Spectral Correspondence Method for Fingerprint Minutia Matching

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Abstract

This paper presents a spectral correspondence method for fingerprint matching. Minutia matching is formulated as recovering the dense sub-block in the corresponding matrix. And then the spectral correspondence method is used for searching the dense sub-block. First, we propose the pairwise adjacency matrix (PAM), whose diagonal elements represent similarities of minutia structures and other elements represent pairwise compatibilities between local minutia structure pair. Second, correct minutia pairs are likely to establish both large similarities and large compatibilities among each other and they form a dense sub-block. Then minutia matching is formulated as recovering the dense sub-block in the PAM. It gives a clear mathematical meaning for “optimal matching minutia pairs”. Third, we recover the dense sub-block based on spectral correspondence method, by using the principal eigenvector of PAM and imposing the one-to-one mapping constraints. Proposed method has stronger description ability and better robustness. Experiments conducted on FVC database demonstrate the effectiveness and the efficiency.

1. Introduction

Minutia-based fingerprint matching methods are the researching focus recently. As minutia features provide inadequate information, most methods are focused on exciting other matching features, such as ridge features [1], phase difference features [2]. Different from the previous papers, this paper provides a novel approach. It uses just minutia features and achieves good results.

Local minutia topologic structures constructed in local areas are less impacted by non-linear distortion and noise. X. Jiang suggests that a local structure constructed by minutiae such as k-nearest structure is more robust in 2000 [3]. X. Chen constructs a topologic structure to increase the tolerance in 2004 [4]. W. Xu grows local triangle structures into a growing area and then fuses them in 2007 [5]. R. Cappelli proposes a new representation called minutia cylinder-code in 2010 [6]. These local minutia topologic structures (simplified as LMTS) use surrounding minutia information and have better description for structural similarity.

Y. Feng proposes a new concept: compatibility of local LMTS pairs [7]. Compatibility refers to the possibility of co-existence of local structure pairs. J. Cao applies compatibility to local minutia star structures and achieves better results [8].

However, how to unify the information of similarity and compatibility? How to describe the optimal LMTS pairs? How to recover the optimal group of LMTS pairs? Based on these considerations, we construct the pairwise adjacency matrix (simplified as PAM). In the PAM the diagonal elements represent similarities of LMTS and other elements represent pairwise compatibilities between LMTS pairs. Correct LMTS pairs are more likely to establish both large similarities within them and large compatibilities among them, thus they form a dense sub-block. Problems of minutia matching are formulated as recovering the main dense sub-block in the PAM. By using the algorithm of spectral correspondence relaxation, we can recover the dense sub-block in the PAM and get the best matching minutia pairs.

Main contributions of this paper are: First, the proposed PAM unifies both similarities information and compatibilities information appropriately. Second, minutia matching is formulated as recovering the dense sub-block in the PAM. It gives a clear mathematical meaning for “optimal matching minutia pairs”. Third, spectral correspondence methods are then used for recovering the dense block. It is efficient and effective. Proposed approach has stronger description ability and better robustness to non-linear deformation and noise.
2. Methodology

2.1. Problem formulation

For point-sets matching, it is common to formulate point matching problem into maximum clique detection in association graph [9]. However, traditional maximum clique model doesn’t perform well for fingerprint matching, as it is more complex.

Here we make some improvements. We take LMTS as basic matching units and the minutia sets as the whole matching parts. We establish the pairwise association graph (PAG), whose nodes represent similarities of LMTS and the weights on the links represent pairwise compatibilities between LMTS. Correct pairs are likely to establish links among each other and thus form a strongly connected sub-graph. Incorrect pairs establish links with the other pairs accidentally, so they are unlikely to belong to strongly connected sub-graphs. We recover correct matching pairs based on how strongly they belong to the main dense sub-graph of pairwise adjacency matrix (PAG).

However, in graph theory, the computation of searching main dense sub-graph is exponential. In order to improve the time efficiency, we build the pairwise adjacency matrix (PAM), whose diagonal elements represent similarities of LMTS and other elements represent pairwise compatibilities between LMTS. Correct minutia pairs are likely to establish large similarities and large compatibilities and they form a dense sub-block. Then minutia matching is formulated as recovering the dense sub-block. By use of spectral correspondence methods [10] and relaxation algorithms [11], we can recovering the dense sub-block and solve the matching problem appropriately.

