Displacement Detection of Structures using a Micro-genetic Algorithm

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Abstract

This study deals with a method to identify displacements on structures using a Micro-genetic algorithm (M-GA). We developed the inverse technique using a Micro-genetic algorithm which can make global solution searches possible as opposed to classical gradient-based optimization techniques such as the Least-square method. The technique described in this paper may allow us not only to detect the base function but also to find unknown displacements of a structure. Example models are simulated to detect unknown displacements and weight values at the same time.

Keywords: *Displacement detection, inverse problems, micro-genetic algorithm, global solution searches*

1. Introduction

In recent years, direct search methods, such as neural networks, genetic algorithms and simulated annealing methods are developed and promisingly applied to the field of structural identification. Among them, genetic algorithms (GA) attract our attention because of the fact that the technique requires significantly small amount of data in dealing with complex problems. This fact is certainly a great advantage over the other methods such as the natural frequency based neural network methods which require an a priori knowledge on both the modal frequencies and shapes to train the neural network. The GA approaches allow us to challenge many nonlinear, discrete, and multimodal optimization and search problems, such as the one studied in this paper. There is a host of papers dealing with GAs in structural damage detection. For instance, Suh *et al.*, [1] presented a hybrid neuro-genetic technique that is able to identify the location and extent of damage in a beam or frame structure using only the frequency information. Mares and Surace [2] demonstrated the ability of the GA to identify damage in elastic structures. Friswell *et al.*, [3] combined the genetic and eigen-sensitivity algorithms for locating damage. Chou and Ghaboussi [4] proposed a GA-based method to determine the location and extent of damage in truss structures from the measured static displacements. Krawczuk [5] presented a wave propagation approach to detect damage in beam structures based on GA and the gradient technique.

Despite the broad spectrum of applications, the conventional GAs usually requires a large number of iterations, and thus a high computational cost. To solve an inverse problem using a GA, it is necessary to carry out iterative forward computations for each chromosome. Therefore, the total time spent in solving the forward problem could be extremely long, usually in the order of magnitude of several thousand iterations or more depending on the complexity of the problem [6]. On the other hand, it can be demonstrated that a uniform micro-genetic algorithm (M-GA) can avoid premature convergence so that it can converge into the near optimal region at a rate much quicker than that of a simple GA. For example, Carroll [7] found that a uniform M-GA is more roust in handing an order-3 deceptive function than the traditional GA methods.

All these studies are applied only to the detection of damages. In this study, we propose a method to identify unknown displacement in structures by processing the static response data combined with the forward analysis. It is known in general that conventional inverse methods such as the Least-square method can accurately detect displacements in simple structures. However, it requires partial derivative processes for different structural types. On the other hand, the M-GA is free from such requirements and thus can yield more accurate results for both static and dynamic conditions than those of the classical gradient-based optimization techniques. This allows for convenient use of M-GA. In this paper, the M-GA is extended to identify displacements of structures.

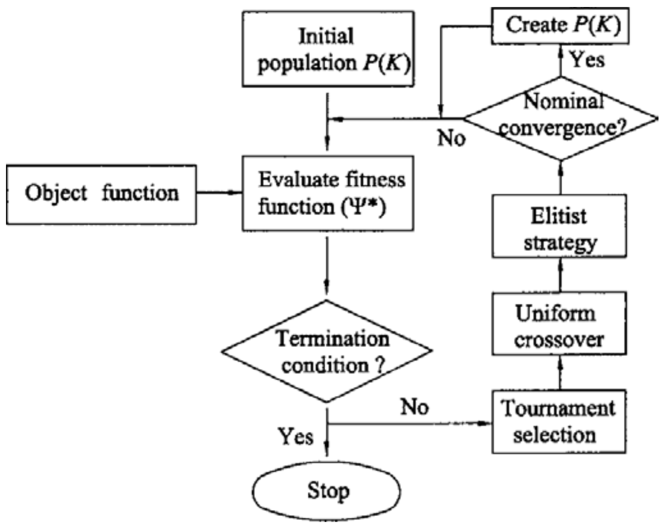

Figure 1. Flow Chart for Identifying the Damage using the Micro-Genetic Algorithm

