

A REMOTE SENSING IMAGE MATCHING METHOD COMBINING GENETIC ALGORITHM WITH LEAST SQUARE MATCHING

Xing Hua XIONG* Zeng Bo QIAN** Ren Xiang WANG*

* Dept. of Photogrammetry & Remote Sensing
Xi'an Research Institute of Surveying & Mapping
No.1 Mid-Yanta Road, Xi'an,
P. R. China, 710054

** Dept. of Information Engineering
Zhengzhou Institute of Surveying & Mapping
No.66 Mid-Longhai Road, Zhengzhou,
P. R. China, 450052

KEY WORDS: Remote Sensing, Image Matching, Genetic Algorithm, Least Square Matching.

ABSTRACT

Image matching is an important task in digital photogrammetry. In the paper, an approach to remote sensing image matching combining genetic algorithm(GA) with least square matching(LSM) is presented to speed up image matching and provide a robust reliable and rather accurate initial value for high-precision subpixel matching. The experiment show that the matching method based on GA is much faster than those based on Sequential Similarity Detection Algorithm(SSDA) and classical Mean Absolute Difference(MAD). Taking our experiment data as an example, the rate of the sum of correlation calculation of MAD to that of GA is at least 34:1, this is to say, the speed of the later is thirty-four times faster than that of the former theoretically.

1 INTRODUCTION

Image matching is an important task in digital photogrammetry. Just as the accuracy and the reliability can determine the performance of image matching, the speed is also a crucial factor in image matching. The two methods are often adopted to decrease the sum of calculation and accelerate image matching. One is to reduce the sum of correlation computation at a lot of non-matched points, such as SSDA. The other is to improve a search strategy to avoid unnecessary calculation, such as Multiresolution Pyramid Structure algorithm (MPSA). A great deal of investigation shows the speed of image matching algorithms mainly depends upon their search strategy. However, the search strategies of MAD and SSDA are both ergodic ones, a lot of time is taken to calculate the correlation values at the non-matching points in order to find the optimal matching point. Therefore, image matching will be greatly increased if the above vain operation is avoided as much as possible. Unfortunately, it is difficult to attain this goal by only using the existing ergodic search strategy without developing new one.

Genetic algorithms (GAs) [J. H. Holland(1975)] are a class of robust parallel adaptive heuristic search/optimization technique based on the Darwin's *Theory of Natural Selection* (better known as *the survival of the fittest*). It can find the near-global optimal solution in a large solution space quickly, and relatively unaffected by the presence of spurious local optima in the solution space. Because of their ability to perform effective search, GAs have been extensively used in many different disciplines[S. M. Bhandarkar (1994), T. Bäck et al(1993), D. Dasgupte and Z. Michalewicz(1997)].

In this paper, we have presented an approach to remote sensing image matching combining GA with LSM. Firstly, the relative accurate matching result is obtained by using genetic algorithm quickly. On the basis of the result above, subpixel location is then acquired by using LSM. The reasons presenting this method are as follows. On the one hand, comparison with MAD and SSDA, genetic algorithms can find near-global optimal solution quickly and robustly by only using a few population and generation; On the other hand, it is true that LSM is an accepted subpixel matching algorithm, but it has to be built upon a reliable initial value satisfying certain precision (not more than 2~3 pixel commonly).

The paper is organized as follows: the next section briefly introduces the basic principle and characteristics of genetic algorithms. The third section describes our proposed image matching method combining GA with LSM. The fourth section reports and compares the results obtained by our approach, a classical SSDA and MAD respectively. The final section concludes the paper and suggests future research directions.

2 GENETIC ALGORITHMS

In order for readers to understand our proposed matching algorithm, the basic principle and characteristics of genetic algorithms will be briefly described in the section. Good tutorials on the subject may be found in [D. E. Goldberg(1989)].

GAs employ a random, yet directed, search for locating the globally optimal solution. They are superior to 'gradient descent' techniques, as the search is not biased towards the locally optimal solution. On the other hand, they differ considerably from random sampling algorithms due to their ability to direct the search towards relatively 'prospective' regions in the search space[M. Srinivas et al (1994)]. In a word, genetic algorithms are a class of intelligent search techniques radically different from classical ones. The differences are based on four principles [D. E. Goldberg(1989)]:

- GAs use a coded representation of the parameters, not the parameters themselves.
- GAs search from a population of solution vectors, not a single solution vector.
- GAs exclusively use values of the function under study, and do not consider auxiliary information, such as the derivative.
- GAs use probabilistic transition rules, not deterministic rules.

