A Study of Identical Twins' Palmprints For Personal Verification

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Abstract — Automatic biometric systems based on human characteristics for personal identification have attracted great attention. Their performance highly depends on the distinctive information in the biometrics. Identical twins having the closest genetics-based relationship are expected to have maximum similarity in their biometrics. Classifying identical twins is a challenging problem for some automatic biometric systems. Palmprint has been studied for personal identification for over seven years. Most of the previous research concentrates on algorithm development. In this paper, we systemically examine palmprints from the same DNA for automatic personal identification and to uncover the genetically related palmprint features. The experimental results show that the three principal lines and some portions of weak lines are genetically related features but our palms still contain rich genetically unrelated features for classifying identical twins.

Keywords: Identical twins, palmprint, biometric, personal identification.

1. Introduction

Biometric systems measuring our behavioral and biological characteristics for personal identification have advantages over traditional token-based identification approaches using a physical key or smart card, and over knowledge-based identification approaches that use a password. Over the last thirty years, various biometric technologies including face, iris, retina, fingerprint and signature, have been proposed, implemented and deployed [1]. Biometric technologies verifying different people are based on the distinctive information in their biometric traits. However, not all biometrics provide sufficient distinctive information to classify identical twins, who have the same genetic expression. Studying identical twins' biometrics is an important topic for biometric authentication.

There are two types of twins, dizygotic and monozygotic twins. Dizygotic twins result from two different fertilized eggs resulting in different Deoxyribo Nucleic Acid (DNA). Monozygotic twins, also called identical twins are the results of a single fertilized egg splitting into two individual cells and developing into two individuals. Therefore, identical twins have the same genetic expressions. The frequency of identical twins is about 0.4% across different populations [3]. Some researchers believe that this is the performance limit of face recognition systems [4].

1.1. From DNA to biometric

DNA contains all the genetic information required to create an organ of a species. The mapping from DNA to the actual expression of an organ is very complex. Firstly, the genetic information is copied from DNA molecule into RNA (Ribo Nucleic Acid) molecule. Then, the RNA is converted into amino acids and the amino acids are converted into functioning proteins. The proteins are assembled to be an organ. In this decoding process, the final products are affected by not only genetic information but other factors as well. As a result, identical twins sharing the same genetic expression have many different biometrics, including fingerprint, iris and retina [5-7]. In fact, some biometrics such as face continually change after we are born. The changes depend on environmental factors such as living style, diet and climate. These environmental factors make identical twins more different as they age. Fig. 1 shows three pairs of identical twins at different ages. The oldest twins in Fig. 1(c) are the most distinguishable.

1.2. Problems of confusion of twins' identities

In spite of the fact that the biometrics of identical twins are affected by many factors, some of them such as facial features are still very similar. Some identical twins share

2

not only similar facial features but also the same signatures. Confusion over their identities has made it difficult for others to know who owns what and who does what. As a result, some identical twins partake in commercial scams such as fraudulent insurance compensation. Most importantly, if one of the identical twins commits a serious crime, their unclear identities cause confusion and uncertainty in court trials.

1.3. Motivations

Classifying identical twins is crucial for all biometric authentication systems. The systems, which cannot handle identical twins, have an obvious security flaw. Fig. 2 depicts the retinas, irises, fingerprints and palmprints of identical twins. The iris and palmprint images are collected using our self-designed devices [8]; the retina images are obtained from Retinal Technologies, (http://www.retinaltech.com/technology.html) with permission to reprint; and the fingerprint images are collected using a standard optical fingerprint scanner. Fig. 2 shows that the retinas, irises and palmprints are distinguishable to human vision. For the fingerprints, to differentiate the images one must pay close attention to the minutiae points (end points and bifurcation points), commonly utilized in fingerprint systems. Based on the position and direction of the minutiae points, the twins' fingerprints are also distinguishable.

In many cases, biometrics are proposed by medical doctors or ophthalmologists [7] but almost all the biometric systems are designed by engineers. The features discovered by doctors or ophthalmologists and the features applied to authentication systems may not be the same. The iris is a typical example [7, 9]. Therefore, the experimental results or observations given by doctors or ophthalmologists about identical twins may not be applicable to automatic biometric systems. Therefore, it is essential to test automatic biometric systems on identical twins. There has been

research in iris, face, voice fingerprint authentication for identical twins [5, 9-13], however, identical twins' palm is ignored. This paper aims at examining an automatic palmprint system on identical twins and identifying their genetically related features.

The rest of this paper is organized as follows. Section 2 presents a palmprint verification algorithm for this study. Section 3 gives our experimental results and analysis. Section 4 offers some concluding remarks.

2. Automatic Palmprint Authentication

In the following experiments, a relatively new palmprint authentication method, called Competitive Code [14] is utilized. We employ this algorithm since it is the most accurate algorithm developed by our team. The basic idea of Competitive Code is to extract the orientation field as features and use angular distance as a matching function. A brief summary of Competitive Code is given below.

1) Six real part of Gabor filters $\psi_R(x, y, \theta_j)$ with different directions θ_j, are applied to a preprocessed palmprint image, $I(x,y)$ [8].

