

AN EFFECTIVE ALGORITHM FOR FINGERPRINT MATCHING¹

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Abstract

Fingerprint matching is one of the most important stages in automatic fingerprint identification systems (AFIS). Traditional methods treat this problem as point pattern matching, which is essentially an intractable problem due to the various nonlinear deformations commonly observed in fingerprint images. In this article, we propose an effective fingerprint matching algorithm based on error propagation. Firstly, ridge information and Hough transformation are adopted to find several pairs of matching minutiae, the initial correspondences, which are used to estimate the common region of two fingerprints and the alignment parameters. Then a MatchedSet which includes the correspondence and its surrounding matched minutiae pairs is established. The subsequent matching process is guided by the concept of error propagation: the matching errors of each unmatched minutiae are estimated according to those of its most relevant neighbor minutiae. In order to prevent the process from being misguided by mismatched minutiae pairs, we adopt a flexible propagation scheme. Experimental results demonstrate the robustness of our algorithm to non-linear deformation.

Key words: fingerprint matching, minutiae, error propagation

1. Introduction

Given a reference representation in database and an input representation extracted from an input image, the matching stage determines the similarity of two fingerprint features and decides whether they are of the same finger. In most AFIS system, the representation of fingerprints is based on minutiae such as ridge ending and ridge bifurcation, with each minutia being characterized by its locations and orientation. With this representation, the matching problem is reduced to a point pattern matching problem. In the ideal case described by Jain [1], the matching can be accomplished by simply counting the number of spatially overlapping minutiae. But in practice, the sensing system maps the three-dimensional finger on to two-dimensional images. Once the location, pressure and direction of impression change, the mapping will change accordingly, which inevitably leads to nonlinear deformation of fingerprint images. Two fingerprint images may have translation, rotation or even nonlinear deformation between them. If the time span between two impressions is long, the images may also change due to cuts on finger or skin disease.

In most systems, fingerprint is represented with a set of minutiae which is called template. The representation itself may be noisy due to presence of spurious minutiae and absence of genuine minutiae. Also, the properties of minutiae such as the location and orientation may be inaccurately estimated due to image degradation and imperfect preprocessing.

Considering all these situations, a good fingerprint matching algorithm should meet the following two criteria:

- Be robust to all kinds of possible deformation which are commonly observed in fingerprints and are hard to model.
- Be robust to small perturbation on minutiae and minutiae properties.

Several approaches have been proposed for point pattern matching [2-5], but these methods did not perform well because they did not make use of the extra information provided by fingerprint minutiae. Presently, most fingerprint matching algorithms based on point pattern matching adopt a two-step strategy: First the correspondence is found, then matching is performed on the aligned templates. In order to solve the problem of correspondence, extra information such as ridge segments [1], spatial properties [6] and local structure [7] of each minutia is applied to provide robustness and reduce searching space.

Transformation parameters can be determined by one correspondence. Due to the presence of noise and deformations, the input minutiae may not be aligned exactly. To improve the performance of matching, various approaches have been proposed: Chen et. al. [8] adopted the concept of tree matching in their approach; Isenor et. al. [9] use graph matching to solve the problem of elastic deformation; Jain and Lee et. al. [10-11] represent the fingerprint with texture information extracted by Gabor filters and the matching is based on Euclidian distance. Recently, Jain et. al. [12] combined texture features and minutiae feature in matching; Vajna [13] combined triangular matching and dynamic time warping to tolerate nonlinear deformation;

In this paper, we present an error propagation based matching algorithm. In the next section, we describe in detail our representation of fingerprint, correspondence estimation, common region estimation and the matching algorithm based on error propagation. In Section 3, we present the experimental results on NIST special database 24. Conclusions are given in Section 4.

2. Fingerprint matching based on error propagation

Before presenting our approach to the problem of fingerprint matching, we will give a short description of our representation. After a fingerprint image is enhanced and thinned with image processing methods, the ridges associated with each minutia are tracked. The tracking procedure stops when the tracking length reaches a certain predefined threshold or another minutia is encountered on the ridge. The ridge sampling method is similar to that of Hong's [6]. In order to overcome the ambiguity that orientation may cause, we use the direction of minutiae as x-coordinate in our sampling instead. Therefore, each ridge is represented by its direction and sampling values. And each minutia is represented by its type, position, direction as well as the ridges it resides (one ridge for an end and three ridges for a bifurcation).

