

Statistical Models for Assessing the Individuality of Fingerprints

Sarat C. Dass, Yongfang Zhu
Department of Statistics & Probability
Michigan State University
East Lansing, MI 48824

Anil K. Jain
Department of Computer Science & Engineering
Michigan State University
East Lansing, MI 48824

Abstract

The problem of fingerprint individuality is as follows: Given a sample fingerprint, what is the probability of finding a sufficiently similar fingerprint in a target population? In this paper, we develop a family of finite mixture models to represent the distribution of minutiae locations and directions in fingerprint images, including clustering tendencies and dependencies in different regions of the fingerprint domain. These models are shown to be a better fit to the observed distribution of minutiae features and give better assessments of fingerprint individuality compared to previous models. Estimates of fingerprint individuality are obtained using the probability of a random correspondence (PRC). For the “12-point match” criteria, a PRC of 9.2×10^{-5} was obtained for the FVC2002 DB1 database when the number of query and template minutiae features both equal 26. The corresponding PRC based on the MSU VERIDICOM database for the same matching criteria is 6.6×10^{-4} .

1 Introduction

The problem of fingerprint individuality is to develop measures that characterize the extent of uniqueness of a fingerprint. Given a sample fingerprint, the question of interest is “What is the probability of finding a sufficiently similar fingerprint in a target population?” An answer to this question requires the development of appropriate statistical models that are able to capture all aspects of variability of the salient fingerprint features. Currently, measures of fingerprint individuality are either unavailable or unsatisfactory due to the inadequacy of the models used for representing the observed distribution of salient fingerprint features. The main challenge here is to satisfactorily model the large intra-class and small inter-class variability of fingerprint features, and be able to compute estimates of individuality from them.

The unavailability of satisfactory measures of fingerprint individuality associated with expert testimony has been the

highlight of several recent court cases: In the case of *Daubert vs. Merrell Dow Pharmaceuticals, Inc.* [5], the U.S. Supreme court ruled that the reliability of expert testimony for identification based on scientific evidence must be established using accepted scientific principles. Following *Daubert*, fingerprint identification was first challenged in the 1999 case of *USA vs. Byron Mitchell* [14] under the fundamental premise that the uniqueness of fingerprints had not been objectively tested and 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.

There have been several previous studies that addressed the problem of fingerprint individuality using probabilistic models on fingerprint features. However, the assumptions made in the previous studies were either ad hoc or did not satisfactorily represent the observed variations of these features in actual fingerprint databases. For example, evidence of over-dispersed uniform distributions for the minutiae locations was demonstrated in [12], whereas in [13], it was shown that the minutiae points tend to form clusters. Pankanti et al [10] start out by assuming a uniform distribution on minutiae locations and directions, but eventually introduce a “correction” to account for this non-uniformity. However, Pankanti’s model underestimates the probability of obtaining exactly k feature matches when compared to what is empirically observed from actual fingerprint databases. Another important observation is that the location and direction of minutiae points are not independent of one another; minutiae points in different regions of the fingerprint domain are observed to be associated with different region-specific minutiae directions. Moreover, minutiae points that are spatially close tend to have similar directions with each other.

To address the issue of individuality, candidate models have to satisfy two important requirements: (i) flexibility, that is, the model can represent the observed distributions of the minutiae features in fingerprint images for different fingerprint impressions in different databases, and (ii) associated measures of confidence and uncertainties can be



Figure 1. Two examples of model fitting on fingerprints from the FVC20202 DB1 database.

