Article

Discriminability of Fingerprints of Twins

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Abstract: A study of the discriminability of fingerprints of twins is presented. The fingerprint data used is of high quality and quantity because of a predominantly young subject population of 298 pairs of twins whose tenprints were captured using a livescan device. Discriminability using level 1 and level 2 features is independently reported. The level 1 study was to visually classify by humans each fingerprint into one of six categories (right loop, left loop, whorl, arch, twin loop, and tented arch). It was found that twins are much more likely (55%) to have the same level 1 classification when compared to the general population (32%). The level 2 study was to compare minutiae (ridge endings and bifurcations). This was done by a minutiae-based automatic fingerprint identification algorithm that provided a score (0-350) given a pair of fingerprints. Scores were computed for corresponding fingers from both twins and non-twins. Five distributions of scores were determined: twins, non-twins, identical twins, fraternal twins, and genuine scores from the same finger. Using the Kolmogorov-Smirnov test to compare distributions, the following inferences are made: twins are different from genuines, twins are different from non-twins, and identical twins are the same as fraternal twins. The main conclusion is that, although the patterns of minutiae among twins are more similar than in the general population, they are still discriminable.

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Introduction

The study of twins has been important in various physiological [1-3] and behavioral [4] settings. Genetic and environmental similarities of twins allow studies such as the effectiveness of drugs, presence of psychological traits, and so forth. By examining the degree to which twins are differentiated, a study may determine the extent to which a particular trait is influenced by genes or the environment.

Because of the lack of sufficient twin data, few twin studies have been carried out in forensics and biometrics. Such studies are important because any modality needs to be evaluated in conditions under which the possibility of error is maximum, that is, the worst-case scenario. Satisfactory performance with twins strengthens the reliability of the method. It also establishes the degree of individuality of the particular trait. Such an individuality measure is relevant from the viewpoint of Daubert challenges in forensic testimony [5].

A significant number of twin pairs (206) have been studied for handwriting [6]. These samples were processed with features extracted and conclusions drawn by comparing verification performances with twins and non-twins. In that study, the conclusion was that twins are discriminable but less so than an arbitrary pair of individuals.

A fingerprint twin study has been previously reported with a small data set of 94 pairs of index fingers [7]. The study showed that the fingerprints of identical twins are distinct and that a state-of-the-art fingerprint verification system can differentiate between twins' fingerprints, though with a lower accuracy as compared to those of non-twins. The study attributed the slight degradation in performance to the dependence of the minutiae distribution on the fingerprint class. An earlier study [8] made use of fingerprints of 196 pairs of twins. In that study, 196 comparisons of level 1 classification were made and when there was a match, a ridge count comparison was made. Level 2 (minutiae) comparisons included only 107 pairs corresponding to the fingerprints of identical twins. The present twin study involves a much larger set of fingerprints from nearly 3,000 pairs of fingers, involving all five finger types.

The question to be answered is whether there exists a higher degree of similarity between individuals who are twins rather than when the individuals are not twins. The goal is to determine whether the fingerprints of twins are more similar to each other than in the case of the general population. Friction ridge patterns contained in fingerprints can be analyzed at several levels of features. Level 1 features correspond to visually observable characteristics commonly used in fingerprint classification, namely, arch, tented arch, left loop, right loop, whorl, and twin loop. Level 2 features correspond to minutiae, which are primarily points corresponding to ridge endings and ridge bifurcations, that are represented as a triple coordinate consisting of x, y, and a direction. Level 3 features include pores within ridges, ridge widths, and shapes.

The analysis reported here was done using only level 1 and level 2 features. The level 1 analysis was done manually by visual inspection. The level 2 analysis was done using an algorithm to compare two fingerprints. Such algorithms are typically used in automatic fingerprint identification systems (AFIS). In the case of fingerprints, we need to ensure some overlap between different portions of the images to always not get an exclusion. For non-twins (and different fingers), test cases can be generated.

