Predicting Fingerprint Recognition Performance from a Small Gallery

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Abstract

Predicting performance of biometrics is an important problem in a real world application. In this paper we present a binomial model to predict fingerprint recognition performance. We use a fingerprint identification algorithm to find the number of corresponding triangles as the match and non-match scores. Then we use these similarity scores in a binomial prediction model, which uses small gallery to predict performance on a large population. The results on the entire NIST-4 database show that our model can reasonably predict large population performance.

1. Introduction

In order to ensure the high confidence in security biometrics such as ear, face, gait, fingerprint, palm, signature and speech are commonly used. Fingerprint has been used for a long time because of its uniqueness and immutability. Depending on an application there are two kinds of fingerprint recognition systems: verification system and identification system [5]. A verification system will store users' fingerprints as sets of minutiae in the database. Then compare a person's fingerprint with her/his own minutiae set to verify if this person is who she/he claims to be. This is a one to one matching problem. The system can accept or reject this person according to the verification result. An identification system is more complex. For a query fingerprint the system searches the whole database to find out if there are any fingerprint minutiae sets saved in the database that can match it. It conducts one to many matching [5].

How does the fingerprint recognition technique work for large population is often asked in a practical application. In this paper we develop a binomial model to predict large population performance based on small gallery. Firstly we calculate the corresponding triangles between each fingerprint in a probe set with every fingerprint in a gallery. Then we use these corresponding values as similarity scores to estimate the distribution of match and non-match scores. After this we use the Cumulative Match Characteristic (CMC) curve to rank all these scores. CMC curve can show different probabilities of recognizing a fingerprint depending on how similar this query fingerprint to its minutiae set compared with other fingerprints in the gallery [6]. Finally we use a binomial distribution to compute the probability that the match score is within rank r. In this paper we only concern about the performance when the rank is 1. Using this model we can predict fingerprint recognition performance when the database size is increased.

In section 2 the related work is presented, details of fingerprint identification technique and prediction model are given in section 3. In section 4, prediction performance based on NIST-4 is described. Finally in section 5 conclusions are provided.

2. Related work

Fingerprint identification problem can be regarded as the verification performed for the probe image with every gallery image in the database. Additionally indexing followed by verification can solve this problem. In Germain et al. [2], they combine indexing and verification together. Their identification approach is based on triangles. For any three noncolinear minutiae they get a triangle. They use length of each side, ridge count and angles as their features. These features are not robust to distortion. So they undermine the performance [8]. Tan and Bhanu [7] propose another approach to solve identification problem, which is also based on triangles. Their approach has two main differences with Germain's. First one is that they use indexing and verification separately. In the indexing step they get top Thypotheses, then use the verification process to verify these hypotheses. Secondly the features they use are: angles, triangle handedness, triangle direction, maximum side, minutiae density and ridge counts. These features are more robust to distortion than Germain's [8].

Binomial model is very suitable for estimating recognition performance when the database size is large. Until now the prediction models are mostly based on feature space or similarity scores. Johnson et al. [4] build a CMC model that is based on the feature space to predict the gait identification performance. L_2 norm and Mahalanobis distance are used to compute similarity within the feature space. They make an assumption about the density that the population variation is much bigger than the individual variation. Sometimes this assumption is invalid. Wayman [9] and Daugman [1] develop a binomial model that uses the non-match distribution. This model underestimates recognition performance for large galleries. Phillips et al. [6] create a moment model, which uses both the match and non-match distributions. Since all the similarity scores are sampled independently, their results underestimate the identification performance. Johnson et al [3] improve this model by using a multiple non-match scores set. They average match scores on the whole gallery. For each match score they count the number of non-match scores that is larger than this match score, which leads to an error. In reality the distribution of match score is not always uniform.

In this paper we use a binomial model to estimate fingerprint recognition performance for large population. We first estimate the similarity scores distributions and then integrate the non-match distribution according to the match score which can find the probability that the nonmatch score is larger than the match score. This is different from Phillips' moment model. It can efficiently solve the problem of underestimate recognition performance.

