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A Method of Fundamental Matrix Estimation Based on NSGA-II and Improved Quasi-affine Transform

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Abstract. *The fundamental matrix is the mainstream solution to computer vision problems such as 3D reconstruction, real-time location and map building. Accuracy and efficiency are two main measurement indexes in fundamental matrix estimation. When the accuracy is not enough, it often needs to be corrected through back-end optimization and other costly ways, and low efficiency will affect the real-time performance of the system. In order to solve this problem, this paper proposes a new estimation method of fundamental matrix based on improved quasi affine transformation. Specifically, based on the QUATRE algorithm, this method first proposes a population cooperation method based on a specific "gene-chromosome" pattern. Secondly, combining the advantages of NSGA-II in solving multi-objective problems, the Pareto dominance relationship of the population chromosome was firstly calculated according to the objective function of mean polarity distance and internal points in the way of NSGA-II, and the crowding degree was also calculated. The operations of population initialization, mutation and crossover in the discrete solution space represented by the homogeneous coordinate system are redefined. The selection operation is then performed according to the elite policy of NSGA-II. In addition, a confidence - based method to determine the number of iterations is proposed to accelerate the algorithm. Experimental results show that the proposed method can effectively eliminate noise and mismatching, and is superior to the current mainstream methods in accuracy and efficiency, and can effectively solve the problem of fundamental matrix estimation.*

Keywords: Polar geometry;Fundamental matrix;Quasi affine transformation;NSGA-II

1. **Introduction.** Fundamental matrix estimation is the key problem to obtain space target information by using Structure from Motion [1, 2], Multi-view Stereo vision [3, 4] and other methods. It is widely used in the cutting-edge research in the field of computer vision, such as image-based Modeling [5, 6], Simultaneous Localization And Mapping [7, 8], Image Segmentation Algorithm [9] , etc.

The three-dimensional spatial information of the target object can be restored from a set of two-dimensional sequence pictures of the same scene taken from different angles and distances, and its theoretical basis is the polar geometric constraint existing between them [10, 11]. The fundamental matrix describes the mathematical relationship between matching feature point pairs in correlation images under polar constraint. Relevant studies can be first seen in algorithms such as camera self-calibration [12, 13]. Let $p_i(x_i, y_i, 1)^T$ and $p_i'(x_i, y_i, 1)^T$ be the homogeneous coordinates of the I $(1 \leq i \leq n)$ feature points matched in the first image I and the second image I', respectively. Equation (1) describes the polar constraint relationship between these feature points.

$$(p_i')^T F p_i = 0 \tag{1}$$

F is the fundamental Matrix, and N is the number of feature points. The estimation of F is an overdetermined problem of equations, which can be solved mathematically for the feature points with a given number of 8. Compared with the general errors of the true points, the errors of the inner points and the outer points can be divided into two categories. Then, to get more accurate estimation results, the key lies in the selection method of 8 pairs of feature points. A set composed of 8 pairs of interior points is called the minimum interior point set, and each set of minimum interior point sets can determine a fudamental matrix estimation model. (1) The stronger the fitting ability of the fundamental matrix estimation model to all feature points, the better the minimum set of inner points. (2) The smaller the average antipode distance calculated by the fudamental matrix estimation model, the better the minimum inner subset.

Accuracy and efficiency are the main indicators to measure the fudamental matrix estimation algorithm. When the accuracy is not enough, it often needs to be corrected

at a high cost [14]. Low efficiency will affect the real-time performance of the system. To solve the above problems, this paper introduces the strategies of intelligent algorithms quasi affine transformation evolutionary (Quatre) [15-18] and multi-objective optimization algorithm (NSGA-II) [19] into the estimation of fundamental matrix.