2) The orientation of a local region is obtained by the competitive rule,

$$k=arg(min_j(I(x,y)*\psi_R(x,y,\theta_j))),\qquad(1)$$

where $j=0, 1, 2, 3, 4$ and 5 and k is called the winning index.

3) Table 1 is used to code the winning indexes. Three bits are used to represent a winning index.

4) Two Competitive Codes are compared by their angular distance. The bit representation of angular distance is defined as,

$$D(P,Q) = \frac{\sum_{y=1}^{N}\sum_{x=1}^{N}\sum_{i=1}^{3}(P_M(x,y)\cap Q_M(x,y))\cap(P_i^b(x,y)\otimes Q_i^b(x,y))}{3\sum_{y=1}^{N}\sum_{x=1}^{N}P_M(x,y)\cap Q_M(x,y)},\qquad(2)$$

4

where $P_i^b\left(Q_i^b\right)$ is the ith bit plane of Competitive Code $P(Q)$; $\otimes$ is bitwise exclusive OR; $\cap$ is bitwise AND; $P_M(Q_M)$ are the mask of $P(Q)$ to denote the non-palmprint pixels and N^2 is the size of Competitive Code. Fig. 3 shows a preprocessed image and the corresponding Competitive Code where different color represents different orientations. We can observe the palm lines in the Competitive Code.

Shorter angular distance represents more similarity between two palmprint images. More computational detail, comparison, and discussion about this method can be found in [14].

3. Experimental Results

We have two possible ways to obtain palmprints generated from the same genetic information. Identical twins' palms are one of them. Left and right palms from the same persons are the other. To make this study more complete, we collect palmprints in both ways. Fig. 4 shows four palmprints from a pair of identical twins. Three of them are similar for human vision but they are still distinguishable. The other is relatively different.

3.1 Database

For this study, we prepare two palmprint databases, twin database and general database. The twin database contains 1028 images collected from 53 pairs of identical twins' palms. The images are collected over half year. Around 10 images are collected from each palm. The age range of the subjects is between 6 and 45. All the images are collected by the self-designed palmprint capture device [8]. The image size is 384×284 with 75 dpi.

The general database contains 7,967 palmprint images from 200 subjects. The palmprint images were collected on two separate occasions. The average time interval between the first collection and second collection was around two months. On each occasion, each subject was asked to provide about 10 images, each of the left palm and the right palm. The image size is also 384×284 and their resolution is 75 dpi.

3.2 Different Types of Palmprint Matchings

To study the similarity between identical twins' palmprints and to obtain a twin imposter distribution, we match the palmprints from the pairs of identical twins' palms (real twin match). We also match the palmprints from the same palms in the general database to obtain a genuine distribution of normal (non-identical) palms. Similarly, we match the palmprints from different palms in the general database to obtain an imposter distribution of normal palms (general match). In addition, we match different person's left palmprints and match different person's right palmprints to obtain a side imposter distribution (side match). We also match the left and right palmprints from the same persons (virtual twin match). For virtual twin match, we flip one of the images to match the other. For the palmprints in the general database, we only match the palmprints from different occasions. The total number of genuine matchings, general imposter matchings, side imposter matchings, virtual twin imposter matchings and twin imposter matchings are 39,673, 15,828,599, 7,894,462, 39,671 and 4,900, respectively; Fig. 5(a) shows these distributions. The genuine distribution along with the four imposter distributions in Fig. 5(a) is used to generate the Receiver Operating Characteristics (ROC) curves given in Fig. 5(b). These figures show that palmprints generated from the same genetic information are significantly correlated and this correlation is neither due to matching between right palms or

6

matching between left palms. However, they still have enough non-genetically related information for classification. For example, if we set the threshold at 0.3725 along with the genuine acceptance rate of 97%, the corresponding false acceptance rate for general imposters is 4.4×10^{-5}% and the corresponding false acceptance rate for identical twin imposters is 2.0×10^{-2}%.

3.3 Identifying the Genetically Related Features.

The previous experimental results demonstrate that palmprints generated from the same genetic information have correlated features. From the observation of Fig. 4, we believe that the strong lines including the principal lines are the genetically related features. The following experiment quantitively justifies this observation.

In this experiment, we successively remove the features points (the winning indexes) associating with the strong lines and use the rest of feature points to perform matching. Using the filter response given in Eq. 1, we can easily identify the strong lines. The corresponding winning indexes are denoted by the masks in Eq. 2. We superimpose the masks to identify the locations of the strong feature points. To provide statistically reliable results, we use virtual twin matchings to investigate the correlated features in this experiment since we have more virtual twin matchings. Virtual twin matchings and real twin matchings are equivalent from genetic point of view since our left and right palms are generated from the same gene as identical twins' palms.

