On the Individuality of Fingerprints: Models and Methods

Dass, S., Pankanti, S., Prabhakar, S., and Zhu, Y.

Abstract

Fingerprint individuality is the study of the extent of uniqueness of fingerprints and is the central premise of expert testimony in court. A forensic expert testifies whether a pair of fingerprints is either a match or non-match by comparing salient features of the fingerprint pair. However, the experts are rarely questioned on the uncertainty associated with the match: How likely is the observed match between the fingerprint pair due to just random chance? The main concern with the admissibility of fingerprint evidence is that the matching error rates (i.e., the fundamental error rates of matching by the human expert) are unknown. The problem of unknown error rates is also prevalent in other modes of identification such as handwriting, lie detection, etc. Realizing this, the U.S. Supreme Court, in the 1993 case of Daubert vs. Merrell Dow Pharmaceuticals, ruled that forensic evidence presented in a court is subject to five principles of scientific validation, namely whether (i) the particular technique or methodology has been subject to statistical hypothesis testing, (ii) its error rates has been established, (iii) standards controlling the technique's operation exist and have been maintained, (iv) it has been peer reviewed, and (v) it has a general widespread acceptance. Following Daubert, forensic evidence based on fingerprints was first challenged in the 1999 case of USA vs. Byron Mitchell based on the "known error rate" condition

mentioned above, and subsequently, in 20 other cases involving fingerprint evidence. The establishment of matching error rates is directly related to the extent of fingerprint individualization. This article gives an overview of the problem of fingerprint individuality, the challenges faced and the models and methods that have been developed to study this problem.

Related entries: Fingerprint individuality, fingerprint matching automatic, fingerprint matching manual, forensic evidence of fingerprint, individuality.

Definitional entries:

1.Genuine match: This is the match between two fingerprint images of the same person.

2. Impostor match: This is the match between a pair of fingerprints from two different persons.

3. Fingerprint individuality: It is the study of the extent of which different fingerprints tend to match with each other. It is the most important measure to be judged when fingerprint evidence is presented in court as it reflects the uncertainty with the experts' decision.

4. Variability: It refers to the differences in the observed features from one sample to another in a population. The differences can be random, that is, just by chance, or systematic due to some underlying factor that governs the variability.

I. Introduction

The two fundamental premises on which fingerprint identification is based are: (i) fingerprint details are permanent, and (ii) fingerprints of an individual are unique. The validity of the first premise has been established by empirical observations as well as based on the anatomy and morphogenesis of friction ridge skin. It is the second premise which is being challenged in recent court cases. The notion of fingerprint individuality has been widely accepted based on a manual inspection (by experts) of millions of fingerprints. Based on this notion, expert testimony is delivered in a courtroom by comparing salient features of a latent print lifted from a crime scene with those taken from the defendant. A reasonably high degree of match between the salient features leads the experts to testify irrefutably that the owner of the latent print and the defendant are one and the same person. For decades, the testimony of forensic fingerprint experts was almost never excluded from these cases, and on cross-examination, the foundations and basis of this testimony were rarely questioned. Central to establishing an identity based on fingerprint evidence is the assumption of discernible uniqueness; salient features of fingerprints of different individuals are observably different, and therefore, when two prints share many common features, the experts conclude that the owners of the two different prints are one and the same person. The assumption of discernible uniqueness, although lacking sound theoretical and empirical foundations, allows forensic experts to offer an unquestionable proof towards the defendant's guilt.

A significant event that questioned this trend occurred in 1993 in the case of Daubert vs. Merrell Dow Pharmaceuticals [1] where the U.S. Supreme Court ruled that in order for an expert forensic testimony to be allowed in courts, it had to be subject to five main criteria of scientific validation, that is, whether (i) the particular technique or methodology has been subject to statistical hypothesis testing, (ii) its error rates has been established, (iii) standards controlling the technique's operation exist and have been maintained, (iv) it has been peer reviewed, and (v) it has a general widespread acceptance [4]. Forensic evidence based on fingerprints was first challenged in the 1999 case of USA vs. Byron Mitchell [8] under Daubert's ruling, stating that the fundamental premise for asserting the uniqueness of fingerprints had not been objectively tested and its potential matching error rates were unknown. After USA vs. Byron Mitchell, fingerprint based identification has been challenged in more than 20 court cases in the United States.

The main issue with the admissibility of fingerprint evidence is that the underlying scientific basis of fingerprint individuality has not been rigorously studied or tested. In particular, the central question is: What is the uncertainty associated with the experts' judgement? How likely can an erroneous decision be made for the given latent print? In March 2000, the U.S. Department of Justice admitted that no

such testing has been done and acknowledged the need for such a study [12]. In response to this, the National Institute of Justice issued a formal solicitation for "Forensic Friction Ridge (Fingerprint) Examination Validation Studies" whose goal is to conduct "basic research to determine the scientific validity of individuality in friction ridge examination based on measurement of features, quantification, and statistical analysis" [12]. The two main topics of basic research under this solicitation include: (i)measure the amount of detail in a single fingerprint that is available for comparison, and (ii) measure the amount of detail in correspondence between two fingerprints.

