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Full Length Research Paper

Implementation of a one-lead ECG human identification system on a normal population

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The electrocardiogram (ECG) is not only a very useful diagnostic tool for clinical purposes, but also is a potential new biometric tool for human identification. The ECG may be useful as a biometric in the future, since it can easily be combined with other biometrics to provide a liveness check with little additional cost. This research focused on short-term, resting, Lead-I ECG signals recorded from the palms. A total of 168 young college volunteers were investigated for identification as a predetermined group. Fifty persons were randomly selected from this ECG biometric database as the development dataset. Then, the identification algorithm developed from this group was tested on the entire database. In this research, two algorithms were evaluated for ECG identification during system development. The algorithms included template matching and distance classification methods. Signal averaging was applied to generate ECG databases and templates for reducing the noise recorded with palm ECG signals. When a single algorithm was applied to the development dataset, the identification rate (that is, rank one probability) was up to 98% (49 out of 50 persons). However, when the prescreening process was added to construct a combined system model, the identification rate increased to 100% accuracy on the development dataset. The combined model formed our ECG biometric system model based on results from the development dataset. The identification rate was 95.3% when the same combined system model was tested on the entire ECG biometric database.

Key words: Biometrics, biometric liveness tests, electrocardiogram (ECG), ECG features, identification, template matching, distance classification.

INTRODUCTION

Biometric techniques provide one strategy for identity verification. Biometrics use anatomical, physiological or behavioral characteristics that are significantly different from person to person and are difficult to falsify. Several biometric systems that have been used commercially for human identity verification are facial geometry, fingerprints, and voice analysis. Unfortunately, these biometric systems may be deceived without liveness check (Willmore, 2002). ECG analysis (Tompkins, 1993; Webster, 1998) is not only a very useful diagnostic tool for clinical proposes, it is also potentially a good biometric for human identification. The ECG differs from person to person because of the position, size, and anatomy of the heart even among normal people. In addition, age, sex, relative body weight, chest geometry, and various other factors create ECG variants among persons with the same cardiac conditions (Simon and Eswaran, 1997). However, modeling those physiological conditions to ECG biometric features are extremely complicated. For instance, ECG features explain only 25.3% of the variability of the BMI (Shen et al., 2005).

Recently applying ECG for biometric identity recognition has drawn more attention in the research community which is expected to be more universal and

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be hard to mimic. Some pioneer studies showed that it is possible to identify people with a one-lead ECG signal on a small population (<30). Biel et al. (1999; 2001) and Israel et al. (2005) used principle components analysis (PCA) method and our previous research applied correlation coefficients to identified 20 arrhythmia persons from the MIT/BIH database (Shen et al., 2002). Current studies have involved various approaches. Khalil et al. (2008) found the most unique signature bearing parts on QRS Complex of ECG for human identification by applying the high-order Legendre Polynomials. Wang et al. (2008) proposed a combined model on autocorrelation (AC) in conjunction with discrete cosine transform (DCT). Also, the discrete wavelet transform was applied for extracting ECG features from wavelet coefficients. Their experimental results demonstrated that the proposed approach worked well for normal 35 subjects, but the accuracy is reduced on 10 arrhythmia patients (Chiu et al. 2009).

It is challenge to applied ECG identification on arrhythmia patients. The previous work by Agrafioti shows that abnormal ECG or ECG with arrhythmia may affect morphological changes of the signal (Agrafioti, 2009), so their proposed method discards PVC windows to increase the robustness. This may alter the classification decision and performance especially when the system had never been trained with such data. Chen et al. introduce complexity-based approach to deal with abnormal ECG for biometric identification purpose (Chen et al. 2007).

In this article, not only is one-lead ECG analysis for human identification investigated with a larger sample size, but also, all of the one-lead ECG signals are recorded from the subjects' palms. Our database indicates that, even though two people are very similar in size, age, and sex, their ECGs are different. Figure 1 shows an example of two persons with the exact same age, sex, weight and height who have completely different ECG patterns.

Background and significance

The ECG fiducial point detection is essential for temporal feature extraction and template generation. Several digital signal processing technologies were utilized on raw ECG signals to detect PQRST fiducial points, including digital filtering, Pan and Tompkins method, first derivative ECG method (that is, dECG) (Kamath, 2007), and the zero-crossing method. In order to accomplish ECG analysis, it is obvious that the R point is the major landmark which needs to be detected first. After digital filtering to limit the ECG bandwidth from 0.01 to 50 Hz, a reliable, real-time QRS detection algorithm is essential to apply. Pan and Tompkins method (Pan, 1985) was used in this research to determine all the R points in order to calculate R-R intervals.

Once the R point is found, the Q and S points are limited within the 150 ms period which is centered by the R point. In addition, the T wave is complete within a 400 ms period backward from the R point, and the P wave is a 200ms advance from the R point. By using these statistical data with the first derivative ECG, the P, Q, S, and T points can be detected by searching minimum (valley) or maximum (peaks) of all the zero-crossing points within the certain window period $[t_{left} : t_{right}]$. For example, to detect P points, t_{left} and t_{right} were set at 200ms and 40ms advance from R points.

The details are described as following equations:

$$[x \quad y]_{Q,S} = \min_{\text{Q, S points}} \{ECG(find(dECG[t_{left} : t_{right}] = 0))\} \ldots \quad (1)$$

$$[x \quad y]_{P,T} = \max_{\text{P,Tpoints}} \{ECG(find(dECG[t_{left} : t_{right}] = 0))\} \ldots \quad (2)$$

where $ECG(t)$ is the de-noised ECG waveform, and $dECG(t)$ is the first derivative of the $ECG(t)$ waveform $dECG(t)$ combines with zero-crossing method to detect PQST points. After fiducial points are correctly detected, each ECG heart beats is segmented for identification. Henceforth, biometric features are able to be extracted and interested ECG templates are created with 50 points before and after P and T points. In this research, template matching, distance classification, and combined models were investigated for ECG-based human identification.