We remove the most 100, 200, 300, 400 and 600 significant winning indexes to generate the general imposter, side imposter and virtual twin imposter distributions shown in Figs. 6(b)-(f), respectively. Fig. 6(a) shows the original imposter

7

distributions for comparisons. To measure the dissimilarity between virtual twin imposter distribution, p and general imposter distribution q, we use Bhattacharyya distance defined as, $B(p,q) = -\log\left(\int \sqrt{p(x)q(x)}dx\right)$. Fig 7(a) shows their Bhattacharyya distances. Similarly, Fig. 7(b) shows Bhattacharyya distances between side and general imposter distributions. Fig. 7(a) illustrates that the dissimilarity of the two imposter distributions decreases when the number of removed winning indexed increases. Comparing the Bhattacharyya distances in Figs. 7(a) and (b), we know that even though we remove more than half of the significant winning indexes, the Bhattacharyya distance between virtual twin and general imposter distributions is relatively large. There are two reasons. Some weak lines are also genetically related. Fig. 8 shows a pair of palm from the same person for illustration. We enhance the small portions for visualization. In addition to the correlation of the weak lines, some winning indexes having weak response are generated from principal lines. To identify the location of the significant winning indexes, we superimpose the masks of all left palmprints in the general database. Fig. 9 gives the distributions of the significant winning indexes. The first 100 significant winning indexes associate with the three principal lines. However, we do not observe any clear structure from others significant winning indexes. According to this finding, the pervious palmprint recognition methods exploiting only the strong lines as features may not be suitable for classifying identical twins [15]. In addition, our finding gives a quantitative evidence for the usage of principal lines for genetic research. However, most of the genetic research about palm lines concentrates only on Simian and Sydney lines shown in Fig 10. [2, 16-18].

4. Conclusion

In this paper, we have systemically examined the palmprints generated from the same genetic information including identical twins' palmprints. This study demonstrates that they can be distinguished by our automatic palmprint identification algorithm. We also give the quantitative evidence to demonstrate that the three principal lines are genetically dependent. This evidence supports the usage of the principal lines for genetic research. It implies that the previous palmprint recognition algorithm exploiting only the strong lines as features may not be able to distinguish identical twins' palmpints. In this study, we also pinpoint that some weak lines are also genetically related. According to our best knowledge, this is the first paper providing a detailed study about identical twins' palmprints for personal identification.

Acknowledgment

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Figures:

Fig. 1   Three pairs of identical twins at different ages

Fig. 2   Different identical twin's biometrics, a) retina, b) iris, c) fingerprint and d) palmprint. The squares and circles on the fingerprint images denote end points and bifurcation points, respectively.

Fig. 3   (a) A preprocessed palmprint image and (b) corresponding Competitive Code.

Fig. 4   Four palmprints from a pair of identical twins.

Fig. 5   Experimental results. (a) Distributions of real twin imposter, virtual twin imposter, side imposter, general imposter and genuine and (b) the corresponding ROC curves.

Fig. 6   (a)-(f), virtual twin, side and general imposter distributions obtained by removing the most 0, 100, 200, 300, 400, and 600 significant winning indexes, respectively.

Fig. 7   (a) The Bhattacharyya distances between general and virtual twin imposter distributions and (b) the Bhattacharyya distances between general and side imposter distributions in Fig. 6(a)-(f).

Fig. 8   Illustration of genetically related weak lines.

Fig. 9   The distributions of the most (a) 100, (b) 200 and (c) 300 significant winning indexes.

Fig. 10   The common palm lines used in genetic research

Tables:

Table 1. Bit representation of the Competitive Code

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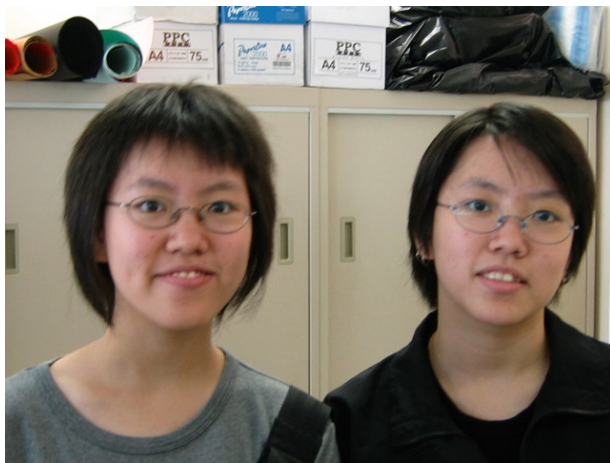
(b)

(c)

