

The improved genetic algorithms for digital image correlation method

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We present a global optimization method, called the genetic algorithms (GAs), for digital image/speckle correlation (DISC). The new algorithms do not involve reasonable initial guess of displacement and deformation gradient and the calculation of second-order spatial derivatives of the digital images, which are important challenges in practical implementation of DISC. The performance of a GA depends largely on the selection of the genetic operators. We test various operators and propose optimal operators. The algorithms are then verified using simulated images and experimental speckle images.

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Digital image/speckle correlation (DISC) has become a popular tool for displacement and strain measurements in recent years due to the advantages of automatic, non-contact, full field, and real time. The method has found valuable and widespread use in many research and engineering applications^[1,2]. In the last decade, a lot of research has been performed in the area of the algorithms for digital image correlation. Various algorithms have been proposed such as differential iteration^[3], double Fourier transform^[4], and gradient-based methods^[5,6]. However, these algorithms often require reasonable initial guess of displacement and deformation gradient. Iterative algorithms also require the calculation of second-order spatial derivatives of the digital images, which increases computation complexity. In addition, the usual gradient-based algorithm can easily be stuck at local minima. In this study, we apply a global optimal algorithm to DISC. When considering global optimization methods for DISC, genetic algorithms (GAs) seem to have attracted considerable attention. The efficiency and the simplicity of the operation are two main attractions of the GAs approach. The new algorithms based on GAs are proposed for DISC in this paper. Although GAs have been applied to DISC^[7], the performance of a GA depends largely on the selection of the genetic operators. We test various operators and propose optimal operators. To develop DISC further, we derive more accurate algorithms based on GAs. The algorithms are then verified using simulated and experimental speckle images.

GAs are stochastic optimization algorithms that were originally motivated by the natural selection mechanism and evolutionary genetics. Unlike the conventional gradient-based searching algorithms, GAs are inherently parallel, and have a reduced chance of converging to the local optimum and would be more likely to converge to the global optimum. A GA starts off with a population of randomly generated chromosomes and advances toward better chromosomes by applying genetic operators, modeled on the genetic processes occurring in nature. During successive iterations, called generations, the chromosomes are evaluated as possible solutions. Based on these evaluations, a new population is formed using a mech-

anism of selection and applying genetic operators such as crossover and mutation. This type of algorithm uses three basic operators: the selection, the crossover, and the mutation. The selection operator works out a new population starting from the current one by encouraging the chromosomes having the strongest fitness (degree of adaptation). The crossover operator uses the information contained in two chromosomes to build two others. The mutation performs a random transformation of a chromosome to bring diversity.

The first problem during the utilization of GAs is the representation of the chromosomes (individuals). There are two kinds of representation in GAs, which are binary coding and real-valued coding^[8]. For real-valued optimization problems, real-valued coding is simply much easier and more efficient to implement, since it is conceptually closer to the problem space. A real-code genetic algorithm (RGA) works without the need of coding and encoding procedures and hence reduces the computation time. Since our goal is to obtain displacements and strains, we choose RGA. Here a chromosome consists of all the variables in correlation coefficient C , which is defined as^[3]

$$C = \frac{\sum_{y=1}^{y=m} \sum_{x=1}^{x=m} f(x, y) \cdot g(x^*, y^*)}{\sqrt{\sum_{y=1}^{y=m} \sum_{x=1}^{x=m} f^2(x, y) \cdot \sum_{y=1}^{y=m} \sum_{x=1}^{x=m} g^2(x^*, y^*)}}, \quad (1)$$

where $f(x, y)$ and $g(x^*, y^*)$ are respectively the undeformed and the deformed subset intensity value,

$$x^* = x + u + \frac{du}{dx} \Delta x + \frac{du}{dy} \Delta y, \quad (2)$$

$$y^* = y + v + \frac{dv}{dx} \Delta x + \frac{dv}{dy} \Delta y, \quad (3)$$

u and v are the displacements for the point P ; $\frac{du}{dx}$, $\frac{du}{dy}$, $\frac{dv}{dx}$, and $\frac{dv}{dy}$ are the derivative terms for the point P .

One gene of a chromosome represents a single parameter of the parameter set $S = (u, v, \frac{du}{dx}, \frac{du}{dy}, \frac{dv}{dx}, \frac{dv}{dy})$. Here

we define S_i ($i = 1, 2, \dots, 6$) as the i th element of S , for example $S_3 = \frac{du}{dx}$ and $S_6 = \frac{dv}{dy}$.

The fitness evaluation function is a measure enabling the evaluation of the suitability of a chromosome. It provides information about how good each candidate solution is. The fitness evaluation results determine the likelihood that a candidate solution is selected to produce candidate solution in the next generation. Our objective is to search the parameter set $(u, v, \frac{du}{dx}, \frac{du}{dy}, \frac{dv}{dx}, \frac{dv}{dy})$ to maximize C . We choose correlation coefficient C as a fitness function.

During the selection, the “parent” individuals aiming at producing the “child” chromosomes are chosen. The first step includes calculating the objective function value at every individual. In our work, the selection of parent chromosomes is done using tournament strategy: initial chromosomes are randomly selected and the “strongest”, i.e. with the highest fitness, is selected for reproduction. We found this scheme is fast, very easy to be implemented, and very effective. This operation is repeated as many times as required by the size of the population.