Our matching algorithm is a three-step method: First, each minutiae in the reference template is matched with each minutiae in the input template and all resulting potential correspondences are used to find several most reliable one, the initial correspondences, using Hough transformation; Secondly, all minutiae surrounding the correspondence are matched and those minutiae pairs whose matching error are less than certain thresholds are added to the MatchedSet; Finally, we adjust the

¹ This work is funded in part by CAS and NSFC(Grant No. 69825105)

matching error of each unmatched minutia according to the information provided by the MatchedSet recursively until the number of elements in MatchedSet stops increasing. A conformation process which checks the consistency of the matching errors of elements in the MatchedSet is made to label and remove the mismatched minutiae after each iteration.

2.1. Correspondence estimation

In the ideal case, the alignment of two point patterns can be precisely decided according to one correspondence. But in practice, we need more candidates to estimate correspondences robustly. To do this, we define two kinds of correspondences: end correspondence and bifurcation correspondence. The similarity criteria are different in the two cases.

Suppose that d and D (we denote the reference and input features by lowercase and capital letters respectively) are the reference and input ridges respectively, d^i and D^i are the i th points on the ridges, and the similarity S of two ends is defined in Equation 1.

$$S = \frac{\sum_{i=0}^L (d^i - D^i)^2}{L} \quad (1)$$

where L is the length of the shorter ridge. Here, nonlinear penalty function is adopted to ignore small deformation and emphasize large deformation because our goal is to find the most consistent area (the region around the correspondence) of the two templates.

The similarity measure of bifurcation is composed of two parts, namely the sum of the similarity scores of the three ridges and the matching error of direction. Suppose that d_0, d_1, d_2 and D_0, D_1, D_2 are the three reference ridges and input ridges, $\theta_0, \theta_1, \theta_2$ and T_0, T_1, T_2 are the orientation of these ridges respectively. Then the similarity measure of two bifurcations is defined in Equations 2 and 3.

$$S = \frac{\sum_{j=0}^2 \frac{\sum_{i=0}^{L_j} (d_{i+j}^j - D_{i+j}^{j \% 3})^2}{L_j}}{4} + \Delta q \quad (2)$$

$$\Delta q = \min_{i=0}^2 (|q_1 - \Theta_{(i+1)\%3} - (q_0 - \Theta_i)| + |q_2 - \Theta_{(i+2)\%3} - (q_0 - \Theta_i)|) \quad (3)$$

Where k is the value of i in Equation 3 when $??$ reaches minimum and $\%$ denotes modulo operation. Before two bifurcations are matching, they must be aligned by directional information of their relevant ridges. In the case of Figure 1, k is equal to 2 which means that the corresponding ridge of ridge 0 in bifurcation A is ridge 2 in bifurcation B.

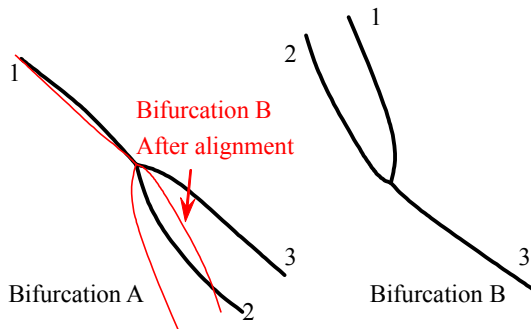


Figure 1. The alignment of bifurcations

In the above two cases, if S is less than a certain predefined threshold T_r , the two minutiae are considered matched. All potential correspondences are labeled in this way and the transformations that they reveal are calculated. Hough

transformation is used to decide the confidence of each pair and K most reliable pairs are selected as the correspondence candidates. Each of these candidates is used to estimate the alignment parameters of two fingerprint templates and the one which leads to maximal matching score is regarded as the genuine correspondence. Obviously, the ridges of the correspondence candidates are of maximal similarity, so the areas around them are supposed to be of maximal consistency.

