Homography Matrix Genetic Consensus Estimation Algorithm[1]

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Abstract

Homography matrix plays an important role in image stitching, camera calibration and other areas of computer vision. This paper presents a novel robust algorithm HM-GCE to estimate homography matrix with principles of genetic algorithm. Related experiments prove its superiority on the robustness, precision and time-consuming compared to the RANSAC algorithm.

1. Introduction

Homography shows the reversible homogeneous transformations between two planes. It is widely used in visual measurement, camera calibration, image stitching and other fields of computer vision. Currently there are mainly three categories of algorithms on the estimation of the homography matrix: 1) Linear estimation methods [1, 2]. Such method is based on minimizing the algebraic distance, with the advantages of simplicity and rapidity, but worse robustness. When there are mismatches, the results of linear estimation is instable; 2) Nonlinear iterative method[3]. Such method is based on minimizing the geometric distance. These methods just execute the iterative optimization on the results of linear estimation, hence it has higher accuracy than liner algorithm does. However ,it does not apply to the situations with mismatches either; 3) Robust estimation methods[4, 5, 6, 7]. Such methods are based on the geometric consistency of the correct matches, that is to meet with the same homography. These methods can also give a satisfactory estimation even when there are numerous mismatches.

Hartley proposed the normalized linear method, to improve the stability of the numerical calculation [1]. Its performance can even be on a par with some common non-linear methods, but still unable to deal with the existence of mismatches. Fischler and Bolles proposed the classical robust estimation algorithm *RANSAC*[4]. *RANSAC* can cope with the situation with numerous mismatches, but it is extremely time-consuming when the ratio of correct matches is small. According to the idea of random sample, many robust algorithms have derived from *RANSAC*, such as *MINPRAN*[5] and *MLESAC*[6]. *MLESAC* algorithm is to maximize the likelihood function characterizing estimation accuracy while *RANSAC* algorithm is to maximize the number of interior point. *MINPRAN* algorithm improves *MLESAC* algorithm by introducing a Bayesian probability, making the estimation is more robust for position error and mismatches. However, *MLESAC* algorithm and *MINPRAN* algorithm did not have significant improvement in the time-consuming. *LMedS*[7] can automatically set the threshold to find out inliers, but it is unable to work when the ratio of mismatches exceed 50%.

This paper presents a novel robust algorithm named Homography Matrix Genetic Consensus Estimation (*HM-GCE*) to do the estimation and prove its superiority on the robustness, time-consuming and accuracy compared to the *RANSAC* algorithm by experiments.

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2. Homography Matrix Genetic Consensus Estimation

Given N point-pairs $\mathbf{x}_i \sim \mathbf{x}_i'$ as the initial point-pair set A in two images, homography estimation is to find out a 3×3 continuous real matrix which has the maximum inliers. Because there are outliers in practice, so the linear and nonlinear iterative methods will not work. If the genetic algorithm is directly applied to the homography estimation, we can not effectively define the crossover and mutation operators in a continuous 3×3 real matrix space. Therefore, this article, in a different point of view, treat four nonsingular point-pairs as a individual in the population, based on the fact that four nonsingular point-pairs solely determines a homography matrix. So each individual determine a solution of homography estimation and arbitrary four nonsingular point-pairs in the initial point-pair set A constitutes the solution space of homography estimation. After this treatment the solution space switches from a continuous space to a discrete space, and the size of the solution space changes from infinity to not larger than C_N^4.

Thus each solution composed by four nonsingular point-pairs corresponds to a individual in population, then it will become easy to implement crossover and mutation operators. This article introduces four definitions: Related Individual, Non-related Individual, Related Solution and Non-related Solution. Related Individuals are composed by four correct matches. Solutions specified by Related Individuals are Related Solutions. There exists at least one mismatch in Non-related Individual. Non-related Solutions correspond to Non-related Individual.

Flow chart of proposed *HM-GCE* algorithm is shown in Fig.1. The structure of *HM-GCE* is as follows, combining the general operation process of genetic algorithm summarized by *Goldberg*[8]:

