

# On The Fundamental Performance For Fingerprint Matching

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## Abstract

Fingerprints have long been used for person authentication. However, there is not enough scientific research to explain the probability that two fingerprints, which are impressions of different fingers, may be taken as the same one. In this paper, we propose a formal framework to estimate the fundamental algorithm independent error rate of fingerprint matching. Unlike a previous work, which assumes that there is no overlap between any two minutiae uncertainty areas and only measures minutiae's positions and orientations, in our model, we do not make this assumption and measure the relations, i.e. ridge counts, between different minutiae as well as minutiae's positions and orientations. The error rates of fingerprint matching obtained by our approach are significantly lower than that of previously published research. Results are shown using NIST-4 fingerprint database. These results contribute towards making fingerprint matching a science and settling the legal challenges to fingerprints.

## 1. Introduction

The foundations of modern fingerprint recognition were established by the research of F. Galton and E. Henry at the end of nineteenth century. Two fundamentally important conclusions were reached through extensive experiments on different age groups within different races [8]: (a) Fingerprints of a person are permanent, i.e., once the fingerprint is fully formed by the seventh month of fetal life, it won't change naturally; (b) Fingerprints of individuals are unique, i.e., no two fingerprints are ever found to be exactly the same. Both conclusions were the building blocks of research in this field over the last century.

After Galton and Henry, work on fingerprint recognition was extended and refined. In the early twentieth century, fingerprints were formally used as valid signs of identity by law-enforcement agencies. Now, in most countries' courts, fingerprint identification is taken positively for a defendant's guilt. People accepted fingerprint identification as science without any doubt. However, recently in *Daubert Hearing* in the U.S. court [5], the *Daubert Opinion* states that: 1) the trial judge must still screen scientific evidence to ensure it is relevant and reliable; 2) the focus, of course, must be solely on

principles and methodology, not on the conclusions they generate; 3) factors the court should consider include: (a) testing and validation; (b) peer review; (c) rate of error; and (d) general acceptance. The opinion governs the admissibility of scientific evidence in U.S. Federal court and many state and local jurisdictions have adopted it.

The second conclusion regarding the uniqueness of fingerprints is challenged because of the *Daubert Opinion*. Despite the fact that all fingerprint examiners believe in it and in reality it has not been found that two fingerprints are exactly the same, it is very difficult to prove it empirically. The millions of sets of fingerprints are never compared against one another for possible duplication. Judge Joyner presented the oral decision on *Daubert Hearing* on September 13th, 1999 [5]. The defense motion to exclude fingerprint evidence and testimony was denied. However, from *Daubert Hearing* to May 22, 2002, there are 37 legal challenges to fingerprints in the United States of America.

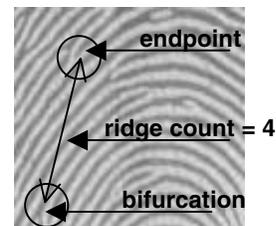


Figure 1. Examples of minutiae and ridge count.

A fingerprint is formed by a group of curves. The most useful features, which include endpoints and bifurcations, are called minutiae. Figure 1 shows examples of an endpoint and a bifurcation in a fingerprint image. Because of its stability, minutiae have been adopted in most existing fingerprint recognition systems. Generally, the similarity of two fingerprints depends on the number of corresponding minutiae. The larger the number of the corresponding minutiae, the more similar the two fingerprints are. From a scientific point of view, we define the error rate of fingerprint matching as: The probability of two randomly chosen fingerprints, which are impressions of different fingers, have sufficient similarity. Obviously, the lower the probability, the more unique the different fingerprints are.

Fingerprint recognition performance is typically determined experimentally. The major limitations of

experimental performance evaluation are [7]: 1) It does not tell us why this is the expected performance. Such an insight can provide fundamental answers to questions such as: a) what are the performance limits? b) How much distortion can be tolerated without degrading performance? c) Is a given matching criterion sufficient to achieve desired levels of performance? d) How many model objects can be accommodated without substantially degrading performance? Without a fundamental understanding of these questions, design of object recognition systems will remain an art rather than a science; 2) Performance obtained experimentally depends on the algorithm and actual implementation of the recognition system, which may result in significant difference of performance.