Fingerprint Data Set

Twins Data Source

The twins data set used in this study consisted of livescan digital images from more than six hundred individuals. This data set is a part of friction ridge image data collected by the International Association for Identification (IAI) at a twins festival held in Twinsburg, Ohio, in August 2003. The friction ridge images of 615 individuals correspond to 298 sets of twins and three sets of triplets. For 5 particular pairs of twins in this set, the friction ridge images of ten family members were also included. (The 298 set includes 5 sets of twins with inconclusive or no DNA analysis results.) For each individual there are ten fingerprints, thus making available 2,980 pairs of twin fingers. In addition, right and left palmprints are included in the database, but not used in this study.

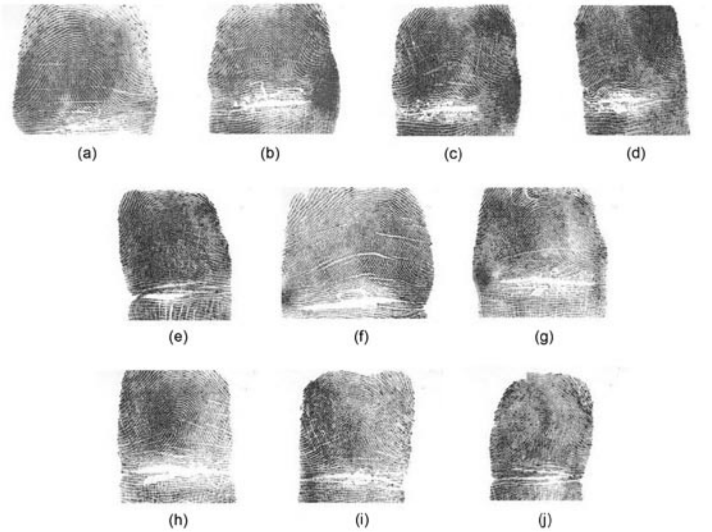


Figure 1

Ten rolled fingerprints from one individual: (a) right thumb; (b) right index; (c) right middle; (d) right ring; (e) right little; (f) left thumb; (f) left index; (g) left middle; (h) left ring; (i) left little.

(a) *(b)*

Figure 2

Fingerprints from a pair of twins. Right thumbs of (a) TX004 and (b) TX005.

Image Type

The images used in this study were all obtained using a livescan scanner. The images were captured at a resolution of 500 pixels per inch (ppi). Figure 1 shows ten rolled fingerprints from one individual. A side-by-side comparison of a pair of twin fingerprints is shown in Figure 2.

Demographic Information

The database contains a folder of images for each individual. A metadata table accompanying each folder gives the demographic information for the individual, code for the individual, and a pointer to his or her twin. The demographic information consists of age, gender, hair color, racial characteristics, whether twins are identical or fraternal, and handedness. The distribution of ages of the twins is given in Figure 3. It can be seen from the peaks in the data that the twins are predominantly in their adolescent years. Thus, the quality of the prints can be expected to be good. The corresponding distribution in the database for each is illustrated in Figure 4.

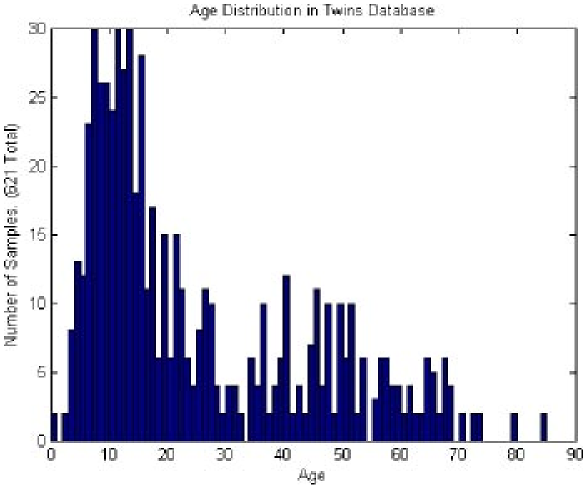
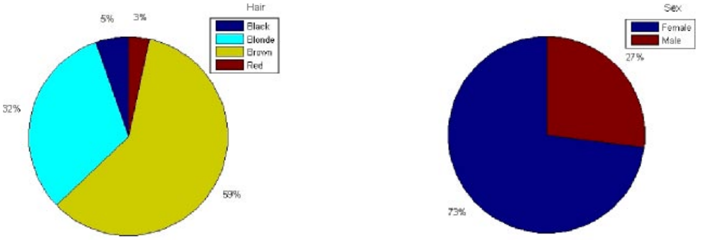