Template matching method

Signals are correlated if the shapes of the waveforms of two signals match one another. The correlation coefficient provides a quantitative measure of how similar the signals look. It is important to note that the amplitude differences of two signals do not affect the correlation coefficient. The equation for the correlation coefficient is:

$$r_{xy} = \frac{\sum_{n=1}^{N} \{x(n) - \bar{x}\}\{y(n) - \bar{y}\}}{\sqrt{\sum_{n=1}^{N} \{x(n) - \bar{x}\}^2 \sum_{n=1}^{N} \{y(n) - \bar{y}\}^2}} \ldots \quad (3)$$

where the value of r_{xy} varies between 1 and –1 depending on the degree of similarity of the shapes of x and y.

LDA distance classification

The distance in R space can be represented as the

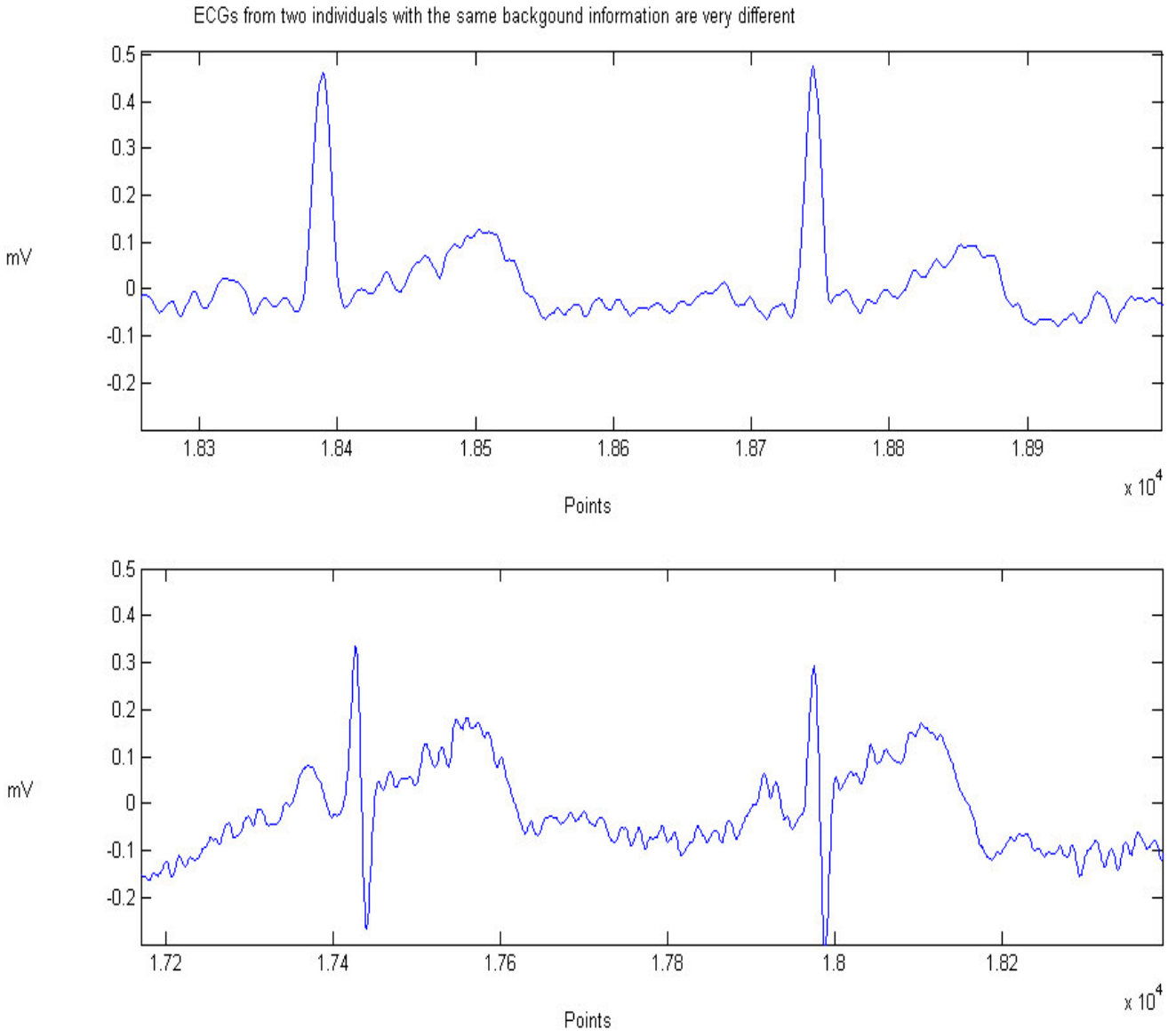

Figure 1. Two subjects (No. 217 and No. 225) have completely different ECG patterns, even though they are the same gender (female), age (21 years old), weight (56.7 kg; 125 lb), and height (170 cm; 5' 7"). The units on the *x* axis are sample data point numbers. The sampling rate of these ECG signals is 500 sps. The units on the *y* axis are millivolts.

similarity between feature vectors x^p and x^q in the Euclidean metric system by:

$$d(x^p,x^q)=\sqrt{\sum_{i=1}^{R}(x_i^p-x_i^q)^2} \quad \ldots \quad (4)$$

However, in the feature space, not all the features are equally weighted. So, this relation can be adjusted by adding a weight vector $w=[w_1,w_2,...,w_R]$.