## 2. Related Work And Contributions

### 2.1. Related Work

Generally, a minutiae-based fingerprint matching algorithm is kind of point matching algorithm. The research on performance of fingerprint recognition belongs to one of the two categories: 1) Find the probability of the amount of details presented in a single fingerprint; 2) Find the probability of the amount of details presented as correspondences in two different fingerprints.

Galton [3] assumed that 24 independent square regions could cover a fingerprint and he could correctly reconstruct any of the regions with a probability of 1/2 by looking at the surrounding ridges. Accordingly, Galton's formulation of the uniqueness of a fingerprint is given by:  $(1/16) \times (1/256) \times (1/2)^{24}$ , where 1/16 is the probability of the occurrence of a fingerprint type, and 1/256 is the probability of occurrence of the correct number of ridges entering and exiting each of the 24 regions. Most research on fingerprint performance is similar to Galton's work, which measures the amount of details in a single fingerprint. A more detailed introduction to this kind of work can be found in [2].

In [6], we use a model-based approach to find the local correspondences between two different fingerprints. An analysis of the probability of finding false correspondences is also introduced. First, we compute  $S$ , the size of the search space, and then compute  $S_l$ , the size of finding one correspondence within some uncertainty area. Based on the assumption that the models are uniformly distributed in the search space, the probability of finding one correspondence is  $S_l / S$ . Using Binomial distribution and Poisson approximation, it can be extended to compute the probability of finding more than one correspondences between two different fingerprints. The problem with this approach is that: 1) the assumption that the models are uniformly distributed in the search space is not realistic; 2) the estimation of error rate in this

approach depends on the recognition algorithm used. It is not suitable to be used if a non-model based recognition approach is used.

An important work was presented in Pankanti et al. [2], which measures the amount of detail needed to establish correspondence between two fingerprints. To estimate the probability of correspondence, they make the following assumptions: 1) only endpoint and bifurcation are considered and they do not distinguish them; 2) minutiae are distributed in a fingerprint uniformly and no two minutiae are very close to each other, so there is no overlap between their uncertainty area; 3) correspondence of a minutiae pair is independent and each correspondence is equally important; 4) fingerprint quality is not explicitly taken into account. The probability that there are exactly  $\rho$  corresponding minutiae between  $n$  query minutiae and  $m$  template minutiae is given by  $\binom{m}{\rho} \binom{M-m}{n-\rho} \binom{M}{n}$ , where

$M=A/C$  and is assumed to be an integer ( $A \gg C$ ),  $A$  is the total area of overlap between the template and query fingerprints after reasonable alignment, and  $C$  is the area of tolerance for uncertainty. Accordingly, the probability of matching  $q$  minutiae in both position and direction is given by  $\sum_{\rho=q}^{\min(m,n)} \left( \binom{m}{\rho} \binom{M-m}{n-\rho} \binom{M}{n} \right) \times \binom{\rho}{q} \times l^q (1-l)^{\rho-q}$ ,

where  $l$  is the probability of two position-matched minutiae having similar direction. This relatively simple model has some problems. *First* of all, the second assumption in their model is not true for the query fingerprint, although it is possible to make it true for the template fingerprint. If the fingerprint quality is 'good', then we can extract minutiae effectively, and the second assumption is true. However, when the fingerprint quality is bad, if we use this assumption to purify the extracted minutiae, we may ignore too many true minutiae. *Second*, their model does not measure the relations between different minutiae, which makes the model unreliable.

### 2.2. Contributions

A major *contribution* of our research is the development of a formal framework for estimating the error rate of fingerprint recognition, so that we may have a fundamental insight into the performance of fingerprint recognition. In our model, we not only assume that the uncertainty area of any two minutiae may overlap each other, but also measure the relations between different minutiae. We address the error rate estimation problem in the following context: 1) Both template and query fingerprint are represented by locations of 2D point features; 2) An instance of a query data is assumed to be obtained by applying some 2D transformations to the template data, considering uncertainty, occlusion and clutter. Our estimation of error rate is fundamental, since it is independent of the particular algorithm used for

recognition system and is validated using *NIST-4* fingerprint database.