The crossover operator is acknowledged as one of the main causes of the efficiency of GAs, it allows us to combine some hopeful schemata and thus quickly progress towards the optimal regions of the search space. The crossover produces new individuals by combining the information contained in the parent chromosomes. Each pair generates two children who replace their parents inside the population. This exploration depends on crossover operator and the crossover probability P_c . Here we choose improved arithmetic crossover operator. The improved arithmetic crossover consists of producing children in a way that every gene in a child is a combination of genes from its two parents.

Let us assume that vector $A = (A_1, A_2, A_3, A_4, A_5, A_6)$ and vector $B = (B_1, B_2, B_3, B_4, B_5, B_6)$ denote the regions of the displacement and strain, respectively, i.e. $A_i \leq S_i \leq B_i$ ($i = 1, 2, \dots, 6$). Assume that S_{o1i} and S_{o2i} are two chromosomes selected for application of the crossover operator, and let $S_{o1i} \leq S_{o2i}$ (if not, exchange S_{o1i} and S_{o2i}). A child S_{ni} can be produced as

$$S_{ni} = \begin{cases} \alpha A_i + (1 - \alpha) S_{o1i}, & \text{if } \text{mod}(\theta, 3) = 0 \\ \alpha S_{o1i} + (1 - \alpha) S_{o2i}, & \text{if } \text{mod}(\theta, 3) = 1 \\ \alpha S_{o2i} + (1 - \alpha) B_i, & \text{if } \text{mod}(\theta, 3) = 2 \end{cases}, \quad (4)$$

where $\alpha \in [0, 1]$ is a random number; $\theta \geq 0$ is a random integer. Improved arithmetic crossover provides some local/hill climbing search (if the parents are on the opposite sides of the hill) capability for a GA, and has a fast convergence speed.

This operator changes the value of a gene S_i , what brings the diversity among the population. This exploration depends on two parameters, the mutation mode of the genes and the probability P_m of applying this operator. If a variable S_i is selected to be mutated, the mutation operator randomly changes the value of this variable by generating a random number within the variation domain of S_i . Like the crossover operator, the mutation is applied with a probability P_m , which is classically fixed to a “small” value throughout the algorithm. Let us assume that $S = (u, v, \frac{du}{dx}, \frac{du}{dy}, \frac{dv}{dx}, \frac{dv}{dy})$ is a chromosome

and $S_i \in [a_i, b_i]$ is a gene to be mutated. We choose a mutation operator, called improved Gaussian. The gene S'_i resulting from the application of different mutation operators is shown as

$$S'_i = S_i + \sigma \left(\sum_{j=1}^{12} r_j - 6 \right), \quad (5)$$

where $\sigma = \frac{1}{6}$, $r_j \in (0, 1)$ is a random number. This mutation operator emphasizes the exploration of the local area surrounding the initial individual.

The algorithm stops when an individual fitness value is 1 or when a maximum number of generations has been run.

It is seen that GAs use three basic genetic operators: selection, crossover, and mutation. The three operators have various algorithms. In fact, we test various algorithms. In Table 1, we list our optimal genetic operators and the other ones used in Ref. [7]. The key parameters for our approach are given in Table 2.

Now we verify the efficiency of our improved GAs method using simulated images and experimental images, and compare it with GAs method used in Ref. [7] (in which the three basic genetic operators are listed in Table 1). The computer-simulated images are generated using an algorithm developed by Zhou *et al.*^[5]. Two typical deformation configurations are used to generate speckle image pairs before and after deformation: 1) rigid body

Table 1. The Three Basic Genetic Operators

Operators	Our Method	Ref. [7] Method
Selection	Tournament Strategy	Roulette Wheel
Crossover	Improved Arithmetic Crossover	Arithmetic Crossover
		Heuristic Crossover
		Simple Crossover
Mutation	Improved Gaussian Mutation	Uniform Mutation
		Non-Uniform Mutation
		Multiple Non-Uniform Mutation

Table 2. The Key Parameters for Our Approach

P_m	P_c	Chromosome Number	Length of Chromosome
0.1	0.6	200	6

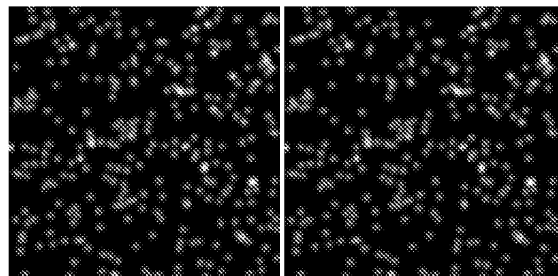


Fig. 1. A simulated speckle image pair with a rigid body translation $u_0 = 0.05$.