This article gives an overview of the problem of fingerprint individuality, the challenges faced and the models and methods that have been developed to study the extent of uniqueness of a finger. Our interest in the fingerprint individuality problem is twofold. Firstly, a scientific basis (a reliable statistical estimate of the matching error) for fingerprint comparison can determine the admissibility of fingerprint identification in the courts of law as an evidence of identity. Secondly, it can establish an upper bound on the performance of automatic fingerprint verification systems.

The main challenge in assessing fingerprint individuality is to elicit models that can capture the variability of fingerprint features in a population of individuals. Fingerprints are represented by a large number of features, including the overall ridge flow pattern, ridge frequency, location and position of singular points (core(s) and delta(s)), type, direction, and location of minutiae points, ridge counts between pairs of minutiae, and location of pores. These features are also used by forensic experts to establish an identity, and therefore, contribute to the assessment of fingerprint individuality. Developing statistical models on complex feature spaces is difficult albeit necessary. In this paper, minutiae have been used as the fingerprint feature of our choice to keep the problem tractable and as a first step. There are several reasons for this choice: Minutiae is utilized by forensic experts, it has been demonstrated to be relatively stable and it has been adopted by most of the commonly available automatic fingerprint matching systems. In principal, the assessment of fingerprint individuality can be carried out for any particular matching

mode, such as by human experts or by automatic systems, as long as appropriate statistical models are developed on the relevant feature space used in the matching. Thus, our framework also extends to the case where matching is performed based on an automatic system. The matching mode in this paper has been selected to be an automatic matcher (see Section V for details) as it is computationally easy to validate the models proposed. In future, our formulation will be extended to include other fingerprint representations and other matching modes as well.

Even for the simpler fingerprint feature, namely minutiae, capturing its variability in a population of fingerprints is challenging. For example, it is known that fingerprint minutiae tend to form clusters [6], [7], minutiae information tend to be missed in poor quality images and minutiae location and direction information tend to be highly dependent on one another. All these characteristics of minutiae variability, in turn, affect the chance that two arbitrary fingerprints will match. For example, if the fingerprint pair have minutiae that are clustered in the same region of space, there is a high chance that minutiae in the clustered region will randomly match one another. In this case, the matches are spurious, or false, and statistical models for fingerprint individuality should be able to quantify the likelihood of spurious matches. To summarize, candidate models for assessing fingerprint individuality must meet two important requirements: (i) flexibility, that is, the model can represent the observed distributions of the minutiae features in fingerprint images over different databases, and (ii) associated measures of fingerprint individuality can be easily obtained from these models.

Several works have been reported in the literature on fingerprint individuality. The reader is referred to the overview by Pankanti et al. [4] on this subject. This article focuses on two recent works of fingerprint individuality where statistical models have been developed for minutiae to address the question of fingerprint individuality. These two works are (1) Pankanti et al. [4], and (2) Zhu et al. [9]. The rest of this paper is organized as follows: Section II develops the problem of biometric recognition in terms of a statistical hypotheses testing framework. Section III develops the statistical models of Pankanti et al. and

Zhu et al. and discusses how fingerprint individuality estimates can be obtained from them. Section IV° describes how the statistical models can be extended to a population of fingerprints. Relevant experimental results based on the NIST Special Database 4 [3], and FVC2002 [2] databases are reported in Section V.

II. The Statistical Test of Biometric Recognition

Fingerprint based recognition, and more generally biometric recognition, can be described in terms of a test of statistical hypotheses. Suppose a query image, Q, corresponding to an unknown identity, I_t , is acquired. Fingerprint experts claim that Q belongs to individual I_c , say. This is done by retrieving information of a template image T of I_c and matching T with Q. The two competing expert decision can be stated in terms of two competing hypotheses: The null hypothesis, H_0 , states that I_c is not the owner of the fingerprint Q (i.e., Q is an *impostor* impression of I_c), and the alternative hypothesis, H_1 , states that I_c is the owner of Q (i.e., Q is a genuine impression of I_c). The hypotheses testing scenario is

$$H_0: I_t \neq I_c \quad \text{vs.} \quad H_1: I_t = I_c. \tag{1}$$

Forensic experts match Q and T based on their degree of similarity (see Figure 1) For the present article, it will be assumed that the degree of similarity is given by the number of matched minutiae pairs, S(Q,T), between Q and T. Large (respectively, small) values of S(Q,T) indicate that T and Qare similar to (respectively, dissimilar to) each other. If S(Q,T) is lower (respectively, higher) than a pre-specified threshold λ , it leads to rejection (respectively, acceptance) of H_0 . Since noise factors distort information in the prints, two types of errors can be made: False match¹ (FM) and false non-match². False match occurs when an expert incorrectly accepts an impostor print as a match whereas false non-match occurs when the expert incorrectly rejects a genuine fingerprint as a non-match. The false match and