Fig. 1
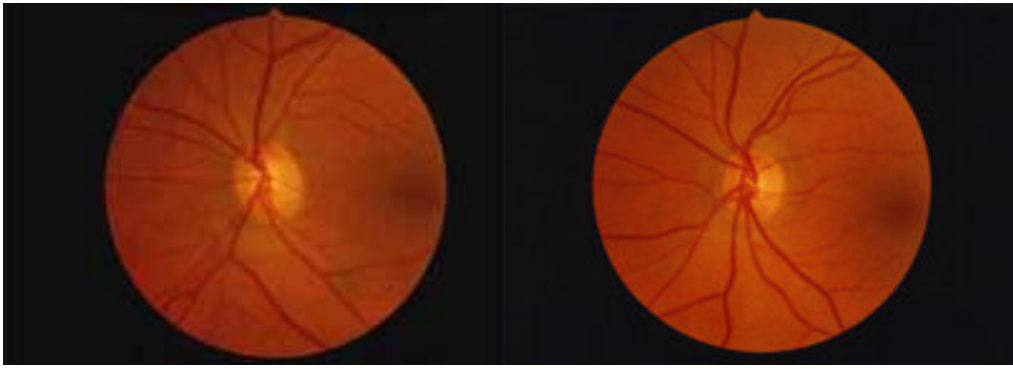
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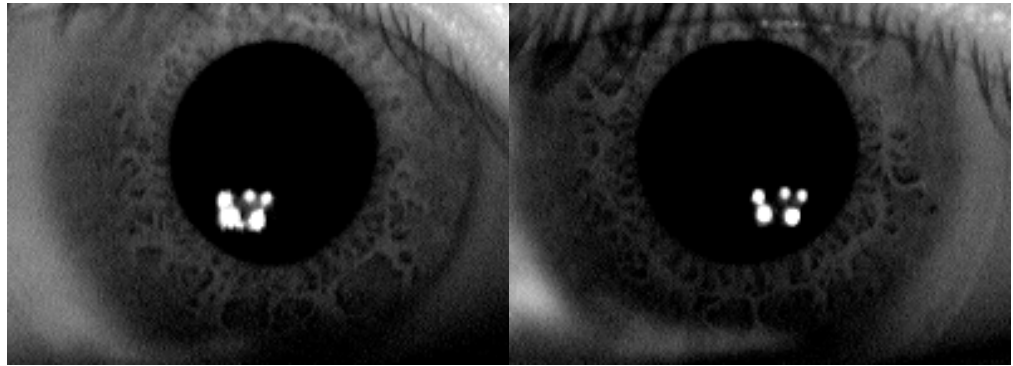
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(c)
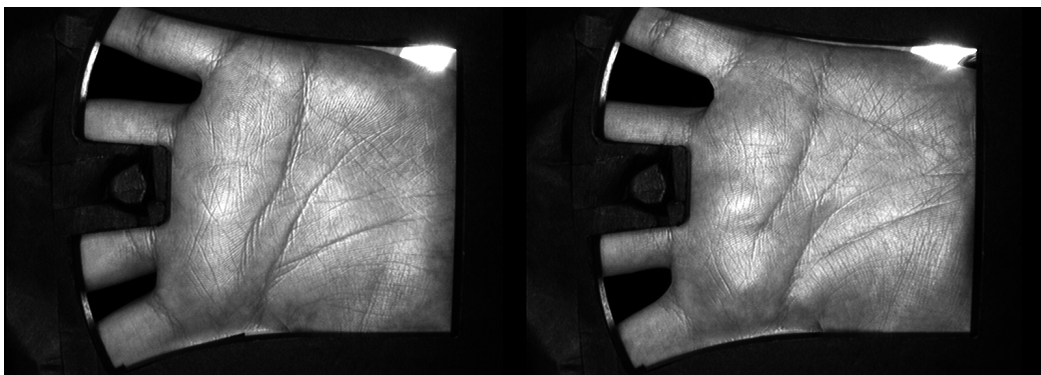
(d)

Fig. 2
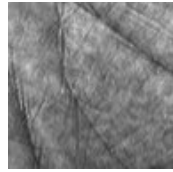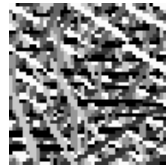
(a)   (b)