In our implementation, we transformed the two templates to polar coordinates. As we have mentioned above, deformation of fingerprint will become larger when a minutia moves away in radial direction [1]. So it will be much easier to implement error propagation in polar coordinates. In the following, triple $t_i (r_i, q_i, a_i)$ and $T_i (R_i, \Theta_i, A_i)$ will be used to represent the i^{th} template minutiae and the i^{th} input minutiae respectively.

2.2. Common region estimation

While deciding the similarity of two patterns, we human often use their common properties to make the judgment. In the light of this idea, we adopt the similarity of the common region as the similarity measurement of the two fingerprints.

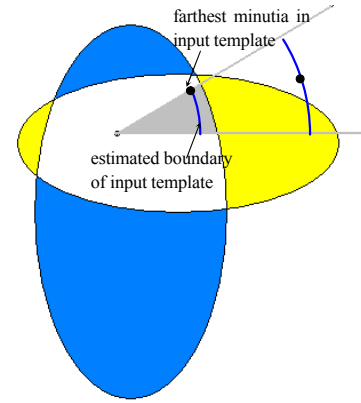


Figure 2. Common region estimation

Figure 2 illustrates our common region estimation method. First, the fingerprint is divided into L sectors, with the correspondence at the center. In each sector, we find the farthest minutia in both referent and input template, indicated by two black dots in Figure 2. Then the arc where the farthest minutia resides is regarded as the boundary of the sector and the inner arc of each sector is regarded as the estimated common region boundary. Finally, the number of minutiae in the common region of both reference template and input template n'_i and N'_i is counted. It is obvious that Larger L will lead to more accurate estimation and more computation as well. A value of 12 is a reasonable choice for L .

2.3. Initialization of MatchedSet

After the two templates are aligned and common region estimated, we initialize the MatchedSet. This procedure is necessary due to following reasons:

- The initialization of the MatchedSet can improve the effectiveness of the algorithm. On the one hand, when the nonlinear deformation of the two templates is small, the number of elements in the initial MatchedSet will be larger than the matching threshold and the algorithm will exit without error propagation. On the other hand, if the two fingerprints are not from the same finger, the number of elements in the MatchedSet will be small and the algorithm will exit with a non-match result.

- If we do not have this initial MatchedSet, error propagation will be based on only one matched pair, namely the initial correspondence, which cannot provide any deformation information.

Implementation of this step is rather simple. First, the correspondence is added to the MatchedSet with zero matching error. Assume that the predefined matching error is $(E_R, E_\Theta, E_A, E_S)$, then each minutia in reference template (r_i, q_i, a_i) is thought to be matched with one minutia in the input template if its position is within the region of $(r_i - E_R, r_i + E_R), (q_i - E_\Theta, q_i + E_\Theta)$, direction is within the region of $(a_i - E_A, a_i + E_A)$ and the similarity score of the two minutiae is less than E_S . If a match is found, the reference and input minutiae are combined as a pair and are added to the MatchedSet and their matching error $(E_{Ri}, E_{\Theta i}, E_{Ai}, E_{Si})$ is recorded as well. When all minutiae in the reference template are traversed, the initialization of the MatchedSet finishes.

One should take care in choosing the error thresholds $(E_R, E_\Theta, E_A, E_S)$ so that only reliable pairs are added to the initial MatchedSet. A confirmation process is also adopted after initialization of MatchedSet as well as after each propagation procedure, which is desirable to solve the inevitable problem of mismatched minutiae pairs. Visual inspection of initial MatchedSet shows that most elements in it are reliable.

