Palmprint Minutia Point Matching Algorithmand GPU Application

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The problem of palmprint application in public security department is described in this paper such as large database and poor quality of the scene palmprint. Firstly, the computational complexity of palmprint feature point matching algorithm is analyzed. The three-level feature points matching algorithm is presented according to the analysis results; secondly, the working process of the three-level feature points matching algorithm is introduced in detail; finally, the algorithm is transformed to GPU (Graphics Processing Units) parallel and the test result is given. The GPU technology is firstly applied to the palmprint recognition in our study. The result showed that the speed of palmprint feature matching compared with others increased by about three times and the speed can increase to more than 15 times with the GPU technology.

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1. Introduction

With the development of biometric identification technology, the palmprint identification technology has attracted more and more attentions and researches. The palmprint recognition and matching have played an important role in the case detection, forensic evidence. It plays a complementary role with the fingerprint recognition and has a broad prospect for application. The palmprint identification technology has higher credibility than other biometric identification technologies. In recent years, many scholars have studied the palmprint automatic identification and matching and put forward a variety of feature recognition methods [1, 2] such as the method based on structure feature [3], the method based on statistical feature, the method based on subspace [4] and the method based on coding [5]. The above method is the palmprint image recognition method mainly based on good image quality and low resolution; but in the criminal investigation field, we need to build the offline high resolution palmprint recognition method because the palmprint database tends to be bigger in the field of criminal investigation. The capability of palmprint identification should satisfy more than one million palmprints at least. For the imperfect palmprint collected in cases, the palmprint feature extraction and matching method base on online low resolution can't meet the demand; therefore, the palmprint recognition research based on high resolution is necessitated in the field of criminal investigation [1, 6]. In 2009, Galton[7] studied the palmprint features and put forward the minutia features. Aiming at the difference between palmprint and fingerprint, Anil K. Jain [8] studied on palmprint feature matching in-depth. Researchers of the Nan Kai University [6] have carried out systemic researches on palmprint feature recognition and matching algorithm and then proposed the solution; but it still needs to be improved whether the matching average speed can overcome maximum database. This paper aims to the research of feature point matching base on high resolution palmprint in criminal investigation field. With the several-level matching mode, we put forward a set of relatively complete palmprint feature point matching method. With the GPU parallel renovated, the speed of palmprint features matching algorithm program can be effectively raised.

2. Palmprint Minutia Feature Matching Algorithm

2.1 Existing Algorithm Computational Complexity

In this paper, the palmprint minutia feature points involve the starting point, the end point, the branch point and the combine point. These minutia feature points have formed the combination of palmprint characteristic. The coordinates and direction as defined is the same as the fingerprint, refer to the ministry of public security, or 774.5 GA - 2008 [9]. The number of palmprint feature point is more than the fingerprint, which is about 1000 or so. With the simple feature matching method, we use a single feature point calculation one time as the basic computing unit. The computational complexity is $m(m-1)...(m-n+1) = \dfrac{m!}{(m-n)!}$ (m ≥ n), in which, m, n refer to the number of feature points both match side. Hong Kong Polytechnic University [10], Nankai University [11], and other institutions researchers proposed local structure matching method similar to the fingerprint matching method. Small local features were seemed as a whole to expect a match object in the target area. Its advantage is represented in its greatly reduction of the computational complexity. The amount of local structure matching calculation is $m*n*p! = mnp!$, p is the number of feature points of local structure. Usually, we take $p = 8$. We can get rid of the most part with low similarity matching points by local structure calculation. Suppose that average filtering rate of local structure matching is $\alpha(\alpha << 1)$, it indicates that the number of may be used in the initial calibration center for the reduced α

times. It doesn't necessary to calculate p points that have matched. The algorithm just only

calculates $\alpha\dfrac{(m-p)!}{(m-n)!}$ time. From the above, we can obtain $\alpha\dfrac{(m-p)!}{(m-n)!}+mnp!<<\dfrac{m!}{(m-n)!}$. Through

local structural matching method, the amount of calculation can be greatly reduced, especially when large amount of data is calculated. A large number of unrelated palmprints can be avoided through the local similarity threshold assessment in local structure matching phase. The number of global matching palmprints will be reduced greatly. It will enable more matching calculation be executed in Unit of time.