(1) A population collaboration method based on specific gene chromosome model is proposed for the estimation of fudamental matrix. Specifically, the matching feature point pair is regarded as a gene and consists of 8 genes, and a chromosome is composed of 8 genes. The fudamental matrix is estimated by this specific population collaboration. (2) The original QUATRE algorithm is improved, and the Pareto dominance relation and congestion strategy of NSGA-II are introduced. The new definition of population initialization, mutation and crossover in the discrete solution space represented by homogeneous coordinate system makes it possible to solve the estimation problem of fundamental matrix. In particular, this algorithm improves the fast non dominated sorting algorithm to realize the Pareto dominance: this algorithm places the chromosome with matching feature number less than 8 in the last layer of Pareto dominance, which is the place where the original Pareto dominance does not have. (3) The elite strategy of NSGA-II is introduced into the selection operation to obtain the selected population. The new species population has higher fitness to the two objective functions and more reasonable chromosome distribution. First, the mutated population and the parent population were merged. According to the order of Pareto rank from low to high (especially, the chromosome with matching feature points less than 8 is put in the last layer of Pareto dominance relation, and the chromosome with matching feature points less than 8 is considered as the worst chromosome) The whole layer population is put into the parent population until all the individuals in a certain layer cannot be put into the parent population. The individuals in this layer are arranged from large to small according to the crowding degree, and they are put into the parent population in turn until the parent population is filled, so as to get a new selected population. (4) This paper proposes a method to determine the number of iterations based on confidence to accelerate the algorithm. Different from the QUATRE algorithm, which uses fixed number of iterations to find the optimal solution, this method calculates the termination conditions in real time based on the given confidence level, which improves the efficiency of the algorithm.

2. **Problem Statement and Preliminaries.** The fudamental matrix estimation methods based on computer vision mainly include linear method, iterative method and robust method.

The typical representative of linear method is the 8-point algorithm and its related extension algorithm. The 8-point algorithm [20] was first proposed by Longuet-Higgins et al. That is 8 pairs of randomly selected feature points were used to calculate the fundamental matrix. This method is sensitive to noise and mismatching. On this basis, Hartley et al. proposed an improved 8-point algorithm [21], which firstly normalized the matching feature points on scale and translation, then calculated the fudamental matrix using 8-point algorithm, and finally carried out inverse regularization operation. Experimental results show that the improved strategy can suppress the noise to a certain extent. However, since 8 pairs of feature points are still obtained by random method, the influence of external points on the estimation results cannot be eliminated fundamentally. Iterative methods mainly include M-estimation method [22] and event deletion method [23]. The feature of M-estimation method is that all feature points are iterated and different weights are given to the outer and inner points. For example, the dynamic penalty weighting mechanism introduced in literature [24]. This method has a good effect on noise suppression, but it is not effective on data sets with many external points. The

event deletion method is improved to some extent, but the computational complexity is still large.

Representatives of robust methods include minimum median method (LMEDS) [25, 26], random sampling consistency algorithm (RANSAC) [27, 28] and its related improved algorithms (for example, higher than minimum subset algorithm HMSS [29]), etc. The LMEDS algorithm is relatively simple and sensitive to noise and mismatching. Xu Jinshan et al. proposed a homography matrix adaptive method [30] based on LMEDS to eliminate external points and shorten the number of iterations. The core idea of RANSAC algorithm is to use the distance from the feature point to the polar line as the basis to test a large number of feature points set, from which to find the optimal result. It is one of the mainstream estimation methods of fundamental matrix at present. But RANSAC algorithm needs a lot of random initialization of the minimum subset. For this problem, HMSS algorithm uses a sampling algorithm higher than the minimum subset to speed up the search of the optimal inner point set. However, the relationship between the accuracy of the algorithm and the size of the set of ideas used is not clear with the HMSS method.

The meta-heuristic optimization algorithms have been shown to be useful to solve many engineering problems. Those promissing optimization algorithms include the Genetic Algorithm (GA) [31, 32], Differential Evolution (DE) [33, 34], Particle Swarm Optimization (PSO) [35, 36], Ant Colony Optimization (ACO) [37, 38], Grey Wolf Optimizer (GWO) [39, 40], Cat Swarm Optimization (CSO) [41, 42], Fish Migration Optimization [43-45] and QUasi-Affine TRansformation Evolutionary (QUATRE) [46-49]. Since the evolutionary algorithm has the characteristic of intelligent optimization in the solution space, this method adopts the improved QUATRE algorithm and NSGA-II algorithmto solve the fundamental matrix estimation problem. Compared with the linear method, the interference of external points caused by noise and mismatching can be eliminated effectively. Compared with the iterative method, it can gather the global optimal solution quickly because of the particle swarm cooperation. Compared with the robust method, the number of subsets extracted can be reduced effectively. The following is the basic concept of QUATRE algorithm.