$$d(x^p,x^q)=\sqrt{\sum_{i=1}^{R}w_i(x_i^p-x_i^q)^2} \quad \ldots \quad (5)$$

The smaller the value of $d(x^p,x^q)$ the closer the distance between vector x^p and x^q. And the distance between two classes, called S_L and S_K, can be described by:

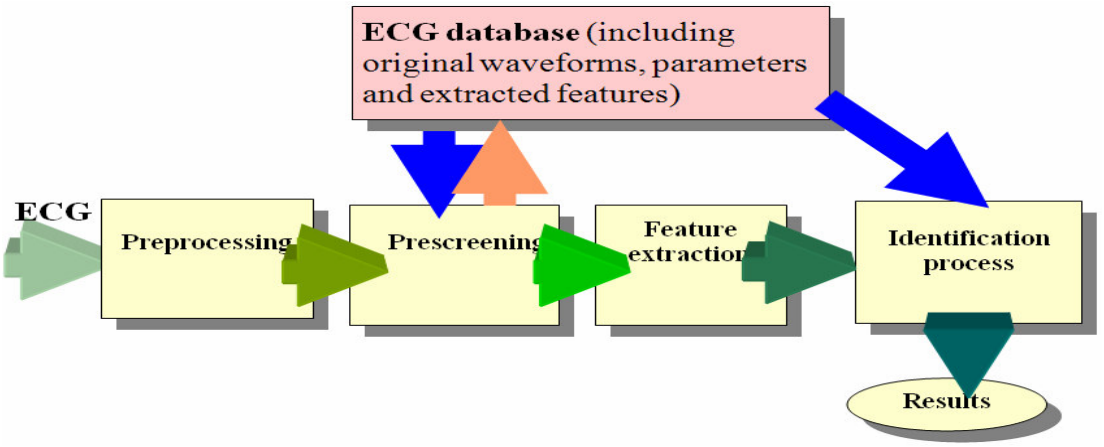

Figure 2. System structure for human identification.

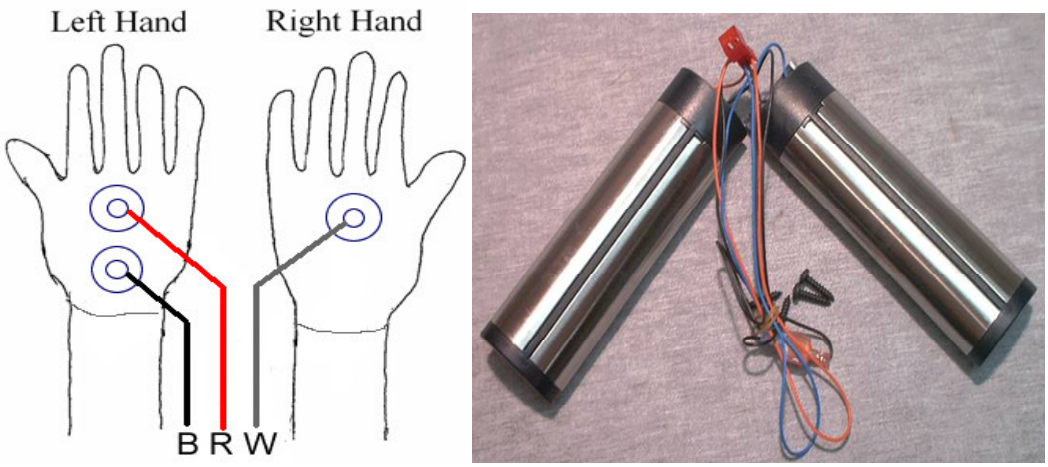

Figure 3. Disposable electrodes were attached to each subject's palms; The measurement layout can be implemented by using dry metal electrodes.

$$D(S_L, S_K) = \frac{1}{m_L \cdot m_K} \sum_{x^p \in S_L} \sum_{x^q \in S_K} d(x^p, x^q) \quad \cdots$$ Where

m_L and m_K are the numbers of feature vectorin S_L and S_K.

System structure

In this research, Lead I ECG signals were recorded from the palms of 168 young college volunteers. Figure 2 shows the block diagram of the human identification system.

EXPERIMENTAL SETUP

Unlike the MIT/BIH database (Goldberger et al., 2000) of ECG signals from cardiology patients, this research focuses on normal, healthy persons. Short-term, resting, Lead-I ECG signals were measured from 168 individuals (113 females and 55 males) to create our ECG biometric database. The ranges of age, weight and height were 19 to 52 years, 45 to 118 kg and 155 to 208 cm, respectively. The interquartile ranges (IQR) of age, weight, and height were 3 years, 13 kg and 15.2 cm, respectively. The subjects' ECG signals were measured and collected with an ECG data acquisition unit (BIOPAC Student Lab PRO system, MP30 with software), electrodes (disposable silver-silver chloride electrodes from BIOPAC Systems, Inc.), and computers (IBM-compatible PCs).

For the lead recording, two electrodes were placed on the left palm and one electrode was placed on the right palm as shown in Figure 3. These subjects were in a resting position and sitting upright, and they were asked to relax with their palms open and resting on their legs. The ECG was recorded for 90 s at a sampling rate of 500 sps for the enrollment process. A calibration procedure was applied by the acquisition software (BIOPAC Student Lab PRO system).

