

## Genetic algorithms in health monitoring of structures

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The development of real-time, in-service structural health monitoring and damage detection technique has recently attracted a large number of academic and industrial researchers. The basic concept of the frequency-based structural health monitoring technique is to monitor the variations in the structural natural frequencies changes caused by the presence of damage. The paper presents results on the identification of damage in composite structures via genetic search technique and changes in natural frequencies. Location and size of the damage are carried out by minimization of an error function involving the difference between calculated and measured natural frequencies. Simulation studies indicate that changes in natural frequencies and genetic algorithm allow to estimate delamination parameters (location and size) very accurate and fast.

### 1. Introduction

The field of system identification has become an essential part of many research and applications activities in the area of mechanical, aerospace, and civil engineering. Early detection of problems such as cracks, delaminations, loss of bond, and corrosion losses can reduce the potential for catastrophic failure, or structural deterioration beyond repair. The increasing complexity of structures and machinery, together with the requirement for rigorous safety and reliability aspects motivates a demand for effective methods for timely location of damages upon and within structures. Many of the recent advances in a damage detection are related to new developments in the area of advanced signal processing. For example, vibration suppression in space structures is very important because such systems are lightly damped, due to the material used and the absence of air damping. For the last ten years the genetic algorithm has become one of the most effective analysis tools available for damage detection. However, in this paper a genetic algorithm is proposed for the detection of both cracks and delaminations.

Genetic algorithm methods are generally very useful when investigating inverse problems, in this case the inverse problem requires the identification of the location and the magnitude of an instance of damage on the understanding that changes in certain key dynamic properties have already been ascertained. It should also be noticed that this sort of genetic algorithm technique allows the identification of damage without so-called

*learning*, which usually has to take place when neural networks are applied, these being rival techniques in this context. The genetic algorithm method is also very attractive in comparison with classical methods because it does not require a solution search within the whole solution space. Instead the algorithm starts from a small initial population of approximated solutions and converges rapidly from thereon.

## 2. Genetic algorithm and objective function

This section illustrates how the genetic algorithm approach can be used to solve what are considered to be continuous parameter estimation problems.

Genetic algorithms are essentially optimisation algorithms which evolve solutions in a manner based on the Darwinian principle of natural selection [1]. They differ from more conventional optimisation techniques in that they work on whole populations of encoded solutions, and each possible solution, (in this case each set of possible model parameters) is encoded as a gene.

The algorithm begins by making a collection of random guesses, noting that this grouping is called the population. Only two pieces of information are required to start the process off namely the size of each chromosome and the number of chromosomes. The latter relates to the population size and the former contains information on the binary code (i.e. the crack depth and location). Each solution is evaluated and scored, and the algorithm then generates a new population of guesses which are more likely to resemble the best-scoring individuals of the current generation. This new population is then evaluated and scored in a similar manner, and, over the course of several generations, the algorithm tends to converge on the failure parameters giving the best global score.

Genetic algorithms are particularly powerful when applied to combinatorial problems, and they use a domain-independent representation in the form of bit-strings to treat the problem in hand. In order to estimate the location of the damage genetic algorithms have been applied in this work, and it is relevant, even if somewhat obvious, to note that the total number of possible combinations for an arbitrary case of damage is, in fact, infinite.

### 2.1. Genetic algorithm

The Genetic algorithm is a search technique based on ideas from the science of genetics and the processes of natural selection. Differences between conventional search techniques and the genetic algorithm (GA) can be summarised as follows [1]:

- the GA operates on a coded form of the task parameters,
- the GA works with a population which represents numerical values of a particular variables,
- the GA only requires the use of an objective function,
- only probabilistic rules of selection are used with GAs.

A simple genetic algorithm consists of three basic operations, these being reproduction, crossover and mutation. The algorithm starts with the randomly generated initial population. The members of this population are usually binary strings called chromosomes. The binary coding system formally allows the use of positive numbers only.