2. Micro-genetic Algorithm

In an effort to reduce the time for finding a global minimum within the entire procedure, Goldberg [8] presented an efficient method that deals with small populations. In this method which is often referred to as the serial GA, the genetic process is restarted with a randomly generated new population while keeping the best outcomes of the previous generation. Then the process is repeated until the prescribed termination condition is satisfied. Based on this method, Krishnakumar [9] and Carroll [10] discovered that the convergence of the M-GA is much faster than that of a simple GA for several test functions.

The M-GA consists of inner and outer loops. The inner loop is the bigger loop encircling the convergence process with the initial generation consisting of K members. For each iteration in the inner loop, the fitness function is evaluated and compared with the prescribed termination condition as shown in Figure 1. From the engineering point of view, the objective of M-GA is to get an acceptable design, *i.e.*, a design whose residual in the fitness function is small compared to the norm of the target intensity. The inner loop is repeated until the termination condition is satisfied. The fitness function is determined by the predefined object function that is based on the forward formulation or the finite element analysis in our case. We use the tournament selection method to select parent genes, which inherits uniform and random genes to their offsprings. Once the parent genes are selected, matings take place using the uniform crossover scheme. In order to prevent the possibility of losing good genes, the elitist strategy is applied. Using these procedural steps, the best member of the population survives in each generation [10]. Since we are dealing with small populations (typically 5 to 6 individuals), the inner loop converges rapidly as compared to the simple GA (30 to 50 initial individuals). However, due to the small number of chromosomes involved in computation, it is unlikely that the process converges into the true value in the first iteration loop. If the inner loop is converging into a nominal value that prevents from further processing, then the process goes out of the inner loop and regenerates a new population by mutating the best members. The purpose of the outer loop is to introduce diversity by mutation, in order to explore other areas in the search space. The new-born generation, selected sequentially by picking genes from the pool of uniform probability, enters the inner loop together with the best gene survived from the previous iteration. It is suggested that the mutation probability should be lowered adaptively as the process converges. The basic algorithm of static motion for the system is written in the form

$$f_i = k_i \cdot x_i \tag{1}$$

Where, f_i, k_i, and x_i denote known and unknown displacement vectors, base shape function vectors, and detective weight vectors, respectively. In the M-GA, the parameters f_i, also mean the known and unknown data, and k_i and x_i are known data per *i*th node. For the kth individual, i.e., for the kth trial function, it can be written in terms of the responses (e.g., displacement) as follows:

$$\Psi = \left[\overline{f}_i - \sum_{i=1}^{n} k_i \cdot x_i \right]^2 \tag{2}$$

Then, the best fitness function can be prescribed by finding the minimum of the variable in a loop among the total individuals

$$\Psi^* = \min\{\Psi\} \tag{3}$$

3. Numerical Example

The uniform micro-genetic algorithm has been implemented for three purposes: To determine (1) the unknown displacement vectors, (2) the weight vectors, (3) the detection of two parameters at the same time. To implement M-GA, the FORTRAN GA driver [11] was used. For numerical demonstrations, a truss-type structure subjected to a concentrated loading is considered. It should be noted that the exact load history is not necessary to be known a priori in order to solve the forward problems. From the practical standpoint, the random load history cannot be exactly estimated, especially for bridge structures subjected to travelling vehicles. If there are no input data available, the input data can be estimated by base shape function vectors based on the Ritz method.