2.2. Spectral correspondence methods

Suppose there are two fingerprint minutia sets P and Q, with \( n_p \) and \( n_q \) minutiae, respectively. \( n_p \) and \( n_q \) local minutia structures can be generated. We can calculate the similarities and compatibilities among these LMTS. Thus the pairwise adjacency matrix (PAM) with \((n_p \times n_q) \times (n_p \times n_q)\) elements can be built using the following formula.

\[
A(i'j'|ii') = \left\{ \begin{array}{ll}
\text{Sim}(L_{ii'}, L_{ij'}) & \text{condition 1} \\
\text{Com}(P_{i'i'}, P_{j'j'}) & \text{condition 2} \\
0 & \text{condition 3}
\end{array} \right.
\]

In the formula, \( L_{ii'} \) indicates the LMTS with minutia \( i \) as center in \( P \) and \( L_{ij'} \) indicates the LMTS with minutia \( i' \) as center in \( Q \). \( \text{Sim}(L_{ii'}, L_{ij'}) \) represents the similarity between \( L_{ii'} \) and \( L_{ij'} \). \( P_{i'i'} \) indicates a LMTS pair, with minutia \( i \) in \( P \) and minutia \( i' \) in \( Q \). \( P_{i'i'} \) has a similar meaning. \( \text{Com}(P_{i'i'}, P_{j'j'}) \) represents the compatibility between pair \( P_{i'i'} \) and \( P_{j'j'} \). \( A(ii'j'|jj') \) represents an element in the PAM. 

Condition 1 indicates that \( i = j \) and \( i' = j' \). That is to say, the element is in the diagonal. Condition 2 indicates that \( i \neq j \) and \( i' \neq j' \). Prior knowledge is used for generating the PAM. As minutia matching is one-to-one matching, minutia \( i \) in \( P \) mapped to both minutia \( i' \) and \( j' \) in \( Q \) is impossible. When condition 3 \( (i = j \text{ and } i' = j') \text{ or } (i \neq j \text{ and } i' = j') \) holds, the element value is 0.

Equivalently, we seek for a set of correct LMTS matching pairs \( M = \{ii'\} \), so as to maximize the PAM score, defined as:

\[
\widetilde{M} = \arg \max_M \sum_{ii'j'j''} A(ii'j'|jj')
\]

(2)

This yields the following binary optimization problem:

\[
\hat{m} = \arg \max_m \sum_{ii'j'j''} (m^T A_m) \text{ s.t. } m^T 1 \leq 1 \text{ and } m^T 1 = 1
\]

(3)

The optimal solution \( \hat{m} \) is the binary vector that maximizes the \( m^T A_m \) score. \( m \) is a row-wise
vectored replica of $A$. The constraints imply that a minutia in $P$ can only be matched to a single minutia in $Q$ or not matched at all. The same applies to each minutia in $Q$.

Leordeanu shows how to apply spectral relaxation to the pairwise matching [10]. Firstly we relax both the mapping constraints and the integral constraints on $m$, such that its elements can take real values in $[0, 1]$. We draw a conclusion that the continuous solution $m^*$ will maximize the $m^T A m$ score that is the principal eigenvector of $A$. We can derive $m^*$ by computing the leading eigenvalue and corresponding eigenvector of $A$, using the following algorithm.

**Algorithm 1** Spectral relaxation iterations.

**Input:** matrix $A$

**Output:** $m^*$, main eigenvector of $A$

1. Initialize $m^*$ randomly
2. Repeat
3. $m^* \leftarrow A m^*$
4. $m^* \leftarrow \frac{1}{||m^*||_2} m^*$
5. Until convergence;

Given the continuous solution $m^*$, we can rewrite it in a $n_p \times n_q$ matrix form and discretize $m^*$ by a greedy approach and derive the optimal solution $\tilde{m}$. It is summarized as following:

**Algorithm 2** Greedy approach for discretization.

**Input:** continuous matrix $m^*$

**Output:** binary matrix $\tilde{m}$

1. Initialize $\tilde{m} = 0$
2. Repeat
3. Find the maximal element $m^*(i,j)$
4. Set $\tilde{m}(i,j) = 1, \forall k$, set $m^*(i,k) = 0, m^*(k,j) = 0$
5. Until $m^* = 0$;

The matching constraints are ignored in the spectral relaxation step and then are induced during the discretization step. After relaxation and discretization, we can gain the optimal matching LMTS pairs.

### 3. Fingerprint Matching

#### 3.1. Building the PAM and spectral relaxation

LMTS are firstly introduced by X. Chen in [4]. A topologic structure is constructed from a minutia $m_i$ and a list of neighbor minutia in a specified circular area. J. Cao uses a dynamic programming strategy to calculate similarities of two LMTS in [8]. Here we use the same strategy and gain the similarity information.