### 3. Technical Approach

In this section, we develop a new model in which we not only measure minutiae's positions and orientations, but also the relations between different minutiae to find the probability of correspondence between fingerprints. To estimate the probability, we make the following assumptions: 1) We do not distinguish endpoint and bifurcation and take both of them as point features; 2) Point features are distributed uniformly in the fingerprints, however, the uncertainty area of different minutiae may overlap; 3) Correspondence of a minutiae pair is independent and each correspondence is equally important; 4) Fingerprint quality is not explicitly taken into account in the model; and 5) The template and query fingerprints are well aligned. Note that 2) is different from that in [2] and 5) is not explicitly stated in [2] although it is one assumption in [2].

Suppose 1) the overlap area of the template and query fingerprints is  $A$ ; 2) the number of minutiae in the template and query fingerprints are  $m$  and  $n$ , respectively; 3) the uncertainty area of a minutia is  $C$ ,  $C=\pi r^2$ , where  $r$  is the radius of the uncertain area; 4) the probability of matching one minutia in the query fingerprint with one minutia in the template fingerprint is  $p$ ,  $p=C/A$ ; and 5) the number of corresponding minutiae in the query fingerprint is  $k$ .

These  $k$  corresponding minutiae in the query fingerprint may correspond to  $i$  minutiae in the template fingerprint, where  $1 \leq i \leq k$ . We can find  $P_{M,N}\{M=i, N=k\}$ , the probability of  $k$  minutiae in the query fingerprint correspond to only  $i$  minutia in the template fingerprint as:

$$i=1, P_{M,N}\{M=1, N=k\} = \binom{n}{k} \binom{m}{1} (I-mp)^{n-k} p^k,$$

$$i=2, P_{M,N}\{M=2, N=k\} = \binom{n}{k} \binom{m}{2} (I-mp)^{n-k} \left( (2p)^k - \binom{2}{1} p^k \right)$$

In general, we can find the probability of  $k$  minutiae in the query fingerprint corresponding to only  $i$  minutia in the template fingerprint as:

$$P_{M,N}\{M=i, N=k\} = \binom{n}{k} \binom{m}{i} (I-mp)^{n-k} H_i$$

$$H_i = p^k, H_i = (ip)^k - \sum_{j=1}^{i-1} \left\{ \binom{i}{j} H_j \right\} \text{ for } i \geq 2 \quad (1)$$

where  $N$  is the number of corresponding minutiae between the template and query fingerprints.

In equation (1), we only consider the position of a minutia in the matching. If we consider both position and direction of a minutia in the matching at the same time, then we have,

$$P_{M,N}\{M=i, N=k\} = \binom{n}{k} \binom{m}{i} (I-mp_d)^{n-k} H_i$$

$$H_i = p_d^k, H_i = (ip_d)^k - \sum_{j=1}^{i-1} \left\{ \binom{i}{j} H_j \right\} \text{ for } i \geq 2 \text{ and } k \geq i$$

$$p_d = \frac{P}{360} \times 2r_i \quad (2)$$

where  $r_i$  is the uncertainty of the minutiae directions.

Figure 1 shows an example of ridge count between two minutiae, which defines the relations between two different minutiae. Obviously, if we measure ridge counts, the matching will be more reliable and the performance of the recognition system will be better. Ridge count changes according to distance between two minutiae, average distance between ridges, orientation of ridges, etc. It is difficult to build a model of ridge counts. However, it is unnecessary for us to know the model of ridge counts explicitly. What we need to know is  $p_r$ , the probability that two ridge counts, which are between a pair of corresponding minutiae in the template and query fingerprints respectively, can be considered as the same ridge count. Because of bad quality fingerprints, it is not easy to develop an effective algorithm to detect ridge counts. Thus, we have to consider the uncertainty of ridge counts in matching. For simplicity, we assume:

$$p_r = \frac{2T_r + I}{r_{max} - r_{min}} \quad (3)$$

where  $r_{max}$  and  $r_{min}$  are the maximum and minimum ridge counts between two minutiae in a fingerprint, respectively, and  $T_r$  is threshold to tolerate the uncertainty of ridge counts in ridge counts matching.

