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On the similarity of identical twin fingerprints ☆

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Abstract

Reliable and accurate verification of people is extremely important in a number of business transactions as well as access to privileged information. Automatic verification methods based on physical biometric characteristics such as fingerprint or iris can provide positive verification with a very high accuracy. However, the biometrics-based methods assume that the physical characteristics of an individual (as captured by a sensor) used for verification are sufficiently unique to distinguish one person from another. Identical twins have the closest genetics-based relationship and, therefore, the maximum similarity between fingerprints is expected to be found among identical twins. We show that a state-of-the-art automatic fingerprint verification system can successfully distinguish identical twins though with a slightly lower accuracy than nontwins. © 2002 Pattern Recognition Society. Published by Elsevier Science Ltd. All rights reserved.

Keywords: Fingerprint; Verification; Identical twins; Performance evaluation; Biometrics

1. Introduction

Biometrics, which refers to automatic identification of people based on their physical or behavioral characteristics is inherently more reliable than traditional knowledge-based (password) or token-based (access card) methods of identification. Traditional methods are prone to fraud because tokens may be stolen and passwords may be guessed. On the other hand, biological characteristics cannot be forgotten, easily shared or misplaced. Moreover, biometrics-based authentication requires that the person to be authenticated be present at the point of authentication to provide his biometric measurement. While the traditional verification methods can establish an absolute "yes/no" verification (either the password provided is correct or it is incorrect), biometrics, on the other hand, determines the degree of "similarity" between the person to be authenticated and the claimed identity. It has been shown that various biometric characteristics are able to establish a "positive verification" with a very high level of confidence.

A number of verification systems based on different biometric characteristics have been developed [1]. For a physical or behavioral characteristics to be useful for verification in an automatic system, it must have the following properties: (i) universality (everyone possesses the characteristic), (ii) permanence (the characteristic remains invariant over life time), (iii) collectible (the characteristic is easy to capture), and (iv) distinctiveness (the characteristic is different for everyone). As the biometrics-based verification is becoming more pervasive, there is a growing interest [2,3] in determining the distinctiveness of biometrics characteristics in order to establish the performance limits of such systems.

The distinguishing nature of physical characteristics of a person is due to both the inherent individual genetic

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diversity within the human population as well as the random processes affecting the development of the embryo [4,5]. Since two individuals can be arbitrarily close with respect to their genetic constitution (e.g., identical twins, the only other genetic relationship that may come close to identical twins is the possibility of human clones. Cloning is a method of producing a baby that has almost the same genetic makeup as its parent [6]), a pessimistic evaluation of identity discrimination based on biometrics may need to rely solely on an assessment of diversity in the traits due to random process affecting human development. Such an assessment strategy would necessarily rely on biometric samples from individuals who are identical/similar in their genetic constitution.

The extent of variation in a physical trait due to random development process differs from trait to trait. By definition, identical twins cannot be distinguished based on DNA. Typically, most of the physical characteristics such as body type, voice, and face are very similar for identical twins and automatic verification based on face and hand geometry will fail to distinguish them. It is, however, claimed that identical twins can be distinguished based on their fingerprints, retina, thermogram, or iris patterns (although, there are conflicting reports on how subtle this distinguishing information is [2]). The focus of this study is to quantitatively determine the similarity of fingerprints in identical twins. We further attempt to assess the impact of this similarity on the performance of automatic fingerprint-based verification systems. Since both, human iris and angiogenesis follow a development pattern similar to fingerprints, we believe the results of this study may be qualitatively applicable to other biometric identifiers such as iris, retina and thermogram (thermogram and retina based person verification is based on features extracted from the underlying vasculature) patterns as well.

2. Fingerprint formation

Fingerprint is the pattern of ridges on the tip of our fingers. It is one of the most mature biometric technologies and is considered a legitimate proof of evidence in courts of law all over the world. Fingerprints are fully formed at about 7 months of fetus development and finger ridge configurations do not change throughout the life except due to accidents such as bruises and cuts on the finger tips. Fingerprints are routinely used by forensic science labs and identification units for criminal investigations. More recently, an increasing number of civilian and commercial applications (e.g., welfare disbursement, cellular phone access, laptop computer log-in) are either using or actively considering to use fingerprint-based verification because of the availability of inexpensive and compact solid state scanners [7] as well as its superior and proven matching performance over other biometric technologies.

Biological organisms, in general, are the consequence of the interaction of genes and environment. It is assumed that the phenotype is uniquely determined by the interaction of a specific genotype and a specific environment. Physical appearance and fingerprints are, in general, a part of an individual's phenotype. In the case of fingerprints, the genes determine the general characteristics of the pattern. Fingerprint formation is similar to the growth of capillaries and blood vessels in angiogenesis [8]. The general characteristics of the fingerprint emerge as the skin on the fingertip begins to differentiate. However, the flow of amniotic fluids around the fetus and its position in the uterus changes during the differentiation process. Thus, the cells on the fingertip grow in a microenvironment that is slightly different from hand to hand and finger to finger. The finer details of the fingerprints are determined by this changing microenvironment. A small difference in microenvironment is amplified by the differentiation process of the cells. There are so many variations during the formation of fingerprints that it would be virtually impossible for two fingerprints to be alike. But since the fingerprints are differentiated from the same genes, they will not be totally random patterns either. We could say that the fingerprint formation process is a chaotic system rather than a random one [8].

How does one assess whether two fingerprints are identical? In order to reliably establish whether two prints came from the same finger or different fingers, it is necessary to capture some *invariant* representation (features) of the fingerprints: the features which over a life-time will continue to remain unaltered irrespective of the cuts and bruises, the orientation of the print with respect to the medium of the capture, occlusion of a small part of the finger, the imaging technology used to acquire the fingerprint from the finger, or the elastic distortion of the finger during the acquisition of the print.