Table 3. The Discrete rms Error for a Pre-Assigned Rigid-Body Translation ($u_0 = 0.01 - 3$ pixel)

Pre-Assigned Values	Our Method		Ref. [7] Method		
	u_0	C -ERR	u -ERR	C -ERR	u -ERR
3.0	6.22×10^{-5}	1.20×10^{-3}	2.10×10^{-4}	2.35×10^{-2}	
1.0	1.83×10^{-5}	3.70×10^{-3}	3.93×10^{-4}	1.03×10^{-1}	
0.5	6.04×10^{-5}	4.74×10^{-4}	5.68×10^{-4}	5.43×10^{-2}	
0.1	1.54×10^{-4}	8.69×10^{-4}	4.29×10^{-4}	3.26×10^{-2}	
0.05	7.31×10^{-5}	3.70×10^{-3}	8.57×10^{-4}	7.97×10^{-2}	
0.01	8.50×10^{-5}	1.50×10^{-3}	7.12×10^{-4}	6.82×10^{-2}	

Table 4. The Discrete rms Error for a Pre-Assigned Rigid-Body Rotation

Pre-Assigned Values	Our Method			Ref. [7] Method			
	ε	C -ERR	u -ERR	v -ERR	C -ERR	u -ERR	v -ERR
$100\mu\varepsilon$	4.15×10^{-5}	4.60×10^{-3}	4.710×10^{-3}	5.48×10^{-4}	1.23×10^{-1}	4.98×10^{-2}	
$10\mu\varepsilon$	3.75×10^{-5}	6.71×10^{-4}	8.29×10^{-4}	6.79×10^{-4}	7.67×10^{-2}	3.28×10^{-2}	

Table 5. The Displacements of Some Points

Points	Our Method		Ref. [7] Method		Newton-Raphson Method	
	u	v	u	v	u	v
100,100	0.652434	-0.325667	1.011290	-0.0859096	0.651579	-0.331544
100,101	0.643931	-0.331009	0.596728	-0.258916	0.643720	-0.332857
100,102	0.648119	-0.331156	0.585168	-0.0197699	0.649813	-0.329185
100,103	0.648045	-0.327258	0.716848	-0.291104	0.649080	-0.331600
100,104	0.648722	-0.332771	0.771599	-0.223612	0.654376	-0.334369
100,105	0.651970	-0.334506	0.632159	-0.322123	0.649672	-0.336277
100,106	0.648050	-0.33275	0.205237	-0.422285	0.651073	-0.336267
100,107	0.649329	-0.337223	0.737482	-0.426862	0.652763	-0.338743
100,108	0.653668	-0.339217	0.808515	-0.325392	0.655339	-0.337737
100,109	0.646450	-0.341121	0.801230	-0.281289	0.647133	-0.342275

translation with $\mathbf{u} = [u_0, 0]^T$; 2) rigid body rotation with $\mathbf{u} = (\varepsilon \cdot y, -\varepsilon \cdot x)^T$. The speckle image pairs are generated with a pre-assigned rigid-body translation ($u_0 = 0.01 - 3$ pixel), and rigid body rotation ($\varepsilon = 10\mu\varepsilon, 100\mu\varepsilon$). Figure 1 shows a simulated speckle image pair with a rigid body translation $u_0 = 0.05$.

For every image pair, the total number of calculated points with fixed positions in original image is 40. We calculate the discrete root mean square (rms) error. The discrete rms error is defined by $ERR = \frac{[\sum_{i=1}^n (y_a - y_e)_i^2]^{1/2}}{n^{1/2}}$, y_a is calculated value, y_e is pre-assigned value. In Table 3,

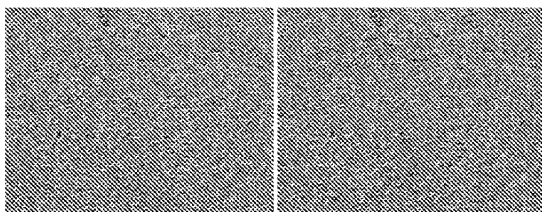


Fig. 2. An experimental speckle image pair with a rigid body translation $u_0 = 0.65$, $v_0 = -0.33$.

we list the discrete rms error for a pre-assigned rigid-body translation ($u_0 = 0.01 - 3$ pixel). In this table, C -ERR denotes the discrete rms error of the cross-correlation coefficient C , and u -ERR is the discrete rms error of the displacement u . In Table 4, we list the discrete rms error for a pre-assigned rigid-body rotation ($\varepsilon = 10\mu\varepsilon, 100\mu\varepsilon$).

After being verified through simulated images, our method is also verified using experimental images. The test speckle pattern is generated through spraying paint onto the surface. An aluminum block is bolted to the base of the X - Y translation table. The specimen is translated in X and Y directions. In Fig. 2, an experimental speckle image pair with a rigid body translation $u_0 = 0.65$ pixel, $v_0 = -0.33$ pixel is shown.

The displacements of some points are calculated by our method, Ref. (7) method, and Newton-Raphson method. The results are listed in Table 5. It can be seen that our improved GAs method is more accurate than the method proposed in Ref. [7].

In this paper, an improved GAs method for DISC is developed, which does not require reasonable initial guess of displacement and deformation gradient and the calculation of second-order spatial derivatives of the digital im-

ages, and thus reduces computation complexity. We test various operators and propose optimal operators. The algorithms are then verified using simulated images and experimental images.

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