1. Initialization. Determine the population size P and subgroup size $p(1 \leq p \leq 20)$; Set the number of generations $G=\infty$; Randomly generate the initial population with composition (P, Q).
2. Individual evaluation. Calculate the fitness of each individual.
3. Population Evolution
   a) Subgroup Partition. Evenly and Randomly divide the population into $n=P/p$ subgroups.
   b) Selection Operator (parent generation). Select 2 parent individuals with greatest fitness from each subgroup.
   c) Crossover Operator. Randomly exchange point-pairs between the 2 parent individuals to

produce 4 intermediate individuals in each subgroup.
   d) Mutation Operator. Implement 5 kinds of mutation on each intermediate individual to generate 20 candidate individuals in each subgroup.
   e) Selection Operator (offspring). Select P individuals from all candidate individuals to constitute the new population.
4. Termination Test. Update G. If G evolutions has been finished, then output the optimal individual of all generations, which has the largest fitness, otherwise transfer to Step 3
5. Refine. Perform the normalized *DLT* and *Levenberg-Marquardt* algorithm on the inliers of the optimal individual to obtain the final homgraphy estimation.
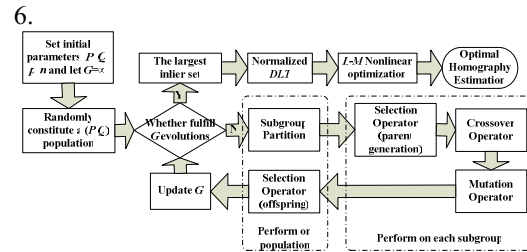6.

Fig.1. Flow Chart of HM-GCE

2.1. Initial Population

Initial population is the basis of population evolution, and the number of related individuals in initial population affects the time-consuming of population evolution to a large extent. Therefore, the introduction of related individuals tothe initial population is of particular importance in improving the efficiency of the algorithm. As the mismatches can be seen as random matches, non-related solutions corresponding to non-related individuals can be seen as random matrixes. Usually the number of inliers corresponding to non-related individuals is much smaller than that corresponding to related individuals. Based on this fact, this article treats a randomly generated individual with more than threshold T_{in} inliers as a related individual. If there are Q related individuals in the population, then the composition of population can be denoted by (P, Q).

2.2. Initial Population

When given a population with (P, Q) constitution, this paper divides it into $n=P/p$ subgroups evenly and randomly. Each subgroup has p individuals. Denote the k_{th} individual in the j_{th} subgroup by $S_{jk}(1 \leq j \leq n,\ 1 \leq k \leq p)$.

2.3. Determination of Fitness

For each individual S_{jk} is composed by four nonsingular point-pairs, we can obtain the corresponding homography matrix H_{jk} through Hartley's normalized linear method[1]. Then we take the number of inliers of H_{jk} as the fitness of individual S_{jk}.

In order to judge whether a point-pair $\mathbf{x}_i \sim \mathbf{x}_i$ is the inlier of homography H_{jk}, we calculate the symmetric Transfer error D_{ijk} as the following formula (1):

$$D_{ijk} = \left\| \mathbf{x}_i' - H_{jk}\mathbf{x}_i \right\|^2 + \left\| \mathbf{x}_i - H_{jk}^{-1}\mathbf{x}_i' \right\|^2 \quad (1)$$

If the symmetric transfer error of D_{ijk} is less than a given threshold Thr, the i_{th} point-pair is considered as the inlier of H_{jk}. Counting up the number of inliers of H_{jk} ,we can get the fitness of individual S_{jk} .

2.4. Selection Operator (parent generation)

In the genetic algorithm, selection operator reflects the thought of "survival of the fittest" in biological evolution. Its purpose is to make the next generation inherit individuals with great fitness.

This article simplifies the selection operator by independently preserving the two individuals with greatest fitness in each subgroup. Here we denote the preserved individuals as S_{j1} and S_{j2} ($1 \leq j \leq n$). After selection operator, the total number of individuals of population changes from pn to $2n$.

2.5. Crossover Operator

In the genetic algorithm, crossover operator plays a very important role in maintaining the population diversity, avoiding a premature convergence to local optimal solution.

Crossover operator in genetic algorithms is achieved through the exchange of individual genes. In the issue of estimating the homography matrix, the individual S_{jk} is formed by four nonsingular point-pairs. So each point-pair is the individual's gene, and we can directly exchange point-pairs of individuals to achieve the crossover operator.

After selection operator(parent generation), each subgroup only remains two individuals S_{j1} and S_{j2}, which respectively contains four point-pairs. This article first generates a random integer q in the interval [1, 3], then randomly exchanges q point-pairs between the individuals S_{j1} and S_{j2}, forming two new individuals denoted by S_{j3} and S_{j4}. Here we preserve all individuals including S_{j1}, S_{j2}, S_{j3} and S_{j4}. So the total number of individuals of population increases from 2n to 4n after crossover operator. Now we denote the m_{th} individual in the j_{th} subgroup by S_{jm} ($1 \leq j \leq n$, $1 \leq m \leq 4$).

