

Palmprint Authentication Using Time Series

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Abstract. Automated personal authentication using biometric features is getting more and more popular for solving the security problems. A new branch of biometric technology, palmprint authentication, has attracted increasing amount of attention because palmprints are abundant of line features and thus low resolution images can be used. In this paper, we propose a new approach for palmprint feature extraction, template representation and matching. Using of time series technologies such as SAX representation and MINDIST calculation is the key to make this new approach simple, flexible and reliable. Experiment shows that this approach can achieve an accuracy of 98.7% when performing one to one verification on a 600 palmprints database. This new approach, which is very computationally efficient, also facilitates the biometric feature fusion as well as palmprint identification using incomplete templates.

1 Introduction

Automated personal authentication using biometric features has been widely studied during the last two decades. Previous research efforts have made it possible to apply biometric systems to practical applications for commercial or security purposes. Among all the existing biometric technologies, fingerprint is the most successful one. However it is still quite difficulty to detect minutiae from dry/wet fingers or fingers from the elders. The high cost of fingerprint sensors has also hampered the social acceptance of this technology. Recently, a novel biometric feature, palmprint [1], has attracted an increasing amount of attention because it has several advantages: palmprints are abundant of line features; low-resolution imaging can be employed; faking a palmprint is quite difficult because the texture is very complicated and one seldom leaves his/her whole palmprint somewhere unintentionally.

Many approaches have been proposed for palmprint authentication [1–7]. These approaches have mainly focused on selecting appropriate features for describing the palmprints. The representation of the features has never been carefully studied. However, in a practical palmprint authentication system, the database might contain templates from millions of people. Choosing a suitable feature representation to make the database small in size and fast responsive to query while keeping high verification accuracy is vital. Also, as multi-biometrics has been proved to be an effective way for improving the reliability of the biometric systems, the convenience and flexibility of using palmprint features as a fusion partner with other different biometric features also needs to be considered.

In this paper, we will propose a new approach for palmprint feature extraction and representation. This new approach makes use of “time series”, a concept which has been widely studied in data mining. The rest of this paper is organized as the follows. Section 2 is a review of the previous palmprint authentication research and a brief introduction to the time series technologies to be used in the paper. Section 3 is the detail description of our approach. Experiments and results are elaborated in section 4. The last section is a conclusion of our work and a discussion on the further work.

2 Related Work

In previous studies, the palmprint features used can be classified into three categories: structural features, statistical features and algebraic features. Typical structural features include principal lines, minutia points and delta points [1, 6]. Statistical features such as texture energy were used in [3, 4, 5], algebraic features such as eigenpalms and fisherpalms were proposed in [2, 7]. Our new approach actually allows adoption of different kinds of features. However, simple statistical features such as gray-level average and variance will be presented in this paper as the key contribution of our work is to use “time series” for the representation of the features.

Time series has been widely studied in data mining [8, 9], bioinformatics [10, 11] and branches of pattern recognition such as biometrics [12, 13]. Technologies such as classification, indexing and motif detection for time series are quite mature. Basically, a time series is a collection of observations made sequentially in time. Nevertheless, as long as the data of interest can be represented sequentially, time series technologies can be applied. In this paper the palmprint features are extracted as data sequences. Time series technologies are applied for the template representation and matching.

One important development in time series research is the introduction of Symbolic Aggregate approxImation (SAX) [14]. SAX is a simple and effective tool for solving most time series problems. The SAX representation is obtained by first transforming the time series into Piecewise Aggregate Approximation (PAA) representation; then predetermined breakpoints are used to map the PAA coefficients into SAX symbols. Basically, SAX converts a real valued data sequence into a string of symbols. MINDIST (minimum distance) is employed to measure the similarity of two SAX symbol strings [14]. In our work, SAX is used for the palmprint template representation and MINDIST is adopted as the matching score of two templates.

