Fingerprint Alignment Using Similarity Histogram

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Abstract. The performance of fingerprint matching algorithm relies heavily on the accuracy of fingerprint alignment. Falsely aligning two feature sets extracted from two finger images of a fingerprint will increase the false rejection rate (FRR). In order to improve the performance of fingerprint matching algorithm, we present a new fingerprint alignment algorithm called similarity histogram approach (SHA). First, we calculate the local similarity matrix based on minutiae and associate ridges between two fingerprints. Then, similarity histograms of transformation parameters are constructed from local similarity matrix. In the end, the optimal transformation parameters are obtained using a statistical method. Experimental results on FVC databases show that our method is effective and reliable.

1   Introduction

Fingerprints have been used as a personal identification tool for a long time. The major reasons are due to their uniqueness and unchangeable properties. A fingerprint is composed of ridges and valleys. In general, the two prominent features used in fingerprints are ridge bifurcations and ridge endings called minutiae. Because of deformation and noise of fingerprints, it is still a challenging task to design a reliable automatic fingerprint matching algorithm.

Many researchers have made progress in the minutiae-based fingerprint matching. Anil K Jain et al.[1] proposed a matching algorithm using minutiae and the information of ridge associated with minutiae. Xudong Jiang et al.[2] presented a matching algorithm based on local and global structures. These researchers used local structure to align the fingerprints. The difference between their algorithms is the different representations of local structures. They selected the most similar local structures as the reference points and get transformation parameters between two fingerprints. However, the accuracy of alignment of fingerprint is greatly affected by the deformation and the noise of two fingerprints. In order to align fingerprints with high accuracy, Anil K Jain's algorithm needs long corresponding ridges, whereas it's very difficult when the fingerprint quality is poor. Xudong Jiang's algorithm may get a false match

when the local structures are small. Luo et al.[4][10] and Dongjae Lee et al.[3] improved these methods. On the alignment stage, they selected more candidates from local structures that have higher similarity. But these approaches increased match time at the same time.

In this paper, we propose a new fingerprint alignment algorithm called similarity histogram approach (SHA). We used minutiae-pairs and associate ridges as local structures. First, we calculate local similarity matrix between two fingerprints. After that, similarity histograms of transformation parameters are constructed from local similarity matrix. At last, we obtain the optimal transformation parameters from similarity histograms based on statistics model. Compared with literature methods, our method is more accurate and robust because the statistical method can effectively reduce random errors caused by noise of original image or caused in the process of extracting minutiae.

This paper is organized as follows. Section 2 introduces the definition of local structure features. Section 3 describes how to create the similarity histogram. Section 4 shows the procedure of obtaining transformation parameters. Section 5 presents our experimental results. In the end, we draw the conclusion in section 6.

2   Local Structure Description

A minutia point and its associate ridge (see Figure 1(a)(b)) detected (refers to methods [4]-[7]) from a fingerprint can be described by a feature vector as follows:

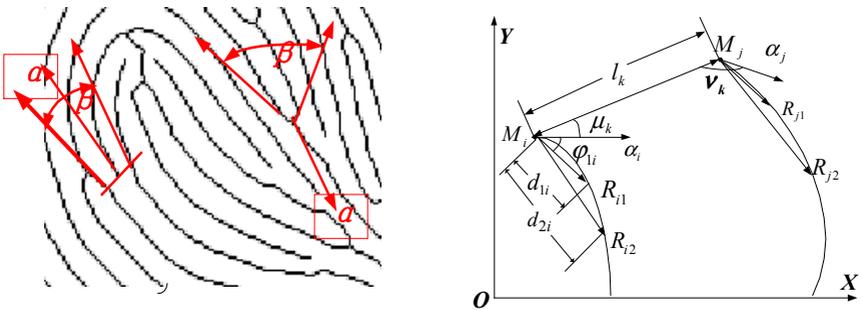$$M_k = (x_k, y_k, \alpha_k, \beta_k, \varphi_{1k}, \varphi_{2k}, d_{1k}, d_{2k})^T$$

Fig. 1. (a) Minutiae point   (b) A local structure

Where x_k and y_k are the coordinates of the minutia M_k, α_k is its local ridge direction, β_k is the difference between directions of two nearest ridges of the minutia point M_k, φ_i (i=1, 2) is the angle difference between α_k and line connecting sample point on the associate ridge with minutiae point M_k, and d_i (i=1, 2) is the distance from minutiae to the sample point. We only use two sample points on each ridge empirically. The feature vector set M, which consists of feature vectors M_k (k=1…N)

of all minutiae detected from a fingerprint, determines the global minutiae structure of the fingerprint.