• **Two-Point Model:** First, let us consider a case, which only uses a pair of minutiae to construct the model. Each pair of minutiae can form a side. Totally,  $i$  minutiae can form  $g_2=iC_2$  sides. Suppose  $M_2$  is the number of models, which are constructed by pairs of minutiae, that are supposed to satisfy all the criteria in the matching and  $P_{2,M}\{\bullet\}$  is the probability of 2-point model, then we have

$$P_{2,M}\{M_2=s | M=i\} = \begin{cases} \binom{g_2}{s} p_r^s (1-p_r)^{g_2-s}, & 0 \leq s \leq g_2 \\ 0, & \text{otherwise} \end{cases} \quad (4)$$

In this case, the expectation of the number of model that satisfy all the criterion in the matching when  $N=k$  is:

$$E\{M_2=s, N=k\} = \sum_{i=2}^{\min(m,n,k)} P_{2,M}\{M_2=s, M=i, N=k\}$$

$$= \sum_{i=2}^{\min(m,n,k)} \{ P_{M,N}\{M=i, N=k\} \times P_{2,M}\{M_2=s | M=i, N=k\} \} \quad (5)$$

Thus, the Probability Distribution Function (PDF) of 2-point model is

$$E\{M_2=s\} = \sum_{k=2}^n \{ E\{M_2=s, N=k\} \} \quad (6)$$

• **Three-Point Model:** A more complex case uses 3 points (triplets of noncolinear minutiae) to build the

model and measure each sides of every 3-point model to predict the performance. Since for each 3-point model, there are three sides and those sides are not independent, they may have effect on other models. It is difficult to get the closed-form equation for  $P_{3,M}\{M_3=s | M=i\}$ , where  $M_3$  is the number of models that are constructed by triplets of minutiae and satisfy all the criterion in the matching and  $P_{3,M}\{\bullet\}$  is the probability of 3-point model. In this work, we use a statistical method to estimate  $P_{3,M}\{M_3=s | M=i\}$  and its 95% confidence interval  $P_{3,M,C=95\%}\{M_3=s | M=i\}$ .

$$E_{C=95\%}\{M_3 = s, N = k\} = \sum_{i=3}^{\min(m,n,k)} P_{3,M,C=95\%}\{M_3 = s, M = i, N = k\} \\ = \sum_{i=3}^{\min(m,n,k)} \{P_{M,N}\{M = i, N = k\}\} \\ \times P_{3,M,C=95\%}\{M_3 = s | M = i, N = k\} \quad (7)$$

where  $C=95\%$  means the 95% confidence interval.

Based on equation (6), we can compute the expectation of Probability Distribution Function (PDF) of the number of 3-point models as,

$$E_{C=95\%}\{M_3 = s\} = \sum_{k=3}^n \{E_{C=95\%}\{M_3 = s, N = k\}\} \quad (8)$$

This is an important result. Although we may find the PDF of the number of n-point model for  $n>3$ , we believe that 3-point model is simple and may provide a simple criterion for evaluating the performance of fingerprint matching.



Figure 2. Sample fingerprints in NIST-4.

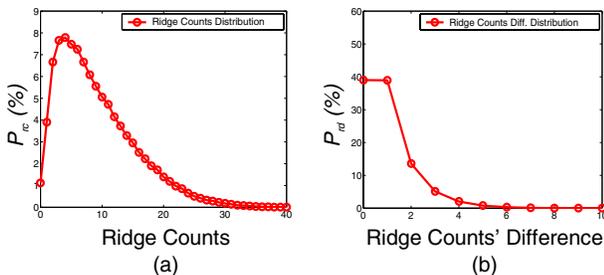


Figure 3. Distribution of (a) ridge counts and (b) ridge counts' difference.

## 4. Experimental Results

### 4.1. Database

The database we use in our experiments is the NIST Special Database 4 (NIST-4) [4], which contains 2000

pairs of fingerprints. Each pair is a different impression of the same finger and is coded as a  $f$  or  $s$  followed by 6 numbers. The size of fingerprints is  $480 \times 512$  pixels. One pair of fingerprints are shown in Figure 2.