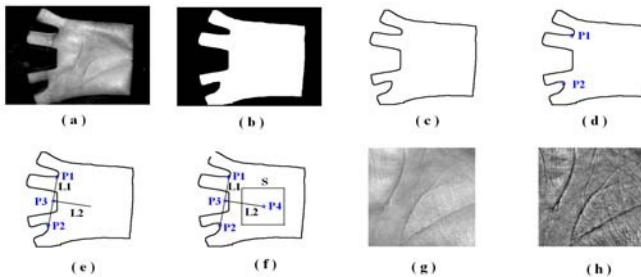


Fig. 1. The palmprint preprocessing

3 Palmprint Representation and Verification

3.1 Palmprint Image Preprocessing

The public palmprint database from the Biometric Research Center, The Hong Kong Polytechnic University, is used in this paper. The palmprints (Fig. 1a) in the database are preprocessed before the feature extraction:

- 1) A threshold is applied to convert the original images into binary images. Isolated pixels are removed. A binarized palmprint is shown in Fig. 1b;
- 2) The palm border (Fig. 1c) is obtained using a border tracking algorithm [21];
- 3) The curvature maxima P_1 and P_2 between the fingers are located using a curvature maxima finding algorithm [22] (Fig. 1d);
- 4) P_1 and P_2 are linked to get line L_1 . Use another line L_2 to pass through the middle point P_3 of L_1 perpendicularly (Fig. 1e);
- 5) A point P_4 is found in L_2 so that the length of $P_3 P_4$ equals to a predefined value. A square S (Fig. 1f) of fixed size (135x135 pixels) is extracted with P_4 as its center (Fig. 1f). S is the region of interest (ROI), from which the features will be extracted;
- 6) The intensity of S is smoothed so that the illumination becomes uniform (Fig. 1h).

Several ROI samples are shown in Fig. 2.

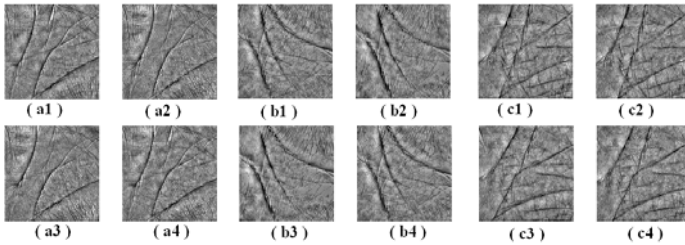


Fig. 2. Extracted ROI squares, (a1) ~ (a4); (b1) ~ (b4); (c1) ~ (c4) are from the same palm

3.2 Feature Extraction and Representation

For time series representation purpose, ROI squares need to be decomposed into sequential data. There are many possible ways of decomposing a 2D image into sequential data. In the MPEG technology, the DCT output of a frame is transformed into sequential data by applying zigzag scan [20]. However, this method is not suitable here. As shown in Fig. 1(f), the ROI square is not rotated according to the direction of L_1 and L_2 . This is because of the low resolution (135x135) of the ROI squares. Distortion and blur caused by the rotation become significant no matter what kind of interpolation method is used. Since the line L_2 has different orientations in different palmprint images, the ROI squares extracted from different palmprint images of the same palm are usually different in direction as shown in Fig. 3.

To solve this problem, we adopt a spiral as the track for the decomposition. The polar equation of a spiral is $r = a\theta^n$. In our implementation, we simply use the Archimedes' spiral with the polar equation $r = a\theta$. a is set to 0.8 empirically. To counteract the effect of direction variation of L_2 , assumed to be θ_0 , we simply include θ_0 in

the polar equation of the spiral as $r = a(\theta + \theta_0)$. Thus, we “rotate” the spiral to adapt the direction of L_2 . It is easy to observe that no matter what θ_0 is, the spiral is invariant in direction with respect to the palm.

