

Fingerprint Minutiae Matching Based on the Local And Global Structures

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Abstract

This paper proposes a new fingerprint minutia matching technique, which matches the fingerprint minutiae by using both the local and global structures of minutiae. The local structure of a minutia describes a rotation and translation invariant feature of the minutia in its neighborhood. It is used to find the correspondence of two minutiae sets and increase the reliability of the global matching. The global structure of minutiae reliably determines the uniqueness of fingerprint. Therefore, the local and global structures of minutiae together provide a solid basis for reliable and robust minutiae matching. The proposed minutiae matching scheme is suitable for an on line processing due to its high processing speed. Experimental results show the performance of the proposed technique.

1. Introduction

Although there exist some image-based [1,2] and graph-based [3,4] fingerprint matching, most fingerprint verification systems required to provide a high processing speed, small template size and high degree of security are so far based on minutiae matching. This is because it is widely believed that the minutiae of the fingerprint are most discriminating and reliable features [5,6]. As in most automatic fingerprint verification / identification systems, we adopt two most prominent kinds of minutiae: ridge ending and ridge bifurcation, which are used by the Federal Bureau of Investigation [7] and can be easily extracted by a computer using techniques such as that proposed in [11,12,15].

The feature vector of minutia generally consists of the minutia type, the coordinates and the tangential angle of the minutia. The automatic fingerprint verification / identification is then achieved with a kind of point pattern matching instead of the fingerprint image matching. Several point pattern matching algorithms have been proposed in the literature [8-10]. Some comments on these algorithms are given in [11,12]. The point pattern matching is generally intractable because the

correspondences between the two point sets of template and input fingerprint are unknown. The minutia correspondences are difficult to obtain due to several factors such as the rotation, translation and deformation of the fingerprints, the location and direction errors of the detected minutiae as well as the presence of spurious minutiae and the absence of genuine minutiae.

A. K. Jain *et. al* proposed an alignment-based matching algorithm in [11,12], in which the ridges associated with the minutiae were used to align the input minutiae with the template minutiae and an adaptive elastic matching algorithm was proposed to match the aligned minutiae. The authors reported good performance. However, this approach results in a large template size because the associated ridges for each minutia must be saved. If only short ridges are saved, the algorithm may results in an inaccurate alignment, or much worse, a false alignment. Another quite different approach proposed by A. K. Hrechak and J. A. Mchugh [13], used the local structure of the minutia to describe the characteristics of the minutiae. This approach owns some advantages in processing speed and robustness to rotated and partial prints. Some improvements of this approach were proposed in [14]. However, the local structure is less distinct feature because it is determined only by a small subset of the minutiae. Prints from different fingers may have quite a few similar local structures and prints from the same finger may only have few similar structures due to the presence of spurious minutiae and the absence of genuine minutiae. Therefore, fingerprint matching based only on the local structure is less reliable.

In this paper, we present a new fingerprint minutiae matching technique based on both the local structures of the minutiae and the global structure of the fingerprints. While comparing two fingerprints, a human expert used to manually examine the local positional relations between minutiae (the local structure of the minutiae) and to confirm the verification finally using the fingerprint unique global position structure consisted of the whole minutiae set. Our approach attempts to automate this human expert behavior. The local structure of a minutia is rotation and translation invariant because it consists of the direction and location relative to some other minutiae. Moreover, the local structure can tolerate reasonable

deformation because it is formed from only a small area of the fingerprint. So the local structures can be directly used for matching and the best matched local structures provides the correspondences for aligning the global structure of the minutiae. The aligned global structure together with the result of the local structure matching finally determines whether the two fingerprints are generated from the same finger.

2. Local structure matching

Generally, a minutia point M_k detected from a fingerprint can be described by a feature vector given by:

$$F_k = (x_k \ y_k \ \phi_k \ t_k)^T, \quad (1)$$

where (x_k, y_k) is its coordinate, ϕ_k is the local ridge direction and t_k the minutia type (ridge ending or bifurcation). Although the ridge orientation has the range $(-\pi/2, \pi/2]$, the minutia can be directed into the range $(-\pi, \pi]$ to increase its discrimination (see Fig. 1).