¹False match is also called the Type I error in statistics since H_0 is rejected when it is true

²False non-match is also called the Type II error in statistics since H_0 is accepted when H_0 is false

non-match rates (FMR and FNMR, respectively), are the probability of FM and FNM. The formulae for FMR and FNMR are:

$$FMR(\lambda) = P(S(Q,T) > \lambda | I_t \neq I_c),$$

$$FNMR(\lambda) = P(S(Q,T) \le \lambda | I_t = I_c).$$
(2)

In case there is no external noise factors that affect the acquisition of Q and T, it can decided without error whether Q belongs to I_c or not based on the premise of the uniqueness of fingerprints. However, the process of fingerprint acquisition is prone to many sources of external noise factors that distort the true information present in Q (as well as T). For example, there can be variability due to the placement of the finger on the sensing plane, smudges and partial prints in the latent that is lifted from the crime scene, non-linear distortion due to the finger skin elasticity, poor quality image due to dryness of the skin and many other factors. These noise factors cause information in Q to be distorted, for example, true minutiae points may be missed and spurious minutiae points can be generated which in turn affects the uncertainty associated with rejecting or accepting H_0 .

The different noise factors can be grouped into two major sources of variability: (1) inter- and (2) intra-class fingerprint variability. Intra-class variability refers to the fact that fingerprints from the same finger look different from one another. As mentioned earlier, sources for this variability includes non-linear deformation due to skin elasticity, partial print, non uniform fingertip pressure, poor finger-condition (e.g., dry finger), and noisy environment, etc. Figure 2 demonstrate the different sources of intra-class variability for multiple impressions of the same finger. Inter-class variability refers to the fact that fingerprints from different individuals look very similar. Unlike intra-class variability, the cause of inter-class variability is intrinsic to the target population. The bottom panel of Figure 1 shows an example of inter-class variability for two different fingerprint images. Both intra- and inter-class variability need to be accounted for when determining whether Q and T match or not. It is easy to see that fingerprint experts will be able to make



(a)



(b)

Fig. 1. Illustrating genuine and impostor minutiae matching (taken from [4]). (a) Two impressions of the same finger are matched; 39 minutiae were detected in input (left), 42 in template (right), and 36 "true" correspondences were found. (b) Two different fingers are matched; 64 minutiae were detected in input (left), 65 in template (right), and 25 "false" correspondences were found.



Fig. 2. Multiple impressions of the same finger illustrating the intra-class variability [2]

more reliable decisions if the inter-class fingerprint variability is large and the intra-class fingerprint variability is small. On the other hand, less reliable decisions will be made if the reverse happens, that is, when intra-class variability is large and inter-class variability is small. In other words, the study of fingerprint individuality is the study of quantification of inter- and intra-class variability in Q and T, as well as to what extent these sources of variability affect the fingerprint expert's decision.

III. Statistical Models for Fingerprint Individuality

The study and quantification of inter- and intra-class variability can be done by eliciting appropriate stochastic (or, statistical) models on fingerprint minutiae. Figure 3 show two examples of minutiae (ending and bifurcation) and the corresponding location and direction information. Two such approaches are described in this section, namely, the work done by Pankanti et al [4] and the subsequent model that was



Fig. 3. Minutiae features consisting of the location, s, and direction, θ , for a typical fingerprint image (b): The top (respectively, bottom) panel in (a) shows s and θ for a ridge bifurcation (respectively, ending). The top (respectively bottom) panel in (a) shows two subregions in which orientations of minutiae points that are spatially close tend to be very similar.

proposed by Zhu et al. [9]. Both works focus on modelling the inter-class fingerprint variability, that is, the variability inherent in fingerprint minutiae of different fingers in a population.

A. Pankanti's Fingerprint Individuality Model

The set up of Pankanti et al [4] is as follows: Suppose the query fingerprint Q has n minutiae and the template T has m minutiae denoted by the sets

$$M_Q \equiv \{\{S_1^Q, D_1^Q\}, \{S_2^Q, D_2^Q\}, \dots, \{S_n^Q, D_n^Q\}\}$$
(3)

$$M_T \equiv \{\{S_1^T, D_1^T\}, \{S_2^T, D_2^T\}, \dots, \{S_m^T, D_m^T\}\},\tag{4}$$

where in (3) and (4), S and D refer to a generic minutiae location and direction pair. To assess a measure of fingerprint individuality, it is first necessary to define a minutiae correspondence between Q and T.



Fig. 4. Identifying the matching region for a query minutiae (image taken from [4] and [9]).