Three sets of ECG databases were generated during enrollment. Because this research surveyed a normal healthy population, all ECG signals were from college students with similar background,

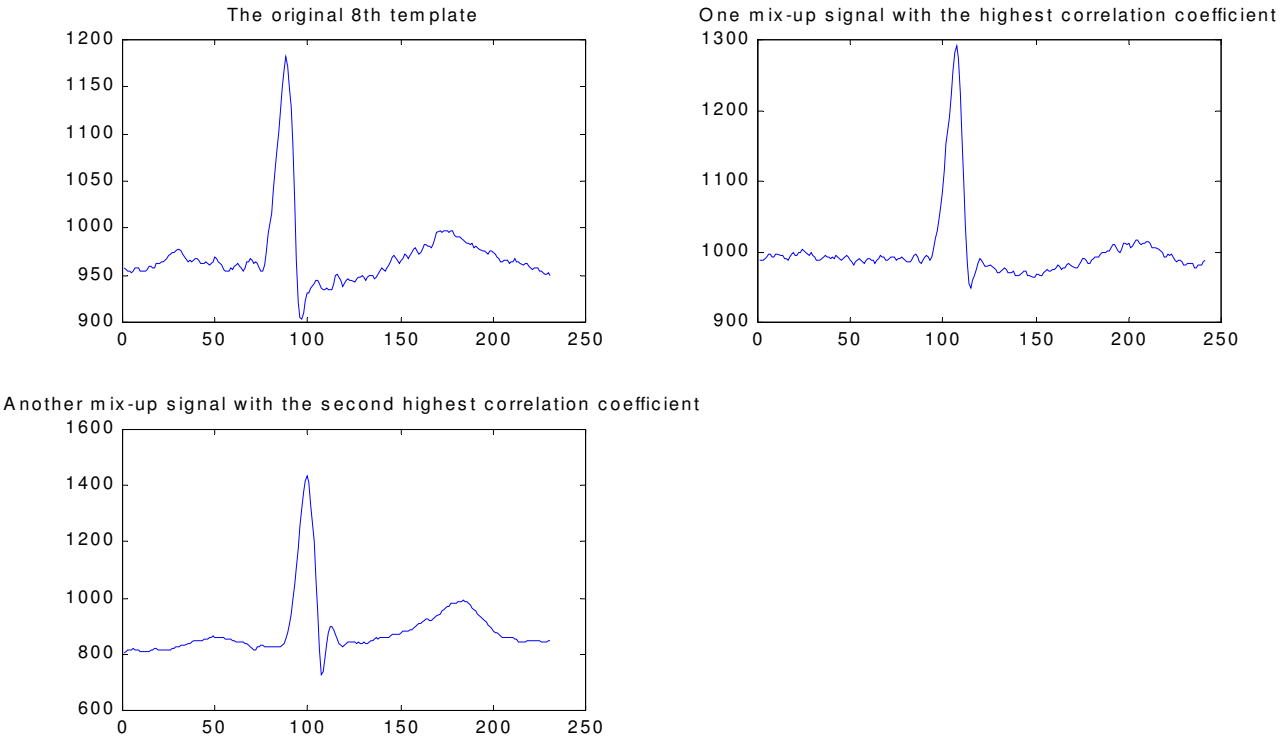

Figure 4. Two similar ECG signals can yield a false positive if only template matching is applied.

such as age and education background. Fifty individuals (33 females and 17 males) were randomly chosen from the database for the system development dataset. Then 20 sequential normal heartbeats were randomly selected by our computer program from each of the 50 individuals in this investigation to form a 1000-beat group as our original ECG database. Next, signal averaging was applied on each 20-heartbeat group to create 50 mean averageheartbeats and 50 median average heartbeats as our second and third databases.

Five methods were used to generate real-time ECG templates (or testing ECG signals). The testing ECG signals were randomly selected from different time slots in the group databases; that is, there is no temporal overlap between the ECG templates and the group database. Five normal heartbeats were picked from each person as testing ECG signals (or real-time ECG templates). Then, each five-beat group was transformed to five different templates by applying signal averaging methods (Tompkins, 1993) for partly eliminating both outliner beats and high frequency interferences: (1) A single heartbeat (randomly chosen without a signal average), (2) A signal-averaged heartbeat using a five-heartbeat-mean method, (3) A signal-median heartbeat using a five-heartbeat-median method, (4) A signal-averaged heartbeat using a three-heartbeat-mean method, and (5) A signal-median heartbeat using a three-heartbeat-median method. Only
one heartbeat was contained in each template. Finally, five input template sets were built.

Preprocessing

ECG preprocessing included selection of appropriate beats and removal of various artifacts. Baseline wander, dc shift, power-line noise, and high-frequency interference were removed (Maglaveras, 1998; Haykin, 2001; Ma et al., 1999). Standard ECG machines have a bandwidth of 0.05 to 150 Hz. However, the noise was so severe for a palm ECG that the signal was band limited to the frequency range between 1 and 50 Hz.

Prescreening

Template matching was used as a prescreening tool. The template (or real-time input) was matched by all the members of the determined group. Correlation coefficients showed to what extent two signals were similar between each template and the pre-determined database. In order to reduce the group size for the identification process, a certain threshold, typically between 0.92 and 0.95, was set on the correlation coefficient to eliminate those members that were not likely candidates. In addition, the maximum size of the candidate group was limited to 10% of the whole sample size. Template matching is limited in its ability to distinguishing among waveforms which are very similar because it ignores amplitude information, which is part of the essential information for identification. An example is shown in Figure 4. ECG machines from all manufacturers use a standard amplitude calibration and a standard bandwidth, so the amplitude and appearance of
the ECG should be the same for a particular individual regardless of when it recorded or what ECG machines it is recorded on.