### 4.2. Parameters

The parameters we used in our estimation include:  $r=15$  pixels,  $C=225\pi$  pixels<sup>2</sup>,  $A=512 \times 480$  pixels<sup>2</sup>,  $p \approx 2.9 \times 10^{-3}$ ,  $r_l = 22.5^\circ$ ,  $p_l \approx 3.6 \times 10^{-4}$ ,  $m=n=60$ . In order to estimate  $p_r$ , we use the Genetic Algorithm (GA) based approach introduced in [1] to find the optimal transformation between each genuine matching in NIST-4 fingerprint database. Based on the optimal transformation, the pairs of corresponding minutiae in two fingerprints of each genuine matching are found. Then, we find  $P_{rc}$ , the distribution of ridge counts, and  $P_{rd}$ , the difference of ridge counts between two fingerprints of each genuine matching. Figure 3 shows these two distributions. From these figures, we have  $P_{rc}\{0 \leq \text{ridge counts} \leq 20\} = 92.5\%$ ,  $P_{rc}\{0 \leq \text{ridge counts} \leq 30\} = 99.3\%$ ,  $P_{rd}\{0 \leq \text{ridge counts difference} \leq 1\} = 78.0\%$ , and  $P_{rd}\{0 \leq \text{ridge counts difference} \leq 2\} = 91.5\%$ . Obviously, different choices of the spread of ridge counts and ridge counts difference may result different estimation of  $p_r$ . To be more conservative, we take the spread of ridge counts and ridge counts difference as 20 and 1, respectively. That is,  $r_{max} - r_{min} = 20$  and  $T_r = 1$ , so  $p_r = 0.15$ .

INPUT: the number of corresponding feature points  $n_c$ ;  
OUTPUT:  $s_i$ , the number of corresponding triangles between the template and query fingerprints;

- 1) For  $i = 1$  to  $n_c - 1$ ; For  $j = i + 1$  to  $n_c$
- 2)     Generate the ridge counts for template and query:  $tr_{i,j}$  and  $qr_{i,j}$ ;
- 3)     Next  $j$ ; Next  $i$
- 4)      $s_i = 0$ ;
- 5) For  $i = 1$  to  $n_c - 2$ ; For  $j = i + 1$  to  $n_c - 1$ ; For  $k = j + 1$  to  $n_c$
- 6)     If ( $|tr_{i,j} - qr_{i,j}| \leq T_r$  and  $|tr_{i,k} - qr_{i,k}| \leq T_r$  and  $|tr_{j,k} - qr_{j,k}| \leq T_r$ )
- 7)          $s_i = s_i + 1$ ;
- 8)     End if;
- 9)     Next  $k$ ; Next  $j$ ; Next  $i$

Figure 4. Basic simulation procedure.

### 4.3. Estimation of $P_{3,M}\{M_3=s | M=i\}$

It is extremely expensive computationally to search all possible situations to find  $P_{3,M}\{M_3=s | M=i\}$ . As  $i$  increases, the size of the search space will explode to  $2^q$  and  $q=iC_2$ . Therefore, we use simulations to estimate its mean and 95% confidence interval. The basic simulation procedure is shown in Figure 4. We performed the tests 100 times. For each test, we repeat the basic simulation procedure  $10^8$  times. Figure 5 shows the 3D surface of estimated  $P_{3,M}\{M_3=s | M=i\}$ . Figure 6 shows the detail of  $P_{3,M}\{M_3=s | M=i\}$  for different value of  $M$  with their 95% confidence interval. We observe that the 95% confidence

interval of the estimated distribution is very small, i.e. the maximum length of 95% confidence interval for each  $M$  in Figure 6 are  $7.9 \times 10^{-6}$ ,  $2.3 \times 10^{-5}$ ,  $4.1 \times 10^{-5}$ , and  $2.0 \times 10^{-5}$ , respectively. Obviously, the results of the 100 tests are very consistent.

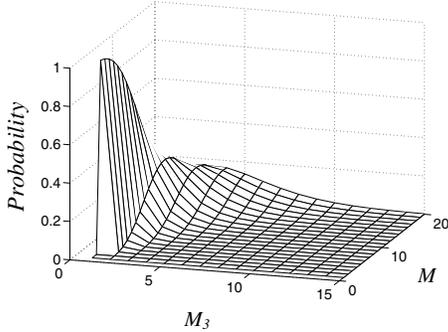


Figure 5. Estimated  $P_{3,M}\{M_3=s | M=i\}$ .