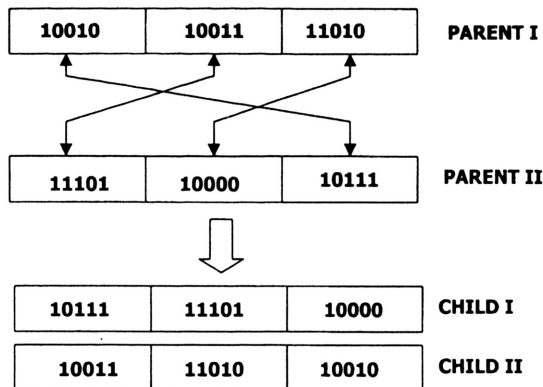
The transition to the real numbers set is achieved by the use of a linear representation from the range:  $[0, 2^N - 1]$  into the range:  $[U_{\min}, U_{\max}]$ . In this operation the resolution which can be worked to is defined by the following equation:

$$\lambda = \frac{U_{\max} - U_{\min}}{2^N - 1}.$$

Particular elements of chromosomes are called genes. In these strings are coded values of a variable, or variables, which can be a solution of the problem of interest in a relevant search space. These variables are then used to evaluate the corresponding fitness value, this being the objective function. In the next step chromosomes are appropriately selected for reproduction. The selection processes can be carried out in various ways. In practice one of the following methods would be used [1]:

- deterministic selection,
- random selection.

Irrespective of the adopted selection method the actual number of selected members will be a function of the fitness of the members. Thus individuals with higher fitness will achieve more copies. In order to minimise any premature convergence for initial populations special scaling methods can be applied [1]. One of the most widely applied methods is linear scaling, as proposed by Bagley [2]. After reproduction the process of crossover is undertaken next. There are many ways of implementing this idea [1]. Generally crossover with one, or many, crossover points can be used and these points are then selected randomly, usually using roulette wheel statistics. In this way certain portions are exchanged between selected *parent* chromosomes, and so two new *children* strings are created. A crossover with two points is illustrated below. In this example two crossover points, and the exchanged parts of the parents have been randomly selected. The genetic form of the two children strings depends on the direction of crossover, with crossover between the two parents potentially in either direction, as shown in the diagram by the double headed arrows.



Taking Parent I as an example it can be seen that the full chromosome is given by 100101001111010. In the diagram above this is divided into three parts, namely, 10010, 10011, and 11010. Alternatively, one might choose to divide the chromosome differently, perhaps like this: 1001, 0100111, and 1010. However, in this research it was decided to work with equal part lengths, as per the first division strategy in which five-bit parts

were chosen. A similar approach is applied to Parent II so that it becomes 11101, 10000, and 10111, as shown above. Therefore, in each case, there is a fifteen-bit string divided into three five-bit parts. The crossover points are defined here as being after five and ten and this gives rise to the crossover strings, as shown in the diagram above, in which Children I and II are generated by means of exchanged five-bit parts from the two parents.

The final process is mutation. Here a particular gene in a particular chromosome is changed randomly. In this context 0 is changed to 1, and vice versa. The process of mutation rarely occurs in nature, and so for this reason the probability of chromosome mutation is necessarily kept to a very low level when using genetic algorithms.

## 2.2. Objective functions

Objective functions are generally based on the following criteria:

- changes in natural frequencies [3, 4],
- changes in mode shapes [5, 6],
- changes in natural frequencies and mode shapes [7],
- changes in amplitudes of forced vibrations [8].

The most popular objective functions based on natural frequency change are the Cawley-Adams criterion [3], and the Damage Location Assurance Criterion (DLAC)[4]. Both of these criteria are based on comparisons between the changes in natural frequencies obtained both from measurements and from calculations.

The Cawley-Adams criterion is formulated as follows [3]:

$$e_s(p, q) = \frac{\delta \Omega_p / \delta \Omega_q}{\delta \omega_q(s) / \delta \omega_p(s)} - 1 \quad \text{if} \quad \frac{\delta \omega_p(s)}{\delta \omega_q(s)} \leq \frac{\delta \Omega_p}{\delta \Omega_q}, \quad (1)$$

$$e_s(p, q) = \frac{\delta \omega_p(s) / \delta \omega_q(s)}{\delta \Omega_p / \delta \Omega_q} - 1 \quad \text{if} \quad \frac{\delta \omega_p(s)}{\delta \omega_q(s)} \geq \frac{\delta \Omega_p}{\delta \Omega_q}, \quad (2)$$

$$e_s = \sum_{p=1}^{m-1} \sum_{q=1}^m e_s(p, q), \quad E_s = \frac{(e_s)_{\min}}{e_s}, \quad (3)$$

where  $\delta \Omega_i$  denotes the actual change in the natural frequency for mode  $i$  in the presence of some form of, as yet, unknown damage,  $\delta \omega_i(s)$  is the theoretical prediction of the change in natural frequency for mode  $i$ , and  $p, q$  define the mode number. The quantity  $e_s$  is defined as the Damage Index.