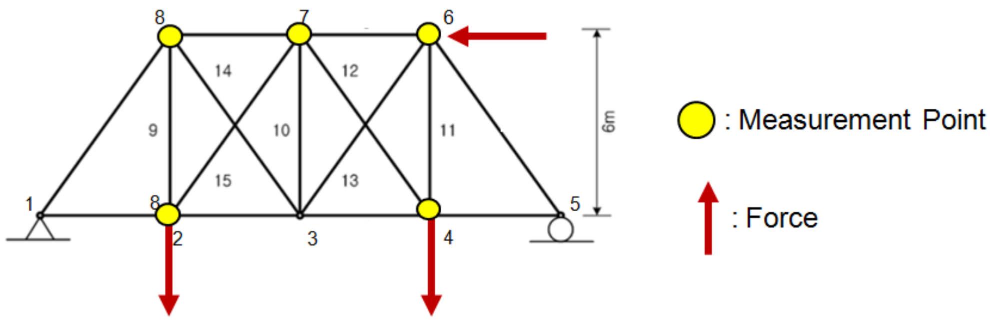

Figure 2. Numerical Example

Figure 2 shows node and element numbers, measurement points, and applied forces of a truss structure for solving the inverse problem using the M-GA. Nodes 3 and 5 are considered as unknown displacements for the detection. In implementation, we play with five individuals and the probability of uniform crossover was set to be 0.5. Figure 3 shows the best and average fitnesses and the mean of Ψ^* for the best member of the population in each generation. The irregular shape of the average fitness is due to the outer loop of the M-GA. For every five generations, the population is restarted, so that the characteristics of the new population are dramatically changed for each outer loop. By comparison, the best fitness function decreases asymptotically to the zero residual value. The entire process is terminated when the condition crosses the threshold value of 1×10^{-4} and it converged after approximately 200 iterations.

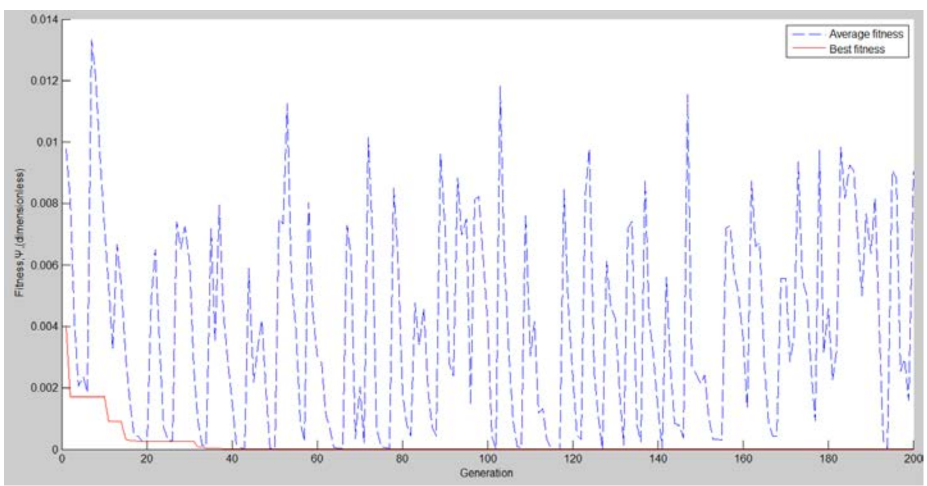

Figure 3. Best and Average Fitnesses of the Best Member of the Population in each Generation. The Irregular Shape of the Average Fitness is due to the Outer Loop of the M-GA

Figure 4 and Table 1 show the comparison of the displacement detections between M-GA and Least-square method at node 3 and 5 of a truss. It can be observed from the figure and figure that displacements detected by M-GA are more accurate than those of the Least-square method. The difference between two approaches at node 4 and 7 increases as shown in Figure and Table 2. Moreover, the Least-square method requires partial derivative processes for different structural types. On the other hand, the M-GA is free from such requirements and thus can yield more accurate results for both static and dynamic conditions than those of the classical gradient-based optimization techniques.