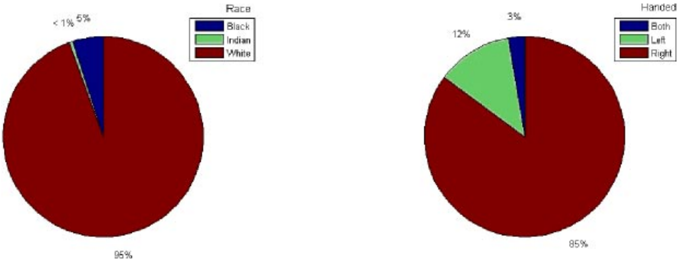
Figure 3

Distribution of ages of twins in database.



(a) *Hair color distribution.*

(b) *Gender distribution.*



(c) *Race distribution.*

(d) *Handedness distribution.*

Figure 4

Distribution of twins' metadata.

Level 1 Study

The first study was to determine the similarities at level 1. An interface was created to present one fingerprint at a time to the subject on a screen. The observer was asked to determine whether the given print belonged to one of six categories: arch, tented arch, right loop, left loop, whorl, and twin loop.

Two individuals independently performed the level 1 classification using six classification types [9]. Their individual classifications were then compared. When there was a disagreement in their decision, a third individual did an arbitration to determine the correct classification. Finally, the classification decisions were validated by two professional friction ridge examiners. The overall distributions of the six level 1 features are shown in Figure 5. There are several ambiguous fingerprints whose classification into the six types cannot be reliably stated even by human experts [9]. However, the distribution obtained provides an indication of how frequently each class is encountered: right loop (30%), left loop (27%), whorl (19%), arch (13%), twin loop (7%), and tented arch (5%).

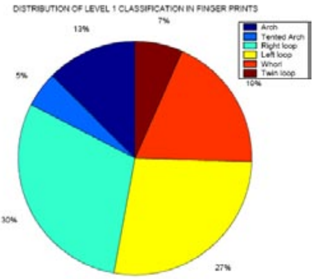


Figure 5

Distribution of level 1 features in database.

The analysis consisted of determining how often the prints of the same finger in a pair of twins matched and a comparison with the case of non-twins. Examples of pairs of prints when they belonged to identical twins and fraternal twins (same hand and finger) are given in Figure 6.

The results were as follows: The percentage of times twins had the same level 1 label for a given finger was 54.68%. The percentage of times non-twins had the same level 1 label was 31.76%. Thus, we can conclude that twins are nearly twice as likely as non-twins to have matching level 1 features. Further, considering only identical twins, the percentage of same level 1 was 56.92% as against 39.44% for fraternal twins. Non-twin frequencies of level 1 are similar to those reported by others [9].

Level 1 features are used only as a coarse method of eliminating candidates from a large database (e.g., AFIS). However, they have little implication on the discriminability of twins because level 1 features are not solely used in the individualization of fingerprints.