Fig. 3
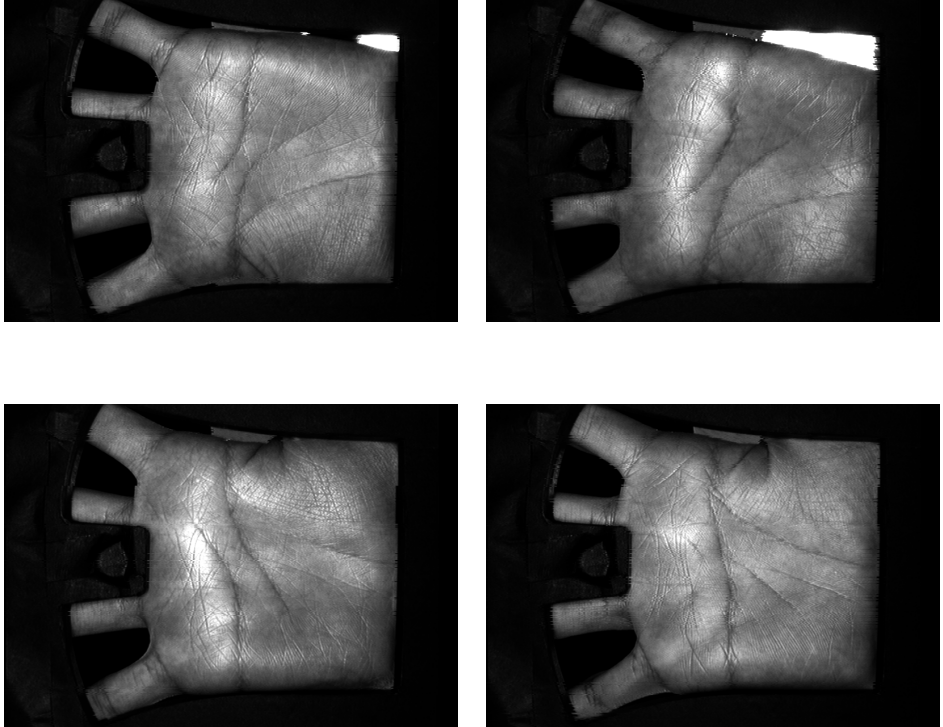
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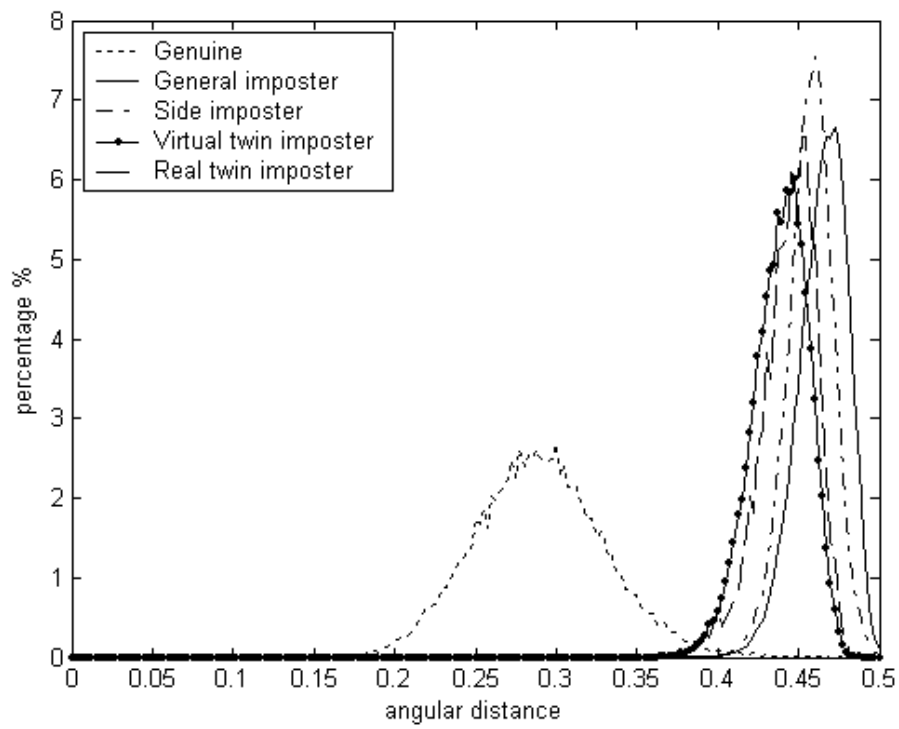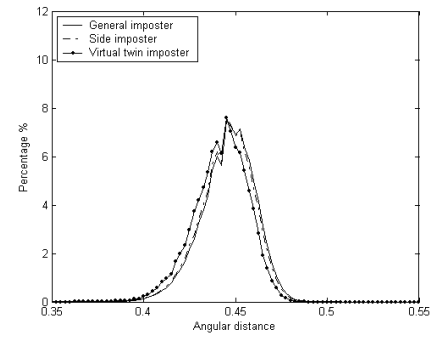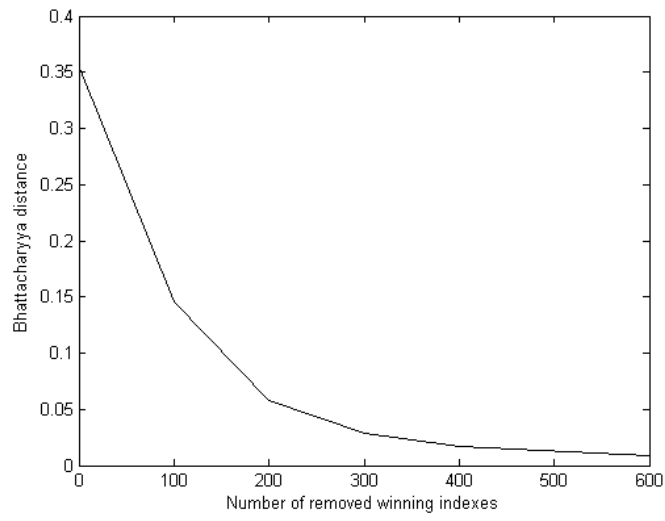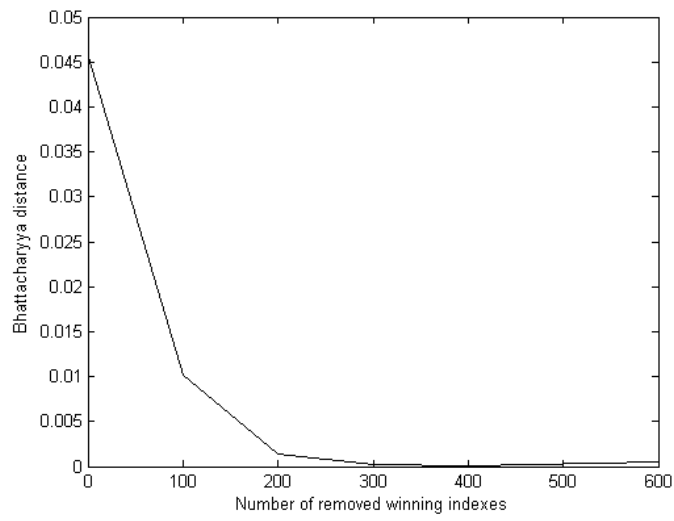