The DLAC criterion was proposed by Messina *et al.* [4] in the form,

$$\text{DLAC}(s) = \frac{|\{\delta \Omega\}^T \{\delta \omega_s\}|^2}{(\{\delta \Omega\}^T \{\delta \Omega\}) (\{\delta \omega_s\}^T \{\delta \omega_s\})}, \quad (4)$$

where  $\{\delta \Omega\}$  is the trial experimental frequency change vector and  $\{\delta \omega_s\}$  is the theoretical frequency change for damage at location  $s$ . In this criterion the quantity  $\text{DLAC}(s)$  is another form of defined Damage Index.



In the literature it is possible to find two criteria based on mode shape change. The first one is called the Modal Assurance Criterion (MAC) [5]. This criterion is given in the following form,

$$\text{MAC}(\phi_i, \phi_j) = \frac{|\phi_i^T \phi_j|^2}{\phi_i^T \phi_i \phi_j^T \phi_j}, \quad (5)$$

where  $\phi_i$  denotes the measurement eigenvector, and  $\phi_j$  represents the calculated eigenvector. The second criterion based on mode shape change is the Co-ordinate Modal Assurance Criterion (COMAC) [6],

$$\text{COMAC}(i) = \frac{\left[ \sum_{j=1}^N |\phi_{i,j}^A \phi_{i,j}^B| \right]^2}{\sum_{j=1}^N (\phi_{i,j}^A)^2 \sum_{j=1}^N (\phi_{i,j}^B)^2}, \quad (6)$$

where  $N$  is the number of mode shapes, and  $\phi_{i,j}^A$  and  $\phi_{i,j}^B$  denote the values of the  $j$ -th mode shape at point  $i$ , for, respectively, measurement data ( $A$ ), and calculation data ( $B$ ).

The Residual Force Criterion (RFC) belongs to those criteria based on natural frequency and mode shape change [7],

$$R_j = \mathbf{K} \phi_{d,j} - \omega_{d,j}^2 \mathbf{M} \phi_{d,j} = \sum_{j=1}^m \alpha_j K_j \phi_{d,j}, \quad (7)$$

where  $\omega_{d,j}$  and  $\phi_{d,j}$  are the  $j$ -th natural frequency and eigenvector, determined experimentally, and  $\mathbf{K}$  and  $\mathbf{M}$  are stiffness and mass matrices of the numerical model.

The Frequency Response Curvature Method (FRCM) is allied to those criteria based on changes in the amplitudes of forced vibrations [8],

$$\alpha_{ij}(\omega) = \frac{x_j(\omega)}{F_j(\omega)}, \quad \alpha''(\omega)_{i,j} = \frac{\alpha(\omega)_{i+1,j} - 2\alpha(\omega)_{i,j} + \alpha(\omega)_{i-1,j}}{h^2}, \quad (8)$$

$$\delta \alpha''_{i,j} = \sum_{\omega} |\alpha''_d(\omega)_{i,j} - \alpha''(\omega)_{i,j}|, \quad \sum_j \delta \alpha'' = \sum_j \delta \alpha''_{i,j}, \quad (9)$$

noting that  $h$  is the distance between locations of interest,  $i$ , and the  $\alpha_{i,j}$  is the receptance measured at the location  $i$ , for an input force at location  $j$ .

The objective function used in this paper is based on the DLAC criterion (see Eq. (4)). Changes in natural frequencies can be considered to be classical damage indicators and have been, without doubt, the most commonly used damage indicator for a long time now. The principal reason for this popularity is that natural frequencies are relatively easy to determine accurately. One sensor, placed on a structure and connected to a frequency analyser, can obviously provide meaningful data for several natural frequencies. Furthermore, natural frequencies are sensitive to all kind of damage, both local and global.

The DLAC values lie in the range 0 to 1, with 0 indicating no correlation and 1 indicating an exact match between the patterns of frequency changes. The value of ( $s$ ) giving the highest DLAC values determines the predicted damage location and size. This correlation coefficient provides superior prediction success rates when compared with the Cawley-Adams algorithm. The use of percentage frequency change data (rather than absolute changes) provides the best results. Problems remain when the level of damage is low. The presence of measurement error must obviously result in some sort of predictive degradation for the damage site, nevertheless experience shows that the method is capable of providing predictions with sufficient confidence to give useful warning of an impending problem. Verification can then be ascertained if the site prediction is subsequently confirmed by experimental measurements, or perhaps by the use of some other alternative predictive criterion.