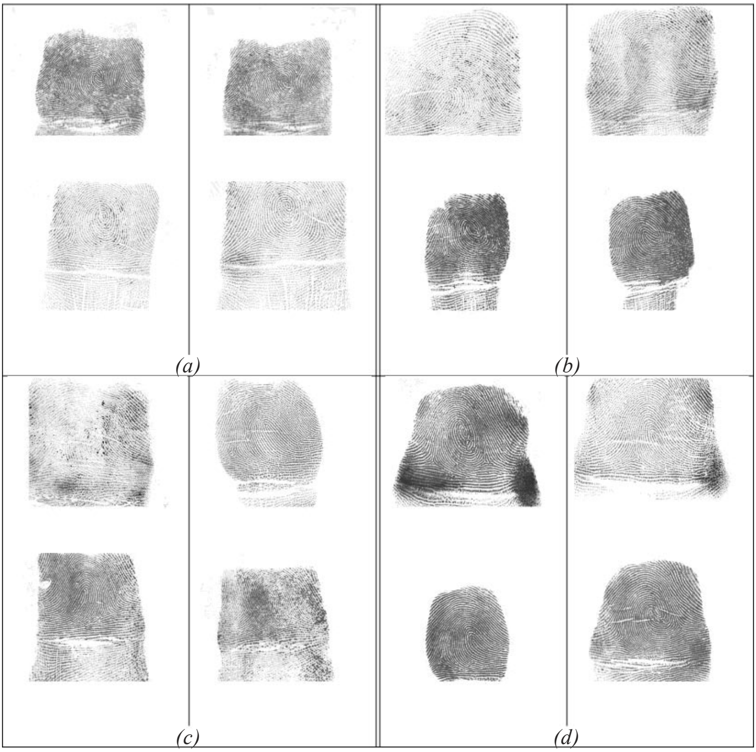


Figure 6

Samples of twins showing both similarity and dissimilarity at level 1: (a) same level 1: identical twins; (b) different level 1: identical twins; (c) same level 1: fraternal twins; (d) different level 1: fraternal twins.

Level 2 Study

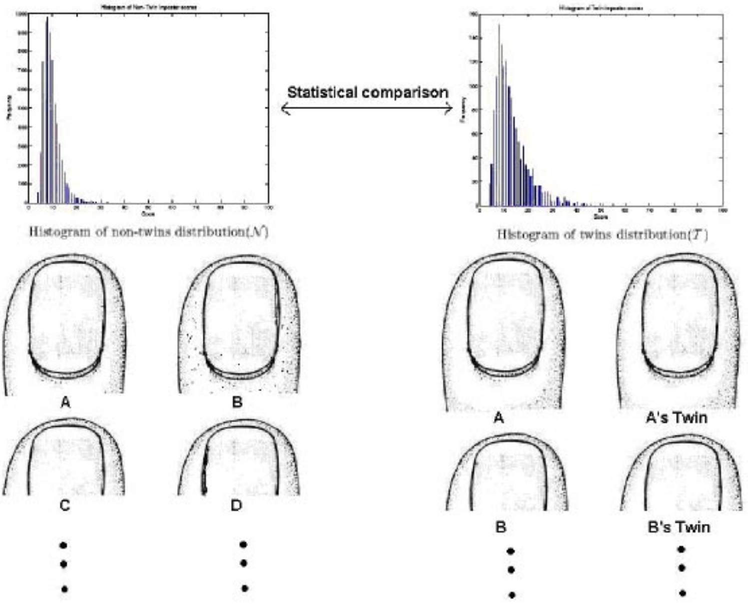
The most important part of the study concerns level 2 features because they are what are primarily used in fingerprint individualization. Level 2 features consist of minutiae that are mostly ridge endings or ridge bifurcations. Each minutia is represented by a 3-tuple (x, y, θ) representing its position and orientation in the fingerprint.

The question to be examined is whether fingerprints of twins are similar when minutiae are used as features. One method of measuring similarity is to use an AFIS-type algorithm that extracts minutiae and obtains a score from the comparison. The approach taken was to use the MIN-DTCT algorithm for detecting minutiae and the Bozorth matcher [10] to determine a score for an input pair of fingerprints, both of which are available from NIST.

We will briefly describe the Bozorth approach to computing a score for the similarity of two fingerprints before proceeding to describe how the scores are to be used. The scoring method uses minutia pairs within a local region of a fingerprint and compares them to corresponding pairs from the other fingerprint. An intra-fingerprint minutiae pair table is constructed to capture relative position and orientation of a pair of minutiae. For each pair of minutiae $\{m_i, m_j\}$ where i and j are minutiae indices, the local model vector is maintained as $[d_{ij}, \beta_i, \beta_k, \theta_{ij}, i, j]$, where d_{ij} indicates the relative distance between minutiae m_i, m_j; β_i, β_j measure the relative angle of the minutiae with respect to the connecting line. Besides these relative measurements, absolute orientation of the connecting line θ_{ij} is maintained for later global consolidation. These pair-wise measurements are made for each pair of minutiae where the connecting distance d_{ij} is less than a fixed threshold. In global consolidation, for a fingerprint pair, the Bozorth algorithm constructs a third table from the two intra-fingerprint tables. This inter-fingerprint compatibility table has potential associations between the two intra-fingerprint minutiae pair tables. This inter-fingerprint compatibility table is now searched for the longest path of linked compatible associations. A score corresponding to this longest path is then generated.