Compatibility between LMTS pairs is used to describe the possibility of co-existence between two LMTS pairs. As each LMTS pair has a transformation vector, we can use the transformation parameters to describe its compatibility. The compatibility between $L_i L_i'$ and $L_j L_j'$ can be defined as:

$$C_{L_i L_i', L_j L_j'} = G \left( D( f(V_{i, i'}, V_{j, j'}) \right)$$ (4)

Here $V_{i, i'} = \left( \Delta x_{L_i L_i'}, \Delta y_{L_i L_i'}, \theta_{L_i L_i'} \right)$

$$G(x) = a \cdot e^{-b x}$$ (6)

$V_{i, i'}$ is the transformation vector from structure $L_i$ to structure $L_i'$. It can be obtained through the least-squares method. $G(x)$ is a monotonically decreasing function. Thus we can gain the compatibility information and then build the PAM.

Using the algorithm 1 proposed in 2.2.2, we can gain the leading eigenvector $m^*$ of PAM, which is also the approximate continuous solution.

Because of the existence of partial overlapping, only subsets of size $n \leq \min\{n_p, n_q\}$ can be matched. Here we set the $m^*$ elements whose value is smaller than the pre-set threshold $\lambda$ to zero. After that we gain the binary matching solution $\tilde{m}$ using the algorithm 2. Thus we can get the optimal matching results.

#### 3.2. Regaining minutiae pairs using MLS model

Isolated minutiae or those minutiae in the border of fingerprint images have few surrounding minutiae. They may be removed at the step of constructing LMTS. It is necessary to regain the lost matches.

C. Liu proposes a minutiae expanding method based on moving least squares (MLS) transformation [2]. Here we use it to regain lost genuine pairs. Parameters of MLS transformation are estimated from matched pairs and are used to transform the model minutia set to the target minutia set. When two minutiae drop into the same tolerance box $(\Delta x, \Delta y, \Delta \theta)$, they are judged as matched. For fingerprints from the same fingerprint, many corresponding minutiae can be retrieved. Meanwhile, for fingerprints from different fingers, few minutiae can be regained as minutiae’s randomness.

#### 3.3. Scoring strategy using Convex Hull

After gaining the matching relationship, we design a new scoring strategy to get the final matching scores. The score evaluation strategy based on convex hull can be represented as follows:

$$\text{Score} = \frac{\tilde{M}}{n_{\tilde{m}}} \cdot \frac{m_{\text{match}}}{(m_{\text{match}}+m_2)}$$ (7)

$\tilde{M}$ represents the maximal PAM score. $n_{\tilde{m}}$ represents the number of initial matched minutiae pairs gained in section 3.2. $m_{\text{match}}$ represents the number of matched points after expanding, and $m_2$ represents the number of unmatched points within the convex hull in $S$. $m_2$ has a similar meaning. It is more reasonable to adopt this new score evaluation strategy.

### 4. Experiments

Comparative experiments are conducted on FVC2004 using different matching algorithms,
including the Grow Fuse method in [5], the Star-Structure approach in [8], and the Minutia Cylinder-Code method proposed in [6]. The minutiae are all extracted by the same approach of Gao proposed in [12]. Due to the low image quality and the limitation of the minutia extraction algorithm, many fake minutiae are extracted, which can be seen in Fig.2.

Partial results are shown in the Table 1. ROC curves on FVC2004 DB1 are shown in Figure 3. The results show that our matching algorithm performs much better than the other algorithms in terms of both EER and FMR. Our method has good robustness to noise and nonlinear deformation. Fig.2 is an example.

![Figure 2: Two fingerprints are from the same finger.](image)

Table 1 Comparative results on database FVC2004: The best results are marked by bold face.

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<tr>
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<th>DB1</th>
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<td>EER</td>
<td>FMR1000</td>
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<tr>
<td>Proposed Method</td>
<td><strong>5.17</strong></td>
<td><strong>19.21</strong></td>
<td><strong>6.78</strong></td>
<td><strong>17.53</strong></td>
<td><strong>3.47</strong></td>
<td><strong>9.54</strong></td>
<td><strong>4.29</strong></td>
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The average matching time is about 12ms. The major time is spent on the similarity calculation of LMTS pairs. There is much room for improvement at this step. This is also the future work.

5. Conclusion

In this paper, we propose the pairwise adjacency matrix, which unifies similarities and compatibilities appropriately. Minutia matching is formulated as recovering the dense sub-block in the corresponding adjacency matrix. It gives a clear mathematical meaning for “optimal matching minutia pairs”. Then the spectral correspondence method is used for searching the dense sub-block. This method makes better use of similarities and compatibilities. It has stronger description ability and better robustness to noise. Experimental results demonstrate the effectiveness and accuracy of our algorithm.

References