Several representations have been used to assess the fingerprint similarity. At a coarse level, a pattern class similarity (Level 1 information) depends upon categorization of the overall fingerprint pattern into a small number of classes; the five major classes are: whorl, right loop, left loop, arch, and tented arch. At a finer level, fingers can also be distinguished based on their ridge thickness, ridge separation, or ridge depths. Ridge count feature measures the number of ridges between two salient points (e.g., core and delta) on a finger. The most widely used measure of fingerprint similarity is based on minute details (minutiae [10] (Level 2 information)) of the ridges: if the relative configuration (e.g., placement and orientation) of ridge anomalies (endings and bifurcations) of two fingers is similar, then their minutiae-based similarity is high (see, Fig. 1). The primary focus of our work is the fingerprint similarity based on the fingerprint minutiae information. In addition to the fingerprint features described in this section, location and densities of the minute sweat pores (Level 3 information) have also been found to contain information helpful for distinguishing individuals [11].

An important question in fingerprint matching is: which characteristics of the fingerprints are inherited? A number of studies have shown a significant correlation in the fingerprint

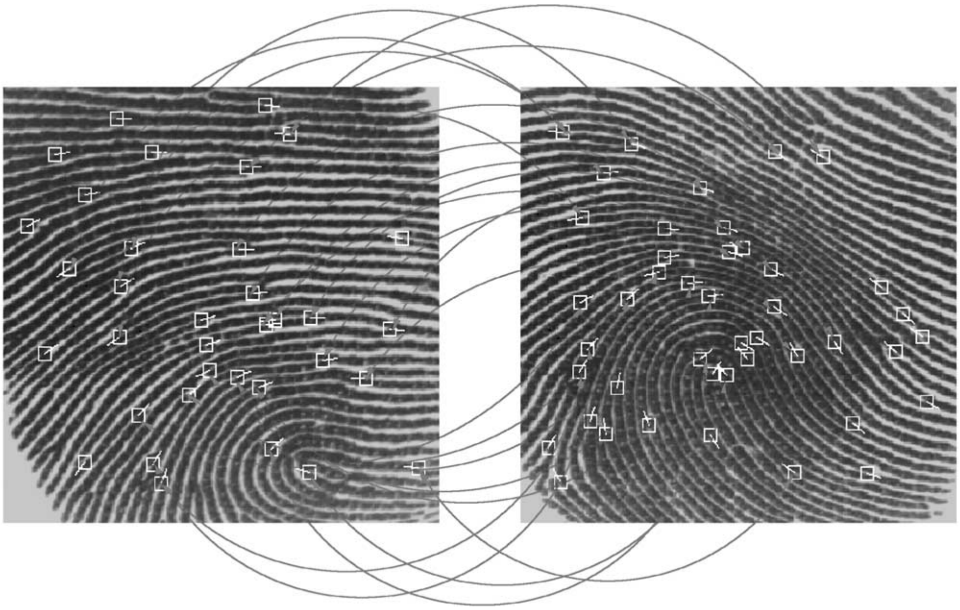

Fig. 1. Relative configuration of ridge endings and branchings between two impressions of the same finger. The minutiae were automatically extracted using the algorithm in [9] and the correspondences were manually determined for illustration.

class (i.e., whorl, right loop, left loop, arch, tented arch) of identical twin fingers; correlation based on other generic attributes of the fingerprint such as ridge count, ridge width, ridge separation, and ridge depth has also been found to be significant in identical twins. In dermatoglyphics studies, the maximum generic difference between fingerprints has been found among individuals of different races. Unrelated persons of the same race have very little generic similarity in their fingerprints, parent and child have some generic similarity as they share half the genes, siblings have more similarity and the maximum generic similarity is observed in the monozygotic (identical) twins, which is the closest genetic relationship [12].

Monozygotic twins are a consequence of division of a single fertilized egg into two embryos. Thus, they have exactly identical DNA except for the generally undetectable micromutations that begin as soon as the cell starts dividing. Fingerprints of identical twins start their development from the same DNA, so they show considerable generic similarity [13]. However, identical twins are situated in different parts of the womb during development, so each fetus encounters slightly different intrauterine forces from their siblings. As a result, fingerprints of identical twins have different microdetails which can be used for identification purposes [12]. It is claimed that a trained expert can usually differentiate between the fingerprints of identical twins based on the minutiae (dis)similarity [12]. Thus, there is anecdotal evidence that minutiae configurations are different in identical twins but to our knowledge, no one has systematically investigated or quantified how minutiae information in identical twins is (un)related in the context of an automatic fingerprint-based authentication system. Daugman [14] claims that left and right irises of the same person while genetically similar can be distinguished by an automatic system even though the machine representations of iris (IrisCode) of genetically similar irises have a smaller degree of freedom as compared to unrelated irises. Daugman evaluated the performance of an iris-based biometric system on genetically identical irises (left and right irises of the same person). The multiple fingerprints of a single individual also share common genetic information and a very common development environment. However, this paper focuses on analyzing the similarity in fingerprint minutiae patterns in identical twin fingers.

Using an automatic fingerprint biometric system [9], we study the (dis)similarity between identical twin fingerprints and compare it to the (dis)similarity between two arbitrary fingerprints. We have confirmed the claim that the identical twin fingerprints have a large class correlation, i.e., if one of the identical twin's fingerprint is a whorl then it is very likely that the other twin's fingerprint will also be of whorl type. We also analyze the correlation between the fingerprint class and the minutiae matching score between two randomly chosen fingerprints. Finally, we stipulate the implications of the extent of the similarity in identical twin fingerprints to the performance of a fingerprint-based person verification system.