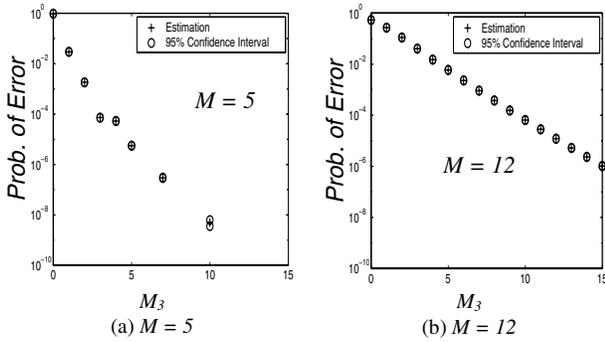


Figure 6. Simulation results of  $P_{3,M}\{M_3=s | M=i\}$  and its 95% confidence intervals.

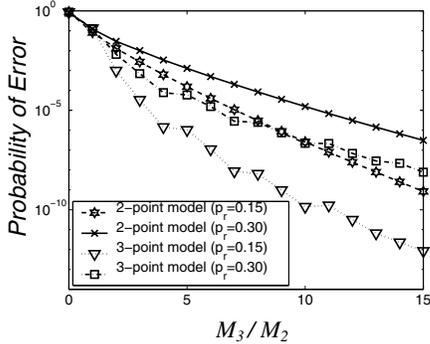


Figure 7. Comparison of different models' estimation.

#### 4.4. Estimation Results

Figure 7 shows the distributions of the 2-point model and 3-point model for  $p_r=0.15$ . We observe that, the 3-point model has more discriminating power than the 2-point model. For example, when  $M_2=M_3=10$ ,  $P_{3,M}\{M_3=10\}=1.4 \times 10^{-10}$  while  $P_{2,M}\{M_2=10\}=2.6 \times 10^{-7}$ . Note that the minimum number of minutiae, which can have  $M_2=M_3=10$ , is 5. It also means that if we use the 3-point model for matching, the probability, with which we can find 10 similar 3-point models between two randomly

chosen fingerprints is about 1 in 7.1 billion. Table 1 shows the error rates for different  $m$ ,  $n$  and  $q$ . We observe that if all the other parameters are fixed, the smaller the number of minutiae in the template and query fingerprints, the lower the probability that they are similar for the same  $q$ . Figure 7 also shows the comparison of the PDFs of 2-point model and 3-point models with different  $p_r$ . The more similar the relations among minutiae, the higher the probability that two fingerprints are from the same finger.

Table 1. Estimated error rate for different  $m$ ,  $n$  and  $q$ .

m	n	$P_{3,M}\{M_3=q\}$			
		8	10	12	15
60	60	$6.5 \times 10^{-9}$	$1.4 \times 10^{-10}$	$3.2 \times 10^{-11}$	$8.5 \times 10^{-13}$
45	45	$3.2 \times 10^{-10}$	$2.8 \times 10^{-12}$	$8.2 \times 10^{-13}$	$1.2 \times 10^{-14}$
36	36	$3.0 \times 10^{-11}$	$1.3 \times 10^{-13}$	$4.7 \times 10^{-14}$	$4.4 \times 10^{-16}$
20	20	$5.1 \times 10^{-14}$	$4.1 \times 10^{-17}$	$2.0 \times 10^{-17}$	$4.1 \times 10^{-20}$

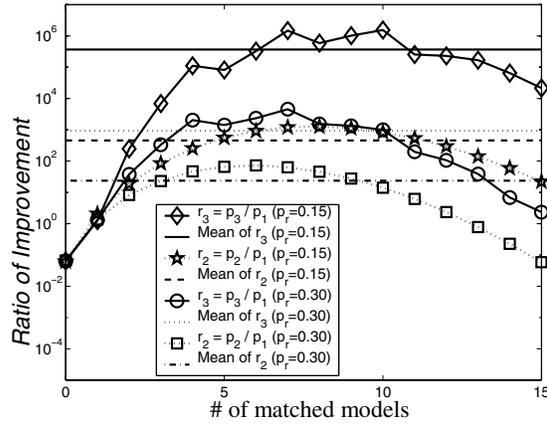


Figure 8. Ratio of estimation results between our approach and Pankanti et al.'s work [2].