2.1. **QUATRE algorithm.** QUATRE is a kind of particle swarm evolution algorithm, put forward by Meng and others, The name comes from the following equation in line 2 which means quasi-affine transform.

$$\begin{aligned} B &= X_{gbest} + c * (X_{r1} - X_{r2}) \\ X &\mapsto M \bigotimes X + \overline{M} \bigotimes B \end{aligned} \tag{2}$$

Equation 2 shows the core idea of the population evolution of the QUATRE algorithm. The first line of the formula indicates that each population particle moves a certain distance toward the random direction expressed by $X_{r1} - X_{r2}$ with the position X_{gbest} of the global optimal particle as the center, where c is the coefficient of the moving step length, and the results are stored in matrix B. The second row indicates that the random perturbation represented by B is randomly applied to the current particle coordinate matrix X in the form of a kind of affine transformation, where the joint search matrix M is obtained as shown in Equation 3. That is, the lower triangular matrix whose element value is 1 is randomly swapped, and then the 0 and 1 elements in each row are randomly swapped $\bar{M}$ is all binary elements in M taking "logical not" operation.

$$\begin{bmatrix} 1 & & & \\ 1 & 1 & & \\ & & \dots & \\ 1 & 1 & \dots & \end{bmatrix} \sim \begin{bmatrix} & 1 & & \\ & \dots & & \\ 1 & & \dots & 1 \\ & 1 & 1 & \end{bmatrix} = M \tag{3}$$

From the point of view of population evolution, it is a process of population evolution including mutation and crossover operation. Therefore, B and M can also be called mutation matrix and crossover matrix respectively. The fundamental matrix estimation problem can be regarded as the optimization problem of selecting 8 pairs of interior points from a given finite matching feature point pair space. The problem space is discrete, and the original QUATRE optimization method is defined in continuous domain. Therefore, the above optimization strategy needs to be improved to solve the fundamental matrix estimation problem. The specific improvement methods are described below.

2.2. **NSGA-II algorithm.** NSGA-II algorithm is a multi-objective optimization algorithm, which was proposed by Deb K et al. It is an algorithm that stratified the population according to the dominant relationship of the solution, obtained the Pareto dominant relationship, then calculated the crowding degree for each layer, and finally used the elite strategy to complete the selection operation. The elite strategy is to merge the mutated population with the parent population. In the order of Pareto level from low to high, the whole layer population is put into the parent population until all individuals in a certain layer cannot be put into the parent population. The individuals in this layer are arranged from large to small according to the crowding degree, and they are put into the parent population in turn until the parent population is filled, so as to get a new selected population. In this way, the chromosome population has higher fitness to the two objective functions, and the chromosome distribution is more uniform and reasonable.

The fast non-dominated sorting and congestion calculation of NSGA-II algorithm reveal the dominant and distribution relationships among matching feature points. It provides information for the mutation operation of the algorithm. The elite strategy of NSGA-II algorithm also provides ideas for the selection operation of this algorithm.

3. **Our method.** This section mainly introduces the fundamental matrix estimation method based on NSGA-II and improved quasi affine transformation. Specifically, this method uses matched feature point pairs to build a population, combines with the optimization ability of particle swarm, the advantages of QUATRE algorithm in solving combinatorial problems and the advantages of NSGA-II in solving multi-objective optimization problems to estimate the fundamental matrix, and the basic process is shown in Figure 1. With matching feature point pairs as input, the first generation population is initialized based on a specific "gene-chromosome" pattern. Then the chromosomes were sequenced based on the internal point rate and the termination conditions of the iteration were calculated. When the termination condition is geted, the algorithm ends and outputs the corresponding estimation value of the fundamental matrix. Otherwise, the population evolves iteratively through mutation, crossover and selection operations.

The fast non-dominated sorting and congestion calculation of NSGA-II algorithm reveal the dominant and distribution relationships among matching feature points. It provides information for the mutation operation of the algorithm. The elite strategy of NSGA-II algorithm also provides ideas for the selection operation of this algorithm.