The key components of genetic algorithms are mainly as follows:

1, ENCODE. One of the keys to genetic algorithm is how to encode each solution(a set of parameters) of a specific problem. In genetic algorithm, These solutions(i.e. individuals) are usually encoded as binary string(called chromosome). A collection of these chromosomes forms a population.

2, FITNESS FUNCTION. The other of keys to genetic algorithm is how to determine fitness function that evaluates the optimality of each chromosome. The goodness of chromosomes is fully determined according to their fitness function value.

3, GENETIC OPERATORS. The main genetic operators are selection, crossover and mutation. The selection only depends upon the fitness value of each chromosome. The higher the fitness value is, the better the performance of chromosome is, and the more the chance of chromosome to be reproduced to the next generation there will be, vice versa. Selection embodies the principle of '*the survival of the fittest*'. The commonly used selection strategies are a roulette wheel selection, a ranking selection and tournament selection. Though reproduction can generate a new population, it can not generate a new individual. Like the evolution of nature, in order to generate a new evolutionary individual, genetic algorithm must also depend on crossover and mutation operators. The crossover operator is an indispensable one in genetic algorithm and the probability of applying crossover is very high generally. The action of this operator is to exchange information between a pair of 'parent' chromosomes selected randomly in terms of the predefined probability of crossover and to generate two 'offspring' chromosomes for the next population. The offspring chromosomes are different from their parents, but they inherit some of their parents' properties to a certain extent. Mutation is to perform random alternation on allele(a value of gene) by some operators, such as bit flip and inversion. Mutation can extend the scope of the solution space and reduce the possibility of falling into local extremes. Contrary to crossover operator, the probability of applying mutation is very low commonly, otherwise, genetic algorithm will degrade into purely random search approach.

4, CONTROL PARAMETER. The control parameters mainly consist of the size of population, the maximum number of generations, the probabilities of crossover and mutation, and the other auxiliary parameters.

5, TERMINATING CRITERION. The convergence speed of genetic algorithm is very slow during the late phases of evolution. Therefore, it is necessary to design a terminating criterion for genetic algorithm generally. There exists no general stopping criterion, the following two ones are usually employed: 1) predefine the maximum number of iterations, and 2) stop if no further improvement in the fitness function value of the best individual is observed for a

certain number of iteration.

A simple structure of genetic algorithm is shown in Figure 1[Z. Michalewicz et al(1997)].

```

Begin
  t ← 0;
  initialize P(t);
  evaluate P(t);
  while(not termination-condition) do
  begin
    t ← t+1;
    select P(t) from P(t-1);
    alter P(t);
    evaluate P(t);
  end
End

```

Fig. 1: The structure of an genetic algorithm

3 THE PROPOSED APPROACH TO IMAGE MATCHING BASED ON GAs and LSM

Our proposed optimization approach to remote sensing image matching consists of the following three steps: (a) Image preprocessing, (b) The relatively accurate initial values that LSM need are obtained by using matching algorithm based on genetic algorithm, and (c) on the basis of the results above, the subpixel location is acquired by using LSM.

3.1 Image Preprocessing

Image preprocessing mainly contains filtering the noise of image itself and adjusting the density differences between matched image and basic image causing the dissimilar imaging conditions, as each of them can make a disadvantageous influence to the performance of image matching. There are many lowpass filtering ways to remove the noise of image itself, a simplest mean value filter is adopted in our method. The approach to adjust the density differences between matched image and basic image is stated as follows.

Let f , m_f , s_f denote the density, mean density and standard deviation of basic image respectively, while g , m_g , s_g represent the density, mean density and standard deviation of matched image respectively. Then the normalization density, f' , g' , are respectively:

$$f' = \frac{f - m_f}{s_f} \quad g' = \frac{g - m_g}{s_g} \quad (1)$$

3.2 The Coarse Matching Method Based on GAs

As mentioned above, the keys to genetic algorithm are how to encode specific solution and to determine fitness function that evaluates the optimality of each solution.