### 3. Numerical examples

The numerical calculations were performed for two cantilever beams. The first example deals with a delaminated composite beam. The beam under consideration is of the following dimensions, length 400 mm, width 20 mm, and thickness 12 mm. It is assumed that the beam is made of twelve layers of glass-epoxy composite, for which the relevant mechanical properties are presented in Table 1. It is assumed that the beam is symmetrical, i.e. that all coupling terms in its governing equation are equal to zero. The orientation angles of the fibres are measured in the x-y plane of the beam and are defined, notationally, by  $(+45/-45)$ . The relative volume fraction of the fibres is defined as being typically 30% .

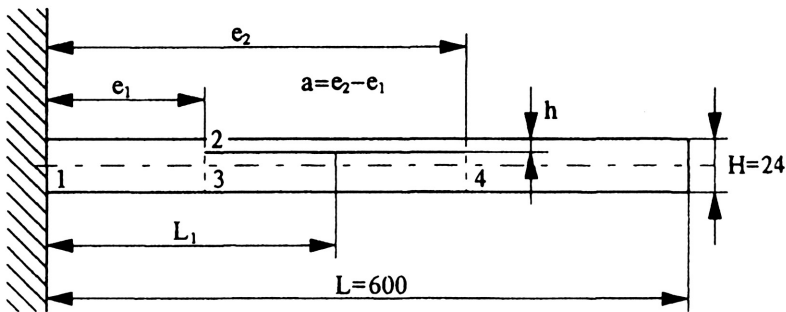


FIGURE 1. Schematic of a cantilevered multi-layer composite beam.

In the case considered here the length of the delamination is equal to 35% of the total beam length and is located between the 6th and 7th layers (i.e. on the neutral axis of the beam). The left end of the delamination is at 100 mm from the fixed end ( $e_1 = L_1/L = 0.25$ ), and the right hand end of the delamination is at 240 mm from the fixed end ( $e_2 = L_2/L = 0.6$ ).

In all cases the population contains 6 members and each member is 33 bits in length (11 for each variable, i.e. locations  $e_1$ ,  $e_2$ , and the location between the layers). During the numerical calculations it is assumed that the crossover probability is 95% and the mutation probability is 0.05% . The delamination length and location are identified

TABLE 1. Material properties of composite material components.

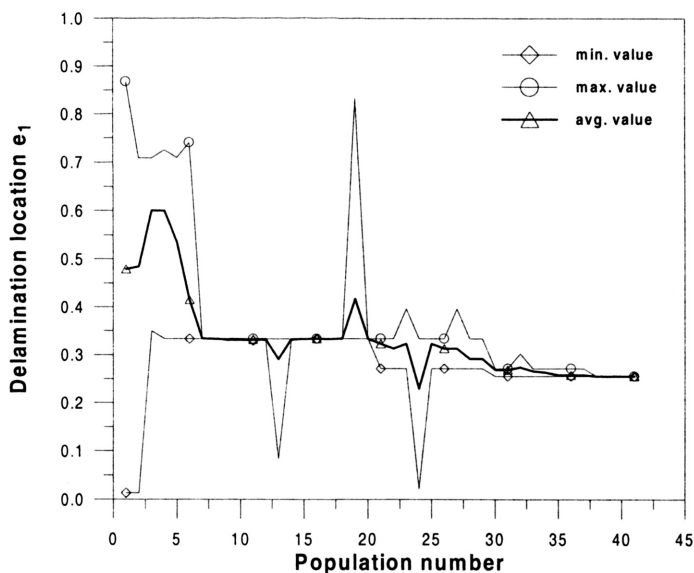
	Matrix-Epoxy	Glass-Fibre
Young modulus	$E_m = 3.43 \text{ GPa}$	$E_f = 66.5 \text{ GPa}$
Poisson ratio	$\nu_m = 0.35$	$\nu_f = 0.23$
Kirchoff modulus	$G_m = 1.27 \text{ GPa}$	$G_f = 27.0 \text{ GPa}$
Density	$\rho_m = 1250 \text{ kg/m}^3$	$\rho_f = 2250 \text{ kg/m}^3$

using the eigensensitivity approach and the first four natural frequencies are used in the numerical tests. Only one run of the genetic algorithm is necessary for each case. Numerical results are presented in Figs. 2-4.