3.1. **Initialization.**

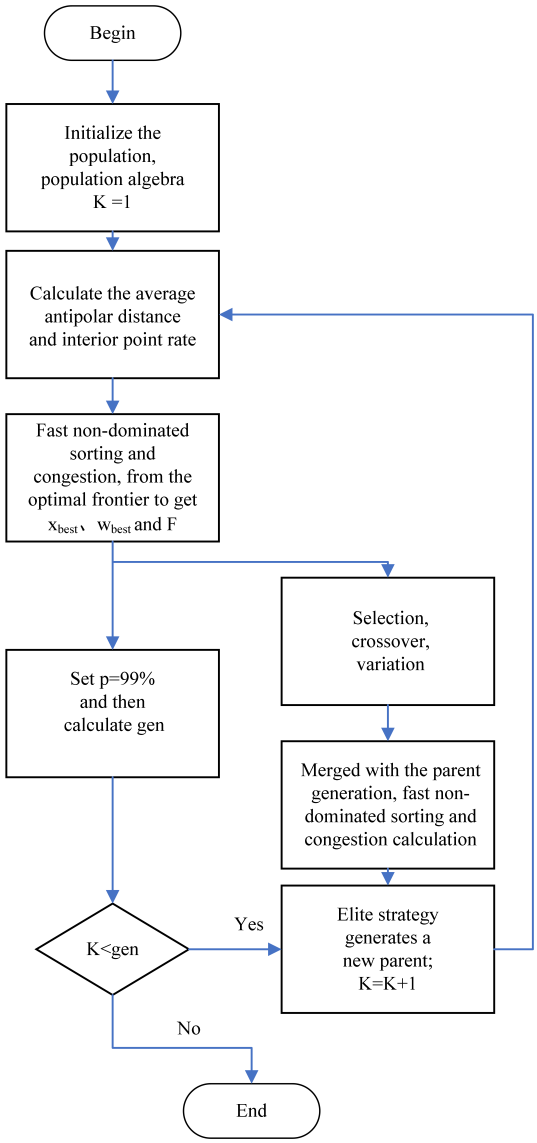


FIGURE 1. Our method flow chart

3.1.1. *Population structure.* Different from the QUATRE algorithm, which generates a specified number of particle swarm initialization with random coordinates in continuous coordinate space, the candidate feature points are known in the fudamental matrix estimation and are usually represented by homogeneous coordinates to simplify the operation. In addition, since 8 pairs of feature points can determine the estimation model of a fudamental matrix, the algorithm will match the homogeneous coordinates of the feature point pairs as genes, and initialize the population by using 8 genes to form a chromosome.

Specifically, A specific feature point recognition algorithm (such as SURF [50]) is used to obtain N pairs of matching feature points in two images at first,and then it is expressed as an $N \times 6$ matrix A as shown in Equation 4 and Equation 5, where $p_{(i,1)}(x_{(i,1)}, y_{(i,1)}, 1)^T$ and $p_{(i,2)}(x_{(i,2)}, y_{(i,2)}, 1)^T$ $(1 \leqslant i \leqslant N)$ are the two homogeneous coordinates of the ith pair feature points respectively.

In order to realize the random selection of NP chromosomes as the first generation of species $X(1)$, can according to the first line of disrupting A, then from A first line of the order every time take eight lines, take NP times in A row, $X(1)$ can be said

for the $NP \times 8$ matrix as shown in Equation 5, the initial population is completed as $x_{(u,v)} = (p_{((u-1)\times 8+v,1)}, p_{((u-1)\times 8+v,2)})$. Each row of $X(1)$ is a chromosome.

$$A = \begin{bmatrix} p_{(1,1)} & p_{(1,2)} \\ \vdots & \vdots \\ p_{(i,1)} & p_{(i,2)} \\ \vdots & \vdots \\ p_{(N,1)} & p_{(N,2)} \end{bmatrix} \tag{4}$$

$$X(1) = \begin{bmatrix} x_{(1,1)} & \cdots & x_{(1,8)} \\ \vdots & \ddots & \vdots \\ x_{(NP,1)} & \cdots & x_{(NP,8)} \end{bmatrix} \tag{5}$$

