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DIVERSITY OF HUMAN FINGER VEIN PATTERNS AND ITS APPLICATION TO PERSONAL IDENTIFICATION

By

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Abstract

Diversity of human finger vein images is shown by extracting their patterns from the right and left index fingers, and middle fingers of 506 person and the usefulness of finger veins patterns for personal identification is shown by evaluating the false acceptance and false rejection rates. These rates depend on the cut-off point. When we set it $C = 0.290$ it is shown in this paper that those rates are estimated to be 0.00000001% and 0.00005%, respectively.

Key Words and Phrases: beta-binomial distribution, biometry, false acceptance rate, false rejection rate, vein patterns

1. Introduction

Our finger veins are not visible and, for example, we do not know whether the image of my right index finger vein is similar to that of my friends, or even to that of my middle finger, or my left index finger. In fact, nothing have been known about numbers, locations and lengths of finger veins. However, recent technologies made it possible to get sharp vein images. Kouno et al. (2000) developed feature extraction of finger vein patterns based on repeated line tracking and Fan and Lin (2004) used thermal images of vein-patterns. Among them we deal with in this paper is the method developed by the Central Research Laboratory, Hitachi, Ltd (Miura et al. (2002, 2004a, 2004b)). The method extracts finger vein images as follows. First a new idea of line tracking is introduced. Second the line tracking is conducted by starting at several random positions to take into account unknown numbers, location and length of veins. Third the finger vein patterns are obtained as the ones having high frequency in the total number of pixels to be tracked.

Figure 1 shows the result of extracted finger vein patterns, represented from Miura et al. (2002). Readers should refer to their paper for details. We extracted vein patterns from the right index and middle fingers and the corresponding patterns from the left fingers of about 500 persons. In this paper we show diversity of human finger vein images and discuss its usefulness for personal identification. The arguments in this paper are mainly based on the evaluation of the false acceptance rate (FAR) and false rejection rate (FRR). Face, Fingerprints, Iris and Voice have been major biometrics that have

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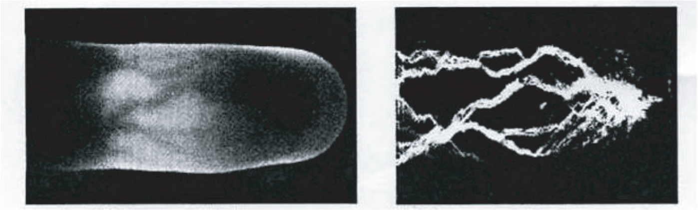

Figure 1: Extracted finger vein image (left) and patterns (right).

been used for personal identification. It is reported that the FAR and FRR of Face are 1% and 10% (Phillips et al. (2002)); of Fingerprints 1% and 0.1% (Wilson et al. (2004)); of Iris 0.0001% and 0.2% (Newton and Phillips (2007)); and FAR and FRR of Voice are 2% and 2% (Reynolds et al. (2005)). The FAR and FRR of the personal identification by finger veins studied in this paper are estimated to be 0.00000001% and 0.00005% when $C = 0.290$ is used for the cut-off point.

2. Diversity of finger vein patterns

The pixels of an extracted vein pattern are classified into three categories; VEIN, AMBIGUOUS, and BACKGROUND where AMBIGUOUS means that the total area of the veins in a pixel is in the range of two threshold values. Two vein patterns are overlapped and are compared pixel by pixel. If a pixel that is classified into VEIN overlaps with a pixel classified into BACKGROUND, the pair of the pixel is said to be mismatched. Note that it is not symmetric, i.e., suppose, for example, that there are two finger patterns, say R and L, which consist of three pixels classified into (AMBIGUOUS, VEIN, BACKGROUND) and (AMBIGUOUS, VEIN, VEIN), then there is no mismatching from R to L, but one mismatching from L to R. The mismatch rate (MMR) is defined as

$$\mathrm{MMR} = \frac{\text{total number of mismatched pairs}}{\text{total number of pixels classified into VEIN in the two finger patterns}}.$$

For example, MMR=1/3 in the above example. The MMR is computed from 506 persons (405 males, 101 females), whose age distribution is given in Table 1.

Table 1: Age distribution of person who are tested.