The feature vector set \mathbf{F} , which consists of feature vectors F_k , $k=1, 2, \dots, N$, of all minutiae detected from a fingerprint, determines the global minutiae structure of this fingerprint. Fingerprint minutiae matching is to find a similarity level between two global minutiae structures, one from the template fingerprint and another from the input fingerprint.

To simplify the description of our algorithm, we define a function $d\phi(t_1, t_2)$ for the difference between two directions or angles, t_1 and t_2 , $-\pi < t_1, t_2 \leq \pi$ as follows:

$$d\phi(t_1, t_2) = \begin{cases} t_1 - t_2, & \text{if } -\pi < t_1 - t_2 \leq \pi \\ 2\pi + t_1 - t_2, & \text{if } t_1 - t_2 \leq -\pi \\ 2\pi - t_1 + t_2, & \text{if } t_1 - t_2 > \pi. \end{cases} \quad (2)$$

The global characteristic of the minutiae x_k, y_k and ϕ_k are dependent on the rotation and translation of the fingerprint. As such, it cannot be directly used for matching. However, we can describe a minutia with rotation and translation invariant feature by using some other minutiae in its neighborhood. For each minutia M_k , the relative distance d_{ki} , radial angle θ_{ki} and minutia direction ϕ_{ki} between minutia M_k and its l -nearest neighborhood minutia M_i calculated by

$$d_{ki} = \sqrt{(x_k - x_i)^2 + (y_k - y_i)^2}, \quad (3)$$

$$\theta_{ki} = d\phi\left(\tan^{-1}\left(\frac{y_k - y_i}{x_k - x_i}\right), \phi_k\right) \quad (4)$$

$$\phi_{ki} = d\phi(\phi_k, \phi_i) \quad (5)$$

are independent from the rotation and translation of the fingerprint. The local structure of a minutia, which is described by the distances, ridge-counts, directions and radial angles of the minutia relative to each of its l -nearest

neighborhood minutiae and the types of these minutiae, describes the minutia rotation and translation invariantly. The feature vector of a minutia M_k that describes its local structure characteristic with its l -nearest neighborhood (here $l=2$) is given by:

$$Fl_k = (d_{ki} \ d_{kj} \ \theta_{ki} \ \theta_{kj} \ \phi_{ki} \ \phi_{kj} \ n_{ki} \ n_{kj} \ t_k \ t_i \ t_j)^T, \quad (6)$$

with the assumption that the minutia i is the nearest and j the second nearest minutia of the minutia k . The ridge-count (number of ridges between two minutiae points) n_{ki} and n_{kj} should be calculated in the minutiae detection phase. Fig. 1 shows a minutia local structure consisted of its l -nearest neighborhood (here $l=2$).

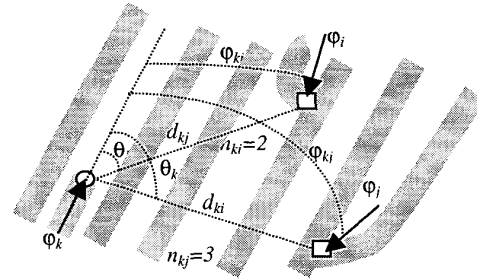


Figure 1. A minutia local structure of 2-nearest neighborhood.

It is easy to see that the local structure feature vector Fl_k is independent from the rotation and translation of the fingerprint. So it can directly be used for matching. Furthermore, the deformation for local structure is not serious because the local structure consists of only a few nearest minutiae. However, errors introduced by minutiae detection cannot be ignored. The matching should be tolerable to such inexactness. Suppose Fl_i^I and Fl_j^T are the local structure feature vectors of minutia i from input fingerprint and of minutia j from template fingerprint, respectively. A similarity level is defined as

$$sl(i, j) = \begin{cases} \frac{bl - W|Fl_i^I - Fl_j^T|}{bl}, & \text{if } W|Fl_i^I - Fl_j^T| < bl \\ 0, & \text{Others} \end{cases} \quad (7)$$