A minutiae in Q, (S^Q, D^Q) , is said to match (or, correspond) to a minutiae in T, (S^T, D^T) , if for fixed positive numbers r_0 and d_0 , the following inequalities are valid:

$$|S^Q - S^T|_s \le r_0 \quad \text{and} \quad |D^Q - D^T|_d \le d_0,$$
(5)

where

$$|S^{Q} - S^{T}|_{s} \equiv \sqrt{(x^{Q} - x^{T})^{2} + (y^{Q} - y^{T})}$$
(6)

is the Euclidean distance between the minutiae locations $S^Q \equiv (x^Q, y^Q)$ and $S^T \equiv (x^T, y^T)$, and

$$|D^Q - D^T|_d \equiv \min(|D^Q - D^T|, 2\pi - |D^Q - D^T|)$$
(7)

is the angular distance between the minutiae directions D^Q and D^T . The choice of parameters r_0 and d_0 defines a tolerance region (see Figure 4), which is critical in determining a match according to Equation 5. Large (respectively, small) values of the pair (r_0, d_0) will lead to spurious (missed) minutiae matches. Thus, it is necessary to select (r_0, d_0) judiciously so that both kinds of matching errors are minimized. A discussion on how to select (r_0, d_0) is given subsequently. In [4], fingerprint individuality was measured in terms of the probability of random correspondence (PRC). The PRC of w matches is the probability that two arbitrary fingerprints from a target population have at least w pairs of minutiae correspondences between them. Recall the hypothesis testing scenario of Equation 1 for biometric authentication. When the similarity measure S(Q, T) is above the threshold λ , the claimed identity (I_c) is accepted as true identity. Based on the statistical hypothesis in Equation 1, the PRC is actually the false match rate, FMR, given by

$$PRC(w) = P(S(Q,T) \ge w \mid I_c \neq I_t)$$
(8)

evaluated at $\lambda = w$.

To estimate the PRC, the following assumptions were made in [4]: (1) Only minutiae ending and bifurcation are considered as salient fingerprint features for matching. Other types of minutiae, such as islands, spur, crossover, lake, etc., rarely appear and can be thought of as combination of endings and bifurcations. (2) Minutiae location and direction are uniformly distributed and independent of each other. Further, minutiae locations can not occur very close to each other. (3) Different minutiae correspondences between Q and T are independent of each other, and any two correspondences are equally important. (4) All minutiae are assumed true, that is there are no missed or spurious minutiae. (5) Ridge width is unchanged across the whole fingerprint. (6) Alignment between Q and T exists, and can be uniquely determined.

Based on the above assumptions, Pankanti et al. were able to come up with the uniform distribution as the statistical model for fingerprint individuality. The probability of matching w minutiae in both position as well as direction is given by

$$p(M,m,n,w) = \sum_{\rho=w}^{\min(m,n)} \left(\frac{\binom{m}{\rho} \binom{M-m}{n-\rho}}{\binom{M}{n}} \times \binom{\rho}{w} (l)^w (1-l)^{\rho-w} \right), \tag{9}$$

where M = A/C with A and C defined, respectively, as the area of overlap between Q and T and $C = \pi r_0^2$ is the area of the circle with radius r_0 . Pankanti et al. further improved their model based on several considerations of the occurrence of minutiae. The ridges occupy approximately $\frac{A}{2}$ of the total area with the other half occupied by the valleys. Assuming that the number (or the area) of ridges across all fingerprint types is the same and that the minutiae can lie only on ridges, i.e., along a curve of length $\frac{A}{\omega}$ where ω is the ridge period, the value of M in Eq. (9) is changed from M = A/C to

$$M = \frac{A/\omega}{2r_0},\tag{10}$$

where $2r_0$ is the length tolerance in minutiae location.

Parameters (r_0, d_0) determine the minutiae matching region. In the ideal situation, a genuine pair of matching minutiae in the query and template will correspond exactly, which leads to the choice of (r_0, d_0) as (0, 0). However, intra-class variability factors such as skin elasticity and non-uniform fingertip pressure can cause the minutiae pair that is supposed to perfectly match, to slightly deviate from one another. To avoid rejecting such pairs as non-matches, non-zero values of r_0 and d_0 need to be specified for matching pairs of genuine minutiae. The value of r_0 is determined based on the distribution of the Euclidean distance between every pair of matched minutiae in the genuine case. To find the corresponding pairs of minutiae, pairs of genuine fingerprints were aligned, and Euclidean distance between each of the genuine minutiae pairs was then calculated. The value of r_0 was selected so that only the upper 5% of the genuine matching distances (corresponding to large values of r) were rejected. In a similar fashion, the value of d_0 was determined to be the 95-th percentile of this distribution (i.e., the upper 5% of the genuine matching angular distances were rejected).

To find the actual r_0 and d_0 , Pankanti et al. used a database of 450 mated fingerprint pairs from IBM ground truth database (see [4] for details). The true minutiae locations in this database and the minutiae correspondences between each pair of genuine fingerprints in the database were determined by a fingerprint expert. Using the ground truth correspondences, r_0 and d_0 were estimated to be 15 and 22.5, respectively. These values will be used to estimate the PRC in the experiments presented in Section V^{14} .

Pankanti et al. [4] was the first attempt at quantifying a measure of fingerprint individuality based on statistical models. However, the proposed uniform model does have some drawbacks. Comparison between model prediction and empirical observations showed that the corrected uniform model grossly underestimated the matching probabilities (see Section V as well as [4]). The inherent drawbacks of the uniform model motivated the research by Zhu et al. [9] to propose statistical distributions that can better represent minutiae variability in fingerprints.