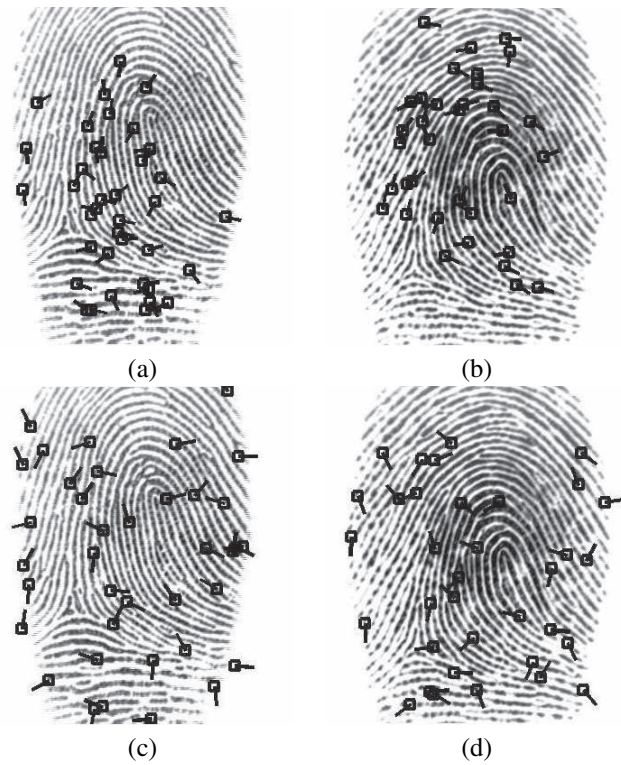


Figure 3. All (X, D) realizations from the proposed model (a-b), and from the uniform distribution (c-d).

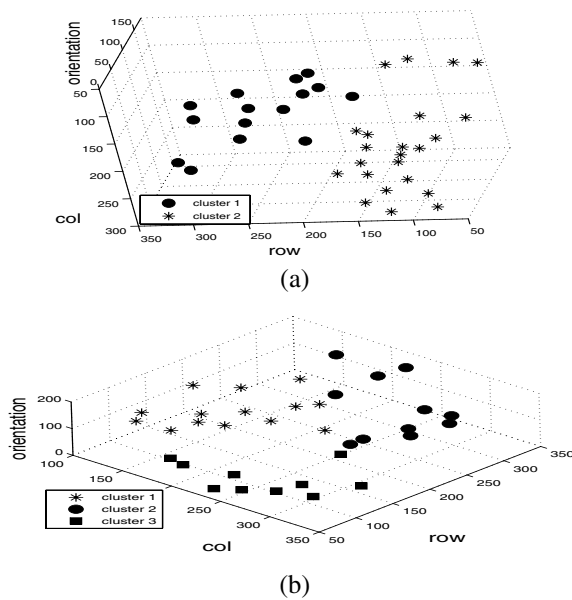


Figure 2. visualization of minutiae feature classification in space (X, D)

easily obtained from these models. We introduce a family of finite mixture models to represent the observed distribution of these features in fingerprint images. For addressing fingerprint individuality, we derive formulas for the probability of a random fingerprint correspondence based on the observed feature match, and demonstrate how these probabilities can be computed from our fitted models.

The rest of this paper is organized as follows: Section 2 describes the finite mixture models proposed for the minutiae features (both location and direction), section 3 compares the simulated impostor matching distributions from the proposed model and the uniform model by [10], section 4 describes how the fitted models can be used to compute the probability of a random correspondence for assessing fingerprint individuality, and section 5 describes the experimental results based on the FVC20202 DB1 [7] and MSU VERIDICOM [10] databases. Summary and discussions are in section 6.

2 Statistical Models On Minutiae Features

Many automatic fingerprint matching systems use minutiae as the salient features for identification since these fea-

tures have been shown to be stable, and can be reliably extracted from fingerprint images. There are many minutiae types observed in fingerprint images [8]. In this paper, we consider only minutiae endings and bifurcations as our salient fingerprint features. The information contained in each minutiae bifurcation or ending consists of the following three components: (i) its location, (ii) its direction, and (iii) the type (either bifurcation or ending). We do not distinguish between the type of the minutiae since this information is not as reliable as the information on location and the direction.

A generic random minutiae location will be denoted by X and its corresponding direction by D . If $S \subseteq \mathbf{R}^2$ denotes the subset of the plane representing the fingerprint domain, the set of all possible configurations for X is the $s = (x, y)$ coordinate points in S . The minutiae direction, D , takes values in $[0, 2\pi)$. Given the total number of minutiae features observed in a fingerprint image is k , say, we develop a joint distribution model for the k pairs of (X, D) , (X_j, D_j) $j = 1, 2, \dots, k$ that accounts for (i) clustering tendencies (non-uniformity) for each (X_j, D_j) , and (ii) dependence between X_j and D_j in different regions of S .