3.1.2. *Fast non-dominated sorting and crowding degree calculation.* Fast non-dominated sequencing: Chromosomes with matching feature points greater than 8 in A are selected as $A1$, and those with matching feature points less than 8 in A are denoting as $A2$. The non-dominated sequencing rank of $A2$ is the lowest, and the crowding degree is infinite. The fast non-dominated sorting process of $A1$ is as follows: calculate two parameters N_x and S_x for each X in $A1$ matrix, where N_x is the number of individuals dominating X in $A1$, and S_x is the number of individuals dominating X in $A1$. The dominating mode is determined according to the Pareto dominating relation: for the components with the minimum multiple objectives, n target components $f_i(i = 1, \ldots, n)$ vector $f(\bar{x}) = (f_1(\bar{x}), f_2(\bar{x}), \ldots, f_n(\bar{x}))$, the solution set U in any given two decision variables $\bar{x}_u$ and $\bar{x}_v$:

(1)If and only if, for $\forall i \in 1, \ldots, n$, have $(f_i(\bar{x}_u)) < (f_i(\bar{x}_v))$, says $\bar{x}_u$ dominate$\bar{x}_v$.

(2)If and only if, for $\forall i \in 1, \ldots, n$, $f_i(\bar{x}_u) \leq f_i(\bar{x}_v)$, and there are at least one $j \in 1, \ldots, n$, make $f_j(\bar{x}_u) < f_j(\bar{x}_v)$, says $\bar{x}_u$ weakly dominant $\bar{x}_v$.

(3)If and only if, for $\forall i \in 1, \ldots, n$, and at the same time $\exists j \in 1, \ldots, n$, make $f_j(\bar{x}_u) > f_j(\bar{x}_u)$, says $\bar{x}_u$ with $\bar{x}_v$ mutually.

The population $A1$ was graded according to the above dominance relationship: (1) Find all the individuals with n_x=0 in the population and store them in set $F1$. (2) For each individual I in the current $F1$, the dominated individual set is S_i, traversal each individual l in S_i and execute $N_L = N_{L-1}$. If $N_L = 0$, the individual l will be saved in set H. (3) The individual in $F1$ is considered as the non-dominant individual at the first level, and H is taken as the current set. The above operation is repeated to complete the grading of $A1$.

Congestion degree calculation: Controlling the uniform distribution of matched pixel pairs through congestion degree is conducive to improving the accuracy of the algorithm. Crowding is the density of individuals around an individual in a population. In this method, the distribution density n_d of the finger matching pixel pairs. The calculation steps are as follows:

(1) Let $n_d = 0$, $n \in 1, \ldots n$.

(2) Perform for each objective function: The individuals of this level are sorted according to the objective function, and f_m^{max} is the maximum value of the individual objective function, and f_m^{min} is the minimum value of the individual objective function.

(3)Calculate $n_d = n_d + (f_m(i+1) - f_m(i-1))/(f_m^{max} - f_m^{min})$, including $f_m(i+1)$ is the individual sorted after an objective function values. The crowding value is obtained.

And then combine $A1$ and $A2$. In this way, all operations of population initialization are completed, the population is stratified and the crowding degree is calculated.

3.2. **Fitness function and termination conditions.** Evolutionary algorithm requires setting an index to measure the merits and demerits of individuals in order to search for the best. In this method, the number of sequence layers and the crowding degree of the sequence layer obtained by fast non-dominant sequencing were used to measure the individual's quality. It is worth noting that the original fast non-dominant sequencing is improved, and the chromosomes with matching feature number less than 8 are placed in the last layer of Pareto dominance relationship. Chromosomes with less than 8 feature spots are considered to be the worst chromosomes. Specifically, for any chromosome, an estimation model of the fundamental matrix can be determined by using the 8 pairs of feature points contained in the chromosome. Through this model, the distance d from any given feature point to the corresponding polar line can be further calculated, and the feature points whose d is less than the given threshold are defined as interior points. Note that in the N pairs of feature points, the number of interior points determined by the corresponding estimation model of a chromosome is N_m, then the interior point rate W of this chromosome can be defined as $W = N_m/N$. The fitness function of inner points can be defined according to the calculation process of W, and the second fitness function can be defined according to equation (10). Then two fitness functions were calculated for the population, and the fitness values were quickly sorted and the crowding degree calculated. According to the calculation results of fast non-dominated sequencing and crowding degree, the higher the number of chromosomes in the sequence layer and the lower the crowding degree value, the better the chromosome, which represents the more inner points, the smaller the mean distance to the opposite pole and the less the surrounding chromosome distribution.The coordinate value of the chromosome with the most internal points in the first layer is expressed by X_{gbest}.