Improvement of the template matching method

Our goal was to find the best match result of databases and templates. Recursively, the template matching method was applied among the three database sets and five template sets, resulting in a total of fifteen dataset matches. Twelve of these dataset matches are two-single-heartbeat matches, and three dataset matches are 20-to-single-heartbeat matches. Our previous study showed the

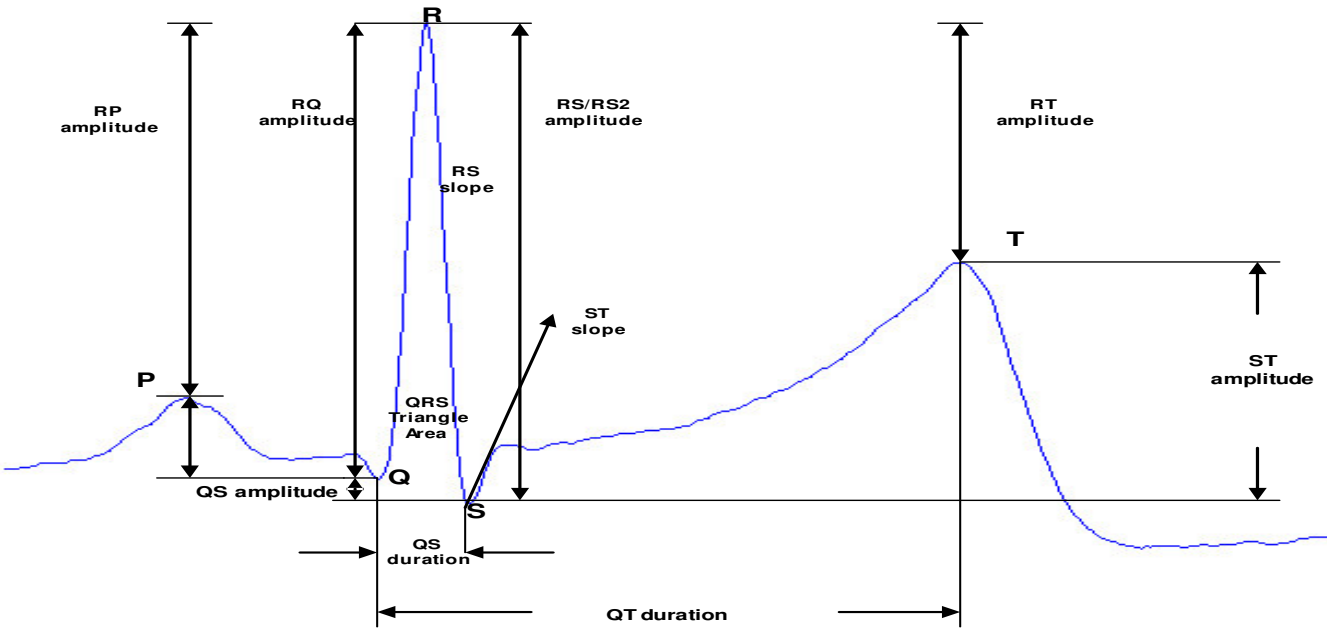

Figure 5. Potential features for classification.

Table 1. Seventeen selected features used for classification.

	Selected features		Selected features		Selected features
1	RQ amplitude	8	RS amp./TS amp.	15	Angle Q
2	QS duration	9	RS2 amplitude	16	Angle R
3	RS amplitude	10	PQ amplitude	17	Angle S
4	ST amplitude	11	QS amplitude		
5	QT duration**	12	RP amplitude		
6	RS slope	13	RT amplitude		
7	QRS triangular Area	14	ST slope		

**The definition of QT duration is different from the clinical definition of QT interval. The QT duration is the time delay between the Q and T point. It has to be normalized with heart rate if not a resting ECG (as is QT interval).

procedure used to obtain 20-to-single-heartbeat matches (Shen, 2002, 2005).

Feature extraction

The 17 ECG features shown in Figure 5 and Table 1 were extracted from ECG waveforms. For comparing among features with different units, all features were normalized using:

$$\text{Normalized feature} = \frac{feature - \min}{\max - \min} \quad \ldots \quad (7)$$

Where max and min represent the maximum and minimum values among 17 features, which came from the development dataset.

These features were selected for identify verification purposes, so some of them may not be meaningful for clinical diagnosis. Most features were extracted from the QRS complex because this waveform is most easily recognized, easy to detect, essential for life, and stable with different heart rates.

The QT time duration depends on heart rate, so normalization must be applied to make sure the QT measurements are usable. One of the commonly used techniques is Bazett's formula, in which the QT interval is adjusted for heart rate by dividing it by the square root of the R-R interval. However, this formula has been criticized for being inaccurate with fast heart rates (Al-Khatib et al., 2003). Our experimental data showed that the Bazett formula fits better with resting heart rate status than the Framingham linear regression equation. In addition, RS2 amplitude is defined as amplitude from point R to the point after 0.024 s delay. An exhaustive test was used to eliminate the bad features or to diminish their weights in order to enhance the identification rate.

Identification process

To avoid misidentification, distance classifications were used in the

Table 2. Template matching results with different template and /or database sets.