Considering the disadvantage of direct binary coding, i.e. there is a greater Hamming distance between consecutive integers(such as 127 and 128) with this encoding strategy, the chromosomes in the population are represented by 16 bits Gray codes string, the first 8 bits of which correspond to the vertical coordinate i of the basic image while the rest correspond to the horizontal coordinate j in the paper. Gray coding is used because it can eliminates Hamming cliffs(the Gray codes of any consecutive integers differ by a single bit) [Keith E. Mathias et al(1994)]. A specified initial population consists of 40 optimal individuals chosen from many seeds in order to find near globally optimal solution with a few populations and generations as quickly as possible. The processes of determining seeds are as follows: 1) Dividing the basic image into many subareas at one quarter size of matching window; 2) Choosing a coordinate point as the seed within each subarea randomly; 3) Evaluating the performance of each seeds with the following fitness function

$fitness(i, j)$; and 4) Selecting the specified number of optimal seeds as initial populations in the whole seeds.

$$e(i, j) = \frac{1}{KL} \sum_{k=-K/2}^{K/2-1} \sum_{l=-L/2}^{L/2-1} \left| f'(i+k, j+l) - g'(k + \frac{K}{2}, l + \frac{L}{2}) \right| \quad (2)$$

$$fitness(i, j) = \left(\frac{1}{1 + e(i, j)} \right)^2 \quad (3)$$

where K and L are the dimensions of matching windows, i and j are the vertical and horizontal coordinates of the center of the matching window in the whole basic image respectively, the beginning point of coordinates lies on the upper left corner of the basic image.

During the population evolution, we have performed elitist and roulette wheel based selection strategies to select mates according to the relative fitness value of each chromosome. Elitist strategy ensures that the best individual in the current generation always survives into the next generation and prevents the inadvertent loss of the best chromosome due to stochastic roulette wheel selection. In the process of crossover and mutation, we have applied uniform crossover and bit flip mutation strategies respectively. The process of the uniform crossover is as follows. First, crossover mask with the same length as parents' is created randomly. Then, the pair of parents selected randomly are exchanged or unexchanged according to the allele of the mask in terms of the crossover probability. If the allele is '1' then exchange, otherwise, unexchange, as shown in Figure 2. Note that a new crossover mask must be randomly generated for each pair of parents. The bit flip mutation is a strategy flipping some allele of the chromosome determined according to the probability of mutation randomly to yield a new generation, as shown in the Figure 3.

| | | | | | | | | | | | | | | | | |
|--------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Parent 1: | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| Parent 2: | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| Mask: | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 1 |
| Offspring 1: | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 |
| Offspring 2: | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 |

Fig. 2: uniform crossover is illustrated.

| | | | | | | | | | | | | | | | | |
|------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Parent: | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 |
| Offspring: | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 |

Fig. 3: mutation is illustrated, positions where bits are flipped are chosen at random.

In order to find a near global optimal solution by using the limited populations and generations as quickly as possible, we assign the size of population, the maximum number of generation, the crossover rate and the initial mutation rate to be 40, 30, 0.95 and 0.02 respectively. In the course of mutation, we have adopted the following adaptive mutation strategy. After 5 successive generations, if no better chromosome can be found, the mutation rate should be increased by 5 times of initial value. After 10 successive generations, if still no better chromosome can be found, the mutation rate should be raised by 5 times of the initial value again. The mutation rate are returned to the initial value providing the optimal fitness value of offspring is improved. After consecutive fifteen generations, if this case is not improved yet, we assume that the best individual in the present population corresponds to an approximate global optimal solution.

3.3 The basic principle of LSM

LSM is an improved least distance correlation algorithm. To compensate for the geometrical and radiometric differences between the two correlation windows, the parameters of transformation have been directly introduced as the values to be determined into least square correlation computation. It is well known that LSM is an accepted high accuracy matching algorithm, but it needs very good initial value. According to experimental results, the accuracy of determination for conjugate points in this way may reach the order of $1mm$ (1/50 to 1/100 pixel) [Zhizhuo Wang (1990)].

Let $g'(x, y)$ and $g''(x, y)$ denote the densities of matched image and basic image respectively. They are composed of both ideal density function and noises. Namely:

$$g'(x, y) = g'(x', y') + n'(x', y') = g'(x'_0, y'_0) + n'(x', y') \quad (4)$$

$$g''(x, y) = g''(x'', y'') + n''(x'', y'') = g''(x''_0 + \Delta x'' + f''_x x''_0 + r''_x y''_0, y''_0 + \Delta y'' + f''_y y''_0 + r''_y x''_0) + n''(x'', y'') \quad (5)$$

where x'_0, y'_0, x''_0, y''_0 denote the initial coordinates of the matched image and the basic image; $\Delta x'', \Delta y''$ denote the increments of the pixel in the basic image; f''_x, f''_y denote the local scale factors of the basic image in x and y direction respectively; r''_x, r''_y denote the local rotation factor of the basic image in x and y direction respectively; Obviously, to obtain the optimal matching results, the below difference must be the least for each pixel.

$$n'(x', y') - n''(x'', y'') = g''(x''_0 + \Delta x'' + f''_x x''_0 + r''_x y''_0, y''_0 + \Delta y'' + f''_y y''_0 + r''_y x''_0) - g'(x'_0, y'_0) \quad (6)$$