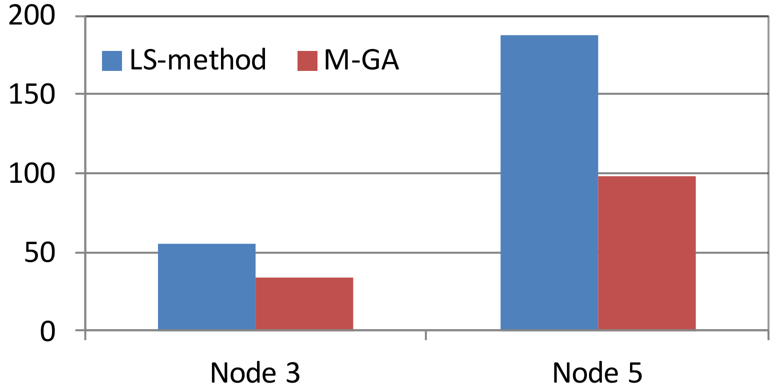

Figure 4. Comparison of the Displacement Detection Errors(%) between M-GA and Least-square Method at Node 3 and 5 of a Truss

Table 1. Comparison of the Displacement Detections between M-GA and Least-Square Method at node 3 and 5 of Truss

		LS-method		M-GA	
Node	measure (mm)	detection (m)	Error (%)	detection (m)	Error (%)
3	-0.00063	-0.00028	55.5556	-0.000415	34.12698
5	0.001242	-0.00109	187.7617	0.000024	98.67963

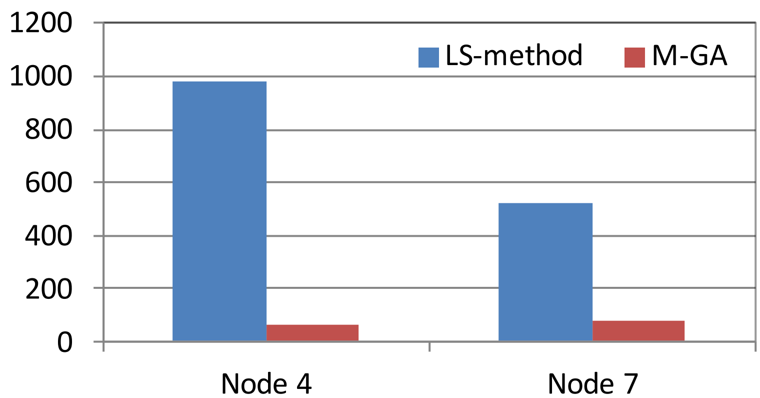

Figure 5. Comparison of the Displacement Detection Errors(%) between M-GA and Least-square Method at Node 4 and 7 of a Truss

Table 2. Comparison of the Displacement Detections between M-GA and Least-square Method at Node 4 and 7 of Truss

		LS-method		M-GA	
Node	measure (mm)	detection (m)	Error(%)	detection (m)	Error(%)
4	-0.00007	0.000615	978.5714	-0.000024	65.71429
7	-0.00013	-0.00081	523.0769	-0.000024	81.53846

4. Conclusion

A displacement identification technique based on the M-GA is developed. The novelty of this work is the use of its response due to the anomalies in a structural system. Since forward problems can be solved by a numerical method, the technique may be applicable to complex problems. The M-GA, in comparison with its predecess or (simple GA) or another conventional searching technique such as the Least-square method is more attractive not only because it can avoid premature convergence but also it converges faster. It is demonstrated in this study that it may be possible to use the described procedure not only to detect the displacement but also to determine unknown weight values in computing by the Ritz method. The effectiveness of the technique is confirmed from the numerical examples.

It is concluded from this study that the approach works well for the numerical experiments tested. Yet, the requirement for executing many forward procedures increases the need for further developing the algorithms for faster convergence and better computational efficiency. However, the examples might be too simplistic to extract conclusions for real-life situations. In order to prove the effectiveness of the technique, it will be necessary to prove the concept from experimental studies.

Acknowledgements

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