Template database	Single heartbeat*** (%)	Five-heartbeat mean (%)	Five-heartbeat median (%)	Three-heartbeat mean (%)	Three-heartbeat median (%)
Twenty heartbeats	42-45/50 (84-90)	45/50 (90)	45/50 (90)	43/50 (86)	44/50 (88)
Mean heartbeat	46/50(92)	49/50 (98)	49/50 (98)	48/50 (96)	48/50 (96)
Median heartbeat	43-45/50 (86-90)	49/50 (98)	49/50 (98)	48/50(96)	48/50 (96)

*** By randomly choosing a single heartbeat as an input template, the results vary with the heartbeat we chose. So, the results are unstable and highly dependent on the chosen heartbeat.

identification process after selecting the possible candidates using the template-matching prescreening. Seventeen features were used for distance classification. The class of an input template can be found by calculating the minimum distances between the feature vectors in an input template and all pre-selected candidates.

Equations (5) to (7) show the mathematical method for finding the distance relationship between two feature vectors and between classes. This method was selected in a combined model for the identification process and used in conjunction with the prescreening process to increase the accuracy of identification.

RESULTS

The template matching method used five different types of template sets to match three different types of database sets. The 15 matching results in Table 2 show that it is not a good idea to pick a single heartbeat randomly as a template because the performance is unstable and highly dependent on the chosen heartbeat. The more heartbeats for signal average processing can provide performance improvement. However, for trade-off on signal quality and system access time, we suggest to capture 5 to 6 continuous heart beats for template making. The entire ECG identification expects to be done within 10 seconds. The best matching results giving 98% accuracy (49 out of 50) occurred when five-heartbeat templates were matched with databases which use averaged heartbeats from 50 to 20-heartbeat groups. That is, the signal averaging approach provided much better template matching performance when the averaged heartbeats were applied to both templates and databases. The templates with more averaged heartbeats offered better performance on the palm ECG biometric system but required more computation time. Even though the signal averaging method removes some high frequencies (Tompkins, 1993), the overall identification rate was still increased. That is, signal averaging removed more interference while preserving biometric traits. Also, there was no difference in using the mean or median as a noise reduction method for template matching.

Without using the entire ECG waveforms, the distance classification calculates the distance from a template feature vector to database feature vectors as described in Equation (6). Exhaustive tests were utilized to determine the appropriate weight vector $w = [w_1, w_2, ..., w_R]$ by ranking these features. The features were eliminated earlier by exhaustive tests; the lower numbers of weights were set. Four levels of weights were used on 17 features. They are 0, 0.2, 1 and 2. However, system performance drops when too many features are assigned to zero (that is, removed). After the weight vector $w = [w_1, w_2, ..., w_R]$ was determined, a 98% (49 out of 50) identification rate was found as the overall performance. In addition, no training process is needed to use distance classification.

The combined system model was investigated using template matching plus LDA distance classification. In Figure 6, the combined system model which unites the template matching method and distance classification was investigated.

There is no training process in this model, so it needs much less time than the previous combined model (DBNN) (Shen, 2005). Hence, the model is more suitable than DBNN for use on a large population.

In the predetermined group with 10, 20, and 50 persons, a 100% identification rate (rank one probability) was also achieved. The rank one probability represents that the identified subjects matched their own templates at the top rank over the entire database. Moreover, the combined system model was further tested in the predetermined group with 100 and 168 people to get 96% and 95.3% identification rates respectively. Figure 7 show that the classification error rate (CER) increased when the number of people in the predetermined group increased. This phenomenon in which the numerical error rate increases when the number of group members increase is fairly typical. The statistical explanation and real data evidence according to the fingerprint biometric can be found in the NIST report to Congress (NIST, 2004).

DISCUSSION

Unlike a clinical ECG database with 12-lead records including limb and thoracic signals, this research focused on palm ECG signals. The ECG recorded from the palms has more noise than the ECG recorded from the torso, but the waveform morphologies are the same as the Lead I ECG. The electromyogram (EMG) interference and baseline wander become more significant when ECGs are recorded from palms; that is, the signal-to-noise ratio