This is the basic error equation of LSM, which can be simplified as follows:

$$V_g = AX - L \quad P_g \quad (7)$$

where $A_i = [S''_x \ S''_x x''_0 \ S''_x y''_0 \ S''_y \ S''_y y''_0 \ S''_y x''_0]$ is a column vector; S''_x, S''_y are gradient of the pixel of basic image in x and y direction respectively; $X = [dx'' \ df''_x \ dr''_x \ dy'' \ df''_y \ dr''_y]^T$ is the correction value vector; dx'', df''_x, dr''_x and dy'', df''_y, dr''_y are correction values of the shift, scaling and rotation coefficient of the pixel in basic image in x and y direction respectively; L is the observation value vector; P_g is the weight matrix of the observation value.

4 IMPLEMENTATION AND COMPARISON

In the course of the coarse matching, we have implemented an approach to image matching based on genetic algorithm on a Pentium III 450 compatible computer. To compare with the proposed approach, we have also implemented two classical MAD and SSDA methods respectively. A pair of aerial optical stereo images, the dimensions of which are 256×256 pixels, are used to evaluate the performance of these three methods. The sizes of matching windows are 36×36 pixels. The parts of the results obtained are shown in Figure 4. Table 1 lists the detailed coordinate values of the 1st and 2nd points obtained by using the above three methods, which contains the consecutive 10 results obtained with genetic algorithm.

From Table 1, the speed of genetic algorithm is obviously one order of magnitude faster than that of MAD or SSDA. This is because both MAD and SSDA are ergodic search method while genetic algorithm is a heuristic non-ergodic one. To be more specific, let $(M \times N)$, $(K \times L)$, S , G and P denote the sizes of the basic image and the matching windows, the numbers of initial seeds, generation and population respectively, while E stands for the number of the individuals generated repeatedly throughout the evolution. Then the total number of correlation computation (T_{MAD} and T_{GA}) of MAD and GAs methods are as follows respectively.

$$T_{MAD} = (M-K+1) \times (N-L+1) \quad (8)$$

$$T_{GA} = S + G \times P-E \quad (9)$$

As mentioned above, genetic algorithms depend upon not only the encoding strategy of solution and fitness function but also their control parameters to a considerable degree. So it is very difficult to obtain an accurate result with genetic algorithm. In general, only a near global optimal solution can be obtained due to limited control parameters. But from our experiments, we found that these approximate results can fully serve as the initial value LSM needs if the control parameters are properly chosen.

In the fine matching stage, on the basis of the above coarse matching results, LSM is implemented within the local search region, the center of which lies on the location given by the coarse matching. The range of local search region are 7×7 pixels, the sizes of matching windows are still 36×36 pixels. Finally, the center of the correlation windows with the minimum matching mean error is accepted as the fine matching location.



Figure 4. the parts of matching results.

| | 1 | | | | | | 2 | | | | | |
|----------------|-----|--------------|-------------|-------|------|----------|-----|--------------|--------------|-------|------|----------|
| | NG | X | Y | RN | RA | Time (s) | NG | X | Y | RN | RA | Time (s) |
| L_Coord | | 180 | 53 | | | | | 116 | 112 | | | |
| R_Coord | | 174 | 52 | | | | | 112 | 107 | | | |
| MAD | | 174 | 53 | 48841 | | 38.63 | | 112 | 107 | 48841 | | 37.63 |
| SSDA | | 174 | 53 | 48841 | | 28.30 | | 112 | 107 | 48841 | | 25.07 |
| GAs | 30 | 173 | 53 | 1274 | 38:1 | 1.26 | 30 | 113 | 107 | 1092 | 44:1 | 1.11 |
| | 28 | 174 | 53 | 1099 | 44:1 | 1.12 | 30 | 112 | 107 | 1160 | 42:1 | 1.15 |
| | 15 | 174 | 51 | 866 | 59:1 | 0.78 | 30 | 113 | 106 | 1019 | 47:1 | 1.00 |
| | 25 | 174 | 53 | 907 | 53:1 | 0.87 | 28 | 111 | 109 | 1101 | 44:1 | 1.10 |
| | 30 | 174 | 54 | 1322 | 36:1 | 1.32 | 18 | 113 | 106 | 831 | 58:1 | 0.80 |
| | 30 | 174 | 52 | 1317 | 37:1 | 1.39 | 26 | 112 | 107 | 1079 | 45:1 | 1.08 |
| | 23 | 175 | 53 | 1036 | 47:1 | 1.01 | 30 | 112 | 108 | 908 | 53:1 | 0.89 |
| | 30 | 174 | 52 | 1297 | 37:1 | 1.28 | 26 | 113 | 105 | 1172 | 41:1 | 1.16 |
| | 30 | 174 | 53 | 1152 | 42:1 | 1.14 | 30 | 112 | 107 | 1119 | 43:1 | 1.09 |
| 30 | 173 | 53 | 960 | 50:1 | 0.97 | 30 | 113 | 106 | 1237 | 39:1 | 1.24 | |
| LSM | | 174.4 | 52.4 | | | | | 112.1 | 106.6 | | | |