$$W = (w_d \ w_\theta \ w_\phi \ w_n \ w_t)^T. \quad (8)$$

The differences between directions and angles in equation (7) should be calculated using equation (2). W is a weight vector that specifies the weight associated with each component of the feature vector. We empirically choose: $w_d=1$; $w_\theta=w_\phi=0.3 \times 180/\pi$; $w_n=w_m=3$. The threshold bl can be $6 \times m$, where m is the number of the component of the local feature vector. The similarity level $sl(i, j)$, $0 \leq sl(i, j) \leq 1$, describes a matching certainty level of a local structure pair instead of simply matched or not matched. $sl(i, j)=1$ implies a perfect match while $sl(i, j)=0$ implies a total mismatch.

Because only a local structure is used to describe a minutia, two fingerprints from different fingers may have quite a few similar minutia local structures. This may result in false acceptance. So the reliability of the matching should be increased further. On the other hand, two fingerprints from the same finger may have only a small number of well-matched local structures because a local structure is described by several minutiae in the neighborhood. Any spurious or dropped minutia in the neighborhood will result in an invalid minutia local structure for matching. Therefore, the minutiae matching based on this local structure is less reliable though the matching is rotation and translation invariant. An idea to improve the reliability is adding the minutiae global structure of fingerprint in the matching process to increase the matching reliability and robustness.

3. Global structure matching

The minutiae global structure of fingerprint described with equation (1) is dependent from the rotation and translation of the fingerprint. To aligning two point set, a corresponding point pair should be found. The best-matched local structure pair can serve such a purpose. Although not all well-matched local structures are reliable and although not each corresponding minutia pair has a well-matched local structure, our experiments showed that the best-matched local structure pair of all local structures of template and input fingerprints are very reliable. The best-matched structure pair ($b1$, $b2$) is obtained by maximizing the similarity level as:

$$sl(b1, b2) = \max_{i, j} (sl(i, j)). \quad (9)$$

The best-matched structure pair, one from the input fingerprint and another from the template fingerprint, serves as a reliable correspondence of the two fingerprints. All other minutiae will be aligned based on this corresponding reference minutiae pair by converting them to the polar coordinate system with respect to the corresponding reference minutia M_b ($b=b1, b2$).

$$Fg_k = \begin{pmatrix} r_{kb} \\ \theta_{kb} \\ \phi_{kb} \end{pmatrix} = \begin{pmatrix} \sqrt{(x_k - x_b)^2 + (y_k - y_b)^2} \\ d\phi \left(\tan^{-1} \left(\frac{y_k - y_b}{x_k - x_b} \right), \phi_b \right) \\ d\phi(\phi_k, \phi_b) \end{pmatrix} \quad (10)$$

The feature vector Fg_k of minutia M_k is rotation and translation invariant and its reliability is dependent only on the minutia M_k itself and the corresponding minutia M_b . Although the reference minutiae points generally can rightly be found, the location and direction errors introduced by the minutiae detection hinders the alignment algorithm to recover the relative pose transformation exactly. Moreover, the nonlinear

deformation of fingerprint that is an inherent property of fingerprint impressions can be accumulated to a large degree. These will make global features of some minutiae of the input fingerprint quite different from those of the template fingerprint. Therefore, the matching should be elastic by using a 3-D bounding box Bg in the feature space instead of an exact matching. However, a large bounding box will increase the possibility of false minutiae matching. The local structure of a minutia which generally has small local deformation, can be used to increase the reliability of the matching for two minutiae within the bounding box. We define the matching certainty level $ml(i, j)$ for minutia i of input fingerprint and minutia j of template fingerprint by:

$$ml(i, j) = \begin{cases} 0.5 + 0.5sl(i, j), & \text{if } |Fg_i' - Fg_j^T| < Bg \\ 0, & \text{Others} \end{cases} \quad (11)$$