In order to ensure the exhaustivity of the algorithm, the population evolution of QUATRE has a fixed number of iterations, $Gen = 10000 \times DN/P$, where NP is the size of the population and D is the dimension of each individual population. Gen can be defined according to the equation 6.

$$gen = \frac{log(1-p)}{log(1-w_{best}^{8})} \tag{6}$$

Where p is the pre-specified confidence (for example, $p = 99\%$), represents the probability that all 8 rows are randomly selected from the feature point set as interior points, and w_{best} is the interior point rate corresponding to X_{gbest}. If the current population algebra K/Gen, the algorithm will be terminated; otherwise, the iterative evolution of the population will continue according to the mutation, crossover, and selection operations described below.

3.3. **Evolutionary strategy.** According to the idea of species evolution, the process of population evolution involves individual changes. Through natural selection, good genes will be preserved and bad mutations eliminated. For the evolutionary algorithm, the current population algebra is K, and the above process is represented by mutation, crossover and selection operations on population $X(K)$ in order to generate a new generation of population $X(K+1)$. Among them, the mutation operation produces the mutation content, the crossover operation realizes the gene change, the selection operation represents the survival of the fittest.

3.3.1. *Variation operation.* Since chromosomes are determined by genes, according to the discussion in Section 3 about the higher the number of chromosomes in the sequence and the lower the crowding value, the better the chromosome is. It can be further derived that the chromosome with the higher the number of chromosomes in the sequence and the

lower the crowding value contains the more excellent genes. Different from the variation method used by QUATRE as shown in equation 1, the present method defines the mutant genes ($P'_{(i,1)}$, $P'_{(i,2)}$)($1 \leq I \leq N'$) as genes mainly from the top R layer chromosomes in $X(k)$, and A small number of genes from the bottom $N' - r$ layer chromosomes, with the total number of N'. The matrix A' composed by this method is shown in equation 7. In order to facilitate the subsequent crossover operation, D genes can be randomly selected from A' as A chromosome, and NP times can be carried out continuously (NP is the size of the population) to obtain the mutant population represented by $NP \times D$ matrix B as shown in equation 8.

$$A' = \begin{bmatrix} p'_{(1,1)} & p'_{(1,2)} \\ \vdots & \vdots \\ p'_{(i,1)} & p'_{(i,2)} \\ \vdots & \vdots \\ p'_{(N,1)} & p'_{(N,2)} \end{bmatrix} \tag{7}$$

$$B = \begin{bmatrix} x'_{(1,1)} & \cdots & x'_{(1,D)} \\ \vdots & \ddots & \vdots \\ x'_{(NP,1)} & \cdots & x'_{(NP,D)} \end{bmatrix} \tag{8}$$

3.3.2. *Cross operations.* The crossover operation is to realize the mutation of the population, which will be carried out in the form of quasi-affine transformation proposed by QUATRE. If the population generated by gene mutation in current population X is denoted as X', then X' should not only retain some genes of X, but also contain some mutant genes from B. The realization method is shown in Formula (3).

$$X' \mapsto M \bigotimes X + \overline{M} \bigotimes B \tag{9}$$

Which cross matrix M, $\bar{M}$ generated method and consistent mentioned in section 2.2, the operator */otimes* said to its left and right two multiplication matrix corresponding to the position of the element, the matrix B, M, X and X' with the same number of columns, M any position in the 0/1 element specifies the X' the corresponding position of the corresponding location of genes from X/B. Since the distribution of the 0/1 element is random, the mutations are also random.

