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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.

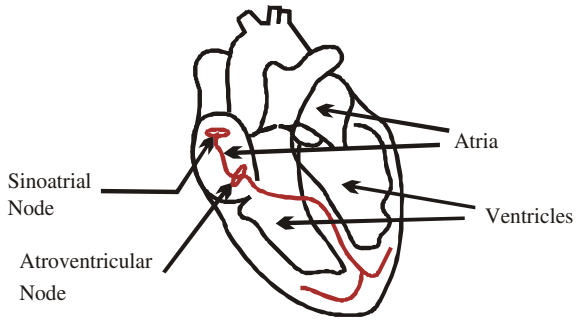

Fig. 1. The heart and its pacemakers: the sino-atrial node is the heart's primary pacemaker and the atrio-ventricular node forces the lag in the depolarization between the atrial and the ventricular contraction.

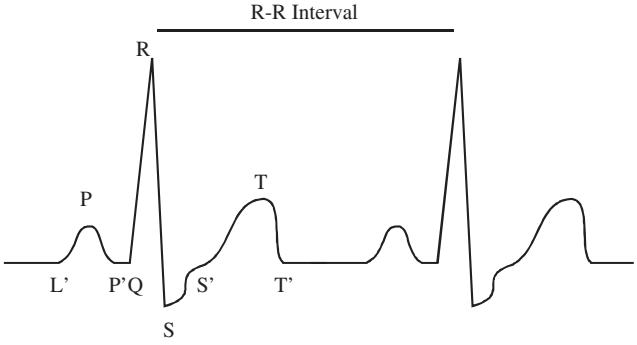

Fig. 2. Ideal ECG signal: this figure depicts two idealized heartbeats.

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