From Figs. 2-4 it can be seen that the genetic algorithm correctly locates the damage and also correctly estimates the size. The convergence to proper results is obtainable in this problem after running no more than 45 populations.

The second example concerns a cracked steel cantilever beam of length 600 mm, width 10 mm, and height 20 mm. In all cases the population contains 6 members, each of length 30 bits (15 for each variable i.e. location and depth of the crack).

A typical convergence plot for a search conducted over both crack parameters (depth and location) is shown in Figs. 6 and 7. The figures indicate convergence well within the 100 generations shown. It is seen that an initially diverse population converges rapidly to the best location, as predicted by 0.1 and crack depth 0.05. The agreement shown here also indicates that the structural model, as well as the crack parameters, have been correctly identified.

FIGURE 2. Delamination location  $e_1$  as a function of the population number.

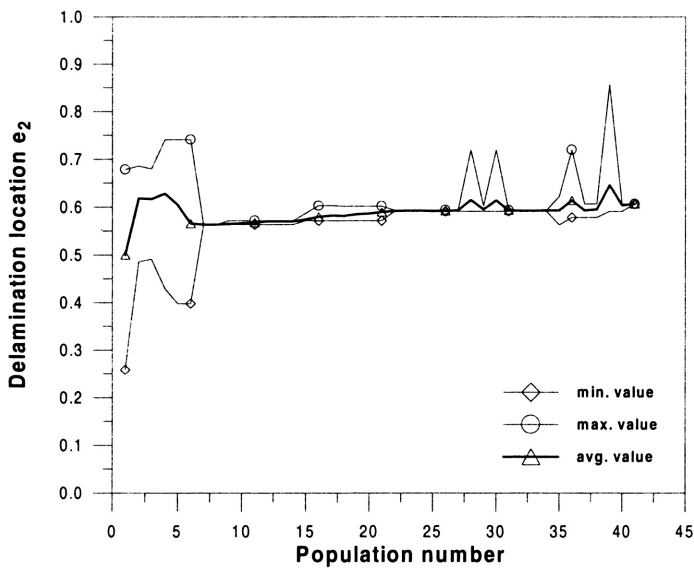


FIGURE 3. Delamination location  $e_2$  as a function of the population number.

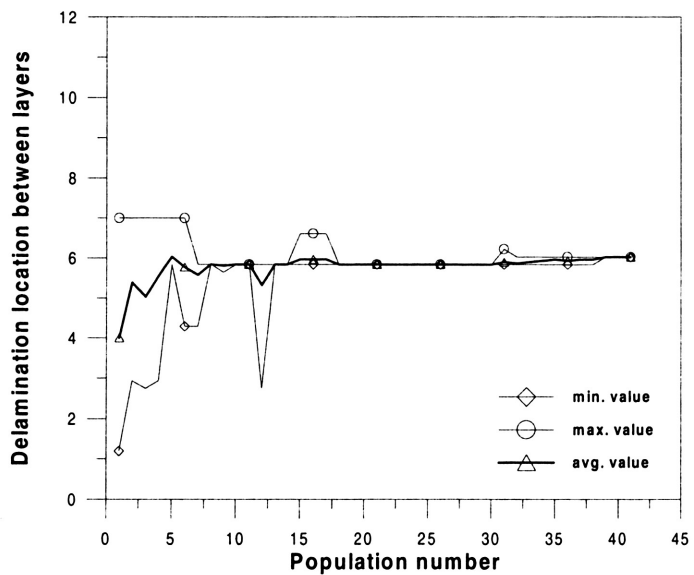


FIGURE 4. Delamination location between layers as a function of number of the population number

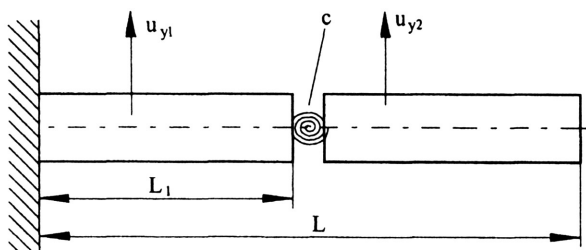


FIGURE 5. Schematic of a cracked cantilever beam.

