

Co-operative Co-evolutionary Genetic Algorithm for Vibration-Based Damage Detection of Two-Dimensional Truss Structure

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Abstract

Vibration-based damage detection, which is a non-destructive method used to detect damage occurred in structures, is based on the fact that vibration characteristics such as natural frequencies and mode shapes of the structures are changed when the damage occurs. This paper presents co-operative co-evolutionary genetic algorithm (CCGA) for vibration-based damage detection in two-dimensional truss structures. The objective function, which is a minimum criterion, is a numerical indicator of the differences between experimental vibration characteristics and numerically calculated vibration characteristics of predicted damage parameters by the finite element method. This numerical indicator is calculated by the concept of residual forces. The damage detection of two-dimensional truss structures are formulated as the test problems. There are three cases of different amounts and members of occurred damage. After simulation runs, the CCGA provides solutions that are obviously better than solutions from previous works using standard genetic algorithms although it uses less numbers generated solutions for solution search. The solutions obtained from the CCGA are almost the same as exact solutions for all test cases. Therefore, by the simulation results, the CCGA is considerably suitable for the damage detection in two-dimensional truss structures.

Keywords: Vibration-based damage detection, Genetic Algorithm, Co-operative co-evolution, Residual force vector, Eigen problem, Truss structure.

1. Introduction

Optimization is a very challenging effort in engineering field in order to satisfy one or several objectives simultaneously. While product designs focus on optimal costs in terms of raw materials availability, processing, reliability, etc. along the product life cycle, non-destructive testing play a crucial maintainability role in order to ensure continuous evaluation and prediction of failure before critical damage becomes disastrous.

Vibration-based damage detection in structure answers both load free testing and long term health-monitoring capability, as proven by extensive findings after the introduction of evolutionary algorithms in solving optimization problem.

A co-operative co-evolutionary genetic algorithm [1] is implemented in this paper to evaluate the level of damage in truss elements of a two-dimensional structure. The exact solutions

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were computed numerically in advance and will be compared with the design variables obtained from repeated tests in order to check the performance of the proposed algorithm.

The following section will review related literatures which contribute fundamental backgrounds to the study, detail the problem solving procedure, and discuss significant finding for future researches.

2. Vibration-Based Damage Detection

Various techniques used to detect damages based on changes in modal properties have been presented and classified despite slow adoption in industry and level of sensitivity to distinguish local and global response [1]. Potential of genetic algorithms seem widely practical in various disciplines. However, other family of evolutionary algorithms will be presented alongside and proven to explain comparable performance while experimented as either a standalone solver [2] or in a hybrid technique [3, 4].

The studied subjects can be a single beam [2], simplified structures [3, 4, 6], or laboratory models [3, 5, 6]. Minimum information of the subject in vibration based approach is based on modal properties consisting of natural frequencies and mode shapes. These properties are therefore the main objectives in order to assess existence of damages in structure and each element while combining fundamental mechanical properties such as mass and stiffness matrices.

Although computer becomes increasingly powerful in terms of processing speed and storage, it is inefficient to explore the whole problem space through individual increment. Problem solver can be computational expensive because of repetitive evaluations of the objective

function. Meanwhile, if the design parameters do not satisfy the termination condition, a new set of variables must be chosen and computed indefinitely. Followed by crossover and mutation or modified operators [7], selection techniques such as tournament selection [3, 6], roulette-wheel selection, or stochastic universal sampling are valuable to approximate the most appropriate set of solutions. Evolutionary algorithms are often the primary choice because of efficient exploration of the design space, use of derivative-free objective function, and therefore avoidance of local optima.

Genetic algorithm has been cited in various disciplines. Researchers may include numbers of design variables, modify variable abstraction technique, combined or alternate different selection method, or assess the performance between different algorithms and criteria. Classification system in vibration based damage detection may be based on linearity of damage, quantification of severity, or applications. Research in various domains proves flexible use of evolutionary algorithms [2]. However, continuing assessment of performance [6] between different approaches can verify the strength in terms of accuracy and performance.