2.2 Three-levels Matching Algorithm

The local structure of the building is a neighborhood structure of a feature point as the center building, as shown in Fig. 1.
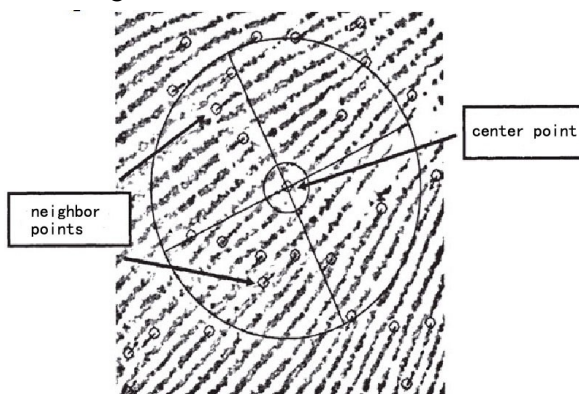

Fig.1 the local structure of near point

The existence of the local structure is universal and the vast majority of feature points can be built on local structure. As all points in the local structure will match each other, the amount of calculation shall still be large. This paper proposes Level 3 matching algorithm. It further reduces the computational complexity by adding special point couple matching before the local structure matching. The concrete method is to use the palmprint adjacent lines parallel to the line to the general approach, so the near feature points is also much close to 0 degree (parallel) or 180 degrees (TIT FOR TAT) direction, as shown in Fig. 2. Define two points to meet distance threshold and angle parallel as a special point couple. At the matching procedure, the specific points couple matching will be executed in palmprint firstly.
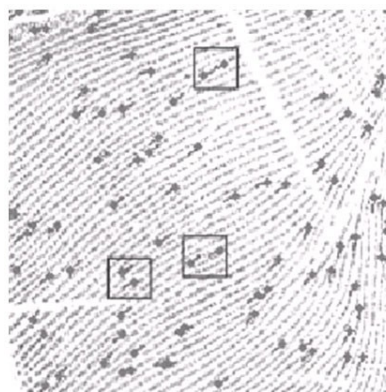

Fig.2 the example of couple point

As the palm mastoid line is relatively smooth, mostly direction of near feature points are often relatively close and the eligible points are widespread in palmprint. Due to the adjacent close distance, two feature points were left and recognized at the same time frequently. Complete palmprint usually can be extracted to special point couple about 100 to 300. As to two identical palmprints, there are a plenty of special point couple that can be effectively matched in an effective area. Because two points are near to each other, the error of relative position and angles of two points will be smaller in the feature extraction. By the two approaching points of parallel or TIT FOR TAT to compose special point couple, we could quickly determine which corresponding point has a possible matching in the initial phase matching. Furthermore, most of useless calculation will be abandoned. The special points couple increase the rapid mode above original secondary matching mode, so its essence does not improve the precision of the algorithm. In the two identical palmprints, the probability of the same extraction are not matching an extraction that almost does not exist, so the special point couple matching just filter the large amounts useless data in the calculation of the late match. On the premise, the mode could not affect the original algorithm precision. It will reduce the amount of calculation.

Known amount of the secondary local structure matching is $C = mnp!$. Given each feature point, the special point couple can be found. The amount of special point couple is $C_1 = m \quad n$. Given the pass rate is k (k < 1), the amount of local structure matching is $C_2 = kmnp!$ In the three-level matching, the total amount of above two parts is $C_1 + C_2 = mn(1 + kp!)$. At that $p! \gg 1$, the efficiency depends on the filtering rate k, $k < 0.1$ in general. We can calculate that the computing speed increase rate is $\dfrac{C}{C_1 + C_2} = \dfrac{p!}{(1 + kp!)} > 10$ in this section.

3 Palmprint Minutia Feature Level 3 Matching Algorithm

3.1 Basic Process of Algorithm

A. read sample palmprint data, calculate special point couple in it, calculate the local structure, convert the polar coordinates and pretreat such as follows:

B. read the archives palmprint data and pretreat such data

C. calculate the similarity between the sample points couple and the archives points couple

D. calculate the similarity between the sample local structures in line with the similarity threshold minutia points and the neighborhood minutia points of the corresponding archives minutia point, get the candidate's corresponding points in line with the local structure similarity threshold.

E. calculate the compatibility weight among the candidate's corresponding point sets according to the method of competition and weighting each other. It can be concluded the point sets of fulfilling threshold requirements. If the point set cannot be fulfilled, end the cycle.