Based on Pankanti et al.'s model, if an expert strictly adheres to the 12-point guideline, there is overwhelming identifying evidence to his/her testimony. The probability of an imposter matching which has 12 minutiae between two different fingerprints is  $7.3 \times 10^{-6}$ . Note that  $7.3 \times 10^{-6}$  is estimated using the parameters based on NIST-4. From Table 1, we observe that  $P_{3,M}\{M_3=12\}=3.2 \times 10^{-11}$  ( $m=60$  and  $n=60$ ). We define:

$$r_3 = \frac{p_3}{p_1} \quad \text{and} \quad r_2 = \frac{p_2}{p_1} \quad (9)$$

where  $p_3$  and  $p_2$  are the probability of the number of 3-point model and 2-point model estimated in this paper respectively and  $p_1$  is the probability of the number of minutiae shown in Pankanti et al.'s work. Figure 8 shows  $r_3$  and  $r_2$  for  $p_r=0.15$  and  $p_r=0.30$  respectively. We observe that the mean of  $r_3$  and  $r_2$  are  $3.68 \times 10^5$  and  $4.56 \times 10^2$  for  $p_r=0.15$  and  $9.34 \times 10^2$  and  $2.37 \times 10^1$  for  $p_r=0.30$ . It shows that the error rate estimated by our

approach is much less than that in Pankanti et al.'s work. The most important reason is that the relations among different minutiae are explicitly modeled in our approach, while in [2] minutiae are considered as individuals.

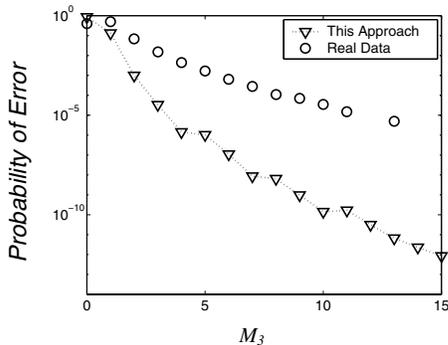


Figure 9. Comparison of theoretical results and real-data results.

#### 4.5. Real Data

In [1], we have designed a Genetic Algorithm (GA) based approach to verify fingerprints. It finds the optimal transformation between two fingerprints. This approach takes into account not only the positions of minutiae, but also the ridges counts between minutiae. The fitness function of the approach is defined by a two-step process. First, it finds the number of corresponding minutiae between two fingerprints for a transformation proposed by the GA. If the number of corresponding minutiae is greater than the threshold, then it finds the number of corresponding 3-point models. We did 200,000×5 experiments to estimate the distribution of the number 3-point models of imposter matching. Figure 9 shows the comparison of the estimated distributions of error rate on real data and the result of our theoretical analysis. The reasons for the difference between these two distributions are: 1) The theoretical model assumes the template and query fingerprints are well aligned, while the alignment in real data matching has some errors; 2) Because of the poor quality images, the minutiae orientation and ridge counts between different minutiae can not be detected precisely; and 3) The overlap area between the template and query fingerprints is less than the entire image area, so that the results on real data are worse than that of the theoretical results.

#### 5. Conclusions

People have long believed that everyone's fingerprints are unique. However, there is very little scientific research on estimating the error rate of fingerprint matching, which is very important for the insight into the performance of fingerprint recognition and its practical applications. Most previous works either measure the amount of details in a single fingerprint or only measure the details of minutiae

in corresponding fingerprints individually. To the best of our knowledge, this work is the first, which not only measures the amount of detail needed to find correspondence between two fingerprints, but also measures the relations between different minutiae. Compared with a previously published research [2], on the average, our model reduces the error rate by a factor of  $4.56 \times 10^2$  for 2-point model and  $3.68 \times 10^5$  for 3-point model respectively. The comparison between the theoretical result and the real-data result, which uses NIST-4 fingerprint database, shows that it still needs much work on fingerprint matching in real-world applications, so that the performance of the existing fingerprint matching algorithm can be close to the theoretical result. The theoretical result of this work provides a framework to find the limit of error rate for fingerprint matching. It not only helps people to understand that fingerprint matching is a kind of science under development, but also helps to settle the legal challenges to fingerprints. Since our approach is independent of the recognition algorithm, it can be used to estimate the error rate of other point based systems in computer vision and pattern recognition.

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