3. Co-operative co-evolutionary genetic algorithm

The co-operative co-evolutionary genetic algorithm (CCGA) explores the search space by utilizing a population which contains a number of species or sub-populations. Each species is independently evolved as the procedure of genetic algorithm. In each species, an individual i

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represents only a decision variable or part of a solution to a problem. A combination of the individual i with corresponding variables or solution parts from other species will lead to a complete solution to the problem where the objective value of the complete solution can then be identified. By partitioning the solution into species, the search space that each species has to cover is significantly reduced compared to the full solution searches. The CCGA produces best performances when there is no coupling between different species at all. For instance, a solution is encoded into a binary chromosome of length 100; the number of possible solutions is $2^{100} = 1.27 \times 10^{30}$. By dividing the binary chromosome into 20 un-coupled species of which each is represented by a 5-bit binary string, the number of possible solutions is then reduced to be only $20 \times 2^5 = 640$. However, if there is coupling between species, search performances deteriorate with increasing coupling strength. Since each species is repeatedly evolved as the procedure of genetic algorithm (GA), the procedure of the GA is firstly explained, and following with the procedure of the CCGA.

3.1 GA procedure

The genetic algorithm (GA) has been extensively explained in [8] and is discussed here to illustrate the basic components and mechanisms of the GA. The standard procedure of the GA can be described as follows.

- 1) Read randomly generated individuals of an initial population from an input file.
- 2) Decode the chromosome of every individual in order to obtain solutions of the problem.
- 3) Calculate objective value f_i of each

individual i in the population.

- 4) Calculate the fitness of each individual, using the obtained objective value.

The fitness (F_i), which is a maximum criterion, of the individual i is directly assigned to be minus f_i and f_i for minimization and maximization problems respectively.

$$F_i = \begin{cases} -f_i, & \text{for a minimization problem} \\ f_i, & \text{for a maximization problem} \end{cases} \quad (1)$$

The fitness F_i is therefore normalized by using the minimum (F_{\min}) and maximum fitness (F_{\max}) of individuals in current population. The normalized fitness NF_i is given by

$$NF_i = \left(\frac{F_i - F_{\min}}{F_{\max} - F_{\min}} \right) \quad (2)$$

The fitness scaling technique is introduced in order to improve performance of search mechanism. The aim of this technique is to make more difference between the maximum and average fitness values to be used in the following selection process by the introduction of a scaling factor which is more than one. The scaled fitness (SF_i) of the individual i can be directly evaluated by the normalized fitness.

$$SF_i = \frac{NF_i}{NF_{avg}} SCF \quad (3)$$

where NF_{avg} is the average of normalized fitness of individuals in the current population while SCF is a pre-defined scaling factor.

- 5) Select a parent population from the current population.

In this paper, a stochastic universal sampling

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(*SUS*) selection is used for the parent selections by consideration of the scaled fitness previously obtained by Eq. (3).

6) Perform a transformation on the parent population using genetic operators, crossover and mutation, to obtain the resulting offspring population.

7) Go back to 2) until a convergence is observed from the solutions found or a fixed number of iterations is reached. It is noted that one loop from 2) to 6) is called one generation of a genetic algorithm run.

By adding the elitism operator, after 4), then a set of fit individuals might be kept without crossover and mutation, and merged with the newly generated individuals from crossover and mutation in 6) to form the new population. Elitism can generally be described as a special way which is incorporated into a genetic algorithm in order to promote the survival of the best individual found. The main reason behind the use of elitism is the fact that there is always a possibility that a crossover or mutation operation might eliminate the best individual found within each generation, subsequently, the best individual in each generation might be worse than that of the previous generation. In order to guarantee that the best solution found from each generation is not lost though the search propagation. The most commonly used elitism is to pass the first n number of best individuals from the current generation to the next generation without crossover and mutation.

3.2 CCGA procedure

The main procedure of the CCGA is as follows.

1) Read randomly generated individuals of an initial population from an input file.

2) Decode the chromosome of every

individual in order to obtain solutions of the problem and calculate objective values of all individuals. The individual having the best objective is assigned to be the current best individual.

3) Start with species counter $s = 1$ and divide an individual in the initial population into a number of parts in which each part represent for each species. The objective value of an individual in the initial population will be the initial objective value of a corresponding individual in each species. The fitness calculation and parent selection will be performed in order to obtain the resulting sub-population of each species.