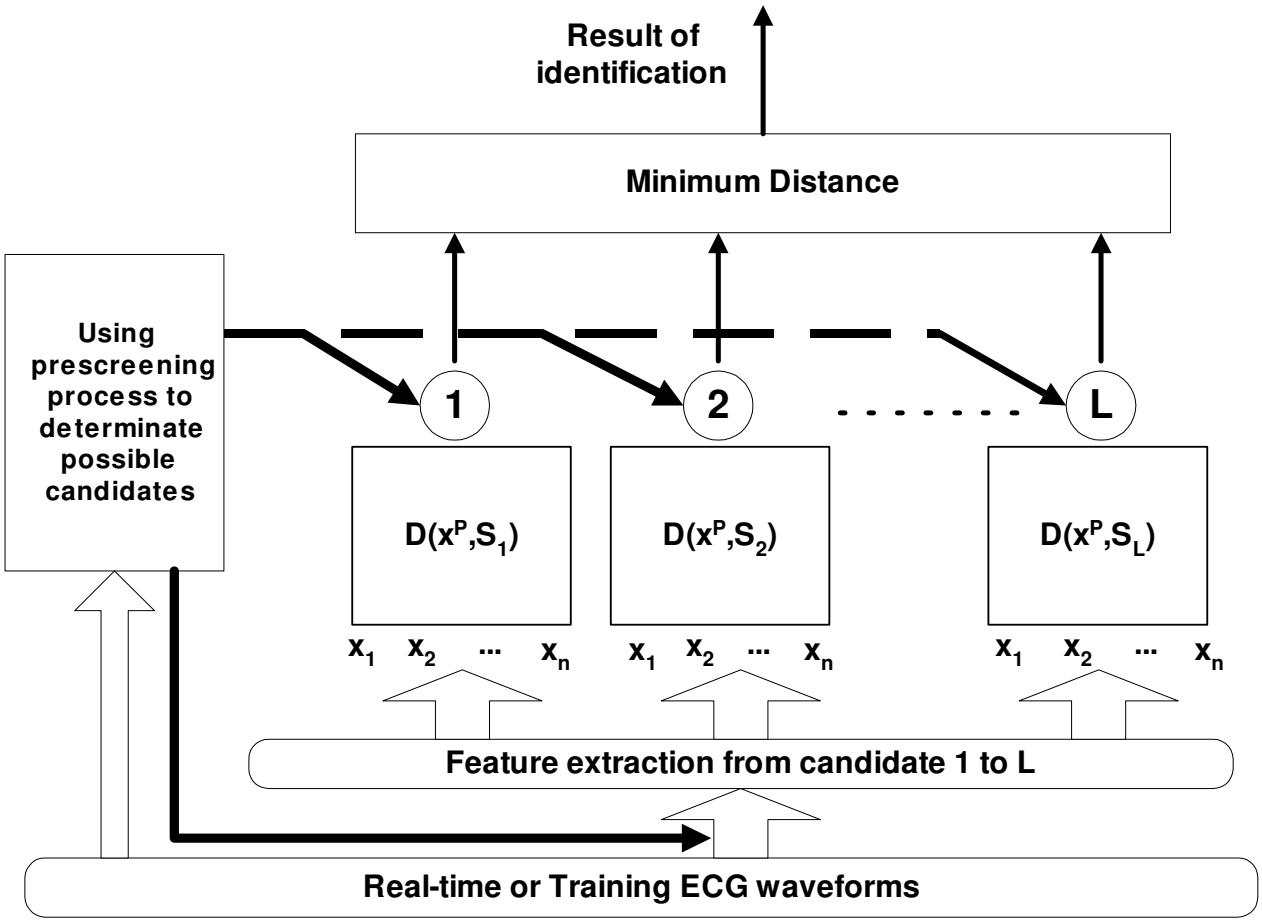

Figure 6. ECG identification model by combining template matching and distance classification.

(SNR) of the palm ECG signal is lower than of the chest ECG signal. However, the big advantages for palm ECG are easy to access, to combine with fingerprint/palm biometrics, and to use mental/dry electrodes. The signal averaging method successfully increased the signal-to-noise ratio thereby improving system performance. However, signal averaging introduces low-pass filtering if the averaged heartbeats are not aligned perfectly, and some identifying features may be distorted by such filtering. Fortunately, benefits gained from reducing interference are much greater than the disadvantages of feature losses using the signal averaging method. Hence, those modified features in the filtered frequency band are insignificant in comparison to the interference from noise.

The feature, angle Q, is not a useful feature because of serious measurement problems. According to Sherwood (1997) and Dubin (2000), Q deflection is small and sometimes absent. Our exhaustive tests confirmed this statement because in our experiments, the accuracy rate always improved if the feature, angle Q, was dropped.

For comparison of identification methods, the major advantage of our combined model (Figure 7) is that no training process needed permitting this technique to be implemented in real-time systems applied to a large population.

Conclusions

This research concentrates on measurements of palm ECG signals from 50 normal healthy persons for human identification. For the combined system model, the identification rate (i.e., rank one probability) was 100% in the predetermined group and 95.3% (160 out of 168 persons) when the same combined system model was tested on the entire ECG biometric database. Based on these results, the Lead-I ECG can be viewed as a potential new biometric for human identity verification. More filter development is desirable for future analysis of palm ECG signals to preserve biometric attributes while improving the signal-to-noise ratio. In addition, the long-term changes of an individual's ECG signals and their implications for implementing a practical biometric system also need to be investigated.