F. calculate the global minute points matching of above candidate's point sets and obtain two palmprint final similarity scores

G. read the archives palmprint in a loop manner till the end of matching; sort the candidate queue according to the similarity scores.

3.2 Special Ppoint Couple Matching

At first, special point couple could be calculated. By searching the neighboring points of each minutia feature points, obtain special point couples of the satisfied threshold requirements. Two feature points as given is (m_i, m_j) and the coordinates are (x_1, y_1, θ_1) (x_2, y_2, θ_2), in which, $x\ y\ \theta$ is rectangular coordinate system position and the angle parameters. If it can meet the requirements of

$$\sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2}\quad 20 ; \min(|\theta_1 - \theta_2|, 360° - |\theta_1 - \theta_2|) \in (0°, 10°)\ \text{or}\ (170°, 180°)$$

In this way, *i* and *j* are the special point couple.

We consider m_i of special point couple as the benchmark, convert the rectangular to the polar coordinates and obtain the m_i, m_j polar coordinates. The polar coordinates of m_i is

$$\begin{pmatrix} r_i \\ \varphi_i \\ \alpha_i \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}, \text{the polar coordinates of } m_j \text{ is } \begin{pmatrix} r_j \\ \varphi_j \\ \alpha_j \end{pmatrix} \begin{pmatrix} \sqrt{(x_j - x_i)^2 + (y_j - y_i)^2} \\ \left(\left(\dfrac{180}{\pi} \times \tan^{-1}\left(\dfrac{y_j - y_i}{x_j - x_i} \right) \right) + 360 \right) \% 360 \\ \theta_j - \theta_i \end{pmatrix}.$$

In the above formula, r is the distance between feature points and the coordinate system center, φ is the direction of feature points and positive angle coordinate system, α is the center of feature point and coordinate system and coordinate positive Angle.

$m_i, m_i^{'}$ points are aligned. The difference degree of special point couple is expressed as the difference of two coordinates:

$$\Delta r = |r_j - r_j^{'}|\ ;\ \Delta\varphi = \min(|\varphi_j - \varphi_j^{'}|, 360° - |\varphi_j - \varphi_j^{'}|) ;\ \Delta\alpha = \min(|\alpha_j - \alpha_j^{'}|, 360° - |\alpha_j - \alpha_j^{'}|)$$

If $\Delta r \leq r_{threshold1}$ $\Delta\varphi \leq \varphi_{threshold1}$ $\Delta\alpha \leq \alpha_{threshold1}$, the corresponding points $(m_i^{'}, m_j^{'})$ is the candidate's corresponding points.

3.3 Local Structure Matching

We use a regular size as Radius to calculate the respective local structure of each candidate's corresponding points. P, Q was given as the matching local structure of samples palmprint and archives. I and j are respective adjacent points in two local structures, the expression is $m_P^i = (r_P^i, \varphi_P^i, \alpha_P^i)$, $m_Q^j = (r_Q^j, \varphi_Q^j, \alpha_Q^j)$. Local structure difference degree is described as follows:

$$\Delta r = |r_P^i - r_Q^j|;\ \Delta\varphi = \min(|\varphi_P^i - \varphi_Q^j|, 360° - |\varphi_P^i - \varphi_Q^j|);\ \Delta\alpha = \min(|\alpha_P^i - \alpha_Q^j|, 360° - |\alpha_P^i - \alpha_Q^j|);$$

the local structure similarity is:

$$sim(m_P^i, m_Q^j) = \begin{cases} \dfrac{(1 - \dfrac{\Delta r}{r_{threshold2}}) + (1 - \dfrac{\Delta\varphi}{\varphi_{threshold2}}) + (1 - \dfrac{\Delta\alpha}{\alpha_{threshold2}})}{3} & \begin{array}{l} \Delta r \leq r_{threshold2} \\ \Delta\varphi \leq \varphi_{threshold2} \\ \Delta\alpha \leq \alpha_{threshold2} \end{array} \\ 0 & others \end{cases}, \text{among}$$

them, $r_{threshold2}\ \varphi_{threshold2}\ \alpha_{threshold2}$ is the difference degree threshold in the corresponding point of the local structure. We assume $r_{threshold2} = 10, \varphi_{threshold2} = 20, \alpha_{threshold2} = 20$. If the

value is not 0, the similarity will be marked down. If the two local structures have *n* corresponding points of matching, n is the natural number, greater than 2, and then the similarity of the local structure is shown as follows: $sim(m_P, m_Q) = \sum_{k=1}^{n} sim(m_P^{ik}, m_Q^{jk})$.