We take each (X_j, D_j) to be independently distributed according to the mixture density

$$f(s, \theta | \Theta_G) = \sum_{g=1}^G \tau_g f_g^X(s | \mu_g, \Sigma_g) \cdot f_g^D(\theta | \nu_g, \kappa_g, p_g), \quad (1)$$

where G is the number of components in the mixture model and $f_g^X(s | \mu_g, \Sigma_g)$ is the probability density function of a bivariate Gaussian random variable with mean μ_g and covariance matrix Σ_g . The density $f_g^D(\theta | \nu_g, \kappa_g, p_g)$ is given by

$$f_g^D(\theta | \nu_g, \kappa_g, p_g) = p_g v(\theta) \cdot I\{0 \leq \theta < \pi\} + (1 - p_g) v(\theta - \pi) \cdot I\{\pi \leq \theta < 2\pi\}, \quad (2)$$

where $I\{A\}$ is the indicator function of the set A , $v(\theta)$ given by

$$v(\theta) \equiv v(\theta | \nu_g, \kappa_g) = \frac{2}{I_0(\kappa_g)} \exp\{\kappa_g \cos 2(\theta - \nu_g)\} \quad (3)$$

is the Von-Mises distribution for modeling angular random variables in $[0, \pi)$ [9] with ν_g and κ_g as the mean angle and the precision of the Von-Mises distribution, and the τ_g 's are non-negative weights summing to one. In (1), Θ_G represents the unknown parameters consisting of G , $(\mu_g, \Sigma_g, \nu_g, \kappa_g)$ for $g = 1, 2, \dots, G$, and the weights τ_g , for $g = 1, 2, \dots, G$. Each component of the mixture model in (1) can be thought of as representing a cluster in the (X, D) space. The minutiae locations corresponding to the g -th cluster have a center at μ_g with cluster shape governed by the covariance matrix Σ_g . We consider four different

parametric forms of Σ_g : (i) $\Sigma_g = \sigma I_2$, (ii) $\Sigma_g = \sigma_g I_2$, (iii) $\Sigma_g = \Sigma$, and (iv) unrestricted Σ_g to represent different shapes of the minutiae location clusters. The density f_g^D corresponding to the minutiae directions of the g -th cluster can be interpreted in the following way: The ridge flow orientation, θ , is assumed to follow the Von-Mises distribution (3) with mean ν_g and precision (inverse of the variance) κ_g . Thus, if κ_g is large, one can expect θ values for the g -th mixture component to be close to the mean orientation ν_g . Minutiae arising from the g -th component, subsequently, have directions that are either θ or $\theta + \pi$, and the density f_g^D assumes that this can happen with probabilities p_g and $1 - p_g$, respectively. Note that the model in (1) allows for the ridge flow orientations to be different in different regions of S (using different ν_g 's and κ_g 's), and at the same time, maintains that spatially neighboring orientations should be similar to each other (same ν_g for orientations from the same cluster).

To estimate the unknown parameters, we develop an algorithm based on hierarchical agglomeration and the EM algorithm for multivariate mixture models. The number of components G was estimated using the BIC criteria [6]. This procedure generalizes the clustering algorithm of [6]. Figure 1 illustrates the fit of the model to two fingerprint images from the FVC2002 DB1 database. Observed minutiae locations (black boxes) and directions (black lines) are shown in panels (a) and (b). Note that we have also incorporated dependence between the minutiae location and direction: If X_j is known to come from the g -th component, then it follows that the direction D_j also comes from the same mixture component. Panels (a) and (b) in figure 2 plot the minutiae features in the (X, D) space where the clustering tendencies of the minutiae features can be visualized. Our algorithm yields G to be 2 and 3 for panels (a) and (b), respectively. Panels (c) and (d) in figure 1 give the cluster assignment for each minutiae feature; the assignment was determined to be the component whose estimated weight τ_g maximized the component weights over g for each minutiae feature.

In order to show the effectiveness of the fit of the models to the observed data, Figures 3 (a-b) show a simulated realization from the fitted models with simulated minutiae locations and directions indicated by black boxes and lines, respectively. Figures 3 (c-d) show a simulated realization when each X 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 1 (a-b)) and simulated minutiae locations and directions from the proposed model (Figures 3 (a-b)) but there is no such agreement for the uniform model. To check the fit of the mixture models to the observed minutiae features, we have developed a goodness-of-fit criteria based on a generalization of Ripley's K function [4]. We have applied

this criteria to fingerprint images in the FVC2002 DB1 and MSU VERIDICOM databases (see Section 5 for details on these databases) and found no evidence of inconsistent fits. We do not present the details here due to space restrictions.