3. Automatic fingerprint identification

Fingerprints are represented as a set of points, where each point corresponds to a minutia in the fingerprint. Each

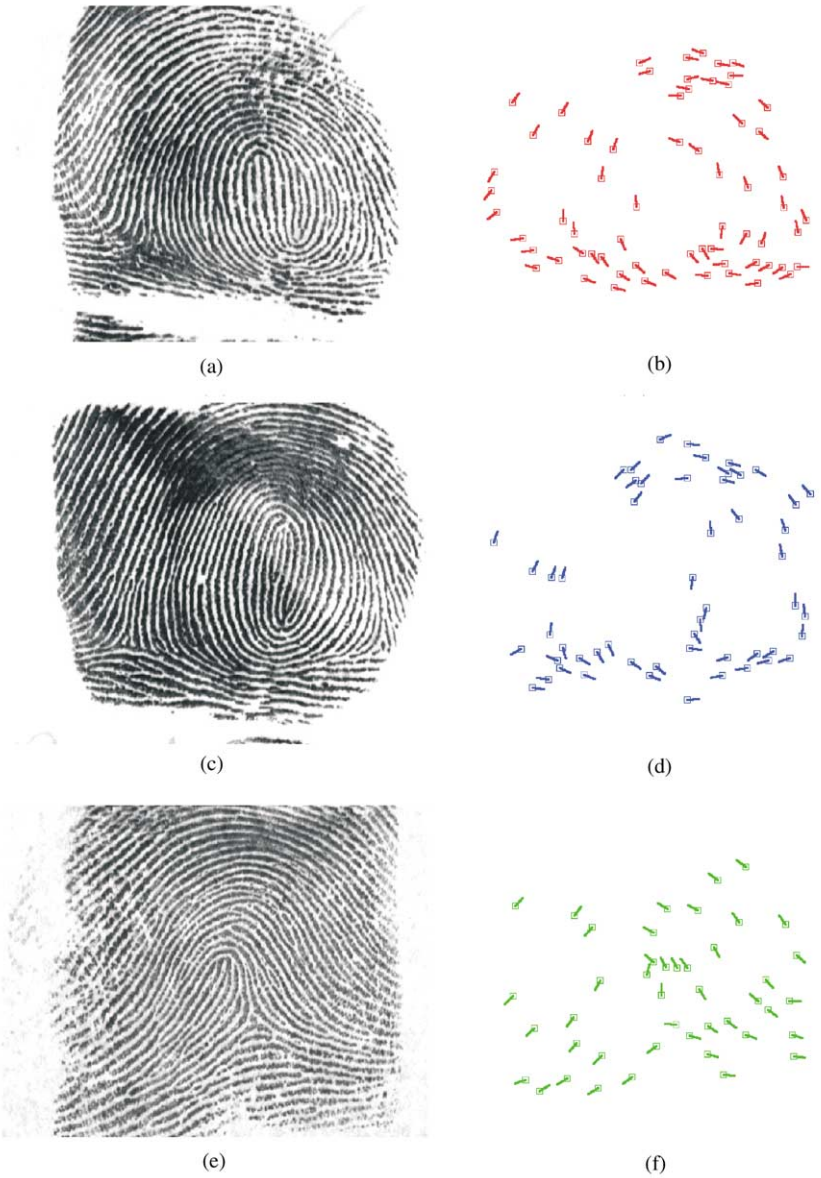

Fig. 2. Minutiae extraction for twins. (a) and (b) are fingerprint images of an identical twin and his/her sibling while the fingerprint in (c) is from another person. (d), (e), and (f) are the minutiae extracted from (a), (b), and (c), respectively using the extraction algorithm in [9].

minutia is characterized by its location, the direction of the ridge on which it resides, and its type (ending, bifurcation, island, etc.). A typical minutiae extraction algorithm first locates the fingerprint ridges and then extracts the minutiae as singular points on the thinned ridge map. In practice, it is not easy for automatic systems to accurately locate ridges in a fingerprint image. The performance of the ridge location algorithm depends heavily on the quality of the fingerprint image. Due to a number of factors such as aberrant formations of epidermal ridges in fingerprints, postnatal marks, occupational marks, problems with acquisition devices, etc., fingerprint images may not always have well-defined ridge structures. Fig. 2 shows the extracted minutiae from some example fingerprints.

Given two representations (minutiae sets), the matching algorithm determines whether or not the associated fingerprints represent the same finger. The matching algorithm in [9] transforms the two minutiae sets to a common frame of reference by an alignment procedure based on translation and rotation (see Fig. 3). The translation and rotation esti-

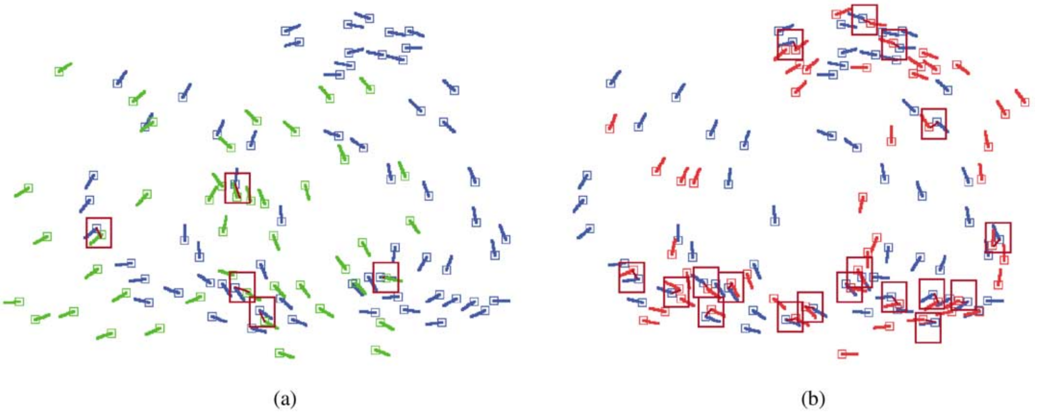

Fig. 3. Minutiae matching for (a) twin–nontwin (matching of Figs. 2(e) and (f), matching score = 3 on a scale of 0–999) and (b) twin–twin (matching of Figs. 2(d) and (e), matching score = 38 on a scale of 0–999). The "matched" minutiae pairs are shown by bounding boxes.

mation is based on properties of the ridge segment associated with a minutia. After the transformation, the matching score is calculated as a function of the number of "matched" (within a tolerance) and "unmatched" minutiae and then scaled to a number between 0 and 999. If this matching score is greater than a prespecified threshold, the verification module accepts the claim that the two fingerprints are impressions of the same finger, and rejects the claim otherwise.