3.4 Method of the Candidate's Corresponding Point Competition Weighting

As the similarity is incompatibility between several candidate local structures, we use the competition weight calculation method to calculate the similarity weighted among each corresponding local structure group and obtain weights of each local structure. As shown in Fig. 3. In Fig. 3a, a sample local structure may be several archives of local structure. In Fig. 3b, the two corresponding local structure groups can realize the matching when they rotate the same corresponding angle; thus the corresponding two center points have high compatibility in the two local structures.

    a. Local Structure Matching   b. Compatible Local Structure
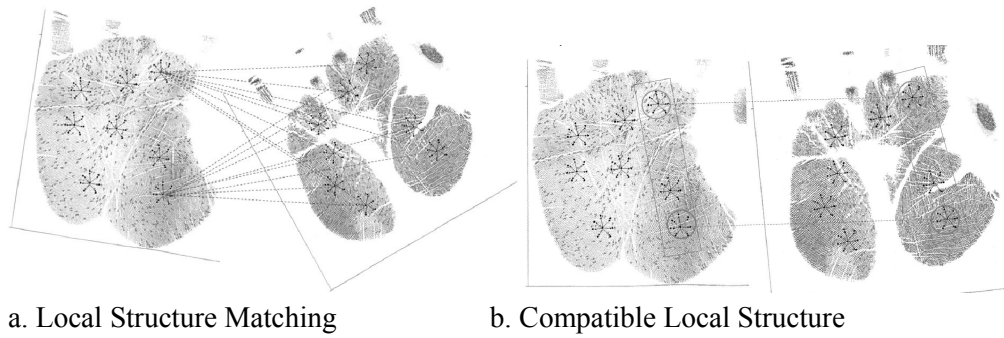
Figure 3: Example of Competion and Weighting

Pairs1 (P1, Q1), Pairs2 (P2 and Q2) are two groups matching local structures. The difference degree between such two groups local structures can be expressed by the difference degree of two center points; the difference degree parameters of two local structure groups are represented as $(\Delta\theta, \Delta x, \Delta y)$; therefore, the similarity between P1 and P2 is expressed as:

$$V(P_1, P_2) = \begin{cases} 0 & |\Delta\theta| > I \ or \ |\Delta x| > X \ or \ |\Delta y| > Y \\ 1 & otherwise \end{cases} \quad I=30, X=20, Y=20;$$

$VS(P_i, Q_i)$ is defined as the local structure competition similarity evaluation value, that is the weight of the local structure. Thus $VS(P_i, Q_i) = sim(P_i, Q_i) + C \times \sum_{j=1, j\neq i}^{n} V(P_i, P_j) \times sim(P_j, Q_j)$. Among the parameters, *n* is a matching number of local structure, *C* is constant, which takes *C*=0.5;

If $VS(P_i, Q_i) \geq 0.2 \sum_{j=1}^{n} sim(P_j, Q_j)$, the local structure that *I* point was used as the center point in line with the similarity filter condition. Use *I* point and the corresponding point in archives as the candidate's calibration point. If there are multiple $VS(P_i, Q_i)$ which are greater than the threshold, we should determine the mutual $V(P_1, P_2)$. If $V(P_1, P_2) \approx 1$, the multiple local structure can be seemed as one group. The maximum $VS(P_i, Q_i)$ would be taken as a calibration center.

3.5 Global Matching

One of the calibration center corresponding points is $A_i\left(x_i, y_i, \theta_i\right), B_j\left(x_j, y_j, \theta_j\right)$. According to the difference of coordinate and angle, the global minute points' coordinate is transformed by rotation and translation. As to each minute points $P_i\left(x_i, y_i, \theta_i\right)$ in the palmprint, upon transformation, a new feature point is shown as follows

$$\begin{pmatrix} x_i' \\ y_i' \\ \theta_i' \\ 1 \end{pmatrix} = \begin{pmatrix} \cos\Delta\theta & -\sin\Delta\theta & 0 & \Delta x \\ \sin\Delta\theta & \cos\Delta\theta & 0 & \Delta x \\ 0 & 0 & 1 & \Delta\theta \\ 0 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} x_i \\ y_i \\ \theta_i \\ 1 \end{pmatrix}.$$

Gi is Euclid distance difference of corresponding points $m_i(x_i, y_i, d_i)$ $m_i'(x_i', y_i', d_i')$ between sample palmprint and archive palmprint through global matching. Then, $G_i = C\sqrt{(x_i - x_i')^2 + (y_1 - y_i')^2 + (d_1 - d_i')^2}$. Define the constant $C=10$; add the differences of all corresponding points, we can obtain a global difference G, $G = \sum\limits_{i=1}^{n} G_i$.