3 A Comparison Between Impostor Matching Distributions

In this section, we demonstrate, via simulation, that the proposed model also results in impostor matching distributions that are closer to the empirical counterpart; the comparison is made with respect to the uniform distribution model on (X, D) . As mentioned earlier, the uniform distribution was the initial distributional model on (X, D) suggested by Pankanti et al [10]. The “corrected” version reported in [10] is a model for the probability of obtaining exactly k feature matches, and is not a distributional model on (X, D) . Therefore, we are only able to simulate from the initial uniform, and not from Pankanti’s corrected model. We do perform a comparison between the probability of obtaining exactly k matches based on our model with Pankanti’s corrected model. However, this is postponed to later since we first require to derive formulas for these probabilities based on our elicited models in Section 4.

Our findings are based on the FVC2002 DB1 and MSU VERIDICOM databases. The FVC2002 DB1 database consists of 100 fingers with 8 impressions per finger resulting in $100 \times 99 \times 8 \times 8 = 633,600$ pairs of impostor fingerprints. Subsequently, the number of minutiae matches for each impostor pair is determined using the matching algorithm reported in [11]. We also fit the proposed models to the 800 fingerprint impressions in this database and obtained one simulated realization of minutiae locations and directions from the fitted models for each finger (each simulated realization consists of k minutiae features where k equals to the observed number of minutiae in a fingerprint impression). Subsequently, the number of minutiae feature matches for each simulated impostor pair is determined using the same matching algorithm resulting in 633,600 simulated impostor matching scores. The empirical and simulated impostor matching scores for the MSU VERIDICOM database are obtained similarly from the 6,543,360 pairs of impostor images. Figure 4 gives a comparison of the number of impostor matches obtained empirically (thick solid line) as well as via simulation from the fitted mixture density models (dot-dashed line). The distribution of the number of impostor matches is also given for the fitted model with uniform distributions on minutiae locations and directions (dotted line). Figure 4 re-emphasizes the fact that the proposed mixture model is more reliable as representations of distributions of minutiae features in observed fingerprint images, resulting in a distribution on the number of impostor matches that better approximates the empirical counter-

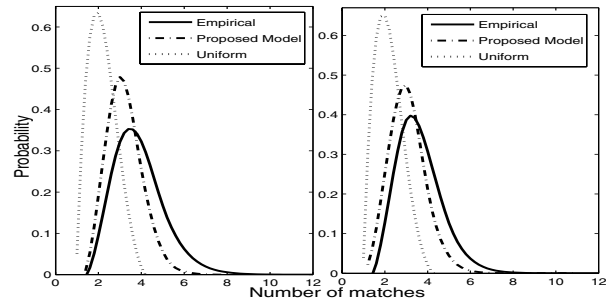


Figure 4. A comparison of the distributions of the number of matching minutiae features: FVC2002 DB1 (left panel) and MSU VERIDICOM (right panel).

part.

4 Probability of a Random Correspondence

Measures of confidence/uncertainty associated with the individuality of fingerprints can be reported in terms of the probability of a random correspondence (PRC). The PRC is the chance that an arbitrary impostor fingerprint from a population of individuals will have corresponding features similar to that of the query. Small (respectively, large) values of the PRC imply that it is unlikely (respectively, likely) that the query features match those of the template of an individual other than the query owner. Let Q (respectively, T) denotes the query (respectively, template) fingerprint image from the individual I_Q (respectively, I_T). We assume that the following quantities are given: The total number of minutiae points, m , in the query Q , the total number of minutiae points, n , in the template T , and the number of matching paired minutiae features, w , between Q and T . Then, the PRC is the probability of obtaining exactly w matches between Q and T when $I_Q \neq I_T$. After several analytical simplifications, we obtain an expression for the PRC given by

$$p^*(w; Q, T) = \binom{n}{w} \cdot (p_m(Q, T))^w (1 - p_m(Q, T))^{n-w}, \quad (4)$$

where $p_m(Q, T)$ is the probability of a random minutiae feature from T matching one of the m minutiae features of Q . It follows that the PRC in (4) corresponds to a binomial probability whose parameters are given by n and $p_m(Q, T)$, respectively denoting the total number of trials and the probability of success in each trial.

