coefficients $\{C_j^h\}$ are a compact representation of the heartbeats in the gallery set. Averaging over all of the heartbeats for a single subject provides the gallery representation $\boldsymbol{C}^h$ against which the probe data are compared.

The probe signal undergoes the same processing steps as the gallery set to derive a representation relative to the basis formed by the dominant eigenvectors. Let $\{X_t^*\}$ denote the raw ECG trace for a probe signal. The processing stream yields a representation of the jth heartbeat as a vector of coefficients in the eigenspace, denoted by $\boldsymbol{C}_j^*$. The best match in the gallery set is the choice of h that minimizes the distance between $\boldsymbol{C}^h$ and $\boldsymbol{C}_j^*$. Let δ denote the distance:

$$\delta = \min\{h\} \| \boldsymbol{C}^h - \boldsymbol{C}_j^* \|$$

If δ is sufficiently small then the heartbeat from the probe signal is judged to match subject h in the gallery set. Voting based on the matches for each heartbeat yields the final classification by subject.

3.3. Limitation of eigenspace attributes

The use of eigenspace attributes has issues that must be addressed. The covariance and the corresponding solution to the

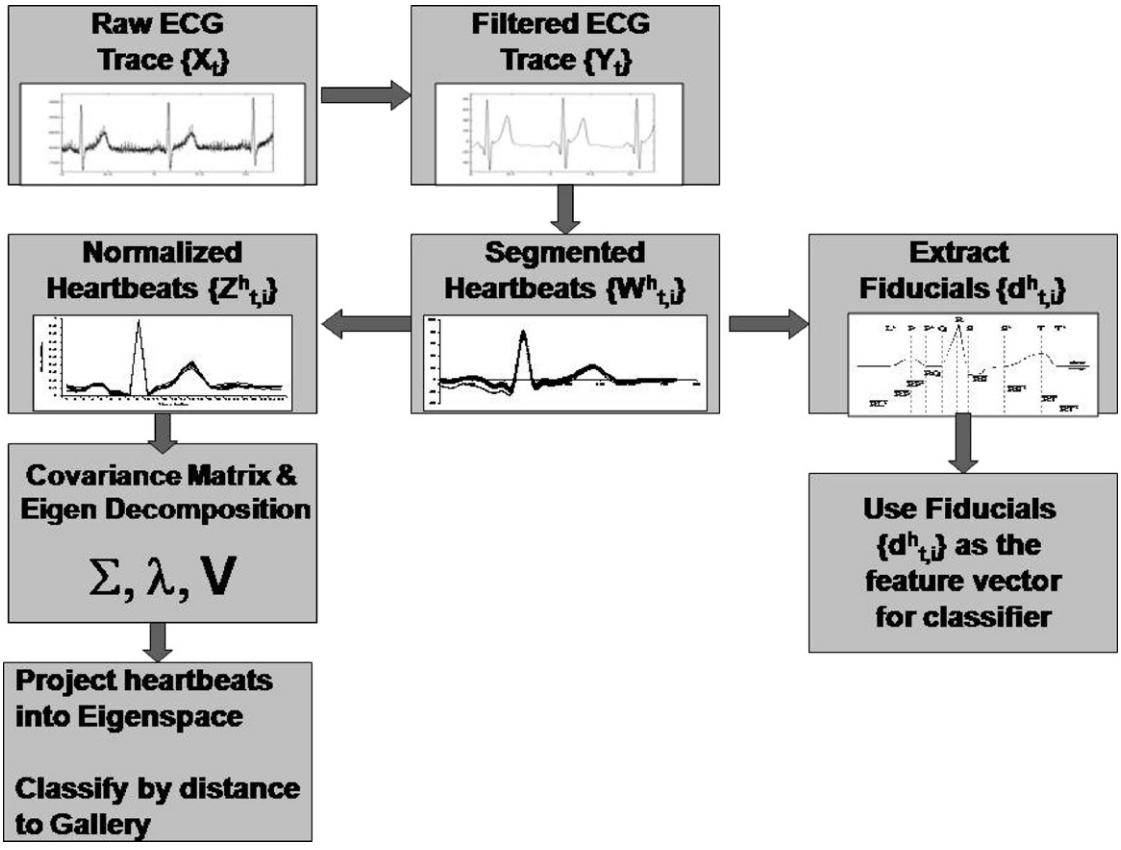

Fig. 7. Initial processing flow includes filtering the ECG signal and segmenting into individual heartbeats.