3.3.3. *Select operation.* The elite policy of NSGA-II is introduced in the selection operation. In this way, the new population has higher adaptability to the two objective functions and more reasonable chromosome distribution. Here are the steps:
(1) K is the algebra of the current population X, the mutant population is X'. First, merge X' and X. Then, the crowding degree of the combined population was calculated, and the whole layer population was placed into the parent population in order of Pareto rank from low to high, until the individuals in the layer could not all be placed into the parent population.
(2) Arrange the individuals in this layer from large to small according to the crowding degree, and place them into the parent population successively until the parent population is filled, so as to get a new selection population.

This completes the selection operation. Among them, the comparison method of chromosome pros and cons is still realized based on the number of sequencing layers and the crowding degree of each layer as described in Section 3.2. After the iteration is stopped, it is necessary to find out the 8 pairs of matching feature points that are used to calculate

the average polar distance from the population after the last selection, that is, the optimal chromosome. This method adopts the chromosome with the smallest average polar distance in the first layer of the population after the last selection as the final output.

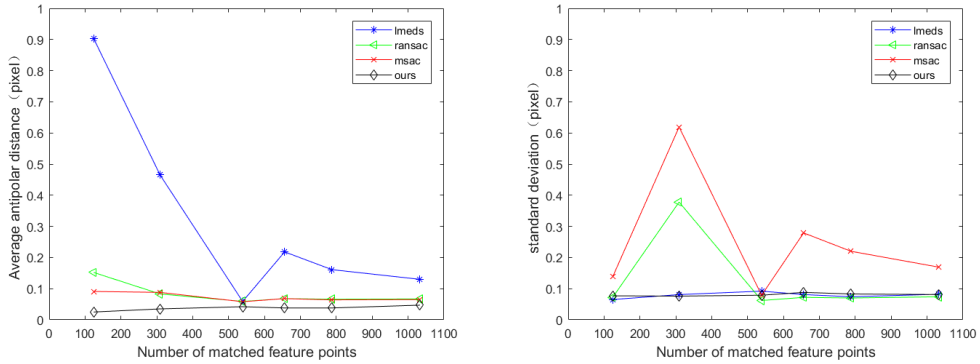
4. **Experiment.** This section will explain and analyze the experiments and results carried out to illustrate the accuracy and efficiency of the method. The experimental data are 30 scenes and a total of 60 pictures (resolution: 1440 × 1080) taken with Xiaomi Mix 2S. All experiments were run on a laptop computer with Intel dual-core i5 processor (2.5GHz) and 16GB memory, and the programming environment was MATLAB R2017A. In order to facilitate presentation, 6 SURF feature points were selected from 30 scenes to pair with typical scenes of different scales, and their numbers were numbered as shown in Table 1.

Firstly, the method is applied to the collected input data, and the fudamental matrix represented by each scene is estimated to test the feasibility of the method. Figure 2 shows the results of Scene 6 and Scene 4 respectively, where line segments are used to connect the matching feature points in the two images. The upper part is the result obtained by using SURF operator, and the lower part is all the interior points determined by the fudamental matrix estimation model based on SURF feature point pairs obtained by using this method. It can be seen that this method can effectively eliminate the mismatched points in SURF matching feature point pairs for solving problems of different scales.

Table 1. Sample data

Picture1	Picture2	The number of matched feature points	After eliminating matched points
252	230	124	98
531	496	309	274
762	706	539	460
1151	1036	656	588
1623	1468	788	713
1663	1551	1033	896

Figure 2. The result of our method applying to scene of No.6 (left) and No.4 (right)



(a) (b)

FIGURE 3. Average antipolar distance (a) and standard deviation (b)

In terms of the overall performance, the proposed method is significantly superior to the other three algorithms in terms of the average distance between poles. In terms of standard deviation, it is comparable to LMEDS, and superior to RANSAC and MASC. Therefore, this method has obvious advantages over the contrast method in terms of accuracy. As can be seen from the longitudinal comparison of different scenes, this method shows better applicability in scenes with more feature points. However, the more feature points, the more time overhead of the algorithm will be. Therefore, the experimental comparison will be made from the efficiency of the algorithm.