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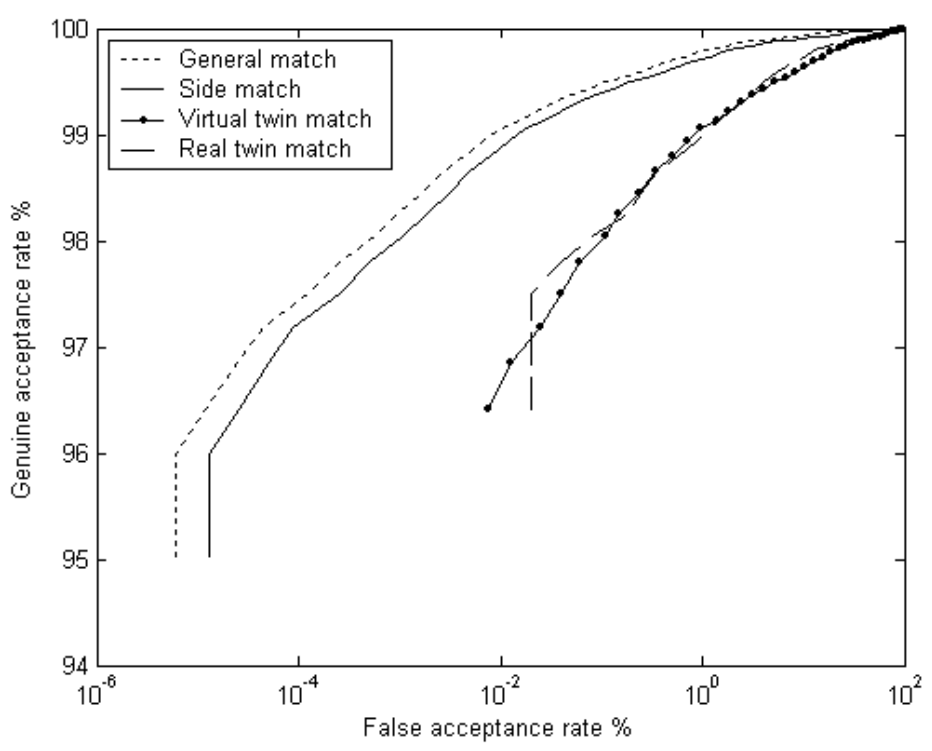
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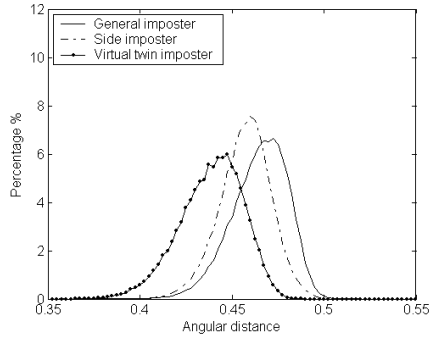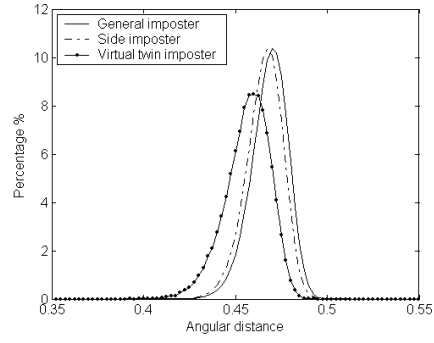
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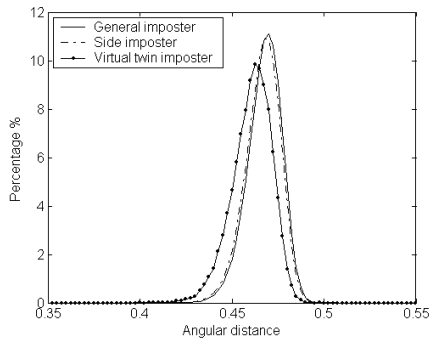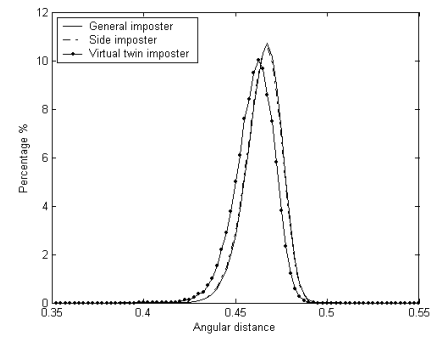