4. Experimental results

An arbitrary subset of the rolled identical twin fingerprints collected for the National Heart, Lung, and Blood Institute (NHLBI) twin study [15,16] was used in our experiments. The fingerprints were acquired using the methods documented in [17]. The fingerprints of the index fingers of 100 pairs of identical twins were scanned using an IBM flatbed color scanner in grayscale mode at 500 dpi resolution. Some of the original fingerprints were in ink while others were taken on a sensitized paper with ink-less fluid. The latter tend to fade with time. Due to differences in paper quality and degradation of the prints over time, several of these fingerprints are of poor quality. We rejected some of the very poor quality fingerprints and used only 94 pairs of identical twin fingerprints in our study. See Figs. 2(a) and (b) for examples of fingerprint images in our twin database.

To study the similarity of identical twins fingerprints, we matched every fingerprint in our twin database with every other fingerprint. See Fig. 2 for examples of minutiae extraction for twin fingerprints. Figs. 3(a), 3(b), and 4 show examples of matching twin–nontwin fingerprints, twin–twin fingerprints, and two impressions of the same finger of a person, respectively. In Fig. 5(a), the dash line shows the twin–twin imposter distribution of matching scores computed by matching a fingerprint with his/her identical twin sibling (twin–twin match), while the solid line shows the twin–nontwin imposter distribution of matching scores between a person's fingerprint and everyone else except his/her twin (twin–nontwin match). The twin–twin imposter distribution was estimated using 188 (94×2) matchings between the 94 twin fingerprint pairs in our identical twin database whereas the twin–nontwin imposter distribution was estimated using 17,484 ($94 \times 93 \times 2$) matchings. Fig. 5(a) shows the twin–twin imposter distribution which is slightly shifted to the right of the twin–nontwin distribution, indicating that twin–twin fingerprints are generally more similar than twin–nontwin fingerprints. The twin–twin and twin–nontwin distributions are found to be significantly different (with 99.99% confidence level) using the Kolmogorov–Smirnov test [18].

A genuine distribution of matching scores is estimated by matching multiple fingerprint images of the same finger. Since we had access to only a single impression of the fingers in our twin database, we had to synthesize the genuine distribution for twin–twin matching. Since the identical twin fingerprints in our database were obtained by rolling inked fingers of the subjects by fairly experienced finger-printers, we expect the genuine distribution characteristics of the twin database to closely correspond to that obtained from a standard public domain fingerprint database (e.g., NIST9 CD No. 1) [19]. This database, consisting of 1800 fingerprint images taken from 900 independent fingers, two impressions per finger, was used to compute the genuine distribution. This genuine distribution along with the two "imposter" distributions in Fig. 5(a) were used to generate the receiver operating characteristics (ROC) [20,21] curves shown in Fig. 5(b). Fig. 5(b) shows that, due to the inherent similarity of twin fingerprints, the ability of the system to distinguish identical twins is lower than its ability to distinguish twin–nontwin pairs. However, contrary to claims made in popular

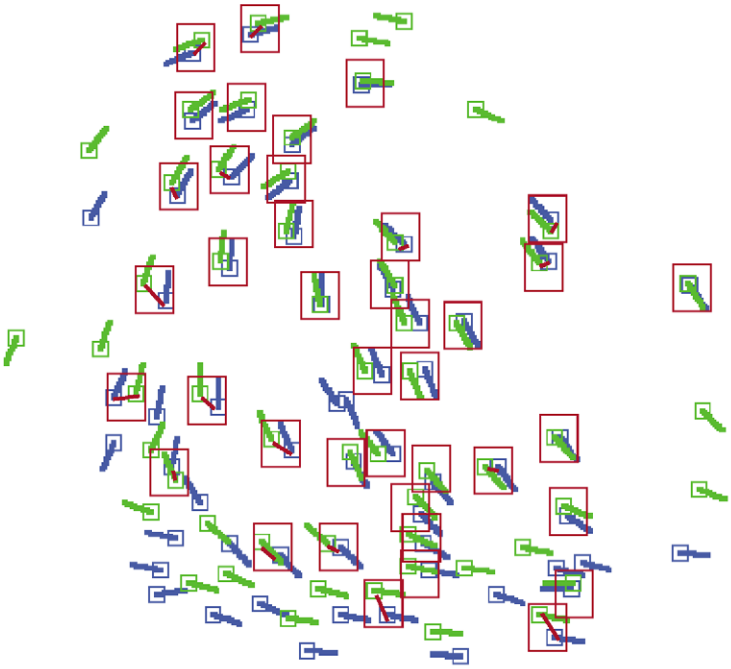

Fig. 4. Minutiae matching for two impressions of the same finger shown in Figs. 6(a) and (b) (matching score = 487 on a scale of 0–999). The "matched" minutiae pairs are shown by bounding boxes.

press [2], the automatic fingerprint verification system can still be used to distinguish between identical twins without a drastic degradation in performance. See Fig. 6 for an illustration. Table 1 shows the trade-off between FARs and FRRs (FAR is also known as false match rate (FMR) and FRR is also known as false nonmatch rate (FNMR) in biometrics [20].) of twin–twin and twin–nontwin matchings for various threshold values on the matching score.