The initial objective calculation of the CCGA in this paper is quite different from the original initial objective calculation by Potter and De Jong [1]. The initial objective calculation in this paper is proposed to reduce computational time and to ensure that the initial best solution for the CCGA is same as that for the GA if starting with a same initial population for an optimization problem.

4) In the current species s , a corresponding full solution of an individual i is obtained by the combination of the individual i with the corresponding parts from other species of the best individual. The objective value of the individual i will be equal to that of the complete solution. If the objective value of the complete solution is better than that of the current best individual, the best individual and its objective value are then updated.

5) Assign fitness, select parents, and perform crossover and mutation to the individuals in sub-population of the current species s as 4) to 6) in the GA procedure, thereafter increase the species counter $s = s + 1$ and go back to 4) until the last species is finished. In the CCGA, the elitism operator can be added into the search mechanism

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after the fitness calculation as the GA.

6) Check termination condition. If the condition is satisfied, report the final best individual as the output solution, otherwise, restart species counter $s = 1$ and go back to 4). It is noted that one loop from 4) to 5) is called one generation of the CCGA run.

In the CCGA, the number of generated solutions from one generation is equal to the number of species times the number generated solutions from one generation of the GA. For the equal numbers of generated solutions, the number of maximum generations, which is used for termination condition, of the CCGA is equal to that of the GA dividing the defined number of species.

4. Calculation of objective function

This section shows how to calculate objective function. The calculation of objective function is adopted from [3] and [9]. The equation of motion of dynamics of a multi degree freedom system is given by

$$[m]\{\ddot{x}(t)\} + [k]\{x(t)\} = \{F(t)\} \quad (4)$$

where $[m]$ and $[k]$ are $(n \times n)$ mass and stiffness matrices and $\{x\}$ and $\{F\}$ are $(n \times 1)$ displacement and applied force vectors.

The j^{th} eigen equation associated with Eq. (4) is given by the following equation

$$[k]\{v_j\} - \lambda_j[m]\{v_j\} = \{0\} \quad (5)$$

where λ_j and $\{v_j\}$ are the j^{th} eigen value and corresponding unit eigen vector.

In the finite element model of the structure, the

matrix $[k]$ can be represented as a sum of the expanded element stiffness matrices of all divided elements.

$$[k] = \sum_{i=1}^N [k]_i \quad (6)$$

where $[k]_i$ represents the expanded stiffness matrix of an i^{th} element and N is the number of divided elements.

Similarly, the matrix $[m]$ is a sum of the expanded element mass matrices of all divided elements.

$$[m] = \sum_{i=1}^N [m]_i \quad (7)$$

where $[m]_i$ represents the expanded mass matrix of the i^{th} element and N is the number of divided elements.

When damage occurs in a structure, stiffness matrix of the damaged structure $[k_d]$ can be expressed as a sum of element stiffness matrices multiplied by stiffness factors associated with each of the N elements α_i ($i = 1, 2, \dots, N$), resulting from the damage.

Then, the stiffness matrix of the damaged structure is given by

$$[k_d] = \sum_{i=1}^N \alpha_i [k]_i \quad (8)$$

The values of the parameters fall in the range 0 to 1. The stiffness factor $\alpha_i = 1$ indicates that the element is undamaged and $\alpha_i = 0$ or less than 1 implies completely or partially damaged element respectively. The experimental natural frequencies and unit amplitude vectors or mode shapes of the

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damaged structure are approximated to satisfy the eigen equation, Eq. (5), of j^{th} mode, therefore the equation can be rewritten as

$$[k_d]\{v_{jd}\} - \lambda_{jd}[m]\{v_{jd}\} = \{0\} \quad (9)$$

where λ_{jd} and $\{v_{jd}\}$ are the approximated experimental eigenvalue and unit eigenvector of j^{th} mode. Moreover, it is assumed that the mass matrix is unchanged due to the damage.