The value of $p_m(Q, T)$ is matcher dependent. Many minutiae matchers including the one we have used in this paper try to maximize the number of matches between any

two pairs of query and template fingerprints, even for impostor pairs. Thus, we expect the value of $p_m(Q, T)$ to be much higher compared to purely random matches between a pair of impostor minutiae features. We propose to estimate $p_m(Q, T)$ by equating the theoretical expected value of the number of matches between a query-template pair to the corresponding observed number of matches obtained by our matching algorithm. One important point to be noted is that the matching algorithm used here never results in zero matches. Thus, we compute the conditional expectation, instead of the unconditional expectation, of the binomial distribution, conditioned on the fact that the number of matches is always greater than 0, and equate this to the observed number of matches between Q and T . The estimation of $p_m(Q, T)$ can be written as:

$$\frac{np_m(Q, T)}{(1 - (1 - p_m(Q, T))^n)} = w_0, \quad (5)$$

where the left- and right-hand terms in (5) are the conditional expectation, and observed number of matches between Q and T , respectively. The value of w_0 can be estimated by simulating minutiae features from the proposed models fitted to Q and T , and then determining the observed number of minutiae matches using the matching algorithm in [11]. Plugging this estimated w_0 value into (5), one can then find a solution for $p_m(Q, T)$.

For a fingerprint database consisting of impressions of N different fingers with L impressions per finger, we wish to find the most representative PRC value for this database. For a fixed query Q , there are a total of $(N - 1)L$ impostor templates, T , corresponding to Q . If, in addition, Q is made to vary, we find a total of $N(N - 1)L^2$ pairs of impostor fingerprint images from the entire database. In that case, the average PRC, $\overline{\text{PRC}}$, corresponding to w minutiae feature matches obtained from the fingerprint database has the expression

$$\overline{\text{PRC}} = \frac{1}{N(N - 1)L^2} \sum_{(Q, T) \text{ impostor}} p^*(w; Q, T), \quad (6)$$

where $p^*(w; Q, T)$ is as defined in (4).

5 Experimental Results

Our methodology for assessing the individuality of fingerprints were validated on two fingerprint databases: FVC2002 [7] and the MSU VERIDICOM [10] databases. For the FVC2002 database, we used the subset DB1 where the fingerprints are obtained using the optical sensor ‘‘TouchView II’’ by Identix. The DB1 database consists of 100 different fingers with 8 impressions per finger. The MSU VERIDICOM database consists of fingerprint images from 160 individuals collected in our laboratory using a

solid state sensor manufactured by Veridicom, Inc. Impressions were acquired from the right index, right middle, left index and left middle fingers for each of the 160 subjects. Four impressions for each of the four fingers were acquired: two impressions were obtained initially, followed by two additional impressions after an interval of six weeks. Thus, $160 \times 4 \times 4 = 2,560$ fingerprint images were obtained.

We compare our results with that of Pankanti et al. [10] where a uniform distribution was assumed for the minutiae locations and the probability of a match between a pair of minutiae directions was assumed to be independent of each other, and independent of the minutiae location matches. We denote the PRC value from the model by Pankanti et al. by PRC_0 . Using the proposed model, we obtain the probabilities of exactly w matches based on the binomial probabilities in (4). The value of $\overline{\text{PRC}}$ was computed using formula (6). Figure 5 gives the results for the FVC2002 DB1 and MSU VERIDICOM databases, respectively. The PRCs are usually computed for an observed number of matches that lie in the right tail of the distributions (for example, 10 or 12) in Figure 5, and thus, models that are close approximations to the empirical distribution especially in the right tails give more reliable estimates of the PRCs. Note that the PRC_0 in the theoretical model suggested in [10] decreases too quickly to zero as the number of matches increases. The uniform distribution on the minutiae location tend to randomly distribute the minutiae features over the entire fingerprint domain (see Figures 3 (c-d)) and consequently, it is less likely that higher number of minutiae matches are obtained as is observed in the empirical data. The assumptions of uniform distribution as well as the independence between minutiae location and direction underestimate the true PRC values, and are generally orders of magnitude smaller compared to the PRCs obtained from the model proposed here. We have also computed the matching probabilities based on mean value of m and n in the two databases and compared the theoretical PRCs with the empirical counterparts. The results are given in Table 1. Note that the value of $\overline{\text{PRC}}$ is much closer to the empirical counterpart compared to PRC_0 .

Next, we compare $\overline{\text{PRC}}$ and PRC_0 for different settings of m , n and w as reported in [10]. Table 2 give the results of this comparison for the FVC2002 DB1 and MSU VERIDICOM databases, respectively; in Table 2, M is defined as the number of non-overlapping cells in the overlapped area between the query and template fingerprint images (see [10] for details). Note that as m or n or both increase, PRCs become larger as it becomes easier to obtain spurious matches for larger m and n values. More importantly, however, is the fact that the $\overline{\text{PRC}}$ s are several orders of magnitude larger compared to PRC_0 .

