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Performance Improvement of the RFM Estimation by Modifying the Initial Population in the Genetic based Optimization

Mojtaba Akhoundi Khezrabad[a*], Mohammad Javad Valadan Zoej[a], Alireza Safdarinezhad[b]

[a] *Faculty of Geodesy and Geomatics Engineering, K. N. Toosi University of Technology, Tehran, Iran.*

[b] *Department of Geodesy and Surveying Engineering, Tafresh University, Tafresh, Iran,.*

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Abstract

Rational Function Models (RFMs) are known as the most famous mathematical transformations used in geometric correction of satellite images. Considering the lack of enough and well-distributed Ground Control Points (GCPs), the structure optimization is a critical step in the terrain-dependent RFM estimation strategy. Heretofore, the binary encoding Genetic Algorithm (GA) optimization method has been used to find the optimal structure of RFMs. However, randomized generation of initial population can directly impact the convergence and also computational costs. In this paper, an approach has been proposed to modify the initial population of the GA algorithm based on the correlations of the column vectors of the least square design matrix. In this approach, probability of the presence of each RFM term in the GA initial population is linearly dependent on its correlation with other terms. Although this method slightly decreases the geometric accuracy, it can fall the processing time by 37.02% on average.

Keywords: Correlation of Column Vector, Genetic Algorithm, Georeferencing, Rational Function Models.

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[*] Corresponding author Tel: +98- 919 005 4956.
Email address: mojtaba.akhoundi@gmail.com.

1. Introduction

Nowadays satellite images are used in a variety of applications such as plants monitoring, updating maps and spatial databases, and so on. In order to extract spatial information from such images, it is necessary to establish a relationship between the image and ground spaces. In order to do this process which is called georeferencing, two general categories of parametric and non-parametric mathematical transformations are usually used. Parametric models are design in a way to be coincident with the imaging geometry. So, in order to use them, internal sensor parameters and raw images are required. However, non-parametric models are just the mathematical transformations that can potentially relate the ground and image spaces. They can be used without the knowledge of internal imaging mechanism and even applied to the resampled images.

Rational Function Models (RFMs) as a well-known non-parametric model are widely used in georeferencing satellite images (Sadeghian et al., 2001; Tao and Hu, 2001). These models are produced by dividing two 3D polynomials, can reach the same accuracies as the parametric models (Jannati and Valadan Zoej, 2015). Generally, RFM's coefficients can be estimated via two different terrain-dependent and terrain-independent strategies. Satellite image providers are usually using the terrain-independent strategy to estimate the RFM's coefficients through Simulated Ground Control Points (SGCPs) generated by sensor models (Fraser, Dial, and Grodecki, 2006). In this strategy, enough and well-distributed SGCPs have been available, and there are no worries about the over-parameterization and ill-posed condition problems. On the contrary, in the terrain-dependent strategy, lack of enough Ground Control Points (GCPs) imposes some computational problems during RFMs estimations. Term selection is known as an efficient approach to find the optimum RFM structure in the terrain-dependent strategy (Moghaddam, Mokhtarzade, and Moghaddam, 2018; Yavari et al., 2012). There is no deterministic approach to find the optimal terms of RFMs, so the metaheuristic optimization methods have been usually used in this area (Moghaddam et al., 2018; Yavari et al., 2012; Zoej et al., 2007). Considering the simple adaption of binary Genetic Algorithm (GA) to the term selection problems, has been used in many studies (Jannati and Valadan Zoej, 2015; Yavari et al., 2012). Despite the simplicity of the binary GA in the RFM term selection optimization, some deficiencies still exist that should be considered. Initial population of the GA should be considered to ensure high-level performance of the GA (Javidi and Hosseinpourfard, 2015). In addition to failure probability of a GA with the badly structured initial population, the slow convergence and also the convergence to local optimum (Cheng et al., 2008) are some consequences of how to design the initial population. So far, some efforts have been done to design approaches which generate a well-spanned initial population in solution space to ensure searching globally in GA (Cheng et al., 2008; Deng, Liu, and Zhou, 2015). Also, some modifications based on innovative reproduction schemes have been developed to catch elite individuals in next generations (Jannati and Valadan Zoej, 2015).