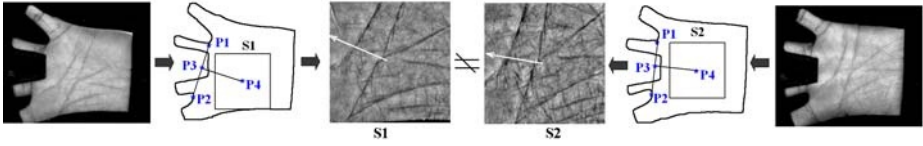


Fig. 3. ROI square direction problem

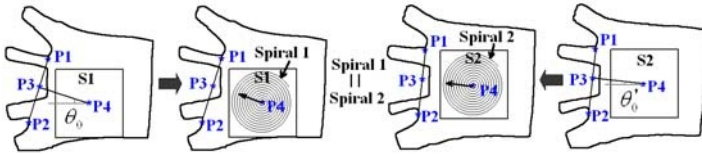


Fig. 4. Use spiral as the feature sequence extraction track

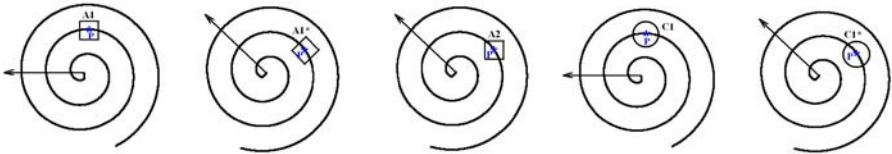


Fig. 5. The problem of using rectangular local area

Fig. 6. Use circular local area

Features are extracted along the spiral. For each point P in the spiral, certain local information at P is used as the feature. Many kinds of local textural features can be used here, such as average intensity, variance, and cross correlation. The shape of the local area has to be carefully selected as the implicit rotation of the spiral must be taken into consideration. Choosing a small rectangle at each tracking point as the local area does not work because rectangle is not rotationally invariant. In Fig. 5, after rotation, A1 changes to A1* instead of A2. To address this problem, we use a circle C as the local area with P as its center so that after rotation C remains invariant (Fig. 6.). The verification accuracy differs when different local texture features are adopted. In this paper, we use average intensity and variance.

For each point on the spiral, the local textural feature is extracted to form the data sequence Q which usually has a quite high dimension (around 2000). Dimension deduction is achieved by converting Q into its SAX representation Q_{sax} [14]. The length and level number of Q_{sax} can be used to control the degree of the dimension deduction [14]. Fig. 7 shows one example of the extracted data sequence and the corresponding SAX representations with different lengths and levels.

The SAX representation Q_{sax} is used as the template of the palmprint. The matching score is obtained by calculating the MINDIST of the two templates. Fig. 8 shows the matching of two templates extracted from two different palmprint images taken from the same palm. The smaller the gray areas are, the smaller the MINDIST is, and the more similar the two palmprints are.

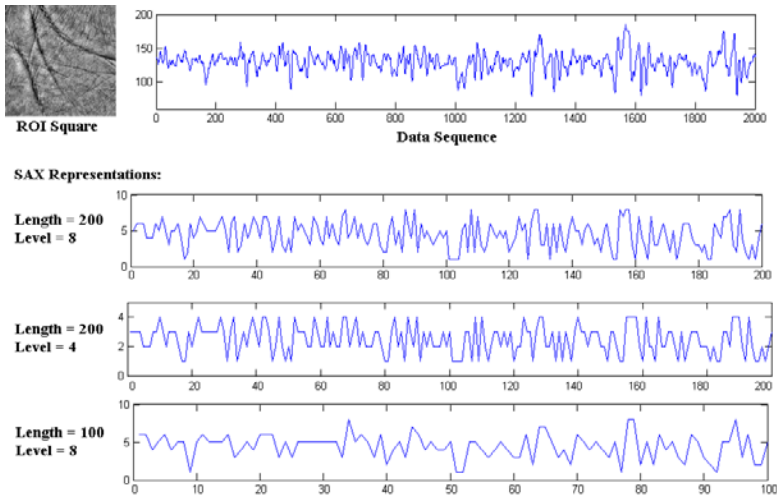


Fig. 7. Data sequence and the corresponding SAX representations with different parameters

Suppose the spiral length is 2000, the radius of C is 5 pixels and intensity average is used as the local feature. The feature extraction process needs around 240,000 additions and 2000 divisions. The computations needed for the SAX conversion and the template matching (MINDIST calculation) are trivial [14]. Compared to the existing methods, the computational complexity of our new approach is considerably low. In an ordinary desktop PC, the time needed for SAX extraction and matching for one palmprint is far less than one second. Thus, our approach is also suitable to be implemented in the relatively slow mobile embedded systems such as PDA.

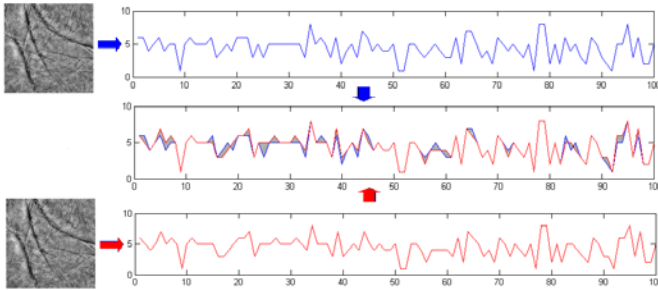


Fig. 8. Palmprint matching using the MINDIST of the SAX representation

4 Experiments and Results

The experiments described in this section are all performed on the PolyU Palmprint Database [15]. The database contains 600 grayscale palmprint images (384x284 pixels; 96dpi) from 100 different palms. Six images from each palm were collected in two sessions, 3 images for each session. The average interval between the two sessions was two months. Three kinds of experiments are performed:

- 1) Accuracy test. The templates for all the palmprints are matched with each other. The verification accuracy is estimated using different features (average intensity & variance), different SAX lengths and different SAX level numbers.
- 2) Fusion test. The templates extracted using different parameters are fused together to investigate the effectiveness of biometric feature fusion.
- 3) Incomplete template identification. Only part of a template (substring of the SAX representation) is used to identify the palmprint from the database.

4.1 Accuracy Test

The templates of all 600 palmprints in the database are extracted and matched (1500 genuine matches, 178200 imposter matches) with each other. Different SAX lengths and level numbers are used and local average intensity and local variance are adopted respectively. The verification accuracy results are listed in Table 1 and Table 2. The ROC curves of several typical test cases are shown in Fig. 9.

Table 1. The verification accuracy using local average intensity

SAX Length	SAX Level	EER(%)	SAX Length	SAX Level	EER(%)
200	10	1.33	200	5	1.51
200	9	1.34	200	4	1.60
200	8	1.51	200	3	1.79
200	7	1.56	100	8	2.01
200	6	1.59	50	8	3.63

Table 2. The verification accuracy using local variance

SAX Length	SAX Level	EER(%)	SAX Length	SAX Level	EER(%)
200	10	3.55	200	5	3.88
200	9	3.56	200	4	3.88
200	8	3.43	200	3	3.30
200	7	3.48	100	8	4.75
200	6	3.68	50	8	6.40

From Table 1 and Table 2 we can see that our new approach has achieved a very high verification accuracy of 98.7%. Also we can see that when the number of the SAX level changes, the verification accuracy does not change abruptly, but the change of SAX length does affect the verification accuracy dramatically. To build a practical biometric system, there must be a tradeoff between the template size and the system accuracy. The experimental results above have shown that longer SAX length is more preferable than bigger SAX level number for a practical biometric system.

SAX representations are small in terms of storage requirement. When SAX length equals to 200 and the level number is 4, each template occupies only 400 bits or 50 bytes. This is one of the advantages of our approach.

4.2 Fusion Test

Multi-biometrics has been proved to be effective for improving the reliability of biometric systems [16, 17]. By using the SAX representation (actually symbol string),

feature fusion (actually string concatenation) can be implemented with ease. The weight of each feature can be easily adjusted by choosing different SAX lengths. In our experiment, we concatenate the SAX representations using different feature extraction schemes (average intensity & variance) to implement a very simple feature fusion. The experiment results are listed in Table 3 in which we can see that the verification accuracy after the fusion is better than using a single feature only. Also, we can see that although test cases II and III have the same SAX length (150) after fusion, the verification accuracy differs a lot. This is because the weight of feature 1 (average intensity) in test case III is higher than that in test case II, and feature 1 (average intensity) is generally more reliable than feature 2 (variance) regarding to the verification accuracy (Table1 and Table2).

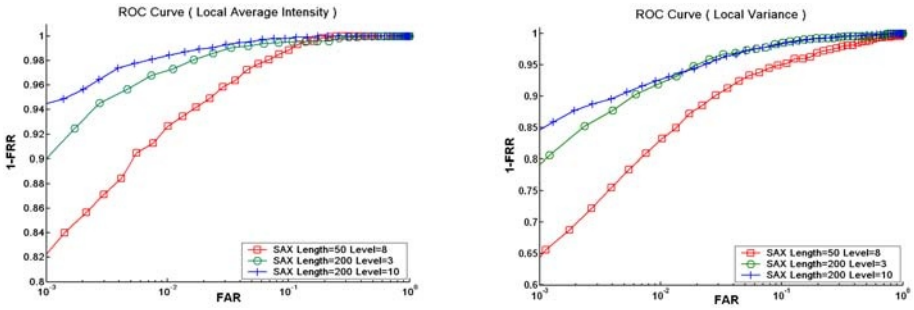


Fig. 9. ROC curves of typical test cases

Table 3. The verification accuracy using feature fusion

Feature 1: Average Intensity			Feature 2: Variance			Feature-Fusion EER (%)	
SAX Length	SAX Level	EER (%)	SAX Length	SAX Level	EER (%)		
100	8	2.01	100	8	4.75	1.99	I
50	8	3.63	100	8	4.75	3.46	II
100	8	2.01	50	8	6.40	1.85	III
50	8	3.63	50	8	6.40	3.08	IV