2.4. Matching based on error propagation

There are two factors that may affect the accuracy of alignment: one is the inaccurate estimation of minutiae properties such as position, type and direction and the other is the nonlinear deformation which is hard, even impossible to model. What make things worse is that these problems are inherent. So what we can do is to work out a flexible matching scheme to compensate for these errors. The detailed description of our algorithm is given below:

1. For each unmatched minutiae $t_i (r_i, q_i, a_i)$ in the reference template, search in the MatchedSet for the *nearest* reference minutia, search for M ($M = 10$ in our implementation) nearest matched reference minutiae, assume $t_j (r_j, q_j, a_j)$, $j = 1, 2, \dots, M$ are the lucky ones and the distance between them is $d(t_i, t_j)$. Assume that the matching error of t_i is $(E_{Ri}, E_{\Theta i}, E_{Ai}, E_{Si})$;

2. Calculate the propagation ratio.

$$Ratio = d(t_i, t_j) / d(t_j, t_i) \quad (7)$$

3. For each minutiae $T_k (R_k, \Theta_k, A_k)$ in the input template,

$$\begin{aligned} & |r_j - R_k| < E_R + Ratio \cdot E_{Ri} \\ \text{if } & |q_j - \Theta_k| < E_\Theta + Ratio \cdot E_{\Theta i} \\ & |a_j - A_k| < E_A + Ratio \cdot E_{Ai} \\ & Similarity(t_i, T_k) < E_S + Ratio \cdot E_{Si} \end{aligned} \quad (8)$$

is satisfied, add the matched pair (t_j, T_k) as well as the matching error to MatchedSet.

4. After all neighbors of each matched minutiae are searched for their matching candidate, a verification procedure is adopted to remove those minutiae pairs whose matching errors are not consistent with those of their neighbours.
5. Repeat step 1 to 4 until the number of elements in MatchedSet does not change any more.
6. The matching score of two templates is defined as [1]:

$$S = \frac{100 \times M \times M}{n_i N_i} \quad (9)$$

where M is the number of elements in MatchedSet, n_i and N_i are the numbers of minutiae in the common region of reference template and input template.

3. Experimental results

Our approach is tested on part of the NIST-24 database, which is specifically designed for studying the plastic distortion and the impact of finger rotation [14]. To verify the effectiveness of our approach rather than that of the preprocessing, we manually choose 1350 fingerprint images (480×420) taken from 45 individuals with reasonable quality as the sample set.

Figure 3 illustrates the matching result of two fingerprint image with all matched minutia pairs connected by line segments. Many lines are observed to be crossed with each other, which denotes that the nonlinear deformation of the two images is large. The matching score is 0.739 in the showed case.

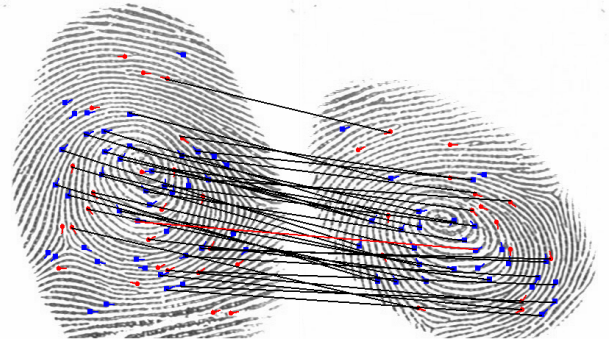


Figure 3. Matching result of two fingerprint images

In the verification experiments, we take 3 fingerprints out of the 30 from one finger as the training set and all remaining fingerprints as the test set. The reason why we choose more than one fingerprint as the training set is that many fingerprint sin the database have very small common region. It is impossible to make a reasonable judgment based on the few minutiae appearing on the common region. Figure 4 illustrates the matching score distribution for fingers of same class and fingers of different classes. The d' value as well as the mean and standard deviation of matching score for fingerprints from the same finger and those of different fingers are listed in Table 1. We can see from these results that the discriminative power of the matching scores is quite high.