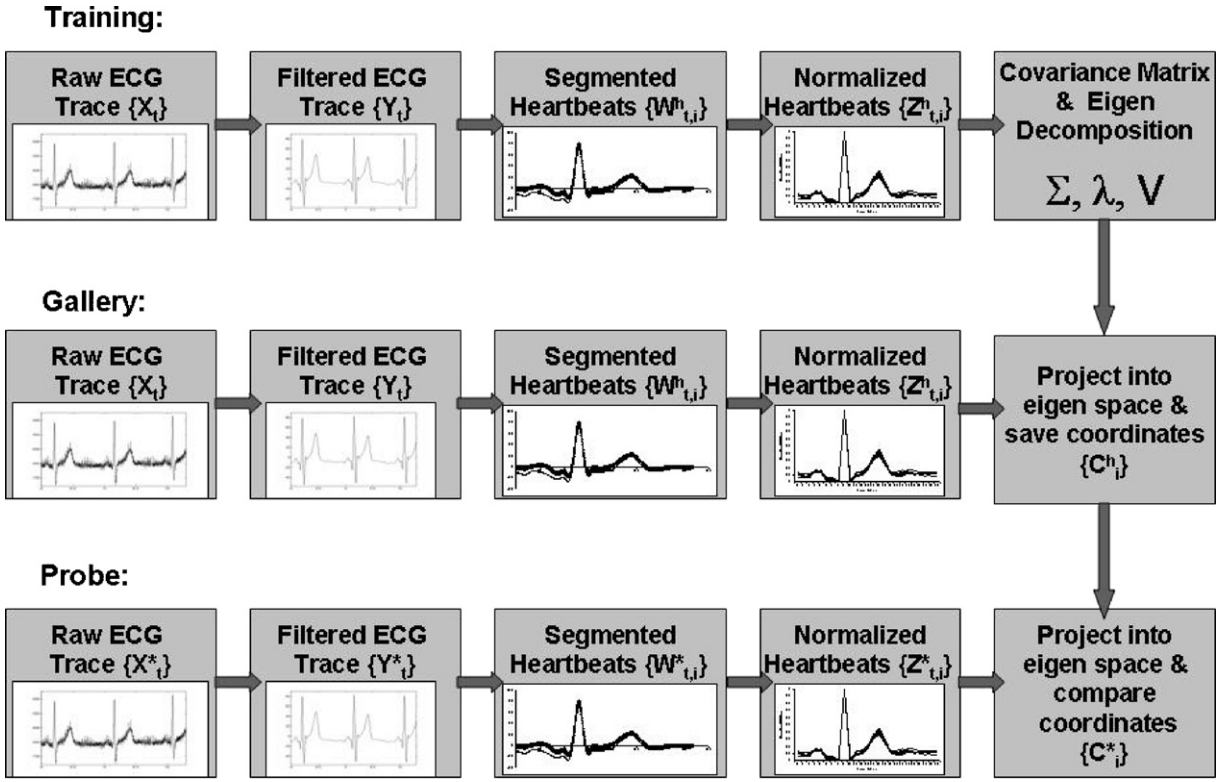

Fig. 8. Processing flow for eigenPulse: the initial processing (filtering, segmentation, and normalization) applies to all ECG signals. The training phase constructs the covariance matrix for the down-sampled heartbeats and computes the eigenvalues and the eigenvectors. The gallery data undergo the same initial processing and the eigen representation is stored for future comparisons. A probe signal is compared to the gallery set to identify a possible match.