4.3 Incomplete Template Identification

The purpose of this experiment is to test whether it is possible to identify the input palmprint by using only part of its SAX representation. As the palmprint images are always taken using low resolution input devices such as webcam, and the distortion of the palm is often more obvious than the fingerprints, so it is quite difficult to control the overall quality of the input palmprint images. However, if we can discard the areas of low quality and use the incomplete template to do the authentication, the palmprint authentication technology will become more practical.

We perform the following experiment: Among the 100 palms, we choose 50 to form a database D . For each palm P_x in D , the master template T_x is obtained by calculating the average value of the SAX representations of 2 (randomly chosen) out of the 6 palmprints of P_x . Then remaining 500 palmprints (palmprints used for master templates generation are excluded) are identified according to D . Thus, there will be

200 genuine identification cases (the palms to be identified are really in D) and 300 imposter cases (the palms to be identified are NOT in D).

For each live template T (SAX symbol string), a substring T_s of T is used for the identification. The start position of T_s in T is randomly chosen. The master template T_m of palm P_m which has a substring bearing the smallest MINDIST (d_{min}) to T_s is found out through sequential search. If d_{min} is smaller than a preset upper-bound threshold d_t , then T is identified as belonging to P_m . d_t is adjusted to find out the smallest possible number of the incorrect identification cases (false acceptance and false rejection). In our experiment, we chose the number of the SAX level to be 10 and the length of the master templates to be 200. The results are shown in Table 4.

Table 4. The accuracy of incomplete template identification

Length(T_s)/Length(T)	Minimum Possible Number of Fail Cases	
100%	1	0.2%
50%	7	1.4%
30%	27	5.4%
20%	51	10.2%
10%	120	24.0%

From the above table we can see that even by using only 30% the live templates, we can still achieve pretty high identification accuracy of 94.6%. Fig. 10 shows the matching of an incomplete template with the corresponding master template. As the length of the master template is short (200) and MINDIST calculation process is very fast, the time needed for the identification process is acceptable even if sequential search is adopted.

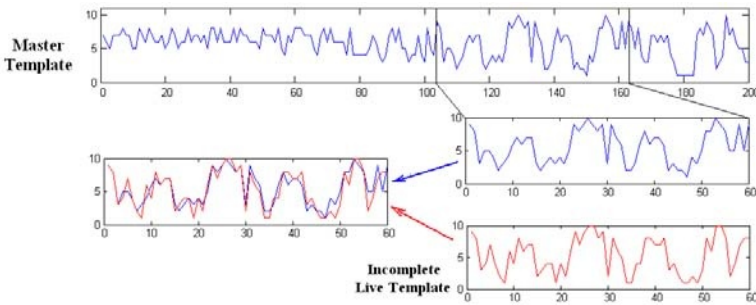


Fig. 10. Incomplete template matching

5 Conclusion and Future Work

We have proposed a novel approach for the palmprint authentication using time series technologies. Using of SAX for the template representation is the key of this new approach. It has the following advantages: first, it is simple to implement and the overall computational complexity is very low compared to previous works; second, it is very flexible as both the local features and the SAX parameters can be adjusted according to different system requirements; third, the SAX representation (essentially

symbol string) makes it very convenient for the implementation of multi-biometrics using feature fusion; fourth, feasibility of the incomplete template matching (substring of SAX) makes this approach more applicable.

However, there are still several problems to be solved. First, the size of the palmprint database used in the experiment is relatively small. Bigger database should be involved to further test the effectiveness of this approach; second, the verification accuracy (98.7%) can still be improved, considering the highest reported results (99.4% in [3], 99.2% in [2]). Using more appropriate local features may improve the accuracy; third, after a careful study of the palmprints for which our approach fails, we find out that most of these palmprints are too bright in certain sub-areas so that the local features are seriously blurred. How to automatically discard these low-quality areas needs to be investigated; fourth, using Dynamic Time Warping (DTW) might help to address the problem of palm distortion and further increase the accuracy [19]; finally, fast string indexing algorithms [18] can be used to improve the efficiency of the incomplete template matching. Also, using non-contiguous SAX slices can make the incomplete template matching more applicable.

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