Age	10-19	20-29	33-39	40-49	50-59	refused to tell	total
numbers	1	149	220	91	41	4	506

Figure 2 shows histograms of the MMR computed from 1,012 (= 506 persons × 2) pairs of identical right index fingers and 255,530 (= 506 × 505) pairs of right index fingers of unrelated individuals, which we call the unrelated finger in the sequel. The figure shows that two histograms are separated, indicating the significant difference of vein patterns of the right index finger between individuals. Figure 3 shows histograms of the MMR computed from 1,012 pairs of right middle finger and right index finger

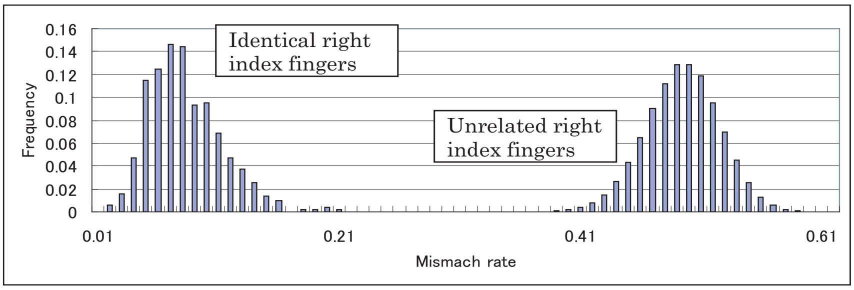

Figure 2: Histograms of mismatch rates (MMR) computed from 1,012 pairs of identical right index finger and 255,530 pairs of unrelated index finger.

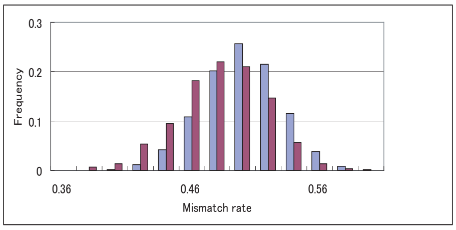

Figure 3: Histograms of mismatch rates (MMR) computed from 1,012 pairs of the right index fingers and middle fingers of identical person (dark) and 255,530 pairs of unrelated individuals (light).

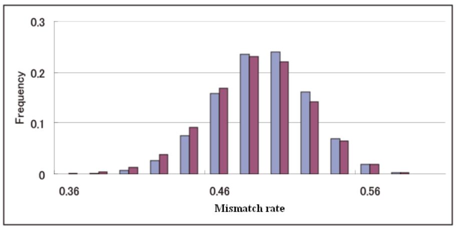

Figure 4: Histograms of mismatch rates (MMR) computed from 1,012 pairs of the right index fingers and left index fingers of identical person (dark) and 255,530 pairs of unrelated individuals (light).

from identical person (dark) and 255,530 pairs of unrelated right index fingers (light). The figure shows that two histograms are almost completely overlapped (Pearson's chi-square χ^2=0.48 with df=13, p-value=1.0000); that the histogram of two fingers of the identical person shifted to left slightly. This indicates that the difference of the vein patterns of the right middle finger and right index finger of identical person is similar to the difference of the vein patterns of the right index fingers of different person. Figure 4 shows histograms of the MMR from 1,012 pairs of the right index fingers and left index fingers of identical person (dark) and that from 255,530 pairs of unrelated right index fingers (light). Again two histograms almost completely overlap ($\chi^2 = 0.018$, df=13 and p-value=1.0000), showing that the difference of the vein patterns of the right index finger and left index finger from an identical person is similar to the difference of the vein patterns of the right index fingers of different individuals. These observations indicate that two fingers are identical if and only if they are the same finger in the same hand of the same person, and all the other cases can be treated simply as unrelated.

The reproducibility of the distributions of the MMR is fairly good. For example, Table 2 shows the means and standard deviations of the distributions of the MMR of unrelated right index fingers that are obtained by measuring 506 individuals 10 times;

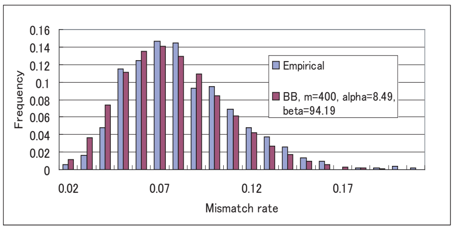

Figure 5: Histograms of mismatch rates (MMR) computed from 1,012 pairs of identical right index finger (empirical) and Beta-Binomial distribution with m=400, α=8.49 and β=94.19.