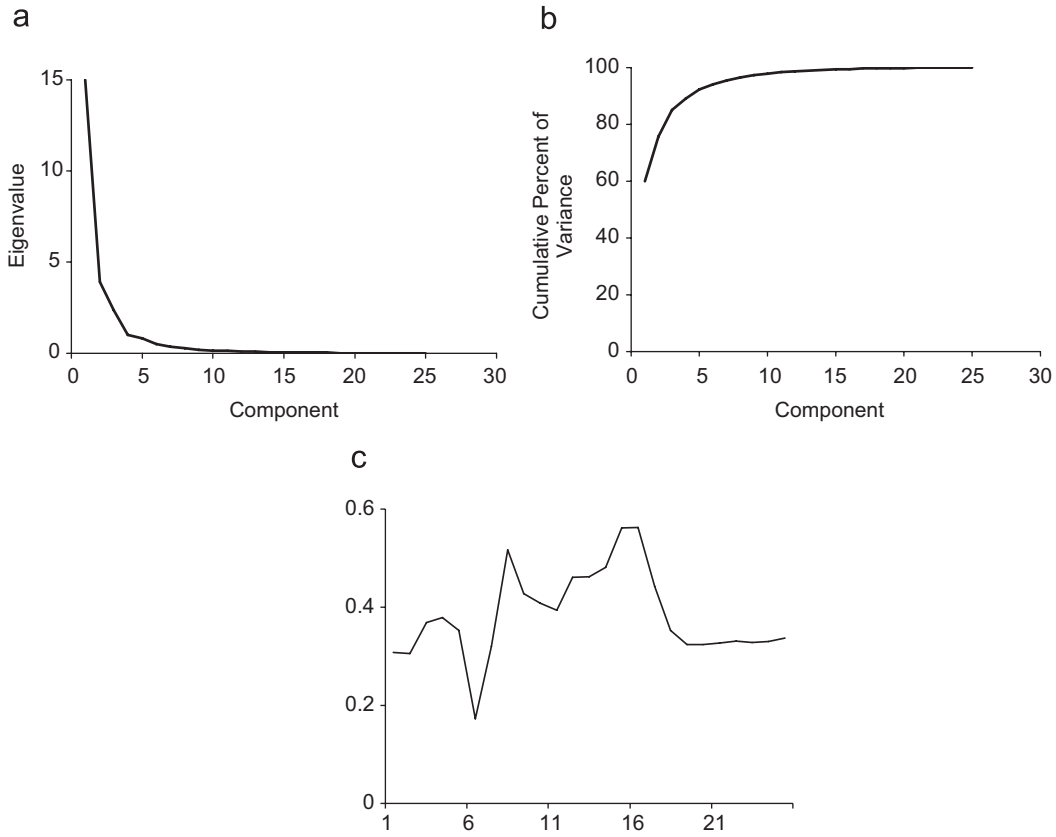

Fig. 9. (a) Eigenvalues for the heartbeat vectors of length 25. (b) The cumulative variance accounted for by the eigenvectors. (c) The average down-sampled heartbeat of length 25.

eigenvalue problem are functions of the training data. If the training data are not representative of the *entire* population, then experiments performed with different data may achieve widely different results. Attribute vectors are generated using an unsupervised approach and understanding what the PCA classifier has learned is difficult. For example, the ECG data are known to vary potential magnitudes with change in electrode placement. Note the differences in the relative heights of the P, R, and T waves between the two graphs (Fig. 3). The normalization procedure described above is designed to mitigate the effect of magnitude differences caused by sensor placement.

4. Experimentation

The ECG data were collected under a rigid protocol [1,3,4]. The 43 male and female subjects ranged in age between 18 and 48. During each session, the subject's ECG was recorded while performing seven 2-min tasks. The tasks were designed to elicit varying stress levels and to understand stress/recovery cycles. Several subjects were repeated to determine session-to-session variations. The eigenPulse experiments used data from the subject's baseline state, which is considered as a low-stress task.

The entire PCA process was performed at each down-sampled resolution. Training, gallery, and probe data were extracted as independent 30 sec data blocks from the 2-min raw task data, where the first and the last 15 sec were avoided to remove sensor and task 'edge' effects. Since only the eigenvectors corresponding to the most significant eigenvalues contain significant information, we used the 60% most significant attributes for identification. For example, the 100-sample resolution equated to using 60 eigenvalues (eigenPulse attributes). A total of 39 from the 43 subjects were enrolled in the system. The unenrolled ECG traces were rejected due to sensor noise.

5. Results and discussion

Previous results [22–25] suggest that there is a correlation between the number of eigenPulse attributes and performance. This hypothesis was tested by computing identification rates at each nominal resolution. Both heartbeat and human identification performance are compared by the nominal attribute length (Fig. 11). The results show the correlation between the percentage of heartbeats classified and the percentage of individuals identified (Fig. 11).