3. Technical approach

We are given two sets of data: gallery and probe. Gallery is a set of fingerprint minutiae saved in the database. For each fingerprint there is one set of minutiae saved in the gallery. Probe is a set of query fingerprints. One finger can have more than one print in the probe set. The fingerprint identification algorithm we used is based on the representation of triangles. For every fingerprint we first extract minutiae. Then randomly choose any three noncolinear minutiae to form a triangle. Thus, one fingerprint can get hundreds of triangles. There are two steps in the identification process: indexing and verification.

3.1. Fingerprint indexing

During the indexing, the features we used to find potential triangles are: minimum angle α_{\min} , median angle α_{med} , triangle handedness ϕ , triangle direction η ,

maximum side λ , minutiae density χ and ridges counts ξ . We compute these features for each fingerprint in the gallery and set up an indexing space $H(\alpha_{\min}, \alpha_{med}, \phi, \eta, \lambda, \chi, \xi)$, the detail explanation of these features can be found in [7].

We compute these features for each query fingerprint and compare them with indexing space H. If the error between them is small enough then we know they are probably the same fingerprint. The output of this process is a list of hypotheses, which are sorted in the decreasing order of the number of potential corresponding triangles. Top T hypotheses are input to the verification process.

3.2. Fingerprint verification

Suppose there are Q and M minutiae in the query and gallery fingerprints respectively. Δ_q and Δ_m are potential corresponding triangles. We assume $F(s, \theta, t_x, t_y)$ is the transformation between query and gallery fingerprints, where s is a scale parameter, θ is a rotation parameter, t_x and t_y are translation parameters. The details of how to estimate the transformation parameters can be found in [7]. If these parameters are less than a threshold then we apply this transformation to the potential corresponding triangles. We compute the distance:

$$d = \frac{\arg\min}{i} \left\{ \left| F\left(\begin{bmatrix} x_{j,1} \\ x_{j,2} \end{bmatrix} \right) - \begin{bmatrix} y_{i,1} \\ y_{i,2} \end{bmatrix} \right\}$$

where $\{(x_{j,1}, x_{j,2})\}$ and $\{(y_{i,1}, y_{i,2})\}$ are two sets of minutiae in the gallery and query fingerprints, j = 1, 2, ...M and i = 1, 2, ...Q. If *d* is smaller than a threshold then we can say that $\{(x_{j,1}, x_{j,2})\}$ and $\{(y_{i,1}, y_{i,2})\}$ are corresponding point. If the number of corresponding points is larger than a threshold then we define Δ_a and Δ_m are corresponding triangles.

3.3. Prediction model

Assume that the size of probe set and gallery are all N. For each fingerprint in the probe set we compute the number of corresponding triangles with every fingerprint in the gallery. The number of corresponding triangles can be used as similarity scores. If we have enough match and non-match scores then we can estimate the Probability Density Function (PDF) of these two distributions. Assume ms(x) and ns(t) represent the distribution of match scores and non-match scores respectively. If the similarity score is higher then the fingerprints are more similar. The error occurs when any given match score is smaller than the non-match scores. The probability that the non-match score is larger than the match score x is NS(x), where

$$NS(x) = \int_{x}^{\infty} ns(t)dt$$
 (1)

We rank all the similarity scores in decreasing order. The probability that the match score rank r is given by the binomial probability distribution:

$$C_{r-1}^{N-1} (1 - NS(x))^{N-r} NS(x)^{r-1}$$
(2)

N is the gallery size. Integrating over all the match scores, we get the probability that all the match scores rank r is:

$$\int_{-\infty}^{\infty} C_{r-1}^{N-1} (1 - NS(x))^{N-r} NS(x)^{r-1} ms(x) dx$$
(3)

In theory the match scores can be any value within $(-\infty, \infty)$. Finally the probability that all the match scores are within rank *r* is:

$$P(N,r) = \sum_{i=1}^{r} \int_{-\infty}^{\infty} C_{i-1}^{N-1} (1 - NS(x))^{N-i} NS(x)^{i-1} ms(x) dx$$
⁽⁴⁾

Here we assume that the match scores and non-match scores are independent and their distributions are the same for all the fingerprints in the gallery. For the identification problem we only consider the situation where rank r = 1 because this can evaluate the performance of identification technique. Then this model becomes:

$$P(N,1) = \int_{-\infty}^{\infty} (1 - NS(x))^{N-1} ms(x) dx$$
 (5)

In this model N is the size of large population whose performance needs to be estimated. Small size gallery is used to estimate the distribution of ms(x) and ns(t).