To quantify the performance degradation of a fingerprint verification system due to the inherent twin–twin similarity in fingerprints, we assume that twin–nontwin imposter distribution is representative of the matchings between unrelated people (nontwins). Suppose a fingerprint verification system was set to operate at a decision threshold of T to satisfy the specified FAR requirements. Now, suppose that identical twins use this automatic fingerprint verification system. Since the twin–twin imposter distribution in Fig. 5(a) is slightly to the right of the twin–nontwin distribution, this will increase the FAR of the system but will have no effect on the FRR. The FAR for identical twins is generally 2–6% higher than twin–nontwin matchings depending on the system operating point (threshold values). The quantitative implication of this in the performance of a fingerprint matching system is as follows. Suppose our system is developed (trained) on fingerprints of unrelated people (nontwins) and is set to operate at, say, a threshold of 20 which corresponds to an FAR of $\sim$ 1% (see Table 1). Now, if 1 million unrelated people (nontwins) used the system, then, based on our empirical distributions, 10,000 people will be falsely accepted while 22,000 people will be falsely rejected. However, if 500,000 identical twin pairs (1 million twins) used the system operating at the same threshold of 20, then 48,000 of these will be falsely accepted while 22,000 people will be falsely rejected. Notice the increase in the false acceptance rate for twins.

To safeguard against "twin fraud", we can set the operating point of our system pessimistically at a threshold of 26 which corresponds to an FAR of $\sim$ 1% for twin–twin matchings and an FAR of $\sim$ 0.3% for twin–nontwin matchings. This raises the FRR to $\sim$ 3.5% as opposed to 2.2% when operating at a threshold of 20. This means that in the worst case scenario (when all the people accessing the system are identical twins), the system will falsely accept 10,000 people out of one million at the expense of falsely rejecting 35,000 people. In the best case (when there are no twins accessing the system), only 3000 people will be falsely accepted while falsely rejecting 35,000 people. In practice, the system will falsely accept between 3000 and 10,000 people (between 0.3% and 1%), depending upon the fraction of twins in our sample population of 1 million while falsely rejecting 35,000 people.

Dermatoglyphics studies have suggested that there is a high class/type similarity in the fingerprints of identical twins. To confirm this claim, we manually classified the 94