2.6. Mutation Operator

From the implementation of crossover operator, we can see that there is only a mutual exchange of point-pairs between individuals. However under some particular situation two individuals S_{j1} and S_{j2} can not form individuals with better performance after exchanging genes. For example, when two individuals are formed by four mismatches, the new individuals S_{j3} and S_{j4} are still composed by mismatches no matter how to exchange point-pairs of individuals S_{j1} and S_{j2}. Obviously it will not be able to provide a accuracy estimation of homography. But mutation operator can cope with this situation here.

In accordance with the thoughts of the mutation operator in the genetic algorithm, we can generate a random integer g between interval [1, 4], and then randomly replace g point-pairs of each preserved individual S_{jm} in population with any other g point-pairs of the initial point-pair set A. However, such a mutation is blind. Since each individual corresponds to a estimation of homography matrix, and it divides all point-pairs into inliers and outliers. Here, we should observe several cases: when some genes of the individual S_{jm} are mismatches, the correctly matched point-pairs exist in both inliers and outliers after division of this individual S_{jm}; when four genes of the individual S_{jm} are all correct matches, the inliers are all correct matches. Still there may be correct matches in the outliers. For these point-pairs, their symmetric transfer error related to S_{jm} specified by formula (1) exceed the threshold Thr , but their symmetric transfer error related to another individual S_{xy} ($x \neq j$ and $y \neq m$) may be below the threshold. Thus, when conducting the mutation operator we should take into account correct matches in both inliers and outliers. This article implements mutation operator by randomly selecting w point-pairs and $4-w$ point-pairs from the inliers and outliers respectively to form the mutated individual. Denote this mutation configuration by (w, $4-w$), where the integer m belongs to interval [0, 4]. So there are five kinds of mutation according to different values of w. After mutation operator, the total number of individuals in the population transforms from of $4n$ to $20n$.

2.7. Selection Operator (offspring)

Through all above operators, we can see that the number of individuals leaps from the initial *pn* to *20n*. To proceed to the next round of genetic consensus estimation, we should maintain the population size *pn*, so we select *pn* individuals with greatest fitness from *20n* individuals as the population of the new generation.

2.8. Determining the number of generations

Try to set the number of generations *G* extremely large to make all the C_N^4 individuals in the solution space appear in the offspring, it is computationally neither infeasible nor necessary. In fact, the number of generations *G* just needs to ensure the appearance probability *C* of a individual composed of four correct matches be large enough. *C* is usually taken as 0.99. Assuming *μ* as the proportion of the correct matches in the initial point-pair set *A*, and the *4pn* point-pairs of the *pn* (*P=pn*) individuals are selected independently, then the number of generations *G* should satisfy the following formula (2):

$$\left(1-\mu^4\right)^{PG}=1-C \qquad (2)$$

Thus, the genetic algebra can be determined by the following formula (3):

$$G = \frac{\log\left(1-C\right)}{P\cdot\log\left(1-\mu^4\right)} \qquad (3)$$

However, the ratio *μ* of the correct matches in the above formula is usually unknown, but when the population size *P* and the probability *C* is confirmed, the number of generations *G* will decrease along with the accretion of the ratio *μ*. Therefore, this article begins from the worst case *μ=0* and *G=∞*. During the process of evolution, record the proportion ρ of inliers of each generation's optimal individual. If ρ is greater than *μ*, set *μ=ρ*, and recalculate *G* by formula (3). Upon completion of *G* generations' evolutions, the algorithm terminates and output the optimal individual of all generations witch has maximum inliers. These inliers are all correct matches if the number of correct matches in the initial point-pair set *A* is large enough. With these inliers, we can perform normalized *DLT* estimation[1] and then execute *Levenberg-Marquardt* nonlinear iterative optimization[3] to obtain the ultimate estimation of homography matrix.

3. Experimental Results

To fully compare *HM-GCE* with *RANSAC*, we use the '2005 datasets' [9] which can be obtained from http://vision.middlebury.edu/stereo/data/.We select the

image from Art datasets and generate a new image by the following ground truth homography matrix $H_†$.

$$H_† = \begin{pmatrix} 0.9848 & -0.1736 & 106.9333 \\ 0.1736 & 0.9848 & -112.2538 \\ 0 & 0 & 1 \end{pmatrix}$$

We first introduce 100 correct matches to the two images through the *SIFT* algorithm[10]. By introducing different numbers of random mismatches to form the different ratios of correct matches, we then compare the performance of *HM-GCE* algorithm and *RANGSAC* algorithm on condition that correct matches are added zero-mean Gaussian white noise with standard deviation *SD*=0,1,2 respectively.

The *SIFT* template in use is provided by the scholar *David Lowe* of the University of British Columbia. It can be obtained from http:// people. cs. ubc. ca/~mbrown. The *RANSAC* algorithm used in the experiment belongs to the template provided by the senior lecturer *Peter Koves* of the University of Western Australia[11].