4. Experimental results

All the fingerprints we use in the experiments are from NIST Special Database 4 (NIST-4). There are 2000 pairs of fingerprints, each of them is labeled 'f' and 's' that represent different impressions of a fingerprint followed by an ID number. Since the fingerprints in NIST-4 are collected by an ink-based method, many fingerprints are of poor quality and some of them even contain characters and handwritten lines. The size of fingerprint image is 480×512 pixels and resolution is 500 DPI.

We choose all these 2000 fingerprints. 'f' images are the gallery and 's' images are the probe set respectively. Matching all these fingerprints pairs we get 2000 match scores. Then we randomly select 20 fingerprints from the gallery and another 20 different fingerprints from the probe set. We match them and obtain 20 non-match scores. Repeat this process for 100 times then we get 2000 non-match scores. Distributions of these 2000 similarity scores are showed in Figure 1 and Figure 2. If the match score is less than a threshold T_m then we believe the fingerprints pair does not match. Since 99.95% non-match scores are less than 12 we choose $T_m = 12$. Using this threshold we can compute the probability of correct verification.

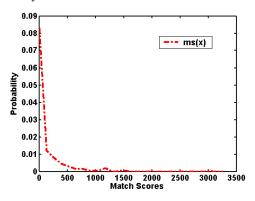


Figure 1. Match scores distribution

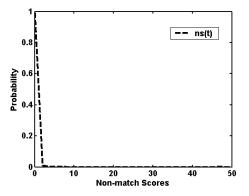
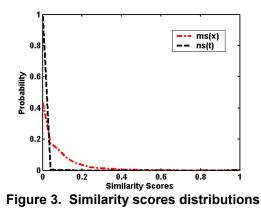


Figure 2. Non-match scores distribution

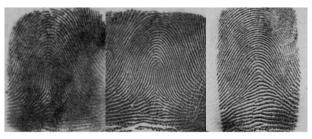


We randomly choose 40 and 50 fingerprints separately from NIST-4 to be our small gallery to predict the

fingerprint recognition performance for the large population. So the sizes of small gallery are n = 40 and n = 50, the size of the probe set is the same as small gallery size. We use the verification technique to compute the similarity scores. Figure 3 shows the distributions of match and non-match scores when n = 50. Sample results are shown in Table 1. The values on the diagonal are match scores, off diagonal values are non-match scores. Usually match scores should be larger than nonmatch scores. For fingerprint s0026 03 the match score is 0, while the non-match score between s0026 03 and f0006 09 is 3, obviously this is not correct. Figure 4 shows these three fingerprints from NIST-4. The quality of s0026 03 is not good. It could not find any corresponding triangle with f0026 03, while it has 3 corresponding triangles with f0006 09.

Table 1. Similarity scores for sample image pairs

	s0031_02	s0006_09	s0015_01	s0026_03
f0031_02	810	4	0	0
f0006_09	0	719	0	3
f0015_01	0	0	106	0
f0026_03	0	0	0	0



s0026_03 f0026_03 f0006_09 Figure 4. Three fingerprints from NIST-4

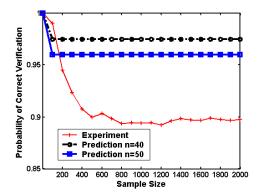


Figure 5. Experimental and prediction performance

Figure 5 shows the experimental and prediction performance results. We use different size of small galleries to estimate fingerprints verification performance on large sample images. We can see that the size of small gallery has effect on the prediction performance. The error reduces with the increase in sample size. So this model can use to predict large population performance.

5. Conclusions

In this paper we use a fingerprint identification algorithm to find the match and non-match scores. We use these scores in a binomial prediction model. The assumption we make for this model is that the match and non-match scores are independent and their distributions are the same for all the fingerprints in the gallery. Based on the results shown in this paper we find that our model can be used to predict large population performance.

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