B. Mixture Models for Fingerprint Features

Zhu et al. [9] proposed a mixture model to model the minutiae variability of a finger by improving Assumption (2) of [4]. A joint distribution model for the k pairs of minutiae features $\{(S_j, D_j), j = 1, 2, ..., k\}$ is proposed to account for (i) clustering tendencies (i.e., non-uniformity) of minutiae, and (ii) dependence between minutiae location (S_j) and direction (D_j) in different regions of the fingerprint. The mixture model on (S, D) is given by

$$f(s,\theta \mid \Theta_G) = \sum_{g=1}^G \tau_g f_g^S(s \mid \mu_g, \Sigma_g) \cdot f_g^D(\theta \mid \nu_g, \kappa_g),$$
(11)

where G is the total number of mixture components, $f_g^S(\cdot)$ is the bivariate Gaussian density with mean μ_g and covariance matrix Σ_g , and

$$f_g^D(\theta \,|\, \nu_g, \kappa_g, \, p_g) = \begin{cases} p_g \, v(\theta) & \text{if } 0 \le \theta < \pi \\ (1 - p_g) \, v(\theta - \pi) & \text{if } \pi \le \theta < 2\pi, \end{cases}$$
(12)

where $v(\theta)$ is the Von-Mises distribution for the minutiae direction given by

$$v(\theta) \equiv v(\theta | \nu_g, \kappa_g) = \frac{2}{I_0(\kappa_g)} \exp\{\kappa_g \cos 2(\theta - \nu_g)\}$$
(13)

with $I_0(\kappa_g)$ defined as

$$I_0(\kappa_g) = \int_0^{2\pi} \exp\{\kappa_g \cos\left(\theta - \nu_g\right)\} d\theta.$$
(14)

In Equation (13), ν_g and κ_g represent the mean angle and the precision (inverse of the variance) of the Von-Mises distribution, respectively (see [9] for details). The distribution f_g^D in Equation 12 can be interpreted in the following way: The ridge flow orientation, o, is assumed to follow the Von-Mises distribution in Equation (13) with mean ν_g and precision κ_g . Subsequently, minutiae arising from the g-th component have directions that are either o or $o + \pi$ with probabilities p_g and $1 - p_g$, respectively.

The model described by Equation (11) has three distinct advantages over the uniform model: (i) it allows for different clustering tendencies in minutiae locations and directions via G different clusters, (ii) it incorporates dependence between minutiae location and direction since if S is known to come from the g-th component, the direction D also comes from the g-th component, and (iii) it is flexible in that it can fit a variety of observed minutiae distributions adequately. The estimation of the unknown parameters in (11) has been described in details in [9].

Figure 5 illustrates the fit of the mixture model to two fingerprint images from the NIST 4 database. Observed minutiae locations (white boxes) and directions (white lines) are shown in panels (a) and (b). Panels (c) and (d), respectively, give the cluster assignment for each minutiae feature in (a) and (b). Panels (e) and (f) plot the minutiae features in the 3-D (S, D) space for easy visualization of the clusters (in both location and direction). The effectiveness of the mixture models can also be shown by simulating from the fitted models and checking to see if a similar pattern of minutiae is obtained as observed. Figures 6 (a) and (b) show two fingerprints whose minutiae features were fitted with the mixture distribution in (11). Figures 6 (e-f) show a simulated realization when each S and D is assumed to be uniformly distributed independently of each other. Note that there is a good agreement, in the distributional sense, between the observed (Figures 6 (c) and (d)) but no such agreement exists for the uniform model.

Zhu et al. [9] obtains a closed form expression for the PRC corresponding to w matches under similar assumptions of Pankanti et al. [4] (barring Assumption (2)). The probability of obtaining exactly w











(d)



Fig. 5. Assessing the fit of the mixture models to minutiae location and direction. Figure taken from [9].





Fig. 6. All (S, D) realizations from the proposed model ((c) and (d)), and from the uniform distribution ((e) and (f)) for two different images ((a) and (b)). The true minutiae locations and directions are marked in (a) and (b). Images are taken from [9].

matches given there are m and n minutiae in Q and T, respectively, is given by the expression

$$p^{*}(w; Q, T) = \frac{e^{-\lambda(Q, T)} \lambda(Q, T)^{w}}{w!}$$
(15)

for large m and n; equation (15) corresponds to the Poisson probability mass function with mean $\lambda(Q, T)$ given by

$$\lambda(Q,T) = m n p(Q,T), \tag{16}$$

where

$$p(Q,T) = P(|S^Q - S^T|_s \le r_0 \text{ and } |D^Q - D^T|_a \le d_0)$$
(17)

denotes the probability of a match when (S^Q, D^Q) and (S^T, D^T) are random minutiae from the mixture distributions fitted to Q and T, respectively. The mean parameter $\lambda(Q,T)$ can be interpreted as the expected number of matches from the total number of mn possible pairings between m minutiae in Qand n minutiae points in T with the probability of each match being p(Q,T).