If $\beta_1, \beta_2, \dots, \beta_N$ are decision variables which are the predicted stiffness factors. By substituting the predicted stiffness factors into Eqs. (4) and (5), an expression residual force vector of j^{th} mode in a function of β_i can be evaluated as follows.

$$\{R_j\} = -\lambda_{jd}[m]\{v_{jd}\} + \sum_{i=1}^m \beta_i [k]_i \{v_{jd}\} \quad (10)$$

The residual vector $\{R_j\}$ will be $\{0\}$, only if a correct set of β_p which shows that $\beta_i = \alpha_i$ for all i , is introduced under the experimentally damaged modal information λ_{jd} and $\{v_{jd}\}$ for a particular mode j .

The $(n \times n)$ residual force matrix $[R]$ is therefore obtained by

$$[R] = [\{R_1\} \{R_2\} \dots \{R_n\}] \quad (11)$$

If all β_i are correct, all elements of the matrix $[R]$ must be 0. Unlike the previous works [5, 6] that the objective function is calculated from only diagonal terms of the residual matrix, in this paper, the objective function f of a set of predicted damage factors is evaluated from all elements of the residual matrix, f is represented by

$$f(\beta_1, \beta_2, \dots, \beta_N) = \sqrt{\sum_{i=1}^n \sum_{j=1}^n R_{ij}^2} \quad (12)$$

where N is the number of elements and n is the number of degrees of freedom.

5. Numerical test

The damage identification problem of two dimensional trusses in Rao et al. [3] was tested to validate the robustness of CCGA and to compare with the finding of previous author. The structure in Fig. 1 is formed by 11 truss elements with the following properties in table 1.

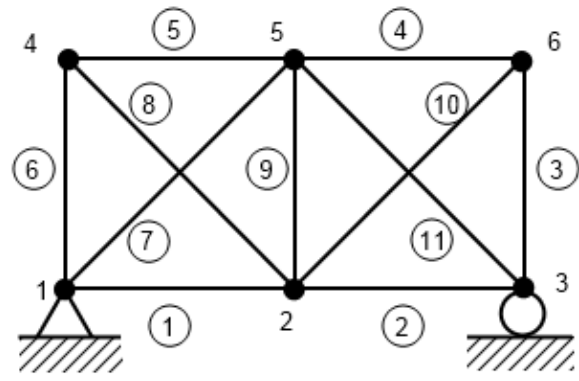


Fig. 1 Truss structure

Table 1 Properties of the truss structure

Young's modulus	E	207	GPa
Density	ρ	7860	kg/m ³
Cross section	A	0.0011	m ²
Length of each bay	l	0.75	m

The modal properties were computed in advance following 3 cases of varying stiffness factor: 1) all members are undamaged; 2) partial damages of 0.7 in element 3 and 0.3 in 6; and 3) complete damage or absence of element 10. Parameter settings of the algorithm are presented in table 2.

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Table 2 Parameter settings

Parameters	Setting and Values
Chromosome coding	Real-value chromosome with 11 decision variables
Number of decision variables in a specie	11
Number of species	Number of decision variables
Population size	20
Number of elite individuals	2 for every specie
Scaling factor	2.0
Selection method	Stochastic universal sampling selection
Crossover method	Simulated-binary crossover ($\eta_c = 15$) with probability = 1.0
Mutation method	Variable-wise polynomial mutation ($\eta_m = 20$) with probability = 0.5
Number of generations	25

The convergence of the solution can be concluded when the fitness value stabilizes, thus, the stiffness factor of each members can be finalized. The solution set converges after 200th iteration in each case (Fig. 2-4).

The comparison in table 3 shows stiffness factor of different elements in function of solving techniques and cases. The difference implies that CCGA can solve more accurately than previous finding using traditional genetic algorithm. Many of the solution also approach close to the exact solution at higher number of decimal point.