Let $M=\{M_i\}(i=1\ldots N)$ denote the minutiae set of a fingerprint.

For every pair of minutiae points M_i and M_j ($1\leq i< j\leq N$) in M, if the Euclidean distance $d(M_i, M_j)$ satisfies with inequality $G_{low}\leq d(M_i, M_j) \leq G_{High}$, where G_{low} and G_{High} are empirically set to 35 and 100. A feature vector $P_k = (l_k, \mu_k, \nu_k, \varphi_{1i}, \varphi_{2i}, d_{1i}, d_{2i}, \varphi_{1j}, \varphi_{2j}, d_{1j}, d_{2j})^T$ is constructed to denote the relationship between M_i and M_j,

Where

$$
\begin{cases}
l_k = d\left(M_{ik}, M_{jk}\right) \\
\theta_k = arctg\left(\dfrac{y_{M_j} - y_{M_i}}{x_{M_j} - x_{M_i}}\right) \\
\mu_k = \left|\alpha_i - \theta_k\right| \\
v_k = \left|\alpha_j - \theta_k\right|
\end{cases}
\tag{1}
$$

The feature vector set P, which consists of feature vectors P_k ($k=0\ldots|P|$), is the local structure set using to construct similarity histogram. It is independent from the rotation and translation of the fingerprint. Generally, a fingerprint has 40~60 minutiae. Therefore, we can get 300~1000 local structures whose numbers are much more than those of other methods. Because SHA is a global alignment algorithm, a large number of local structures are needed.

3   Construction of Similarity Histogram

3.1   Local Similarity Matrix Calculating

To simplify the description of our algorithm, we define a vector operator F as $F(A)=(|a_1|,|a_2|,\ldots|a_n|)^T$, where A is a vector $(a_1, a_2, \ldots a_n)^T$.

Let $P^{(1)} = \{P_h^{(1)}\}(h = 0\ldots|P^{(1)}|)$ denote the input minutiae structure set and $P^{(2)} = \{P_l^{(2)}\}(l = 0\ldots|P^{(2)}|)$ denote the template minutiae structure set computed using above method. Suppose $P_h^{(1)}$ and $P_l^{(2)}$ are the local structure feature vectors of minutiae-pair h from input fingerprint and minutia-pair l from template fingerprint. The difference of $P_h^{(1)}$ and $P_l^{(2)}$ is defined as $\Delta P_{hl} = F(P_h - P_l)$, If each element of ΔP_{hl} is smaller than b_0, the similarity degree between $P_h^{(1)}$ and $P_l^{(2)}$ is defined as follows:

$$
S(h,l) = \begin{cases}
c_0 - \sqrt{\Delta P_{hl}^T \Delta P_{hl}} & if \ \sqrt{\Delta P_{hl}^T \Delta P_{hl}} < c_0 \\
0 & Others
\end{cases}
\tag{2}
$$

If any one element of ΔP_{hl} is greater than or equal to b_0, we set $S(h,l) = 0$. The threshold values of b_0, c_0 are empirically set to 15   50. The similarities of local structures constitute a matrix, which size is $|P^{(1)}| \times |P^{(2)}|$.

For each similarity $S(h,l)$, we get the local structures $P_h^{(1)}$ and $P_l^{(2)}$ of two lines respectively connecting the minutiae $M_i^{(1)}$ and $M_j^{(1)}$, $M_i^{(2)}$ and $M_j^{(2)}$. There are two possible correspondences. If $M_i^{(1)}$ is corresponded to $M_i^{(2)}$ and $M_j^{(1)}$ is corresponded to $M_j^{(2)}$, we call it a first pairing. In contrast, it is called a second pairing.

For a second pairing, we define the difference of $P_h^{(1)}$ and $P_l^{(2)}$ as:

$$\Delta P'_{hl} = (|l_h^{(1)} - l_l^{(2)}|, |\mu_h^{(1)} - v_l^{(2)}|, |v_h^{(1)} - \mu_l^{(2)}|, |\varphi_{1i}^{(1)} - \varphi_{1j}^{(2)}|, |\varphi_{2i}^{(1)} - \varphi_{2j}^{(2)}|,$$
$$|d_{1i}^{(1)} - d_{1j}^{(2)}|, |d_{2i}^{(1)} - d_{2j}^{(2)}|, |\varphi_{1j}^{(1)} - \varphi_{1i}^{(2)}|, |\varphi_{2j}^{(1)} - \varphi_{2i}^{(2)}|, |d_{1j}^{(1)} - d_{1i}^{(2)}|, |d_{2j}^{(1)} - d_{2i}^{(2)}|)^T$$

So we can also calculate another similarity $S'(h,l)$ using formula 2.