IV. Incorporating Inter-Class Variability via Clustering

The above PRC was obtained for a single query and template fingerprint pair. An important difference between the proposed methodology and previous work is that mixture models are fitted to each finger whereas previous studies assumed a common distribution for all fingers/impressions. Assuming a common minutiae distribution for all fingerprint impressions has a serious drawback, namely, that the true distribution of minutiae may not be modeled well. For example, it is well-known that the five major fingerprint classes in the Henry system of classification (i.e., right-loop, left-loop, whorl, arch and tented arch) have different class-specific minutiae distributions. Thus, using one common minutiae distribution may smooth out important clusters in the different fingerprint classes. Moreover, PRCs depend heavily on the composition of each target population. For example, the proportion of occurrence of the rightloop, left-loop, whorl, arch and tented arch classes of fingerprints is 31.7%, 33.8%, 27.9%, 3.7% and 2.9%, respectively, in the general population. Thus, PRCs computed for fingerprints from the general population will be largely influenced by the mixture models fitted to the right-loop, left-loop and whorl classes compared to arch and tented arch. More important is the fact that the PRCs will change if the class proportions change (for example, if the target population has an equal number of fingerprints in each class, or with class proportions different from the ones given above). By fitting separate mixture models to each finger, it is ensured that the composition of a target population is correctly represented.

The clustering of mixture models reduces the computational time for obtaining the PRC for a large population (or database) of fingerprints without smoothing out salient inter-class variability in the population. To formally obtain the composition of a target population, Zhu et al. [9] adopt an agglomerative hierarchical clustering procedure on the space of all fitted mixture models. The dissimilarity measure between the estimated mixture densities f and g is taken to be the Hellinger distance

$$H(f,g) = \int_{x \in S} \int_{\theta \in [0,2\pi)} \left(\sqrt{f(x,\theta)} - \sqrt{g(x,\theta)}\right)^2 dx \, d\theta.$$
(18)

The Hellinger distance, H, is a number bounded between 0 and 2, with H = 0 (respectively, H = 2) if and only if f = g (respectively, f and g have disjoint support). Once the clusters are determined (see [9] for details), the mean mixture density is found for each cluster C_i as

$$\bar{f}(x,\theta) = \frac{1}{|C_i|} \sum_{f \in C_i} f(x,\theta).$$
(19)

The mean parameter $\lambda(Q, T)$ in (16) depends on Q and T via the mean mixture densities of the clusters from which Q and T are taken. If Q and T, respectively, belong to clusters C_i and C_j , say, for i, j = $1, 2, \ldots, N^*$ with $i \leq j$ and N^* denoting the total number of clusters, $\lambda(Q, T) \equiv \lambda(C_i, C_j)$ with the mean mixture densities of C_i and C_j used in place of the original mixture densities in (17). Thus, the probability of obtaining exactly u matches corresponding to clusters C_i and C_j is given by

$$p^{*}(u; C_{i}, C_{j}) = e^{-\lambda(C_{i}, C_{j})} \frac{\lambda(C_{i}, C_{j})^{u}}{u!}.$$
(20)

and the overall probability of exactly u matches is

$$p^{**}(u) = \frac{\sum_{i \le j} |C_i| |C_j| p^*(u; C_i, C_j)}{\sum_{i \le j} |C_i| |C_j|}.$$
(21)

It follows that the overall PRC corresponding to w matches is given by

$$\overline{\text{PRC}} = \sum_{u \ge w} p^{**}(u) \tag{22}$$

In order to remove the effect of very high or very low PRCs, the $100(1-\alpha)\%$ trimmed mean is used instead of the ordinary mean as in (21). The lower and upper $100\alpha/2$ -th percentiles of { $p^*(u; C_i, C_j)$, $1 \le i, j \le N^*$ } are denoted by $p_C^*(u; \alpha/2)$ and $p_C^*(u; 1-\alpha/2)$. Also, define the set of all trimmed $p^*(u; C_i, C_j)$ probabilities as $\mathcal{T} \equiv \{ (i, j) : p_C^*(u; \alpha/2) \le p^*(u; C_i, C_j) \le p_C^*(u; 1-\alpha/2) \}$. Then, the $100(1-\alpha)\%$ trimmed mean PRC is

$$\overline{\mathsf{PRC}}_{\alpha} = \sum_{u \ge w} p_{\mathcal{T}}^{**}(u) \tag{23}$$

where

$$p_T^{**}(u) = \frac{\sum_{(i,j)\in\mathcal{T}} |C_i| |C_j| p^*(u; C_i, C_j)}{\sum_{(i,j)\in\mathcal{T}} |C_i| |C_j|}$$
(24)

In Section V, we have used the trimmed mean with $\alpha = 0.05$.