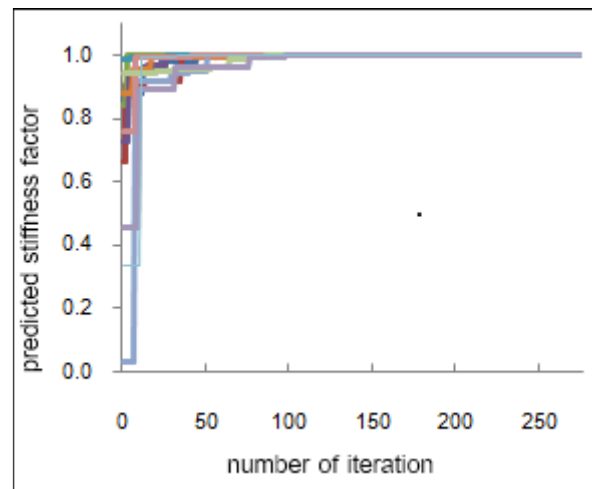


Fig. 2 Stiffness factor in case 1

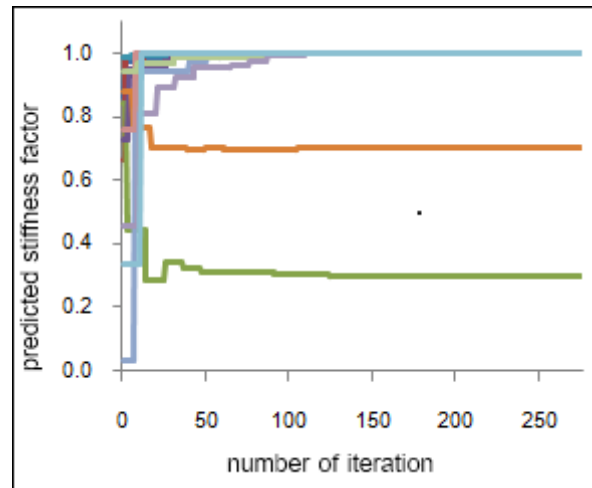


Fig. 3 Stiffness factor in case 2

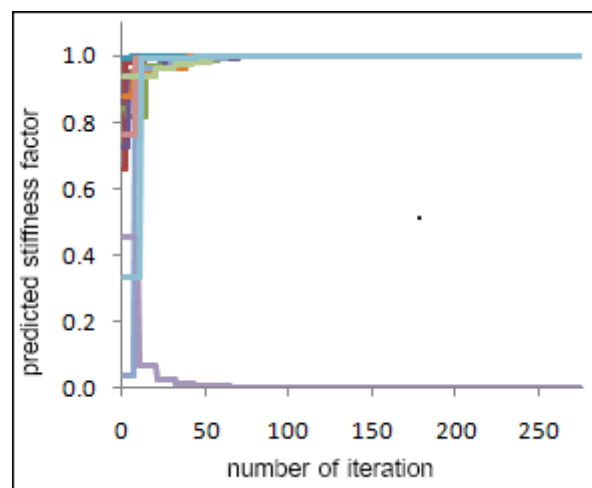


Fig. 4 Stiffness factor in case 3

Table 3 Comparison of stiffness factor in each case with simulated results and Rao et al. [3]

Element	Case 1			Case 2			Case 3		
	Exact	Rao et al.	CCGA	Exact	Rao et al.	CCGA	Exact	Rao et al.	CCGA
1	1	0.9882	1.00000000	1.0	0.9974	0.99999983	1	0.9882	0.99999959
2	1	0.9982	0.99999996	1.0	0.9784	0.99999953	1	0.9941	0.99999990
3	1	0.9833	0.99999964	0.3	0.3176	0.29989888	1	0.9804	0.99999944
4	1	0.9941	0.99999999	1.0	1.0000	0.99999963	1	1.0000	1.00000000
5	1	0.9902	1.00000000	1.0	0.9892	0.99999995	1	0.9941	0.99999999
6	1	0.9990	0.99999921	0.7	0.6920	0.70003016	1	0.9723	0.99999998
7	1	0.9912	0.99999980	1.0	0.9970	0.99999984	1	0.9920	0.99999987
8	1	1.0000	0.99999992	1.0	0.9361	0.99998622	1	0.9991	0.99999998
9	1	0.9981	0.99999959	1.0	1.0000	0.99999374	1	1.0000	0.99999995
10	1	1.0000	0.99998890	1.0	0.9853	0.99999739	0	0.0009	0.00000055
11	1	0.9983	0.99999990	1.0	0.9967	0.99999998	1	1.0000	0.99999996

6. Conclusion

Based on the findings on performance in terms of mathematical model as well as numerical experiments, CCGA satisfies this case of vibration-based damage detection better than conventional genetic algorithm. Therefore, more cases should be examined and compared to other algorithms in order to alternate or to cooperate different approaches efficiently.

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