In this paper, a new approach is proposed to generate GA's initial population based on available GCPs to estimate RFMs. The main idea of the proposed method is founded on an assumption that dark areas of solution space can be recognized by correlation analysis of the design matrix column vectors of the equation set. So, the probability of the presence of dark area solutions will be decreased which prevents precise searching of these areas. Dark areas are an idiom for solutions that have a low level of probability of success. The proposed approach is dynamically adapted to available GCPs. In other words, a specific method is used to randomly generate initial population based on composition of GCPs and their spatial distributions. This article is organized into five sections. In next section, the proposed approach is presented. The data used is described in the third section. While in the fourth section, the implemental details and the results are presented, the last section concludes.

2. Methodology

Geometric correction of satellite images can be applied via geometric transformations. RFMs are known as the most popular 3D interpolative transformations which have been widely used in this area. An RFM is comprised of the ratio of two often 3D polynomials (Equation 1).

$$l=\frac{P_1(X,Y,Z)}{P_2(X,Y,Z)} \qquad s=\frac{P_3(X,Y,Z)}{P_4(X,Y,Z)}$$

$$P_m(X,Y,Z)=\sum_{i=0}^{n}\sum_{j=0}^{n-i}\sum_{k=0}^{n-i-j} a_{m,i,j,k}X^iY^jZ^k \tag{1}$$

Here, $[l, s]$ are digital coordinates of a point in image space, $[X, Y, Z]$ are the corresponding 3D coordinates in ground space, $a_{m,i,j,k}$ are the Rational Polynomial Coefficients (RPCs) and n is the order of 3D polynomials. In RPCs estimation procedures, the terms $a_{2,0,0,0}$ and $a_{4,0,0,0}$ is set to a fixed value (one) in order to avoid rank deficiency of equation set.

Satellite image providers, usually use third order of 3D polynomials to build up RFMs and consequently estimate the RPCs. Considering the terrain-independent strategy used by image providers, there is no challenge in the estimation of third-order RFMs with 78 coefficients. However, when limited number of GCPs are available, estimation of RPCs of high order RFMs in terrain-dependent strategy will face challenges such as singularity or ill-posed conditions. Optimal term selection is a technical way to deal with such over-parameterization problems. Heretofore, GA and some other meta-heuristic optimization procedures have been used to find optimal terms of RFMs in the terrain-dependent strategy. All developed methods try to find an optimal term permutation for each satellite image based on available GCPs. But the search domain is vast. Considering third-order 3D polynomials, 278 term compositions would exist. Obviously, too many of these permutations are not good solutions that can be named as the dark areas of the solution space. A tuned optimization method should intelligently ignore probable dark areas and spent time searching for better solutions. So, numerous modifications have been developed to improve such optimization algorithms.

In this paper, a method is proposed to balance the existence probability of each gene (an RFM's term) in the first generation of the GA. This method avoids the dark areas of the solution space in the initial population, which expediates the GA convergence. To do so, before the generation of initial population, an equation set including all possible RFM's terms (third order 3D polynomials) is formed through available GCPs. Obviously, zero and negative degrees of freedom or even ill-posed condition would probably happen in this step, but the equation set need not to be solved. In fact, just the values of the design matrix of the equation set are needed for next steps. The rest of this section is dedicated to explain the detail of the proposed method.

Equation (2) shows the standard form of the equation set to be solved using the linear parametric least square adjustment model.

$$L+V=A\times\Delta \tag{2}$$

Here, L is the observation vector which is filled by image observations (l, s), V is the residual vector, A is the design matrix that is strictly filled by the derivations of observation models from the unknown values, and Δ is the vectors of unknowns (RPCs).