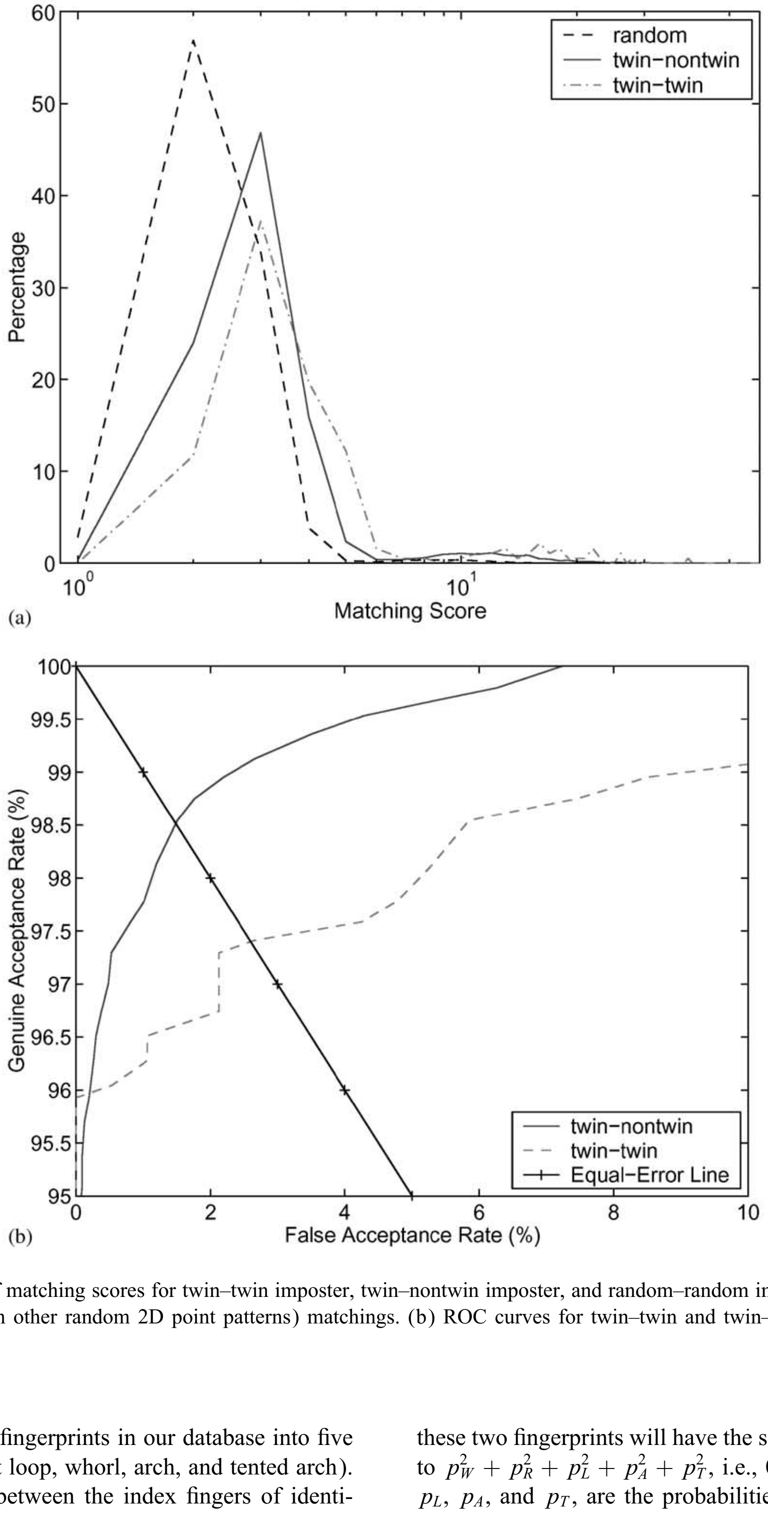

Fig. 5. (a) Distribution of matching scores for twin–twin imposter, twin–nontwin imposter, and random–random imposter (random 2D point patterns are matched with other random 2D point patterns) matchings. (b) ROC curves for twin–twin and twin–nontwin minutiae pattern matchings.

pairs of identical twin fingerprints in our database into five classes (right loop, left loop, whorl, arch, and tented arch). The class correlation between the index fingers of identical twins (fraction of identical twin pairs whose index fingerprints have the same class label) is found to be 0.775 (based on Table 2). If we randomly choose two index fingerprint images from a large database, the probability that these two fingerprints will have the same class label is equal to $p_W^2 + p_R^2 + p_L^2 + p_A^2 + p_T^2$, i.e., 0.2718, where p_W, p_R, p_L, p_A, and p_T, are the probabilities of a fingerprint chosen at random belonging to the class of whorl, right loop, left loop, arch, and tented arch, respectively. Thus, there is only 0.2718 chance that two randomly chosen index fingers will have the same type which is much lower than the 0.775

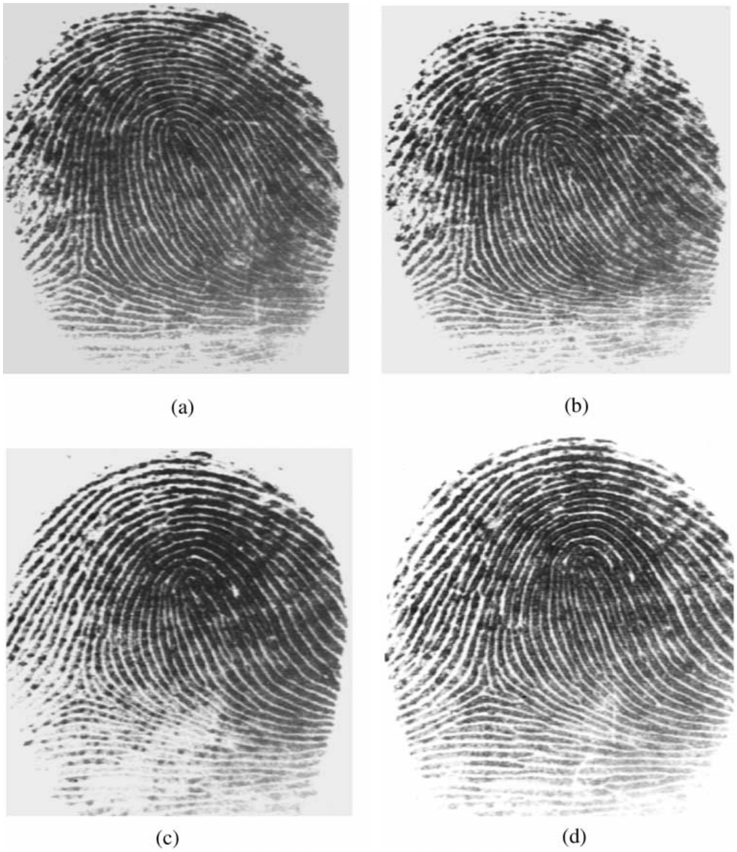
(a) (b) (c) (d)

Fig. 6. Fingerprint images of identical twin sisters captured using an optical scanner from Digital Biometrics Inc., (a) and (b) are two impressions of the same finger of one twin and (c) and (d) are two impressions of the corresponding finger of her sibling. Matching scores between (a) and (b) is 487, and between (c) and (d) is 510. The matching score between (a) and (c) is 24, and the matching score between (b) and (d) is 4. The fingerprints of both the twins here have the same type (right loop) and look similar to untrained eyes. Fingerprint experts, as well as our automatic fingerprint verification system can, however, easily differentiate the twins.

Table 1
False accept and false reject rates with different threshold values for the twin–twin and twin–nontwin matchings in the identical twin database

Threshold	FRR (%)	FAR (twin–twin) (%)	FAR (twin–nontwin) (%)
16	1.05	8.51	2.20
20	2.20	4.79	1.02
24	3.00	2.13	0.48
26	3.49	1.06	0.29

Table 2
The natural proportion of occurrence of each of the five major fingerprint classes in the index finger (based on an unpublished 1995 report by Frank Torpay of Mitre Corporation using data extracted from the FBI's Identification Division Automated Services database of 22,000,000 human-classified fingerprints)

Whorl (W) (p_W)	Right loop (R) (p_R)	Left loop (L) (p_L)	Arch (A) (p_A)	Tented arch (T) (p_T)
0.3252	0.3638	0.1703	0.0616	0.0779

chance that the fingerprints of two identical twins will have the same class label.