3.2   Creating Similarity Histogram Function

The transformation between two fingerprints is rotation, scaling and translation. We suppose the scaling is constant because the images in the most applications are acquired from the same device. Therefore, only rotation and translation parameters need to be calculated. We describe how to creating similarity histogram function (SHF) of rotation parameter. The procedure of SHF of translation parameters is omitted in this paper because both of the means are similar.

The rotation between the local structures can calculated as:

$$\Delta \alpha_1 = \frac{\left(\alpha_i^{(1)} - \alpha_i^{(2)}\right) + \left(\alpha_j^{(1)} - \alpha_j^{(2)}\right)}{2} \tag{3}$$

$$\Delta \alpha_2 = \frac{\left(\alpha_i^{(1)} - \alpha_j^{(2)}\right) + \left(\alpha_j^{(1)} - \alpha_i^{(2)}\right)}{2} \tag{4}$$

$\Delta \alpha_1$ is the rotation angle of first pairing, and $\Delta \alpha_2$ is the rotation angle of second pairing.

Now we define a function $f(\Delta \alpha)$, which is called histogram similarity function of the variable $\Delta \alpha$. It can be described as follows:

$$f(\Delta \alpha) = \sum_h \sum_l \left(S(h,l)\delta(\Delta \alpha - \Delta \alpha_1) + S'(h,l)\delta(\Delta \alpha - \Delta \alpha_2)\right) \tag{5}$$

Where $\delta(t)$ is general impulse function.

4   Obtaining Transformation Parameters

On the ideal condition, if the two fingerprints are acquired from the same finger, the similarity histogram has only a very sharp peak (see Figure 2). We can get the optimal rotation parameter according to the peak. However, due to the noise, the histogram distribution is always anomalous. Therefore, $f(\Delta\alpha)$ has to be smoothed before computing the optimal rotation parameter $\Delta\alpha$.

Let W_g denote a Gaussian mask window whose length is $2d+1$, W_g consists of c_i ($i=1...2d+1$, $d \geqslant 0$, $c_i \geqslant 0$, $\sum c_i = 1$). The new similarity histogram fuction $\overline{f}(\Delta\alpha)$ is calculated as the convolution of $f(\Delta\alpha)$ and W_g.

$$\overline{f}(\Delta\alpha) = f(\Delta\alpha) \otimes W_g \tag{6}$$

Where "$\otimes$" denotes the convolution operation. Figure 2 shows $f(\Delta\alpha)$ and $\overline{f}(\Delta\alpha)$.

Empirically, the window size of W_g is set 7. The element of W_g can be calculated by (see Figure 4):
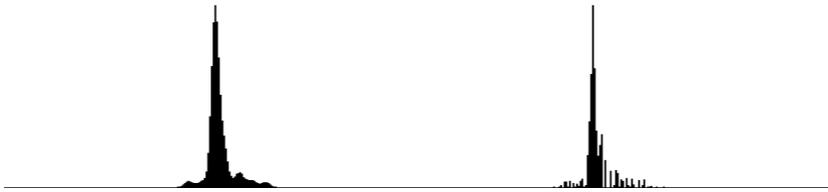
$$c_i = 0.5(1-\cos(\pi i/d))/2. \ (i=1...2d+1) \tag{7}$$

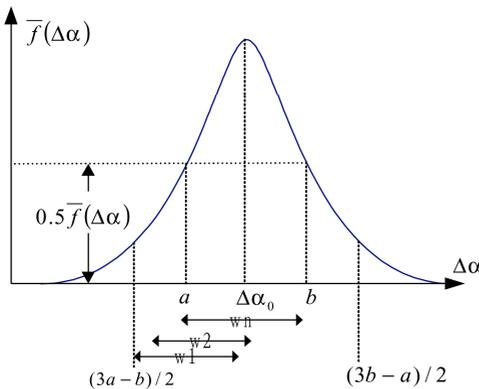**Fig. 2.** (a)Similarity Histogram   (b) Smoothed similarity histogram

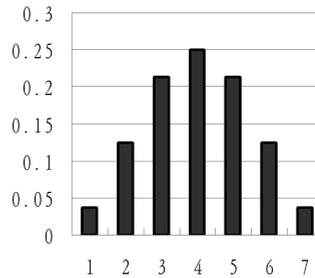**Fig. 3.** Optimal window searching   **Fig. 4.** Gaussian masking window

To obtain the optimal parameter $\Delta\alpha_{opt}$, we used a statistic method proposed by Jeng-Horng Chang, et al.[8]. According to the characteristics of SHF, there exist some differences with it.