4. GPU Acceleration of Algorithm

The characteristics of mutually independent calculation of multiple palmprint and multiple feature points can ensure minimize communication of parallel computing; thus we try to transform the above algorithm on GPU, which mainly aims at the steps of large calculation amount, including special point couple matching and the local structure matching.

Special point matching and local structure matching, in addition to algorithm instructions, the input and output of GPU, data loading and distribution are the same. GPU calculation main steps are shown as follows:

A. set the presetting value of data size, used for launch a GPU kernel every time. According to the presetting value, divide the palmprint data block.

B. load the archive palmprint data blocks in memory.

C. copy the palmprint from memory to the global memory of GPU device.

D. store archive data blocks in texture memory of GPU to improve the use of GPU for palmprint matching speed.

E. launch GPU computation. Calculate the coordinate's transformation of minute points and the difference of special point couples (or the difference of local structure).; end the GPU computing

F. determine the candidate point of next step calculation in CPU according to the calculation difference degree.

5. Test and Results

5.1 Accuracy Tßest

We cut out 5000,20000,100000,5000000, four groups' data as a test template library. From the dataset of matched, we selected 20 scene matched with archives and 20 archives matched with archives.

Data size	Ranking 1	Ranking≤10	Ranking≤50	Ranking≤100	Ranking＞100
5000	18	1	1		
2*10⁴	17	2		1	
1*10⁵	13	4	2		1
5*10⁵	8	5	3	1	3

Table 1: Accuracy Test of Scene Matching with Archives

Data size	Ranking 1	Ranking≤10	Ranking≤50	Ranking≤100	Ranking＞100
5000	20				
2*10⁴	18	2			
1*10⁵	17	2	1		
5*10⁵	17	1	1	1	

Table 2: Accuracy Test of Archives Matching with Archives

From the above tables, the accuracy of algorithm has a little increase than the former two-level algorithm.

5.2 Speed Test

We used more than 640 thousand people palmprint database collected from the public security organ of Beijing City for the speed testing and the results are as follows.

5.2.1 Computing Time Test of the Secondary Algorithm and Three-Stage Algorithm

CPU version of three-stage algorithm compares with secondary algorithm that unused special point match. According to different size of palmprint computation time see the table below.

data size	100	1000	2000	10000	50000	200000	600000
Secondary(s)	1.635	15.842	28.954	150.078	680.350	2735.137	8004.064
three-stage(s)	0.540	5.049	9.786	48.095	235.057	936.962	2807.838
speed up ratio	3.027	3.138	2.959	3.120	2.894	2.919	2.851

Table 3: Computation Time of Two-Level and Three-Level Feature Matching Algorithms

From the above table, using special point couple to match can sharply increase matching speed, the speed up ratio of the different scale data approach linear.

5.2.2 GPU Speed up Ratio Test Relative to CPU

Test the CPU version and GPU version of the palm three-level matching algorithm. The GPU version is Nvidia GTX580 and the CPU version is Intel core i5. Using the same sample palmprint to compare with different sizes of palmprint database.

data size	100	1000	2000	10000	50000	200000	600000
CPU(s)	0.540	5.049	9.786	48.095	235.057	936.962	2807.838
GTX580(s)	0.638	2.229	3.053	6.336	14.953	56.874	170.257
speed up ratio	0.85	2.27	3.21	7.59	14.73	16.47	16.492

Table 4: Computation Time of CPU and GPU Algorithm

From the above table, the algorithm uses GPU acceleration with the increase of data size; and the speed up ratio can be greatly improved.

6. Conclusion

This algorithm has high accuracy for minute feature points matching based on the high resolution palmprint image. The three-level matching algorithm compared with the original algorithm can improve the matching speed. It can meet the large capacity of palmprint database comparison demanded by the public security organ and other special department. This algorithm is suitable for large-scale parallel computing, especially for the mass thread of parallel computing based on GPU. The algorithm based on GPU while compared with the algorithm based on CPU, can increase the speed significantly under the same accuracy.

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