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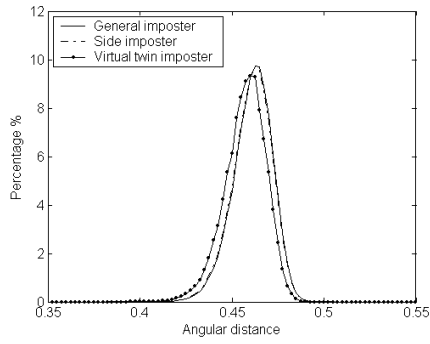
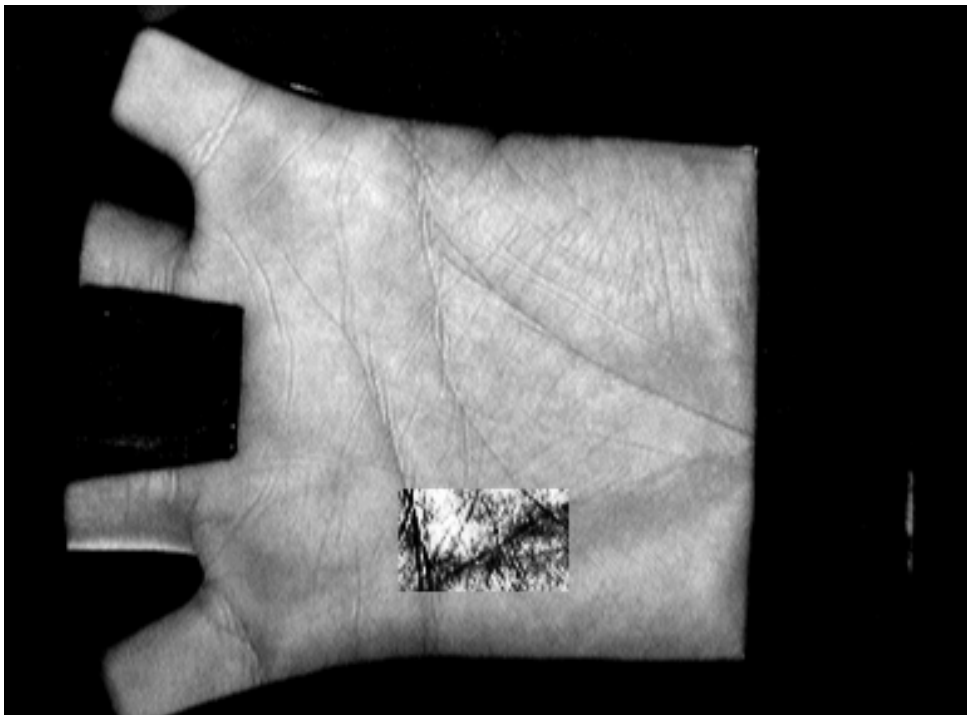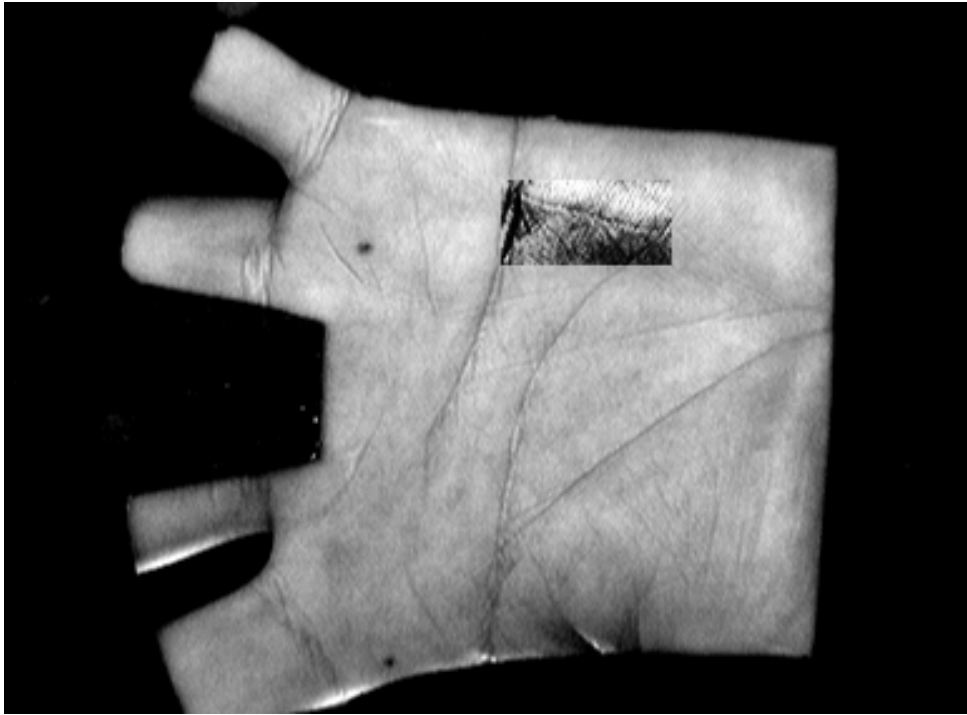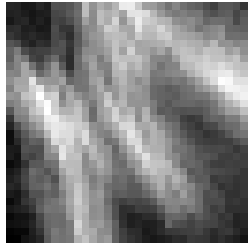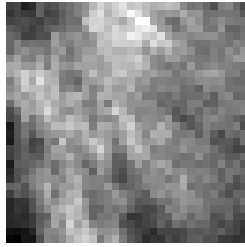(e)   (f)