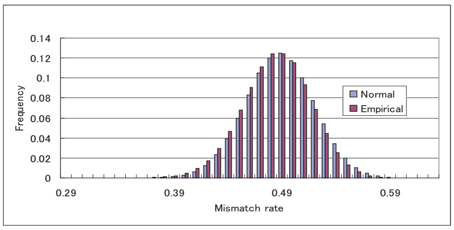

Figure 6: Histograms of mismatch rates (MMR) computed from 2,555,300 unrelated pairs of right index finger (empirical) and normal distribution with mean=0.4859 and s.d.=0.0308.

in each time the mean and the standard deviation are computed from 255,530 pairs of unrelated index fingers. The table shows that the variabilities of the mean and s.d. throughout those 10 examinations are negligible.

Table 2: The means and standard deviation (s.d.) of the distributions of the mismatch rates (MMR) in 10 repeated examinations: in each examination the mean and s.d. are computed from 255,530 unrelated pairs of the right index finger.

	1	2	3	4	5	6	7	8	9	10	pooled
mean	0.485	0.485	0.486	0.486	0.486	0.486	0.486	0.486	0.486	0.486	0.486
s.d.	0.031	0.031	0.031	0.031	0.031	0.031	0.031	0.031	0.031	0.031	0.031

3. Personal identification

3.1. Statistical model

Suppose that a finger vein pattern of an individual is registered and a new finger pattern is arrived. Figure 2 suggests that we may judge that the new arrival is unrelated if MMR $> C$, and identical to the registered if MMR $\leq C$ for some cut-off point C. The goodness of this personal identification is evaluated by the false rejection rate (FRR) and false acceptance rate (FAR); defined by FRR=Pr(MMR$> C \mid$ identical fingers) and FAR=Pr(MMR$\leq C \mid$ unrelated fingers).

We introduce a mathematical model to evaluate the FRR and FAR from the data. Let m be the total number of pixels classified into VEIN in the two vein patterns, and X_i be a binary variable taking 1 with probability P if the i^{th} pair of the pixels is mismatched and 0 otherwise, where P represents the true mismatch rate. The mismatch rate P is estimated by

$$\bar{X} = \frac{1}{m} \sum_{i=1}^{m} X_i,$$

which is equivalent to the MMR defined in Section 2. Since a vein is connected, $X_1, \ldots, X_m$ would not be statistically independent. Furthermore m is unknown and depends on the length of the veins. These characteristics must be taken into account in the modeling. We assume that P is a random variable following a beta distribution of parameters α and β, and that m is also a random variable following a Poisson distribution with mean λ, and that for given $P = p$ and m, $X_1, \dots, X_m$ are conditionally independent and identically distributed with a Bernoulli distribution with $\Pr(X_i = 1 | P = p, m) = p$. It follows under these assumptions that for given m, $m\bar{X}$ follows a beta-binomial distribution and that the mean, variance and the third central moment of $\bar{X}$ are given. Since mean λ of the Poisson distribution in this problem is larger than 100, we may well approximate m by λ and the unconditional mean, variance and the third central moment of $\bar{X}$ are approximated as follows.

$$E(\bar{X}) = \pi, \qquad V(\bar{X}) \approx \pi(1-\pi)\frac{\phi}{1-\phi}\left(1 + \frac{1}{\lambda}\frac{1-2\phi}{\phi}\right),$$

$$E\big(\bar{X} - E(\bar{X})\big)^3 \approx \frac{\pi(1-\pi)}{(1+\phi)(1+2\phi)}\left(\phi\big(3(\pi-1) + 2\phi(\pi-2)\big) + \frac{3}{\lambda}(\pi - \phi - 1)\right),$$