V. Experimental Results

The results in this section are taken from Zhu et al. [9]; the interested reader is referred to more details discussed in the paper. The methodology for assessing the individuality of fingerprints are validated on three target populations, namely, the NIST Special Database 4 [3], FVC2002 DB1 and FVC2002 DB2 [2] fingerprint databases. The NIST fingerprint database [3] is publicly available and contains 2,000 8-bit gray scale fingerprint image pairs of size 512-by-512 pixels. Because of the relative large size of the images in the NIST database, the first image of each pair is used for statistical modeling. Minutiae could not be automatically extracted from two images of the NIST database due to poor quality. Thus, the total number of NIST fingerprints used in our experiments is F = 1,998.

21 Mixture Model								
	Freeman-Tukey			Chi-square				
p-value	NIST (1,998)	DB1 (100)	DB2 (100)	NIST (1,998)	DB1 (100)	DB2 (100)		
p-value > 0.01 (Mixture accepted)	1,864	71	67	1,569	65	52		
p-value ≤ 0.01 (Mixture rejected)	134	29	33	429	35	48		
Uniform Model								
	Freeman-Tukey			Chi-square				
p-value	NIST (1,998)	DB1 (100)	DB2 (100)	NIST (1,998)	DB1 (100)	DB2 (100)		
p-value > 0.01 (Uniform accepted)	550	1	0	309	1	0		
p-value ≤ 0.01 (Uniform rejected)	1,448	99	100	1,689	99	100		

TABLE I. Results from the Freeman-Tukey and Chi-square tests for testing the goodness of fit of the mixture and uniform models. Entries correspond to the number of fingerprints in each database with p-values above and below 0.01. The total number of fingerprints in each database is indicated in parenthesis. Table entries are taken from [9].

For the FVC2002 database, also available in the public domain, two of its subsets DB1 and DB2 is used. The DB1 impressions (images size = 388×374) are acquired using the optical sensor "TouchView II" by Identix, while the DB2 impressions (image size = 296×560) are acquired using the optical sensor "FX2000" by Biometrika. Each database consists of F = 100 different fingers with 8 impressions (L = 8) per finger. Because of the small size of the DB1 and DB2 databases, a minutiae consolidation procedure was adopted to obtain a master (see [9] for the details). The mixture models were subsequently fitted to each master.

Zhu et al. developed a measure of goodness of fit of hypothesized distributions to the observed minutiae based on a chi-square type criteria. Two tests were considered, namely, the Freeman-Tukey and Chi-square tests. The results for the goodness of fit for two hypothesized distributions, namely, mixture and uniform models are reported in Table I. For all the three databases, the number of fingerprint images with p^{22} values above (corresponding to accepting the hypothesized distribution) and below the threshold 0.01 (corresponding to rejecting the hypothesized distribution) were obtained. Note that the entries in Table I imply that the mixture model is generally a better fit to the observed minutiae compared to the uniform; for example, the mixture model is a good fit to 1,666 images from the NIST database (corresponding to p-values above 0.01) based on the Freeman-Tukey test. For the Chi-square test, this number is 1,784. In comparison, the uniform model is a good fit to only 905 and 762 images, respectively.

The distributions of m and n for the three fingerprint databases are shown in Figures 7 (a), (b) and (c), respectively (the distribution of m and the distribution of n are identical, and hence only one histogram is obtained). The mean m (and n) values for the NIST, FVC2002 DB1 and FVC2002 DB2 databases are approximately 62, 63 and 77 respectively (For the FVC databases, m and n are reported as the mean number of minutiae centers in each master).

Zhu et al. compared the PRC obtained by [9] with those of Pankanti et al. [4]. The query and template fingerprints in the NIST and FVC databases are first aligned using the matcher described in [5], and an overlapping area between the two fingerprints are determined. In order to compute the PRCs, the mixture models are restricted onto overlapping area (see [9] for more details). Table III gives the PRCs corresponding to the mean m, mean n and mean overlapping area for the NIST and FVC databases. The empirical PRC is computed as the proportion of impostor pairs with 12 or greater matches among all pairs with m and n values within ± 5 of the mean in the overlapping area. The empirical probabilities of at least w matches are obtained by counting the number of fingerprint pairs with 12 or more matches divided by the total number of pairs. Thus, one should note that the empirical probability is matcher dependent. Since fingerprint individuality is assessed based on minutiae location and direction only, the matcher of [5] was used which depends only on minutiae information.

Note that as m or n or both increase, the values of PRCs for both the models become large as it



Fig. 7. Empirical distributions of the number of minutiae in the (a) NIST database, (b) master prints constructed from the FVC2002 DB1 database, and (c) master prints constructed from the FVC2002 DB2 database. Average number of minutiae in the three distributions are 62, 63 and 77, respectively. Figure taken from [9].

becomes much easier to obtain spurious matches for larger m and n values. Additionally, Table III illustrates an important fact: The PRCs based on the mixture models are orders of magnitude larger compared to Pankanti's model and closer to the empirical probability of at least w matches. Note also that the mean of λ s (the theoretical mean number of matches) are closer to the empirical counterpart (mean number of observed matches) compared to Pankanti's model. This demonstrates the adequateness of the mixture models for the assessment of fingerprint individuality. While the mixture models is more

Database	(m,n)	Mean Overlapping Area (pixel ²)		
NIST	(52,52)	112,840	413	
FVC2002 DB1	(51,51)	71,000	259	
FVC2002 DB2	(63,63)	110,470	405	

TABLE II. Table giving the mean m and n in the overlapping area, the mean overlapping area

and the value of M for each database.