We believe that the global similarity of fingerprints (shown as class/type similarity) is, to a certain extent, responsible for the local similarity (shown in the matching performance). Consider two fingerprints that belong to the same class (e.g., right loop). Since the minutiae can exist only along the ridges (although at random locations), the matching score between these two fingerprints is likely to be higher than the matching score between two sets of random point patterns. To study the correlation of class

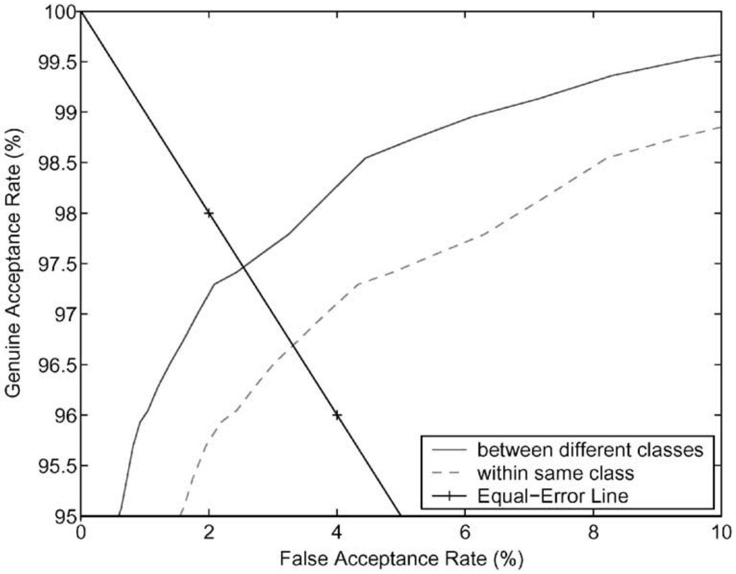

Fig. 7. Effect of fingerprint class type on the matching score.

Table 3
False accept and false reject rates with different threshold values for the within-class and between-class matchings in the NIST4 database

Threshold	FRR (%)	FAR (within-class) (%)	FAR (between-class) (%)
16	1.05	10.65	6.11
20	2.20	6.30	3.24
24	3.00	3.83	1.82
26	3.49	3.01	1.39

information with the matching performance, we used the NIST4 database [22] which has 4000 fingerprint images collected from 2000 independent fingers with 800 fingerprints from each of the five classes. The ground truth about the fingerprint class was marked in the NIST4 database by an expert at NIST.

The between-class and within-class distributions were computed from about 130, 000 matchings each by matching the 3600 good quality fingerprints in the NIST4 database with each other. The genuine distribution computed from the NIST9 database was used here so that the FRRs could be directly compared with Table 1. The ROCs for between-class and within-class matchings are shown in Fig. 7 and Table 3 shows the corresponding trade-off between FARs and FRRs for different thresholds on the matching score. Note that the matching performance is better for fingerprints belonging to different classes compared to fingerprint belonging to the same class. Also, the magnitude of the shift between the two ROCs in Fig. 7 is of the same order of magnitude as the one manifested in Fig. 5(b) (also compare Table 3 with Table 1). Thus, we have shown that the minutiae-based similarity of identical twin fingerprints, is of the same order as the similarity between unrelated people who have the same fingerprint class label. Hence, we conclude that the larger similarity observed in identical twins is due to the high class correlation in their fingerprint types.

5. Conclusions

One out of every 80 births results in twins and one-third of all the twins are monozygotic (identical) twins [14]. Some identical twins have been reported to be involved in fraud, which can be called as “twin fraud”, since people mistake the identities of the identical twins. The childhood mischief by the identical twins of switching places on their teachers and taking each other’s exams may grow into serious criminal activities in adulthood such as buying a single insurance for identical twin siblings or claiming welfare benefits twice when only one sibling is unemployed. There have been cases reported where an identical twin was sentenced for a crime that was committed by his/her sibling [2]. Fertility treatments have resulted in an increase in the identical twin birth rate (in fact, according to a study by Robert Derom [2], the identical twin birth rate is about twice as high for women who use fertility drugs). Further, because of the medical advances in the treatment of premature babies, population of identical twins is increasing.

We have shown that even though identical twin fingerprints have large class correlation, they can still be distinguished using a minutiae-based automatic fingerprint verification system though with slightly lower accuracy than nontwins. Our results suggest that the marginal degradation in performance may be related to the dependence of the minutiae distribution on fingerprint class.

What are the implications of our empirical results in person verification applications? In authentication applications, marginal degradation in accuracy performance will have almost no effect on "evil" twins posing as impostors. In large scale fingerprint based verification applications, a small degradation in authentication accuracy may imply a significant degradation in the recognition accuracy. Further, if the degradation in the performance is dependent on the class correlation which in turn depends on the genetic constitution (as suggested by the dermatoglyphics studies), it may imply that benefits reaped by composition of ten-finger information may have been overestimated in the literature. Further, the magnitude of performance degradation of a minutiae-based fingerprint matcher may depend upon the genetic relationship among a target population corpus. Both of these effects may need further investigation; more research is necessary for class-independent minutiae-based matchers. Since the accuracy performance of a minutiae-based fingerprint matcher degrades with genetic similarity in the population, alternative representations of fingerprints should be explored that can be combined with the minutiae representations to yield a more accurate automatic fingerprint matching system [23]. Finally, fingerprint classification applications used for the binning of population to increase efficiency of fingerprint-based search may not be very efficient in genetically related population.

6. Summary

Although, the word "fingerprint" is popularly perceived synonymous with individuality, uniqueness of fingerprints is not a fact but an empirical observation. With the stipulation of widespread use of fingerprints, however, there is a rightfully growing public concern about the *basis* underlying individuality of fingerprint. Lending erroneous legitimacy to these observations will have disastrous consequences, especially, if fingerprints (and other biometric identifiers) be ubiquitously used to establish positive person identification for reasons of efficiency, convenience, and reliability to fight growing identity fraud in the society. Further, the increasingly automated fingerprint matching systems use not the entire discriminatory information in the fingerprints, but only a parsimonious representation extracted by a machine unsupervised by human expert.