where

$$\pi = \frac{\alpha}{\alpha+\beta}, \qquad \phi = \frac{1}{\alpha+\beta}.$$

3.2. Estimation

3.2.1. Estimating the FRR

Parameters α, β and m are estimated to be 8.49, 94.19 and 400 by applying the method of moment (see, for example Bickel and Doksum, 1976, p.92) to the MMR data from 1,012 (= 506 persons × 2) pairs of identical right index fingers. Figure 5 shows the histogram and fitted conditional beta-binomial distribution conditioned on $m = 400$; showing the fitting is fairly good ($\chi^2 = 0.09$, df=19, p-value=1.0000). The FRR are computed based on the fitted conditional beta-binomial distribution for selected values of the cut-off points and those values are given in the second column of Table 3. The table shows that those value are in order of $10^{-6} \sim 10^{-7}$.

3.2.2. Estimating the FAR

The means and s.d. of the 10 examinations in Table 2 is so close that we pooled those data, and obtained estimates $\hat{\alpha} = 369.593$, $\hat{\beta} = 391.116$ and $\hat{m} = 400$ from 2,555,300 unrelated pairs of right index finger altogether. When $\alpha + \beta$ is large, the beta-binomial distribution is approximated by a normal distribution; in particular, the approximation is good when $\alpha/(\alpha+\beta)$ is close to 0.5. Figure 6 shows the histogram from 2,555,300 unrelated pairs (empirical) and fitted normal distribution $N(0.4859, 0.0308^2)$, showing that the fitting is pretty good. The FAR is computed by using the fitted normal distribution and selected cut-off points. Those values of FAR are summarized in the third column of Table 3. The table shows that orders of those values are in $10^{-9} \sim 10^{-12}$, depending on the cut-off point. To show the confidence on the estimated FRR 95% confidence intervals (c.i.) of the FAR are obtained from 10,000 bootstrap samples consisted of 1,000 samples drawn randomly with replacement from each of 10 populations in Table 2 and are listed in the fourth column of Table 3.

Table 3: Estimated false acceptance rate (FAR) and false rejection rate (FRR).

Cut-off point	FRR	FAR	95% c.i. of FAR	
0.270	3.16E-06	1.31E-12	6.32E-13	2.56E-12
0.275	2.03E-06	4.10E-12	2.07E-12	7.80E-12
0.280	1.30E-06	1.25E-11	6.41E-12	2.45E-11
0.285	8.23E-07	3.73E-11	2.00E-11	6.96E-11
0.290	5.20E-07	1.08E-10	5.82E-11	1.94E-10
0.295	3.27E-07	3.07E-10	1.74E-10	5.49E-10
0.300	2.04E-07	8.47E-10	4.84E-10	1.46E-09
0.305	1.27E-07	2.28E-09	1.35E-09	3.85E-09
0.310	7.86E-08	5.97E-09	3.69E-09	9.81E-09

3.3. Risk of personal identification

The value of the cut-off point C must be decided from FRR and FAR when we use the above device for personal identification. Similarly to the type I and type II errors in the theory of the statistical testing hypothesis, FRR and FAR compete, i.e., when the cut-off point C increases FRR decreases, whereas FAR increases, and vice versa. The FAR should be more important in practice than FRR for the purpose of preserving security. In addition we will show here that the FAR is directly related to the risk for personal identification. Note that the main concern of the user of the device would be the risk that if the person passes the device and yet he/she is not identical to the registered, i.e., *cheater* could impersonate the registered person for some malicious purpose. The risk may be represented by means of probability, Pr(different | passed), and be estimated as follows. Let Pr(identical) (Pr(different)) be the probabilities that the new person is identical (different) to the registered person, where Pr(identical) + Pr(different) = 1. Then it follows from the Bayes theorem that

$$\Pr(\text{different} \mid \text{passed}) = \frac{\text{FAR} \cdot \Pr(\text{different})}{\text{FAR} \cdot \Pr(\text{different}) + (1 - \text{FRR}) \Pr(\text{identical})}.$$

If we have no information on Pr(identical) and Pr(different), it would be natural to set $\Pr(\text{identical}) = \Pr(\text{different}) = 0.5$. Thus

$$\Pr(\text{different} \mid \text{passed}) \simeq \text{FAR},$$

since $\text{FAR} \ll \text{FRR} \ll 1$. If highly suspicious, we may set $\Pr(\text{identical}) = 0.0001$. Then we have in the ranges of FRR and FAR in Table 3

$$\Pr(\text{different} \mid \text{passed}) \simeq \Big(\Pr(\text{different}) / \Pr(\text{identical})\Big)\text{FAR},$$

It shows again that the risk for personal identification is proportional to the FAR. It would be worthy to note that, even if highly suspicious, i.e., $\Pr(\text{identical}) = 0.0001$, we have $\Pr(\text{different} \mid \text{passed}) = 4.10E - 8$ from Table 3, still very small, when the cut off point is set to be $C = 0.275$.