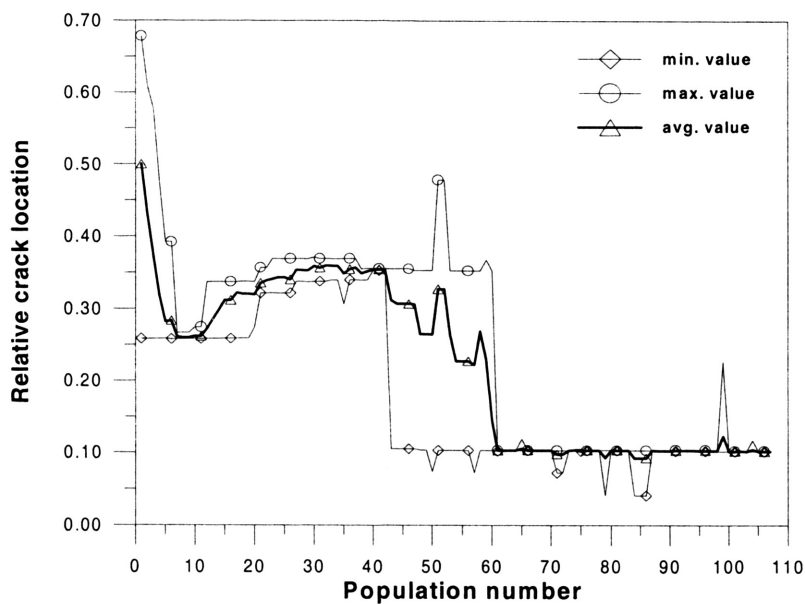


FIGURE 6. Relative crack location as a function of population number.

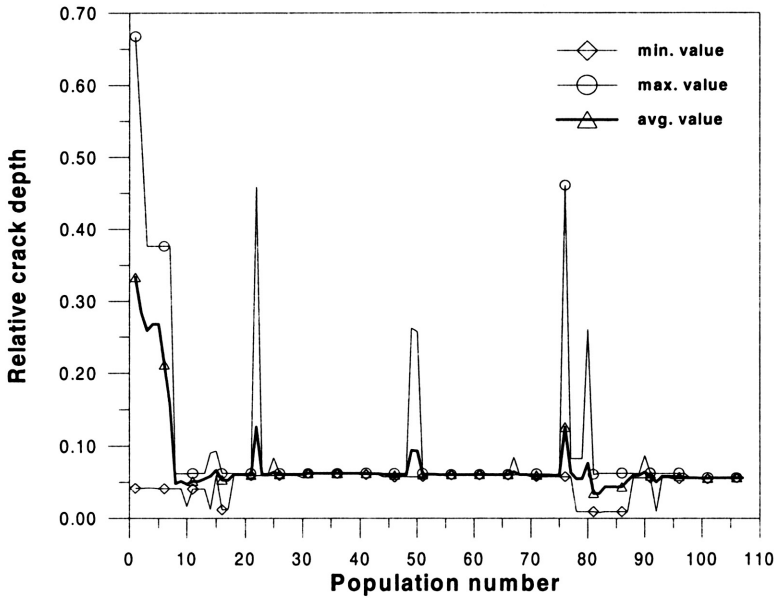


FIGURE 7. Relative crack depth as a function of population number.

#### 4. Conclusions

A genetic algorithm has been applied to the determination of the location and the magnitude of a delamination and also of a crack, both in a cantilever beam structure. Some modifications to the genetic algorithm have also been suggested in order to improve general searching efficiency. The examples illustrated shows overall high efficiency, and numerical stability, in the identification of damage.

This technique can be used for the analysis of a mechanical system in order to accurately determine the location of an example of damage and also a useful measure of its magnitude.

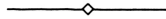
The results that have been obtained in this work are promising, particularly because the number of calculations needed for failure detection is much less than those required for classical search algorithms. For this reason the requisite computational time can be minimised.

Future work should be devoted to the implementation of naturally observable processes within this algorithm. It is intended that other vibration criteria, as applied to structural health monitoring and based on mode shape changes and also on the amplitudes of forced vibrations, will be investigated as possible objective functions. Such comparative analysis should indicate which damage indicator is most sensitive to changes in the stiffness of a structure as caused by damage.

The intention is eventually to employ such a method as a basis for an overall health monitoring system, and to this end two of the authors of this paper have already investigated several important models of failures, both in isotropic and anisotropic materials [9-11]. It is expected that unifying damage detection methodologies will ultimately emerge from this maturing programme of research.

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