Fig. 6

(a)

(b)

Fig. 7

Fig. 8
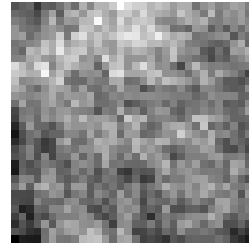
(a)　　　　　　　(b)　　　　　　　(c)

Fig. 9
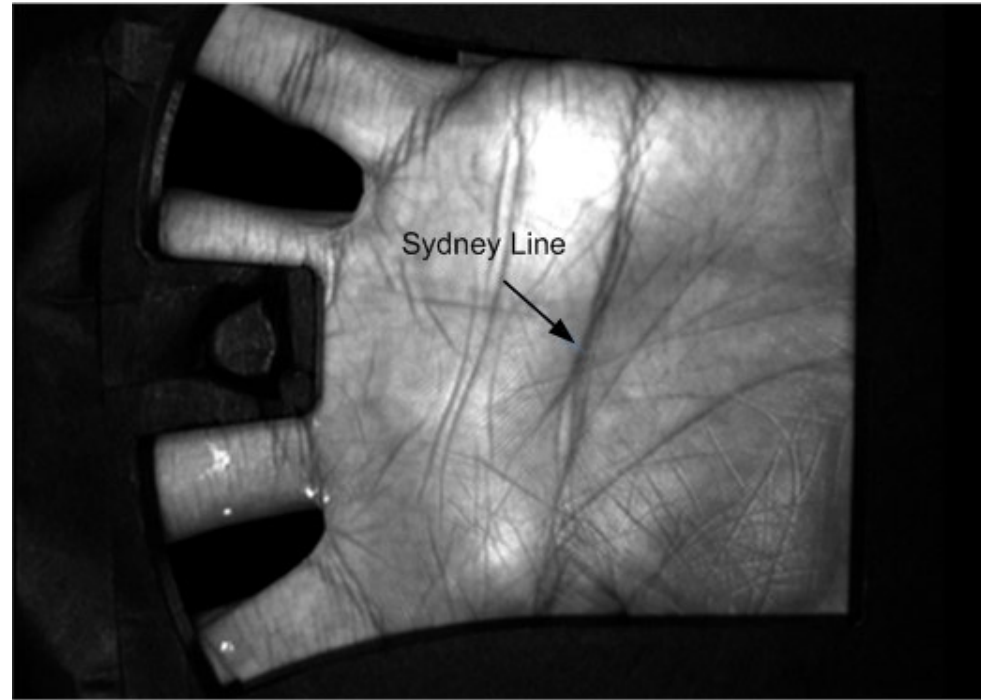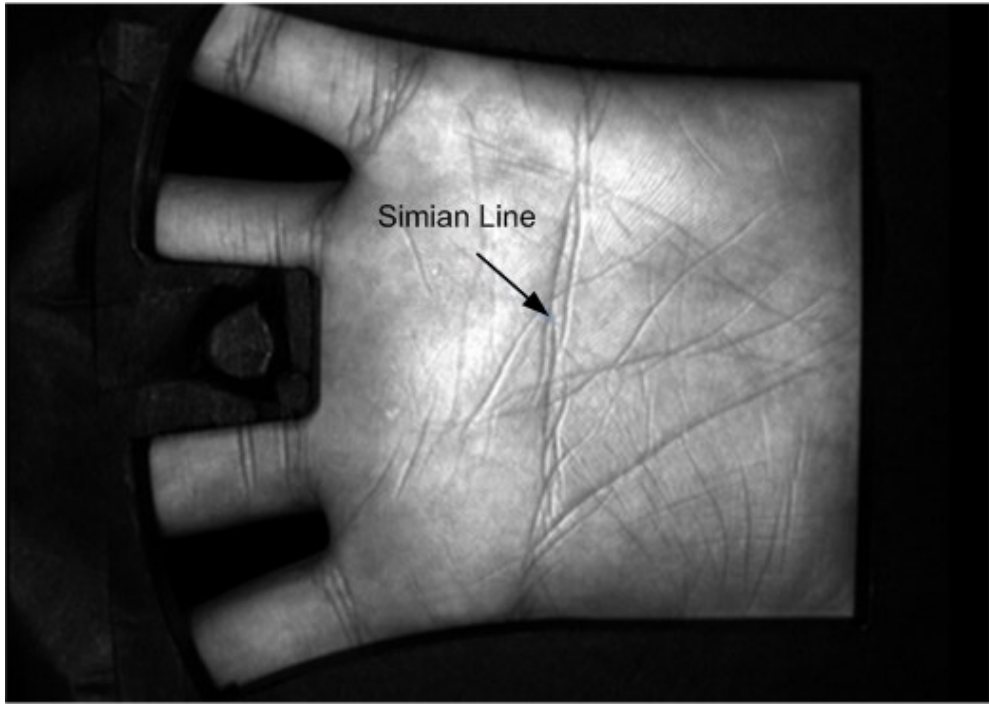
Fig. 10

Table 1

Original values	Bit 1	Bit 2	Bit 3
0	0	0	0
1	0	0	1
2	0	1	1
3	1	1	1
4	1	1	0
5	1	0	0