3.4. Universal unequalness of the human finger vein

Also FAR is useful to assess universal unequalness of the human finger vein. Suppose N be the size of population that we consider. N may be, for example, the size of the populations in Tokyo ($N \sim 12$ millions), the populations in Japan ($N \sim 120$ millions) or the populations in the world ($N \sim 6.5$ billions). Suppose that one person is chosen randomly from the population and registers his/her finger vein to this device. Then "how many persons are there in the population who are going to be judged as "identical" to this person ?" would be an interesting question. The question is answered as follows. Suppose that we number all the persons of the population as $1, 2, \ldots, N$, and suppose the person 1 registers his finger vein without loss of generality. Let Y_i be the random variable defined as

$$Y_i = \begin{cases} 1, & \text{person } i \text{ is judged as "identical" to the person 1,} \\ 0, & \text{otherwise,} \end{cases}$$

for $i = 2, \ldots, N$ and $Y = \sum_{i=2}^{N} Y_i$. Then the expected number of the persons who is supposed to be judged as "identical" to the person 1 is

$$\mathrm{E}(Y) = \sum_{i=2}^{N} \mathrm{E}(Y_i) = (N-1)\mathrm{FAR} \simeq N \cdot \mathrm{FAR}.$$

Table 4 lists this expected values for some selected values of C and N. We may esteem those values in the table as the index of universal unequalness of personal identification by means of finger veins. From the table, for example, the universal unequalness of the human finger vein would be statistically guaranteed in Japan, when we set C as $C \leq 0.310$. On the other hand, if we want to ensure the universal unequalness of the finger vein in the world, we would have to set C as $C \leq 0.290$.

Table 4: Expected value of the number of persons who judged as "identical" to some specific person in the N populations.

Cut-off point c	$N = 1$ million	$N = 10$ millions	$N = 100$ millions
0.270	0.00000	0.00001	0.00013
0.275	0.00000	0.00004	0.00041
0.280	0.00001	0.00013	0.00125
0.285	0.00004	0.00037	0.00373
0.290	0.00011	0.00108	0.01080
0.295	0.00031	0.00307	0.03070
0.300	0.00085	0.00847	0.08470
0.305	0.00228	0.02280	0.22800
0.310	0.00597	0.05970	0.59700

4. Discussion

We investigated the diversity of human finger vein patterns by comparing the right and left index fingers and middle fingers of about 500 persons and considered its usefulness for personal identification. The validity of our personal identification is evaluated by two probabilities inherent to the device, the false rejection rate (FRR) and the false acceptance rate (FAR). From the FRR and FAR, we can estimate the reliability of the personal identification by the human finger vein.

The personal identifications are also reported by the human iris patterns. For example, Daugman and Downing (2001) gave through investigation on the randomness of unrelated human iris patterns of 2.3 million different pairs of eye images and considered its use for personal identifications. They measured the Hamming distance between unrelated iris patterns and observed that the distribution of the Hamming distance is well approximated by the binomial distribution. In the present manuscript, on the other hand, we observed that the distribution of the mismatch rate of the finger veins cannot be approximated fairly by binomial distribution. Instead, we consider the beta-binomial distribution for the mismatch rate, reflecting the feature of the over-dispersion.

Comparing the distribution of our mismatch rate between unrelated finger veins to that of the Hamming distance of iris pattern given in Daugman and Downing (2001), the estimated standard deviation is 0.0308 in our study, while it is 0.032 in Daugman and Downing (2001). This result implies that the diversity among the different persons of the human finger vein is similar to that of the iris pattern, and our method also may be utilized for the personal identification.

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