The *Skewness* of a window w is defined as:

$$\beta(w)=\mu_3(w)/\sqrt{\mu_2^3(w)} \tag{8}$$

Where $\tilde{m}_w = \dfrac{\sum_{i \in w} \Delta\alpha \times \overline{f}(\Delta\alpha)}{\sum_{i \in w} \overline{f}(\Delta\alpha)}$, $\mu_n = \dfrac{\sum_{i \in w}(i-\tilde{m}_w)^n \overline{f}(\Delta\alpha)}{\sum_{i \in w} \overline{f}(\Delta\alpha)}$

First, we find the initial value $\Delta\alpha_0$ where $\overline{f}(\Delta\alpha_0)$ reaches maximum value of SHF. After that, we can get an interval [a, b] that satisfies with $f(\Delta\alpha) \geq 0.5\overline{f}(\Delta\alpha_0)$ and is centered at $\Delta\alpha_0$.

Second, we get a searching interval *[(3a-b)/2, (3b-a)/2]* which has the same center as [a, b] and double length of [a, b]. We use a searching window with length (b-a). Searching windows starts by placing the leftmost point at *(3a-b)/2*. We move the window one bin at a time until rightmost point arrive at *(3b-a)/2*. Figure 3 shows an example.

Therefore, the optimal window is $w_0 = \min\|\beta(w)\|$. The final optimal parameter can be calculated as $\Delta\alpha_{opt} = \tilde{m}_{w_0}$.

5   Experimental Results

The experiments make use of the databases provided by FVC2000 [9]. To verify the robustness and empirical usefulness of the algorithm, we randomly select some fingerprints from those databases, manually rotate them by an angle, and calculate the rotation parameters with our algorithm. We compare the standard deviation of errors of SHA with that of local alignment algorithm (The algorithm of Luo et al. in [4] is selected). The experiments show that the accuracy of SHA is much better than that of Luo et al. (see Figure 5). In this figure, X-axis denotes the rotation degrees.
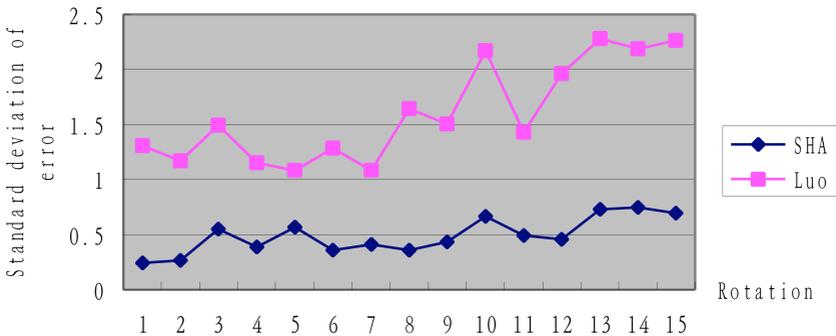

Fig. 5. The comparison of the accuracy of alignment

Our goal is to improve the performance of the matching algorithm. We test our algorithm and Luo's on the database FVC2000 and FVC2002. Table 1 shows the performance of two algorithms. The definition of the EER, ZeroFMR and ZeroFNMR show in [9]. We can clarify that our algorithm based on similarity histogram is more effective.

Table 1. Performance evaluation on FVC Database

Database		SHA			Luo		
		EER	Zero FMR	Zero FNMR	EER	Zero FMR	Zero FNMR
FVC 2000	Db1	2.74%	5.64%	100%	4.39%	21.0	100%
	Db2	0. 81%	1.87%	100%	3.27%	20.0%	100%
	Db3	8.93%	25.6%	100%	10.4%	31.7%	100%
	Db4	1.73%	4.98%	100%	6.08%	42.1%	100%
FVC 2002	Db1	2.60%	5.32%	100%	6.75%	25.4%	100%
	Db2	1.32%	4.56%	100%	3.63%	12.1%	100%
	Db3	4.55%	13.1%	100%	5.97%	15.2%	100%
	Db4	3.13%	7.77%	100%	7.26%	16.9%	100%

The experiment is done on a PC with PIII800 processor. The average matching time is 0.018s.

6   Conclusion and Discussion

We have described a new fingerprint alignment algorithm based on similarity histogram. This algorithm is a kind of global alignment algorithm. This method can also handle other point-pattern matching problems very well. Experimental results show that it can greatly reduce errors during computing transformation parameters, and it is a reliable and effective method.

We observe the accuracy of SHA is decreased seriously when there are no enough minutiae. Increasing sample points on associate ridges can take some effect. This algorithm can't tolerate very large deformations. In the feature, we will spend more time and energy on these problems.

Acknowledgements

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