With the introduction of the local structure similarity level in the global matching we can choose a relatively large bounding box, $Bg = (8 \pi/6 \pi/6)^T$, to tolerate the fingerprint deformation. Moreover, equation (11) provides a soft decision instead of the simple “matched” or “unmatched” result. To avoid a minutia being doubly used for matching, $ml(i, j)$ is set to be zero if there exists any k , that $ml(i, k) > ml(i, j)$ or $ml(k, j) > ml(i, j)$. The matching degree of the input and template fingerprints, called matching score Ms , will then be determined by the ‘average’ matching certainty level of the minutiae defined by:

$$Ms = 100 \times \frac{\sum_{i, j} ml(i, j)}{\max\{M, N\}}, \quad (12)$$

where M and N is the number of the minutiae for template and input fingerprints, respectively. Two fingerprints will be verified as from a same finger if their matching score is higher than a threshold.

4. Experimental evaluation

A set of fingerprint images captured with a Veridicom CMOS sensor of size 300×300 pixels, which contains 1,504 fingerprint images from 188 different individuals with 8 images for each finger, is used in the experiments. The captured images vary in quality, direction and position. The minutiae for each fingerprint image were obtained with our minutiae detection algorithm proposed in [15]. Each fingerprint in the set was matched with the other fingerprints in the set. So, a total of 2,260,512 matchings have been performed. The distributions of matching scores for the same fingers and for different fingers are shown in Fig. 2. The mean values ms , md , and standard deviations sds , sdd of the matching score for same and different fingers are also shown in Fig. 2. In

addition, a statistical metric d' , which gives an indication of the separation between the two distributions [12], is also given in Fig. 2.

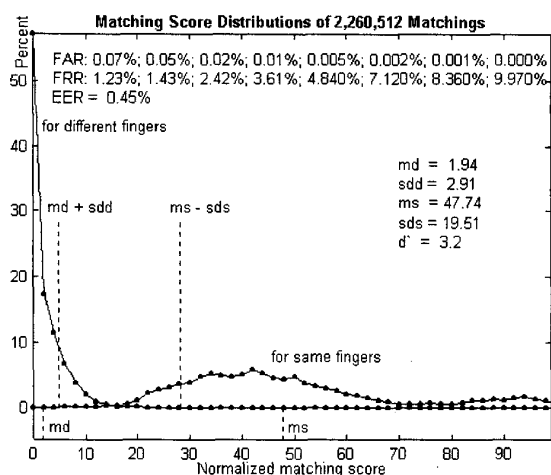


Figure 2. Statistical results of 2260512 matchings.

From the Fig. 2 we see that by setting different values of the threshold on the matching score we can obtain different false acceptance rate (FAR) and false reject rate (FRR). Some FARs and the corresponding FRRs by setting different values of the threshold are given in Fig. 2. We achieved an EER of 0.45%. In the experiments, we found that the low matching scores for some of the same fingers are due to the insufficient amount of common regions of the fingerprint pairs. This is because the area of the CMOS sensor is quite small (only 0.6×0.6 inches). Therefore only a partial fingerprint can be obtained from the sensor. In practice, a substantial decrease on both the FAR and the FRR can be obtained if a sufficient amount of common region (>60%) of template and input fingerprints is ensured. The processing time for minutiae matching is not fixed. It depends on the number of the minutiae. The average processing time of the 2,260,512 matchings is 0.0016 seconds on a PC Pentium II 450 MHz.

5. Conclusion

This study described a new fingerprint matching technique based on both the local and global structures of the fingerprint minutiae. The local structure is rotation and translation invariant and can tolerate reasonable deformation because it covers only a small area of the fingerprint. Therefore, the local structures can be directly used for matching and the best-matched local structure provides the corresponding reference for aligning the global structure of the minutiae. The aligned global structure matching together with the result of the local structure matching finally determines whether the two

fingerprints are generated from a same finger. With a relative large bounding box in the global structure matching, the matching algorithm can tolerate, to some extent, the nonlinear deformation of the fingerprint. The employment of the local structure similarity level in the global matching reduces the contribution of possibly false matched minutiae in the global structure matching due to the use of a relatively large bounding box.

The usefulness of the proposed approach was confirmed in the experiments conducted, which showed good performance in reliability, accuracy and processing speed.

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