The column vectors of the design matrix are directly related to equations set condition. In other words, the correlations among the column vectors of the design matrix can be considered as a sign of ill-posed level or even rank deficiency. So, in the proposed approach, after forming the design matrix with the available GCPs, correlation matrix of the design matrix's column vectors (C) is estimated through Equation (3).

$$C=\begin{bmatrix}1 & c_{1,2} & \cdots & c_{1,78}\\ c_{2,1} & 1 & \cdots & c_{2,78}\\ \vdots & \vdots & \ddots & \vdots\\ c_{78,1} & \cdots & c_{78,77} & 1\end{bmatrix}_{78\times 78},\quad C_{i,j}=\frac{\sum_{k=1}^{m}(a_{k,i}-\bar{a}_{-,i})(a_{k,j}-\bar{a}_{-,j})}{\sqrt{\sum_{k=1}^{m}(a_{k,i}-\bar{a}_{-,i})^2\sum_{k=1}^{m}(a_{k,j}-\bar{a}_{-,j})^2}} \tag{3}$$

In Equation (3), $a_{i,j}$ are the elements of design matrix, $\bar{a}_{-,i}$ is the mean value of the i^{th} column of design matrix and m is total number of equations (2× number of GCPs). The correlation matrix is a square matrix and the dimension of this matrix equals the maximum number of RFM terms (78 for the third order of 3D polynomials).

Considering C as the correlation matrix, the probability of each RFM's terms (P_i) is estimated by Equation (4).

$$\begin{gathered} P_i = S\times\left[1-\frac{\Sigma c_i}{\max(\Sigma c)}\right]+O,\qquad i=1,2,\cdots,78\\ \Sigma c=[\Sigma c_1,\Sigma c_2,\dots,\Sigma c_{78}]\\ \Sigma c_i=\sum_{j=1}^{78}\left|c_{j,i}\right| \end{gathered} \tag{4}$$

In Equation (4), Σc_i is sum of the absolute elements of i^{th} column of C, Σc is a vector containing the Σc_i (i =1, 2,…, 78), and also the S and O are scale and offset parameters respectively. The scale and offset parameters are used to increase the flexibility of P_i (i=1, 2, …, 78) estimations. The scales and offsets parameters can adjust the upper and lower probability of genes in the initial population. So, in the evaluation step, three different scales and offsets have been used to analyze the efficiency of these tuning parameters. It should be noted that the scale and offset parameters should be selected in a way that all genes' probabilities (P_i (i=1, 2, …, 78)) remain in the standard range of probability ([0~1]).

Hence, P_i can be considered as the activation probability of i^{th} gene (term) in chromosomes of the GA initial population. To generate the initial population based on these activation probabilities, the term correspond to P_i is activated only in a limited number (P_i×NP) of randomly selected chromosomes of the initial population. The NP is total number of individuals in the GA populations. The other steps of GA are exactly the same as standard form of its implementation procedures. It should be mentioned that the values of P_i depend on number of GCPs and their distribution in the ground coordinate space that is used in the RFM term selection process. So, it is expected that the proposed approach can be adapted to each term selection problem based on available dataset.

In the standard GA adapted with the RFMs term selection, each binary chromosome is an independent terms composition. Total number of terms of each chromosome is proportional to the number of activated genes in that chromosome. In fact, if a gene in a specific chromosome is activated, the corresponding term of that gene exist in the chromosome. During the execution of GA, for each chromosome a merit function would be estimated. The merit function in the RFM term selection process is the inverse of the Root Mean Square Errors (RMSE) estimated over the GCPs. To do so, usually total numbers of GCPs are divided into 3 categories. The Control Points (CoPs) used for RPCs estimation, GA Check Points (GACPs) that are used to evaluate each chromosome through merit function, and some Independent Check Points (ICPs) that are separated for final evaluations are the mentioned categories.

3. Data

In this article, an image of IKONOS taken from Hamedan on the seventh day of October 2000 has been used. Ground coordinates of 74 points of this image have been determined using a 1:1000 map of the area. Figure (1) shows the position of the CoPs, GACPs, and ICPs with red triangles, blue circles, and green crosses respectively.