The Bozorth score is typically in the range of 0~50 for impostor scores and can be as high as 350 for genuines. Other AFIS algorithms have similar scores but have different ranges.

Scores for the two populations of non-twins and twins, both for the same finger, were obtained using the scenario depicted in Figure 7. The results can be evaluated in two ways. First is to simply place thresholds on the scores so as to make “hard” decisions on whether the fingerprints were the same or different, and the second is to make a “soft” comparison of the distributions of scores.



(a) *(b)*

Figure 7

Comparing fingerprints of (a) non-twins and (b) twins using level 2 features.

The scores provided to the matcher can be thresholded to provide a hard decision of being the same or different. The thresholds would be derived from genuine and impostor distributions. Here the genuine distribution would come from multiple fingerprints of the same finger as shown in Figure 8(e). The resulting error rates are shown in Table 1.

	FP Error Rate	**EER Threshold**
Non-twins	2.91%	18
Twins	6.17%	26

Table 1

False positive rate with twins and non-twins using Bozorth matcher.

The error rates are dependent upon a choice of threshold, such as the equal error rate (EER) threshold used in Table 2. To remove this dependency, we can instead obtain a distribution of the scores of twins and compare it to the distribution for non-twins. This will also help us take into account the entire range of values rather than values relative to a single threshold.

Comparing Distributions

Many statistical tests exist to compare two distributions. These tests answer the question, Can we disprove, with a certain required level of significance, the null hypothesis that the two distributions are drawn from the same population? [11] Some of the most common tests used to quantify the difference in the distributions are chi-square, Kolmogorov-Smirnov, student-T, and ANOVA. Among these, the Kolmogorov-Smirnov test assumes nothing about the distribution and also can be used on unbinned distributions. Hence, it is presented here.

The Kolmogorov-Smirnov (KS) test can be applied to obtain a probability of similarity between two distributions. The KS test is applicable to unbinned distributions that are functions of a single independent variable, that is, to data sets where each data point can be associated with a single number [11]. The test first obtains the cumulative distribution function of each of the two distributions to be compared and then computes the statistic, D, which is a particularly simple measure: it is defined as the maximum value of the absolute difference between the two cumulative distribution functions. Therefore, if comparing two different cumulative distribution functions $S_{N1}(x)$ and $S_{N2}(x)$, the KS statistic D is given by $D = \max_{-\infty<x<\infty} |S_{N1}(x) - S_{N2}(x)|$. What makes the KS statistic useful is that its distribution in the case of the null hypothesis (data sets drawn from the same distribution) can be calculated, at least to useful approximation, thus giving the significance of any observed nonzero value of D. The significance level of an observed value of D is given approximately [11] by equation 1.

$$P_{KS} = Q_{KS}(\sqrt{N_e} + 0.12 + (0.11/\sqrt{N_e})D) \qquad (1)$$

where the $Q_{KS}(\cdot)$ function is given by (see [11] for details):

$$Q_{KS}(\lambda) = 2\sum_{j=1}^{\infty}(-1)^{j-1}e^{-2j^2\lambda^2}, \text{ such that: } Q_{KS}(0) = 1,\ Q_{KS}(\infty) = 0 \qquad (2)$$

and N_e is the effective number of data points, $N_e = N_1 N_2 (N_1 + N_2)^{-1}$, where N_1 is the number of data points in the first distribution and N_2 is the number in the second.