Fig.2(a)、Fig.3(a) and Fig.4(a) show that *HM-GCE* is more robust than *RANSAC* because *HM-GCE* can detect more inliers at each ratio of correct matches. Fig.2(b)、Fig.3(b) and Fig.4(b) show that elapsed time of *HM-GCE* is slightly greater than that of *RANSAC* at large ratios of correct matches .However at low ratios of correct matches, *HM-GCE* takes much less time than *RANSAC* does. Fig.2(c)、Fig.3(c) and Fig.4(c) show that *HM-GCE* is more accurate than RANSAC because *HM-GCE* has lower estimation error at each ratio of correct matches. The estimation error is defined by $\|H_{est}- H_†\|_F$ in Frobenius norm where $H_†$ is the ground truth homography matrix and H_{est} is the estimation of homography matrix.
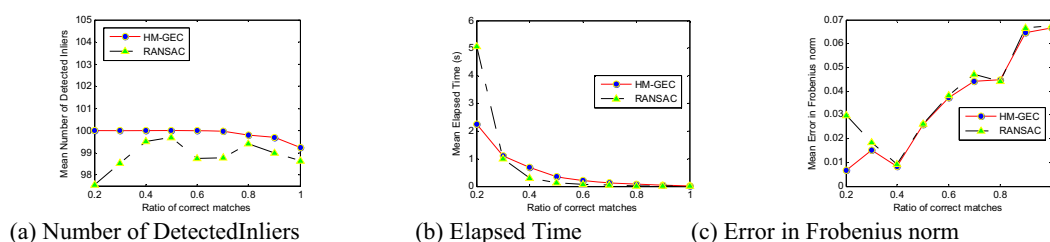
4. Conclusion

In this paper, we introduce the genetic consensus estimation algorithm to the estimation of homography matrix, and design the corresponding selection operator, crossover operator and mutation operator according to the particularity of the homography estimation. In this way ,the *HM-GCE* algorithm can not only retain the efficiency produced by the parallel search of genetic algorithm but also make it easy to implement through making the solution space of homography matrix discrete. The results of realated experiments in the paper also proved that *HM-GCE* algorithm has stronger robustness and less time-consuming than *RANSAC* algorithm dose in the homography estimation.
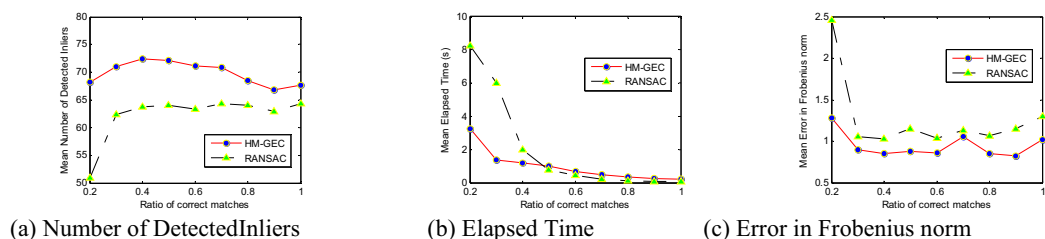
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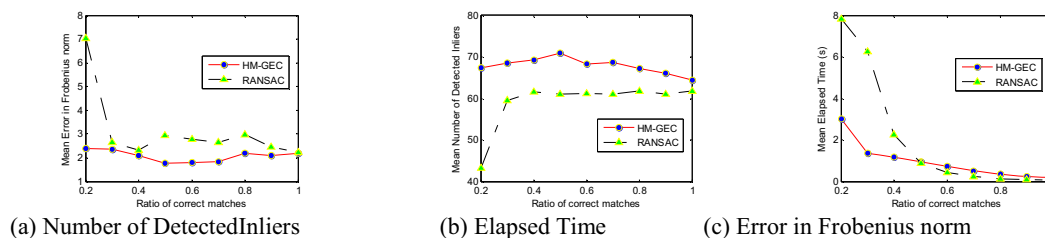
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(a) Number of DetectedInliers   (b) Elapsed Time   (c) Error in Frobenius norm

Fig. 2. Results of homography estimation by HM-GCE and RANSAC with SD=0.

(a) Number of DetectedInliers   (b) Elapsed Time   (c) Error in Frobenius norm

Fig. 3. Results of homography estimation by HM-GCE and RANSAC with SD=1.

(a) Number of DetectedInliers   (b) Elapsed Time   (c) Error in Frobenius norm

Fig. 4. Results of homography estimation by HM-GCE and RANSAC with SD=2.