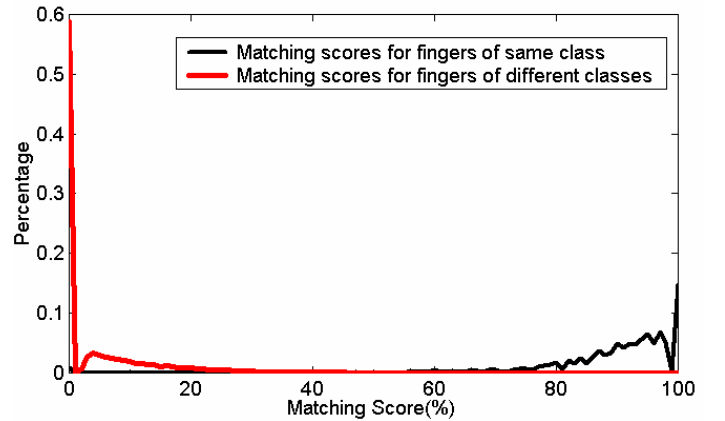


Figure 4. Distribution of matching scores for fingerprints from same class and different classes

d'	6.56
Mean (same)	88.32
Standard Deviation (same)	14.93
Mean (different)	5.65
Standard Deviation (different)	9.76

Table1. d' and Means and Standard Deviations of the matching scores for fingerprints from the same class and that from different classes

A false acceptance occurs when two images from different fingers are matched, and a false rejection occurs when two images from the same finger are not matched. Table 2 lists several False Acceptance Rate (FAR) and False Reject Rates (FRR) at different thresholds. The Equal Error Rate (EER) is about 2.01% in our experiments. Figure 5 illustrates the Receiver Operating Characteristic (ROC) Curve of our test.

False Acceptance Rate(FAR)	False Reject Rate (FRR)
2.01%	2.01%
1%	2.5%
0.1%	5.3%
0.01%	15%

Table2. FARs and FRRs at different thresholds

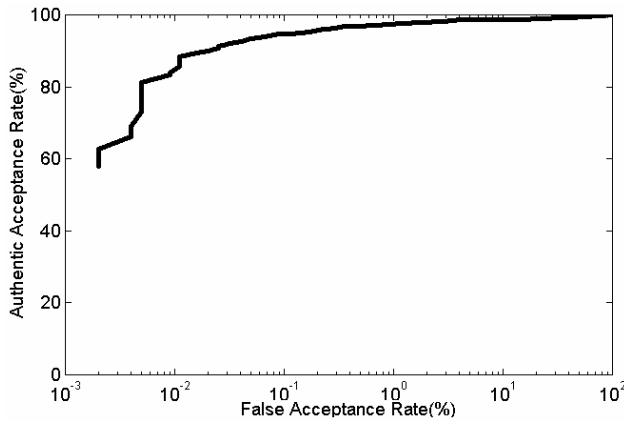


Figure 5. ROC Curve

The identification rates of our algorithm on NIST-24 database under different numbers of best matches are demonstrated in Table 3.

Number of best matches	Identification rate
1	98.44%
2	98.75%
3	99.00%

Table 3. Identification rates at different numbers of best matches

The average matching time from one pair of templates is less than 0.1 second on a PC with Pentium III 450MHz CPU and 128M RAM. Experimental statistics show that the initialization of MatchedSet contributes much to effectiveness of the algorithm.

Our test results are not comparable with that of [1], as the database and test protocol are not the same. Anyway, from above figures and tables, we find that our algorithm can provide robustness to deformations.

4. Conclusions

In this article, we have proposed a fingerprint matching algorithm based on error propagation. Our algorithm makes use of matching pairs of ends and bifurcations, thus provides more reliable alignment of two templates. Further, the similarity of the common region is used as the similarity measure of two fingerprint templates. Finally, the concept of error propagation is

applied to track nonlinear deformation adaptively. Experimental results indicate the effectiveness and robustness of our algorithm and it does meet the response-time and accuracy requirements for an automatic fingerprint verification system.

Although experimental results reveal that our approach is promising, what they also reveal is that there are still some problems to be solved. We list some of them in the following on which our future work will focus.

- The definition of minutia similarity. The image itself changes much when large deformation is observed. All features extracted from the image, including ridge segments, may also change in this situation. That is why the similarity of genuine paired ridges is sometimes smaller than that of different ridges. What is invariant or insensitive to fingerprint deformation is an open issue;
- How to reduce the similarity of two templates from different fingers? We find through visual inspection of the mismatched fingerprints that fingerprints of the same type tend to be confused with each other. The solution to this problem will need more effort.

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