Table 1. The matching results. NG, L_Coord, R_Coord, and RN denote the number of evolution, the coordinate of the point within the matched image, the coordinate of the real point matching with L_Coord, and the sum of correlation computation respectively, while RA denotes the rate of the MAD to the GAs in the sum of correlation computation.

5 CONCLUDING REMARKS

In the paper, we have presented a fast image matching method combining GAs with LSM. The method makes full use of the characteristics of both GAs and LSM. The convergence of genetic algorithm is fast during the early evolution, and the result obtained can fully serve as the initial value LSM needs if the control parameters can be properly selected and adjusted. On the other hand, the accuracy of LSM is very high, but LSM needs a satisfactory initial value. To analyze the performance of genetic algorithm, we have also implemented two coarse matching methods based on canonical MAD and SSDA. It can be seen the experimental results obtained in this study that the speed of genetic algorithm is indeed much faster than that of either MAD or SSDA and the results are also satisfactory.

Genetic algorithm is a very young developing bionic technique, and it is also a very promising search/optimization technique acknowledged by many experts in different areas. People have been researching why genetic algorithm is useful and how it works during the past 20 years or more. Our work is only the beginning, and there must be many problems deserving of further investigation. For example, how to choose and adjust the control parameter of genetic algorithm to obtain more robust and reliable matching results? In some cases, a satisfactory result can not always be

obtained with only a few population and generation, as the quality of result depend greatly upon the control parameters of genetic algorithm in the circumstances.

REFERENCES

- J. H. Holland, 1975, *Adaptation in Nature and Artificial Systems*. The University of Michigan Press, Ann Arbor, MI, 1975.
- D. E. Goldberg, 1989, *Genetic Algorithms in Search, Optimization and Machine Learning*. Addison Wesley, Reading, Massachusetts.
- M. Srinivas, and L. M. Patnaik, 1994, Adaptive Probabilities of Crossover and Mutation in Genetic Algorithms. *IEEE Trans. on SMC*, Vol. 24, No. 4, April, 1994, pp. 656-666.
- T. Baeck F. Hoffmeister and H. P. Schwefel, 1993, *Application of Evolutionary Algorithms*. Technical Report No. SYS-2/92 of the Systems Analysis Research Group at the University of Dortmund, Department of Computer Science, 1993. <ftp://lumpi.informatik.uni-dortmund.de/pub/EA/paper/ea-app.ps.gz>
- D. Dasgupte and Z. Michalewicz Eds, 1997, *Evolutionary Algorithms in Engineering Applications*, Berlin: Springer, 1997.
- P. Andrey and P. Tarroux, 1994, Unsupervised Image Segmentation Using A Distributed Genetic Algorithm, *Pattern Recognition*, 27(5), 1994, pp. 659-673.
- S. M. Bhandarkar, Y. Q. Zhang and W. D. Potter, 1994, An Edge Detection Technique Using Genetic Algorithm-based Optimization. *Pattern Recognition*, 27(9), 1994, pp. 1159-1180.
- M. S. Shyu and J. J. Leou, 1998, A Genetic Algorithm Approach to Color Image Enhancement. *Pattern Recognition*, 31(7), 1998, pp. 871-880.
- K. Mathias and D. Whitley, 1994, Transforming the Search Space with Gray Coding. *Proc. of the 1st IEEE Int' l Conf. on Evolutionary Computation, ICEC' 94*, Orlando, Florida, USA, IEEE Press, 1994, pp: 513-518.
- Z. Michalewicz and M. Michalewicz, 1997, *Evolutionary Computation Techniques and Their Application*. In 1997 IEEE International Conference on Intelligent Processing Systems(ICIPS' 97), Oct. 28-31, 1997, Beijing, China, pp. 14-25.
- Zhizhuo Wang, 1990, *Principles of Photogrammetry (With Remote Sensing)*, Publishing House of Surveying and Mapping, Beijing, China, May 1990, 452-455.