Our objective is to match the theoretical and empirical distributions of the impostor matches using appropriate sta-

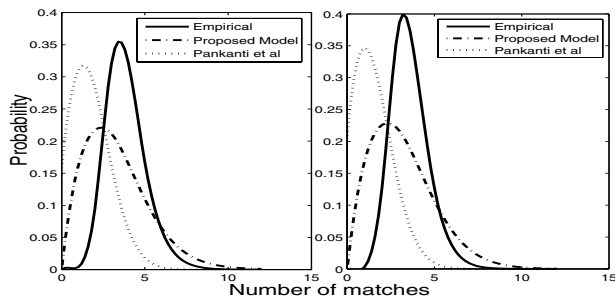


Figure 5. Comparing the distributions of the number of minutiae matches based on different models for FVC2002 (left panel) and MSU VERIDICOM (right panel)

Table 1. A comparison of the PRCs with the empirical probabilities at mean m and n values for the FVC2002 DB1 and MSU VERIDICOM databases.

Database	m, n, w	Empirical PRC	PRC_0	\overline{PRC}
FVC2002 DB1	27, 27, 5	0.167	0.024	0.107
MSU VERID	24, 24, 5	0.216	0.018	0.100

tistical models on the minutiae features based on a certain matcher implementation. We judge a model to be more accurate if it produces results closer to the empirical distribution. Thus, in our case, we deem the mixture models to be a more accurate representation of the observed data than the uniform model, especially in the right tail area. Our eventual goal is to obtain reliable fingerprint individuality estimates for a population of individuals. In such a case, we would collect a sample of fingerprints from the population, fit the mixture model to each fingerprint in the sample and check to see if the matcher implementation results in a theoretical distribution that is close to the empirical counterpart. This requirement emphasizes the need for flexible models to accommodate all possible feature variability in a large number of fingerprint images as is demonstrated by the mixture model. Once successful, we would be able to predict the matcher performance and individuality estimates without having to actually perform millions of impostor matchings for the entire population.

Table 2. A comparison of \overline{PRC} and PRC_0 for different m, n and w based on FVC 2002 (upper panel) and MSU VERIDICOM (lower panel).

(M, m, n, w)	PRC_0	\overline{PRC}
(115, 26, 26, 26)	2.8×10^{-41}	1.6×10^{-17}
(115, 26, 26, 12)	1.2×10^{-9}	9.2×10^{-5}
(149, 36, 36, 36)	4.9×10^{-56}	7.2×10^{-27}
(149, 36, 36, 12)	4.0×10^{-7}	9.3×10^{-4}
(177, 46, 46, 46)	5.5×10^{-70}	9.9×10^{-37}
(177, 46, 46, 12)	2.1×10^{-5}	3.3×10^{-3}
(45, 12, 12, 12)	4.6×10^{-18}	6.5×10^{-9}

(M, m, n, w)	PRC_0	\overline{PRC}
(104, 26, 26, 26)	5.3×10^{-40}	1.6×10^{-13}
(104, 26, 26, 12)	3.9×10^{-9}	6.6×10^{-4}
(176, 36, 36, 36)	5.5×10^{-59}	1.1×10^{-17}
(176, 36, 36, 12)	6.1×10^{-8}	5.6×10^{-3}
(248, 46, 46, 46)	1.3×10^{-77}	1.2×10^{-41}
(248, 46, 46, 12)	5.9×10^{-6}	1.5×10^{-2}
(70, 12, 12, 12)	1.2×10^{-20}	1.2×10^{-8}

6 Summary and Conclusions

A novel family of finite mixture models is proposed as a flexible and reliable way of representing minutiae variability in fingerprint images. These models better represent clusters of features observed in fingerprint images compared to the uniform distribution. Consequently, the theoretical distribution of the number of impostor matches obtained using the proposed models is much closer to the empirical counterpart, and gives rise to more reliable individuality estimates. We note that fingerprint individuality estimates depend heavily on the type of matcher used, and propose a procedure that explicitly takes the matcher implementation into account. We believe that accounting for the matcher implementation explicitly in the mathematical formulation of fingerprint individuality has not been previously addressed in the literature.

Note from the impostor matching distributions (Figure 4) and the theoretical probabilities of obtaining exactly k matches (Figure 5) that there are still differences between our theoretical models and the empirical counterparts. Our future work will focus on improving the models presented here further by considering some kind of dependence between the observed minutiae features instead of assuming

independence between them. We also plan to develop models that give the probability of obtaining exactly k matches in the genuine case, which in turn will determine the likelihood of a genuine versus impostor match.

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