5. **Main Results.** in order to evaluate the accuracy of the algorithm, a comparative experiment will be carried out on the polar distance d as described in Formula (4).

$$d = \frac{1}{2}\left(\sqrt{\frac{(p'^T F p)^2}{(FP)_1^2 + (FP)_2^2}} + \sqrt{\frac{(p^T F p')^2}{(F^T P')_1^2 + (F^T P')_2^2}}\right) \tag{10}$$

Where F is the fudamental matrix obtained through the evaluation method, P and P' are the two points of the feature point pair respectively, and (*)1 and (*)2 represent the first and second components of the vector * respectively.

5.1. **Accuracy comparison and analysis.** Using the mean oppose-pole distance and standard deviation as measurement indexes, comparative experiments can be carried out on LMEDS, RANSAC, MSAC and this method. Specifically, each algorithm will be run 100 times in all experimental scenarios, and each time equation 10 will be applied to all interior points determined by the algorithm, and the results will be averaged. Figure 3 shows the experimental results of each algorithm in Scenes 1 to 6. The horizontal axis of the left figure represents the 4 algorithms and the 6 scenarios applied (from left to right, Scenes 1 to 6), and the vertical axis represents the average polar distance. The horizontal axis of the right figure is the number of SURF feature points of each scene (Scene 1 to Scene 6 from left to right), and the vertical axis is the standard deviation.

5.2. **Efficiency comparison and analysis.** In addition to accuracy, the algorithm can also be evaluated from the aspect of running efficiency. The average running time of the above algorithms in the comparative experiment described in Section 4 was recorded, as shown in Fig. 4. In the figure, the horizontal axis represents the four algorithms and the six scenarios applied (Scene 1 to Scene 6 from left to right), and the vertical axis represents the average running time (unit seconds). It can be seen that the operation efficiency of this method still takes less time when the number of feature point matches

gradually increases. With the increase of the problem size (i.e. the number of feature point pairs), the proposed algorithm can converge to the optimal solution faster than other algorithms due to particle swarm cooperation.

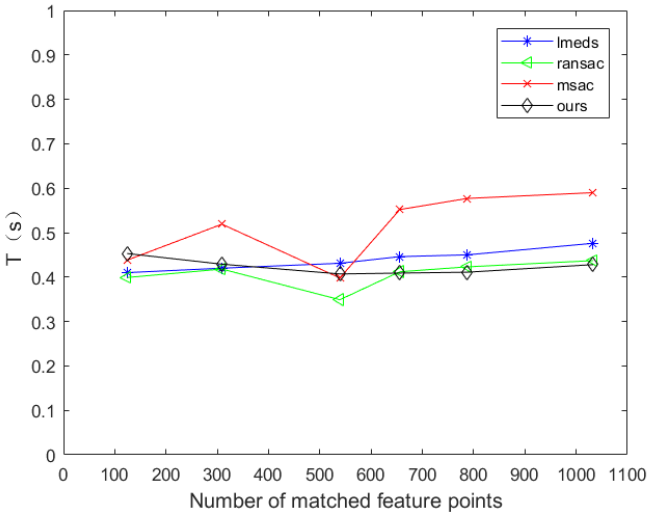


FIGURE 4. Running time of the experiment

6. **Conclusions.** In this paper, we propose an improved estimation method for the fudamental matrix of quasi affine transformation, which combines the optimization ability of particle swarm optimization and the advantage of QUATRE algorithm to solve combinatorial problems to estimate the fudamental matrix. To be specific, firstly, a population cooperation method based on a specific gene-chromosome pattern is proposed for fudamental matrix estimation. Secondly, the methods of population initialization, mutation and crossover in the discrete solution space represented by the homogeneous coordinate system are redefined, which makes it possible to use the framework of QUATRE algorithm to solve the problem of fudamental matrix estimation. In addition, a confidence - based method to determine the number of iterations is proposed to accelerate the algorithm. Compared with the traditional method, the proposed method can effectively eliminate the noise and the outer point interference caused by mismatching, and has the advantages of fast optimization and solution. Experimental results show that this method is superior to the current mainstream estimation methods in accuracy. In terms of efficiency, it is better than other algorithms after the number of feature points gradually increases. In general, the proposed method shows good performance after combining the advantages of NSGA-II multi-objective optimization and QUATRE algorithm to solve combinatorial problems.

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