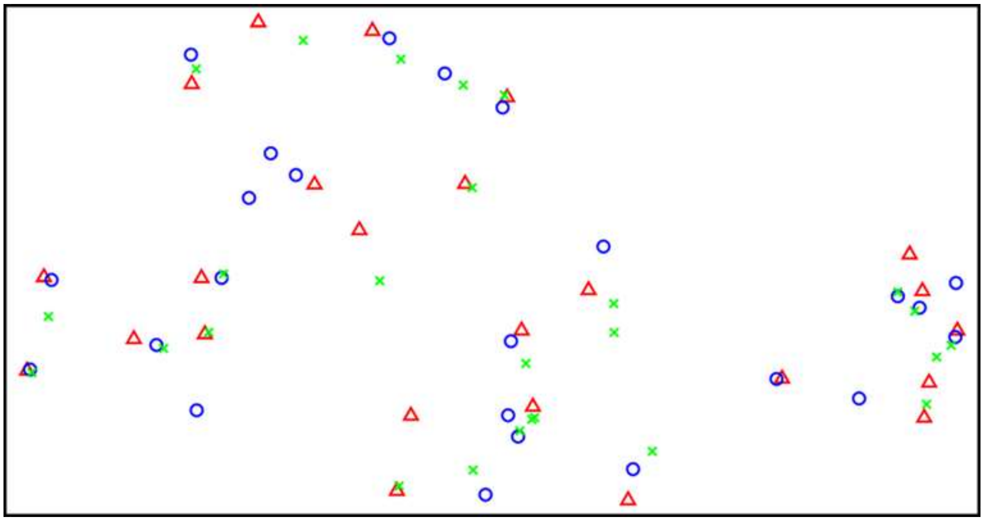

Figure 1. Distribution of the CoPs (red triangles), GACPs (blue circles), and ICPs (green crosses) in the image.

Table (1) shows some information about the image.

Table 1. Information about the data

Band	Panchromatic
Product	GEO
Off-nadir angle	20.4º-47.4º
Sampling interval	1 meter

4. Implementation and Results

In this article, in order to compare the standard GA and the proposed method, common parameters have been used for both methods. These parameters are shown in Table (2).

Table 2. Common implemental parameters of the GA and the proposed method

Chromosome length	78 bits
Selection	tournament
Crossover	uniform
Mutation probability	0.001
Merit Function	1/RMSE GACPs

The proposed method has been evaluated in three cases in which the scale and offset parameters vary. These cases are expressed in Table (3).

Table 3. Proposed method's cases in the terms of the scale and offset

Case	Scale	Offset	Lower Probability	Upper Probability
1	1.19	0.15	0.15	0.85
2	1.69	0	0	1
3	1	0	0	0.59

Due to the random nature of the GA, the results of each pair of processes could be different even if all the parameters are exactly the same. Hence, each of the four mentioned cases (the standard GA and three cases of the proposed method) are repeated five times and the average values obtained from these repetitions are shown in Tables (4-7). As shown in Figure (1), all the cases are trained and evaluated using 24 CoPs, 24 GACPs, and 26 ICPs.

Table 4. Results of the Standard GA

Size of population	RMSE CoPs (pixel)	RMSE GACPs (pixel)	RMSE ICPs (pixel)	Number of iterations	Processing time (S)
100	0.90	0.94	1.08	62.2	1.63
200	0.75	0.68	0.81	80.0	3.32
300	0.73	0.67	0.74	84.0	5.14
400	0.72	0.68	0.68	76.8	6.38
500	0.72	0.64	0.69	88.6	9.21

Table 5. Results of the first case of the proposed method (S=1.19 and O=0.15).