Database	(m,n,w)	Empirical		Mixture		Pankanti	
		Mean no. of matches	PRC	Mean λ	PRC	Mean λ	PRC
NIST	(52,52,12)	7.1	3.9×10^{-3}	3.1	4.4×10^{-3}	1.2	4.3×10^{-8}
FVC2002 DB1	(51,51,12)	8.0	2.9×10^{-2}	4.9	1.1×10^{-2}	2.4	4.1×10^{-6}
FVC2002 DB2	(63,63,12)	8.6	6.5×10^{-2}	5.9	1.1×10^{-2}	2.5	4.3×10^{-6}

TABLE III. A comparison between fingerprint individuality estimates using the (a) Poisson and mixture models, and (b) Pankanti et al. [4].

adequate at representing minutiae variability, the PRCs obtained are far too large indicating a large amount of uncertainty in declaring a match between a fingerprint pair. One way to reduce the PRC is to add more fingerprint features when performing the identification. Fingerprint individuality assessment can then be made by developing appropriate statistical models for these features.

VI. Summary and Future Work

In this article, an overview of the challenges involved in assessing the individuality of fingerprints is presented. Two works have been discussed. Pankanti's model is the first attempt at modeling the observed minutiae distribution via statistical models whereas Zhu et al. developed more flexible models that adequately describe all minutiae characteristics. There are many open problems that still remain unsolved. Both works have only addressed the issue of inter-class minutiae variability. Appropriate statistical models for modeling the intra-class minutiae variability are still very few in the literature. A very important source of intra-class variability is the quality of the query and template images, and work still needs to be done to investigate how PRCs change with quality of the fingerprint image. It is also important to develop statistical models for more complex fingerprint features. In this case, one can use more useful matching criteria that utilize richer fingerprint features.

In this article, the PRCs have been related to the false match rates. Another measure of fingerprint individuality should be related to the false non-match rates. Eventually, a measure of fingerprint individuality should be a optimal combination of the two measures of errors.

VII. Acknowledgments

The authors would like to thank Prof. Anil Jain for introduction of the fingerprint individuality problem to the authors and for many subsequent discussions that has helped us in our research in this area. This article was written under the support of the NSF DMS grant 0706385.

References

- [1] Daubert v. Merrel Dow Pharmaceuticals Inc, 509 U.S. 579, 113 S. Ct. 2786, 125 L.Ed.2d 469 (1993).
- [2] D. Maio, D. Maltoni, R. Cappelli, J. L. Wayman, and A. K. Jain. FVC2002: Fingerprint verification competition. In *Proceedings of the International Conference on Pattern Recognition*, pages 744–747, 2002. Online: http://bias.csr.unibo.it/fvc2002/databases.asp.
- [3] NIST: 8-bit gray scale images of fingerprint image groups (FIGS). Online: http://www.nist.gov/srd/nistsd4.htm.
- [4] S. Pankanti, S. Prabhakar, and A. K. Jain. On the individuality of fingerprints. *IEEE Trans. Pattern Analysis and Machine Intelligence*, 24(8):1010–1025, 2002.
- [5] A. Ross, S. Dass, and A. K. Jain. A deformable model for fingerprint matching. *Pattern Recognition*, 38(1):95–103, 2005.
- [6] S. C. Scolve. The occurence of fingerprint characteristics as a two dimensional process. *Journal of the American Statistical Association*, 74(367):588–595, 1979.
- [7] D. A. Stoney and J. I. Thornton. A critical analysis of quantitative fingerprint individuality models. *Journal of Forensic Sciences*, 31(4):1187–1216, 1986.

- [8] U. S. v. Byron Mitchell. Criminal Action No. 96-407, U. S. District Court for the Eastern District of Pennsylvania, 1999.
- [9] Y. Zhu, S. C. Dass, and A. K. Jain. Statistical models for assessing the individuality of fingerprints. IEEE Transactions on Information Forensics and Security, (3):391-401, 2007.
- [10] S. L. Sclove, "The Occurrence of Fingerprint Characteristics as a Two Dimensional Process", Journal of American Statistical Association, Vol. 74, No. 367, pp. 588-595, 1979.
- [11] D. A. Stoney and J. I. Thornton, "A Critical Analysis of Quantitative Fingerprint Individuality Models", Journal of Forensic Sciences, Vol. 31, No. 4, Oct 1986, pp. 1187-1216.
- [12] U.S. Department of Justice document SL000386, March 2000. Online: http://www.forensicevidence.com/site/ID/ID_fpValidation.html