The magnitude of the distinctive information in a fingerprint is also being a suspect recently. A leading pop article [24] states that "the fingerprints may be unique in the sense that, as Leibniz argued, all natural objects can be differentiated if examined in enough detail". Cole further argues that uniqueness may be valid when *entire* prints are compared but not for prints depicting small portions of a finger; the print size is even more significant in the view of the newer chip-based fingerprint sensors which cover a small portion of the finger (unlike the nail-to-nail rolled inked fingerprints used in many criminal fingerprint investigations). A recent WSJ article [2] speculates that identical twin fingerprints are 95% similar. The same article also quotes a security expert stating "identical twins would probably pass most of (biometric which includes fingerprint) security technology". Finally, a recent (1993) US Supreme Court Daubert vs Merrell hearing started a closer scrutiny of the UK Home Office observation in 1893 that fingerprints are unique. Although the supreme court conceded that fingerprints are unique, it subsequently sought (through DOJ) to sponsor a systematic study to examine a sound and indisputable scientific basis of the fingerprint individuality information.

Thus, uniqueness of fingerprints is not a bygone conclusion. Nor this empirical observation has been systematically studied. Obviously, there is an enormous public interest in this crucial and contemporary topic. We attempt to explore answers to some of these fingerprint individuality questions. More specifically, the objective of our work is to examine the fingerprint individuality information in the context of an automated fingerprint matching system. We accomplish this objective by considering a worst case situation of monozygotic twin fingerprints. Further, we validate our results by estimating the statistical significance of our results and by forwarding the evidence that the correlation in fingerprint minutiae representations from identical twin fingers is due to the fingerprint class correlation in identical twin fingerprints (which has been previously studied). Finally, we lay out the implications of our results in terms of identity verification and identification systems. To our knowledge, all these aspects of fingerprint individuality information have never been examined before.

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References

[1] A.K. Jain, R. Bolle, S. Pankanti (Eds.), BIOMETRICS: Personal Identification in Networked Society, Kluwer, New York, 1999.

[2] D. Costello, Families: the perfect deception: identical twins, Wall Street J. Feb. 12th 1999.

[3] Problem identifications, http://onin.com/fp/problemidents.html

[4] R.G. Steen, DNA and Destiny: Nature and Nurture in Human Behavior, Plenum Press, New York, 1996.
[5] N.L. Segal, Entwined Lives: Twins and What They Tell Us About Human Behavior, Plume, New York, 2000.
[6] M.D. Eibert, Human Cloning: Myths, Medical Benefits and Constitutional Rights, U & I Magazine, 1999, available at http://www.humancloning.org/users/infertil/humancloning.htm
[7] Veridicom, Inc., Fingerprint Authentication Technology Enabling Secure E-commerce, http://www.veridicom.com/
[8] E.P. Richards, Phenotype vs. Genotype: Why Identical Twins Have Different Fingerprints? http://www.forensic-evidence.com/site/ID_Twins.html
[9] A.K. Jain, L. Hong, S. Pankanti, R. Bolle, An identity authentication system using fingerprints, Proc. IEEE 85 (9) (1997) 1365–1388.
[10] F. Galton, Finger Prints, McMillan, London, 1892.
[11] A.R. Roddy, J.D. Stosz, Fingerprint features-statistical analysis and system performance estimates, Proc. IEEE 85 (9) (1997) 1390–1421.
[12] H. Cummins, C. Midlo, Fingerprints, Palms and Soles: An Introduction to Dermatoglyphics, Dover Publications Inc., New York, 1961.
[13] W. Bodmer, R. McKie, The Book of Man: The Quest to Discover our Genetic Heritage, Viking, 1994.
[14] J. Daugman, Recognizing persons by their Iris patterns, in: A.K. Jain, R. Bolle, S. Pankanti (Eds.), BIOMETRICS: Personal Identification in Networked Society, Kluwer Academic Publishers, New York, 1999.
[15] E. Splitz, R. Mountier, T. Reed, M.C. Busnel, C. Marchaland, P.L. Roubertoux, M. Carlier, Comparative diagnoses of twin zygosity by SSLP variant analysis, questionnaire, and dermatoglyphics analysis, Behav. Genet. 26 (1) (1996) 56–63.
[16] T. Reed, D. Carmelli, R.H. Rosenman, Effects of placentation on selected type a behaviors in adult males, in the National Heart, Lung, and Blood Institute (NHLBI) twin study, Behav. Genet. 21 (1991) 9–19.
[17] T. Reed, R. Meier, Taking dermatoglyphic prints: a self-instruction manual, Am. Dermatoglyphics Assoc. Newslett. 9 (Supp.) (1990) 18.
[18] W.H. Press, S.A. Teukolsky, W.T. Vellerling, B.P. Flannery, Numerical Recipes in C, The Art of Scientific Computing, Cambridge University Press, Cambridge, 1992.
[19] NIST Special Database 9. NIST 8-bit Gray Scale Images of Fingerprint Image Groups (FIGS), http://www.nist.gov/srd/nistsd9.htm
[20] UK Biometric Working Group, Best Practices in Testing and Reporting Biometric Device Performance, Version 1.0, March 2000. http://www.afb.org.uk/bwg/bestprac10.pdf
[21] J.L. Wayman, Multi-finger penetration rate and ROC variability for automatic fingerprint identification systems, Technical Report, San Jose State University, 1999.
[22] NIST Special Database 4. NIST 8-bit Gray Scale Images of Fingerprint Image Groups (FIGS), http://www.nist.gov/srd/nistsd4.htm
[23] A.K. Jain, S. Prabhakar, L. Hong, S. Pankanti, Filterbank-based Fingerprint Matching, IEEE Trans. Image Process. 9 (5) (2000) 846–859.
[24] Simon Cole, The myth of fingerprints: A Forensic Science Stands Trial, http://www.linguafranca.com/print/0011/feature_fingerprints.html, 2000

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