Fig. 11 illustrates two important relationships contained within the eigenPulse data. First, the intrinsic dimensionality of the ECG data is considerably smaller than 250 attributes [26–28]. Second, the down-sampling performs more noise reduction than information truncation. This is evidenced by the lack of correlation between the number of attributes and heartbeat classification performance except at the lowest resolution. And, a slight increase in heartbeat classification is observed with reduced resolution.

The raw PCA results are not as good as the fiducial discriminant functions (86% of the heartbeats versus 91%, respectively). However, if the fiducial performance included the 35% of the *failed to enroll* individuals, fiducial classification would fall to 65% for individuals. So, over the entire population eigenPulse performed better than fiducial attributes for human identification.

Even though the PCA system is capable of classifying all of the heartbeats, the classification performance still needs to be improved. One method is to remove poorly recorded heartbeats, outliers, from the datastream. Culling outliers increases collection times because

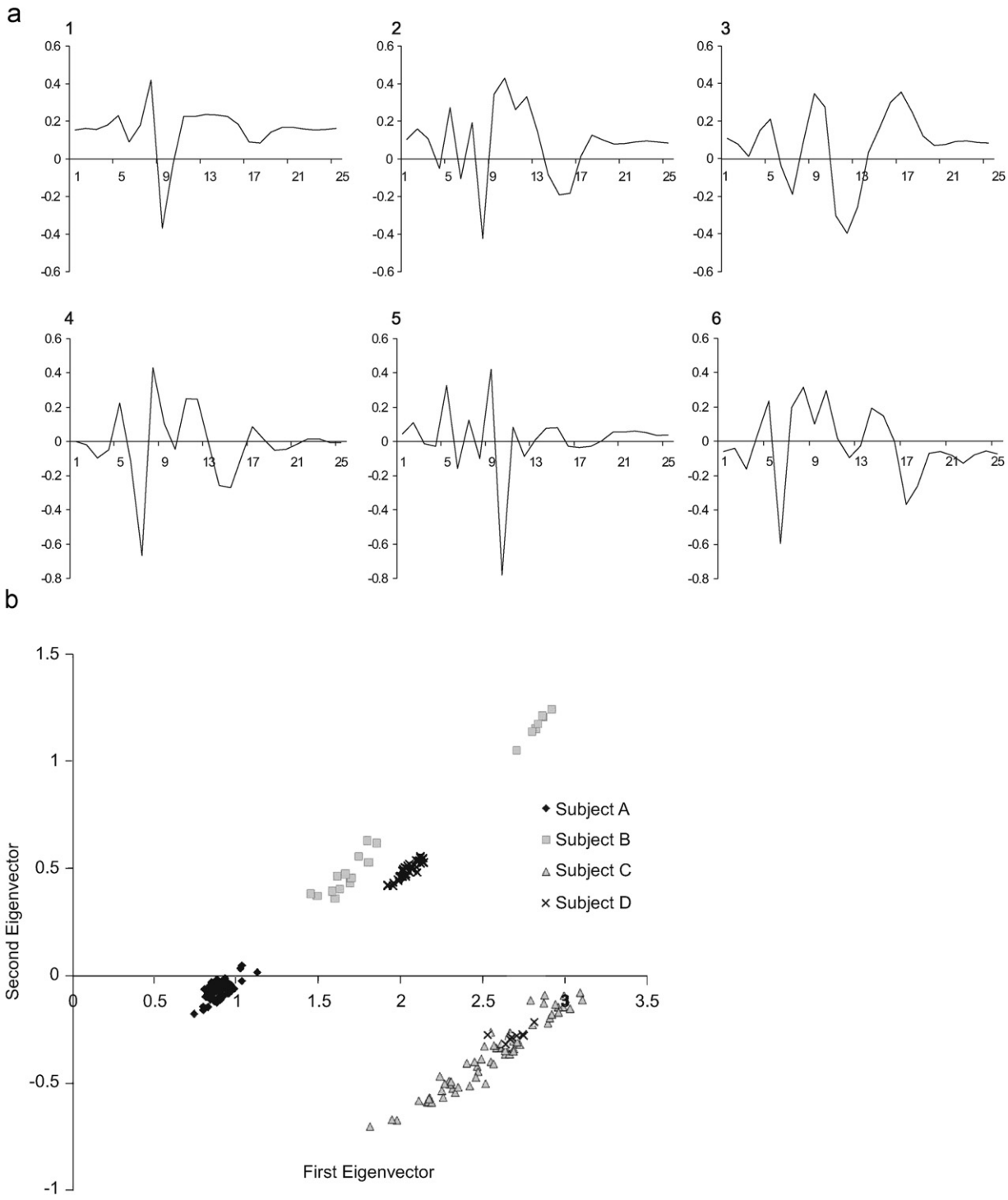

Fig. 10. (a) The eigenvectors corresponding to the six largest eigenvalues for down-sampled heartbeats of length 25. (b) Heartbeats from four subjects from Fig. 3 projected onto the eigenvectors corresponding to the two largest eigenvalues.