Size of population	RMSE CoPs (pixel)	RMSE GACPs (pixel)	RMSE ICPs (pixel)	Number of iterations	Processing time (S)
100	0.78	0.80	1.21	62.4	1.60
200	0.71	0.74	1.12	66.0	2.66
300	0.74	0.70	1.04	78.4	4.85
400	0.72	0.72	1.09	75.2	6.16
500	0.74	0.67	1.01	84.4	8.66

Table 6. Results of the second case of the proposed method (S=1.69 and O=0).

Size of population	RMSE CoPs (pixel)	RMSE GACPs (pixel)	RMSE ICPs (pixel)	Number of iterations	Processing time (S)
100	0.78	0.84	1.24	49.6	1.35
200	0.79	0.81	1.20	61.8	2.47
300	0.76	0.75	1.14	60.4	3.69
400	0.75	0.76	1.16	70.8	5.73
500	0.69	0.76	1.15	75.0	7.67

Table 7. Results of the second case of the proposed method (S=1 and O=0).

Size of population	RMSE CoPs (pixel)	RMSEGACPs (pixel)	RMSE ICPs (pixel)	Number of iterations	Processing time (S)
100	1.48	1.27	1.89	44.2	1.04
200	0.77	0.70	1.03	50.2	1.97
300	0.78	0.67	1.00	55.0	3.20
400	0.76	0.68	0.98	55.8	4.32
500	0.74	0.65	0.99	59.0	5.70

In the first case of the proposed method, none of the genes in the initial population is converged. Hence, the terms with extremely low probabilities can be present in the optimal RFM, or the terms with higher probabilities can be absent. So, all the terms have to converge in the iterative process of the GA. This increases computational costs and needs more time to be processed. In the second case, the genes with the highest and lowest probabilities are converged to one and zero respectively even in the initial population. This causes the processing time to decrease significantly. In the third case, the genes with the highest correlation are converged to zero when the initial population is created. This is the best case in terms of computational costs and processing time. Table (8) compares the proposed method with the standard GA. In this table, the percentage of the improvement in the processing time, number of iterations that are needed for the algorithm to be converged, and the RMSE ICPs are shown.

Table 8. Comparison between the proposed method and the standard GA

Size of population	Amount of reduction in processing time (%)			Amount of reduction in convergence iterations (%)			Amount of increase in RMSE ICPs (%)		
	case 1	case 2	case 3	case 1	case 2	case 3	case 1	case 2	case 3
100	2.02	17.50	36.24	-0.32	20.26	28.94	11.40	14.32	74.74
200	20.03	25.77	40.82	17.50	22.75	37.25	37.75	47.71	27.61
300	5.61	28.15	37.72	6.67	28.10	34.52	39.85	52.92	35.21
400	3.36	10.18	32.23	2.08	7.81	27.34	59.81	70.98	43.31
500	5.95	16.68	38.10	4.74	15.35	33.41	46.20	65.19	43.19

The proposed method has increased the RMSE error at ICPs. On average, the amount of error for the first, the second, and the third cases has increased by 39.00%, 50.22%, and 44.81% respectively. These increases might be the result of selection of some inappropriate terms or the removal of some appropriate terms in the initial population. In other words, although the highly correlated terms are not suitable for RFMs, at least one term might be selected from such terms. Also, the proposed method calculates high chances for the terms with lower correlations. However, some of these terms are inappropriate for the optimal RFM, due to the area topography, imaging geometry, and the image's errors. However, the proposed method does not consider these issues. Moreover, the average increase in error is less than half a pixel (0.29, 0.37, and 0.38 pixels for the first, the second, and the third cases respectively). Hence, the proposed method might still be accurate enough for many satellite images applications.

5. Conclusion

In this article, a method for reducing the computational costs of the standard GA is proposed. This method uses the design matrix of RFMs to calculate the probability of presence of each term in the optimal RFM. The probability of each gene determines number of chromosomes of the initial population in which this gene is activated. After producing the initial population, the optimal terms are determined through the same process as the standard GA. The proposed method is evaluated in three cases and all of the cases have decreased the processing time. However, this method has fallen the geometric accuracy of the models, but these models might be accurate enough for many photogrammetric purposes.

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