Analysis of Results

A set of 298 pairs of twins was used to carry out the experiments. The fingerprints were rolled fingerprints with 10 prints (corresponding to 10 fingers) per person. The total number of prints used was 298 x 2 x 10 = 5,960 (i.e., 2,980 twin pairs). Of these, 740 were prints of fraternal twins and the remaining 2,240 were those of identical twins. The following five distributions were obtained.

1. Twins: The fingerprint of an individual was matched with the corresponding fingerprint of his or her twin. The number of comparisons made was 2,980. Let us denote the distribution of scores from matching twins as *T*.

2. Non-Twins: In this case, an individual's fingerprint was compared with the corresponding fingerprint of all other people who were not his or her twin. The total number of comparisons possible was 10 (ten prints) x 596 (total individuals who are twins) x 594 (leaving out the individual and his or her twin) = 3,540,240. Of these, 6,660 were used for the experiments. The distribution of scores from non-twins is denoted as *N*.

3. Identical Twins: This involved matching fingerprints of identical twins (255 pairs of twins) and is denoted as *I*.
4. Fraternal Twins: This involved matching fingerprints of fraternal twins (42 pairs) and is denoted as *F*.
5. Genuine: Pairs of fingerprints that belong to the same finger were compared against each other to obtain the Genuine distribution. The FVC2002 Db1 data set was used to obtain this particular distribution, due to lack of multiple rolled fingerprint samples of the same finger in the Twins' database. A total of 100 fingers with 8 samples of each finger constituting a total of 800 prints were present in the FVC2002 Db1 database. These were also obtained as livescan images at 500 ppi, similar to the Twins' dataset.

Histograms of the Bozorth scores for each of the five cases described are shown in Figure 8.

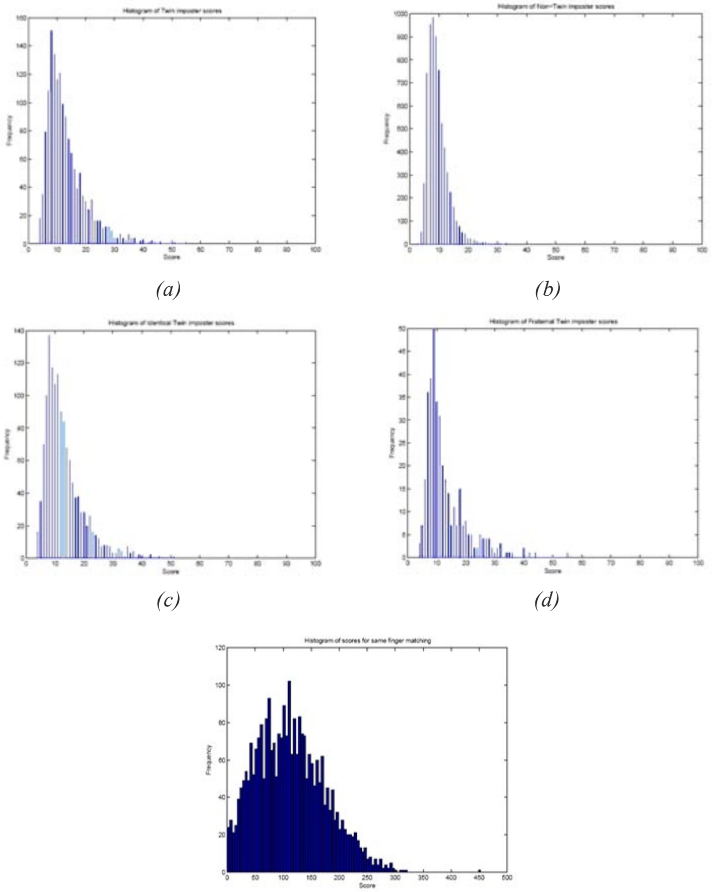
Statistical Comparison

The Kolmogorov-Smirnov test was performed to compare the distributions and to obtain a significance level that the distributions are drawn from the same population. Table 2 summarizes the results. The value shown in each cell indicates the significance level with which it can be said that the two distributions are drawn from the same population.