a large pool of heartbeats is required to generate a good sample. However, we are exploring outlier removal methods that compare heartbeats to the idealized eigenvector representation. This approach will provide a method for excluding anomalous recordings attribute to instrument error or noise, while retaining heartbeats that arise from unusual physiological properties (e.g. double peaks, missing P waves). In addition, robust methods for estimating the covariance matrix will reduce the influence of outliers in the training data [29].

A second avenue for improving eigenPulse is to employ a more sophisticated classifier. The results reported above relied on simple Euclidean distance of the eigen representation of the probe heartbeat to the corresponding representation in the gallery set and all heartbeats were classified. Investigation of the features space, however, indicates that some individuals exhibit multi-modal data rather than a simple, compact cluster (Fig. 10b). By using a different classifier, such as a self-organizing neural network, these types of clusters

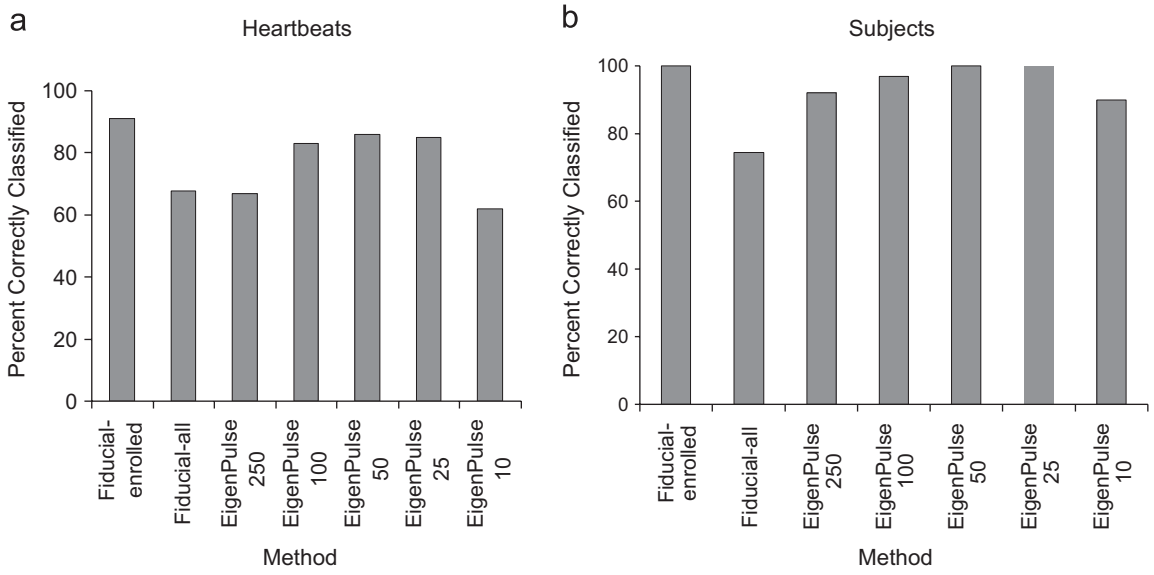

Fig. 11. Classification performance for the various methods: (a) classification of individual heartbeats and (b) classification of subjects based on voting from the heartbeat classification.

can be handled more effectively [30]. In short, we are exploring a variety of methods for improving eigenPulse performance.

6. Summary

This paper presents a new method for human identification using the individual's electrocardiogram (ECG). The method, which we call eigenPulse, exploits PCA that is common with traditional biometrics such as fingerprint and iris. The advantages of our eigenPulse processing are the increase in enrollment rate, the elimination of the fiducial extraction step, and the access to a larger attribute set. All of these eigen decomposition advantages allow the eigenPulse process to operate over larger groups of individuals than previously reported fiducial-based processing. The paper compares the current eigenPulse processing to those experiments previously reported [1].

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