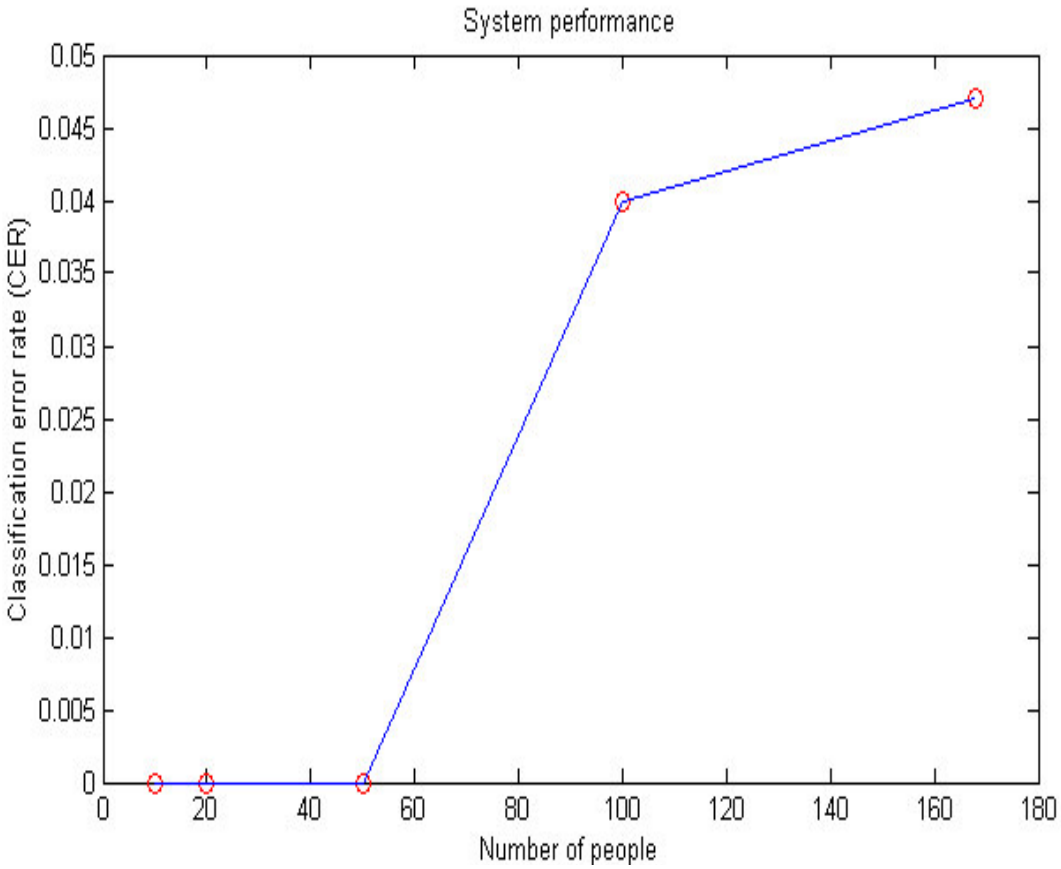

Figure 7. Classification error rate (CER) increased when the number of people in the predetermined group increased.

FUTURE WORK

In this research, only static ECG identification was studied. The current waveform analysis and recognition on ECG biometrics may not be robust on exercise ECGs with unavoidable heart rate increase. Hence, more heart-beat resistance features may come from time-frequency, frequency and other signal decomposition methods. More exquisite equipment and advanced artificial intelligent algorithms would be very helpful to discover other significant ECG features for future human identification.

REFERENCES

Agrafioti F, Hatzinakos D (2009). ECG biometric analysis in cardiac irregularity condition, SIViP, 3: 329-343.

Al-Khatib SM, LaPointe NMA, Kramer JM, Califf RM (2003). What clinicians should know about the QT interval, JAMA, 289: 2120-2127.

Balakrishnama S, Ganapathiraju A (1998). Linear discriminant analysis – A brief tutorial, Institute for Signal and Information Processing, Department of Electrical and Computer Engineering, Mississippi State University, pp. 1-8.

Biel L, Pettersson O, Philipson L, Wide P (1999). ECG analysis: A new approach in human identification, IMTC/99. Proc. of the 16th IEEE Instrumentation and Measurement Technology Conference, 3: 557-561.

Biel L, Pettersson O, Philipson L, Wide P (2001). ECG analysis: A new approach in human identification, IEEE Trans. on Instrumentation and Measurement, 50 (3): 808-812.

Chen S, Thakor NV, Mower MM (2006). Ventricular fibrillation detection by a regression test on the autocorrelation function." Med. Biol. Eng. Comput., 25: 241-249.

Chen SW (2007). Complexity-measure-based sequential hypothesis testing for real-time detection of lethal cardiac arrhythmias, EURASIP J. Advanc. Signal Process., 2007: Article ID 20957.

Chiu CC, Chuang CM, Hsu CY (2009). Discrete wavelet transform applied on personal verification with ECG signal, International Journal of Wavelets, Multiresolution and Information Processing (IJWMIP), 7 (3): 341-355.

Dubin D (2000). Rapid interpretation of EKG's, V ed. Cover Publishing Company, Tampa, Florida, Pp. 368-369

Goldberger AL, Amaral LAN, Glass L, Hausdorff JM, Ivanov PCh, Mark RG, Mietus JE, Moody GB, Peng CK, Stanley HE (2000). PhysioBank, PhysioToolkit, and PhysioNet: Components of a New Research Resource for Complex Physiologic Signals. Circulation, 101(23): e215-e220.

Haykin S (2001). Adaptive filter theory. 4th Ed., New Jersey: Prentice-Hall, pp. 313-322

Israel SA, Irvine JM, Cheng A, Wiederhold MD, Wiederhold BK (2005), ECG to identify individuals. Patt. Recog., 38: 133-142.

Kamath C, Ananthapadmanabhayuyu TV (2007). Modeling QRS Complex in dECG. IEEE Trans. Biomed. Eng., 54(1): 156 - 158.

Khalil I, Sufi F (2008). Legendre Polynomials based biometric authentication using QRS complex of ECG. In: Intelligent Sensors, Sensor Networks and Information Processing, 2008. ISSNIP 2008. Int. Conf., on, pp. 297-302.

Ma WK, Zhang YT, Yang FS (1999). A fast recursive-least-square adaptive notch filter and its applications to biomedical signals, Med. Bio. Eng. Compt,, 37: 99-103.
Maglaveras N (1998). ECG pattern recognition and classification non-linear transformations and neural networks: a review. Int. J. Med. Inf., 52: 191-208.
NIST report to Congress (2004). http://www.itl.nist.gov/iad/894.03/fing/pact1102.pdf.
Pan J, Tompkins WJ (1985). A real-time QRS detection algorithm. IEEE Trans. Biomed. Eng. BME, 32(3): 230-236.
Shen TW, Tompkins WJ (2005). Biometric Statistical Study of One-Lead ECG Features and Body Mass Index (BMI), 27th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC05), pp. 1529-1533.
Shen TW (2005). Biometric Identity Verification Based on Electrocardiogram (ECG), Ph.D. Dissertation, University of Wisconsin, Madison.
Shen TW, Tompkins WJ, Hu YH (2002). One-lead ECG for identity verification, 2nd Joint Conference of the IEEE Engineering in Medicine and Biology Society and the Biomedical Engineering Society, pp. 62-63.
Tompkins WJ (1993). Biomedical Digital Signal Processing, Prentice-Hall, p. 368.
Webster JG (1998). Medical instrumentation, application and design. New York: Wiley, pp. 1-72.