	Genuine vs Twin	**Identical vs Fraternal**	**Twin vs Non-Twin**	**Genuine vs Non-Twins**
Kolmogorov-Smirnov (probability)	0.0010	0.9999	0.1174	0.0004

Table 2

Kolmogorov-Smirnov test between different distributions. All pairs of distribution except identical vs fraternal were found to be different from each other.



(a) *(b)*

(c) *(d)*

(e)

Figure 8

Histograms of Bozorth similarity scores: (a) twins T (2980 values); (b) non-twins N (6660 values); (c) identical twins I (2550 values); (d) fraternal twins F (420 values); (e) genuine G (2800 values).

The hypotheses tested, their significance, and conclusions are given below.

1. Test 1:
    a. Hypothesis: Similarity of fingerprints of twins is the same as the similarity between genuine prints of the same finger.
    b. Significance level: .1% (refer to column 1 in Table 2).
    c. Deduction: Hypothesis is rejected because it is less than 5% significance. It is concluded that the similarity of fingerprints of twins is different from that between genuine prints of the same finger.
2. Test 2:
    a. Hypothesis: Similarity of fingerprints of identical twins is the same as the similarity between fingerprints of fraternal twins.
    b. Significance level: 99.99% (refer to column 2 in Table 2).
    c. Deduction: Hypothesis is accepted because it is stronger than 95% significance. It is concluded that the similarity of fingerprints of identical twins is the same as the similarity between fingerprints of fraternal twins.
3. Test 3:
    a. Hypothesis: Similarity of fingerprints of twins is the same as the similarity between non-twins.
    b. Significance level: 11.74% (refer to column 3 in Table 2).
    c. Deduction: Significance is not less than 5% to reject the hypothesis. It can, however, be said that the conclusion is not in favor of the hypothesis and hence the similarity of fingerprints of twins is different from the similarity between arbitrary fingers.

Further, the distributions being positive can be modeled with gamma distributions. The corresponding probability density functions are shown in Figure 9, which are gamma distributions corresponding to twins, non-twins, and same finger distributions.

A slight shift in the twins' distribution in comparison to the non-twins' distribution can be observed.

Summary and Conclusion

A study of the discriminability of the fingerprints of twins has been presented. Using a larger set of samples than used in previous studies, the similarities of the fingerprints of twins were studied. Livescans and younger ages of the subjects ensured good-quality prints thereby allowing the focus to be on the inherent individuality of fingerprints and one that was not affected by image quality issues.

Two studies were conducted using fingerprint features at levels 1 and 2. The level 1 results, obtained by human visual comparison, show that twins' fingers have a higher probability of having the same classification (42%) than in the case of non-twins (25%).

Level 2 features were studied using a minutiae-based matching algorithm that provides a similarity score. Distributions of scores were compared using the Kolmogorov-Smirnov test. The statistical inferences from the level 2 study are:

1. The similarity of fingerprints of twins is different from that between genuine prints of the same finger.
2. The similarity of fingerprints of identical twins is the same as the similarity between fingerprints of fraternal twins. This indicates that genetic influence on the formation of minutiae in identical twins is the same as the influence among fraternal twins.
3. The similarity of fingerprints of twins is different from the similarity between arbitrary fingers.

The implications of the study are (1) there is more similarity between twin fingers than in the case of two arbitrary fingers, (2) there is no significant difference between the fingerprints of identical and fraternal twins, and (3) twins can be successfully discriminated using fingerprints. The net result of the findings is that the argument for the individuality of fingerprints is strengthened.

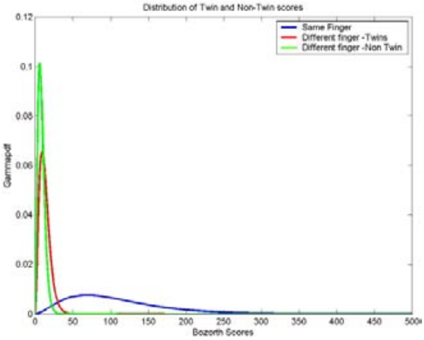


Figure 9

Probability density functions of fingerprint scores modeled as gamma distributions.

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