

Evolutionary Algorithm in Identification of Stochastic Parameters of Laminates

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Abstract. The paper deals with the identification of material constants in multi-layered composites. Simple and hybrid (with laminas made of different materials) laminates are considered. Material constants are presented in a stochastic form to model their uncertainty. The Evolutionary Algorithm based on such representation of the data is used as the global optimization method. Chromosomes are represented by multidimensional random vectors consisting of random genes in the form of independent random variables with the Gaussian density probability functions. The stochastic optimization problem is replaced by a deterministic one by evolutionary computing of chromosomes having genes consisting of mean values and standard deviations. Modal analysis methods are employed to collect measurement data necessary for the identification. The Finite Element Method in stochastic version is used to solve the boundary-value problem for laminates. Numerical examples showing efficiency of the method are presented.

1 Introduction

Composites are materials constructed by joining (at least) two materials together on the macroscopic level. They usually consist of the matrix and the reinforcement. The resultant properties of composites depend on: i) the properties of phases; ii) the volume fraction of the reinforcement; iii) the distribution of the reinforcement in the matrix; iv) the geometry of the reinforcement.

The most commonly used group of composites are laminates – fibre-reinforced composites made of many layers (plies). The fibres are usually situated directionally in each ply of the laminate, but have different directions in particular plies. There are two main reasons of the popularity of laminates: i) the high strength/weight (or stiffness/weight) ratio, especially in comparison with the conventional, usually isotropic materials; ii) the possibility of designing the material properties according to the requirements by manipulating the components materials, stacking sequence, fibers orientation and layer thicknesses.

The cost of laminates quickly increases with their strength. To find the balance between cost and required properties, the plies in laminates may be composed of more than one material [1]. The laminates obtained in such a way are called the hybrid ones. The interply hybrid laminates with plies composed of two different materials are considered in the present paper. The internal

layers are built of a weaker and cheaper material while the external layers are made of a high-stiffness but more expensive material.

The aim of the paper is to identify material constants in multilayered, fibre-reinforced composites (laminates). Simple and hybrid laminates are taken into account. An identification problem can be formulated as the minimization of some objective functions depending on measured and calculated state fields. The identified material constants of laminates are assumed to be non-deterministic ones due to the manufacturing process. The uncertainties are introduced to decrease discrepancies between real structures and their mathematical model. The uncertainties can be introduced by using different granularity models, like interval numbers, fuzzy numbers or in the stochastic way [3]. The identification of the material constants in laminates with interval and fuzzy representation of the design variables was presented in [4, 5].

In the present paper the stochastic approach to identification is taken into account. The parameters are modelled by means of random variables characterized by probability density functions. The classical approach to the solution of such problems is based on stochastic programming [6]. In the proposed the evolutionary algorithm with stochastic representation of genes is used as the global optimization method.

2 The Formulation of the Stochastic Identification Problem

A general non-linear stochastic programming problem can be described as searching for a random vector [7]:

$$\mathbf{X}(\gamma) = [X_1(\gamma), X_2(\gamma), \dots, X_i(\gamma), \dots, X_n(\gamma)] \quad (1)$$

which minimizes the objective function $F(\gamma) = F(\mathbf{X}(\gamma))$ and satisfies the constraints:

$$P[g_j(\mathbf{X}) \geq 0] \geq p_j, j = 1, 2, \dots, m. \quad (2)$$

The probability space (Γ, \mathcal{F}, P) plays the basic role in the theoretical model of random phenomena [10]. The set Γ is called the space of elementary events and it represents all the possible simplest outcomes of a trial associated with a given random phenomenon. \mathcal{F} is a σ -algebra of subset of the set Γ and the elements of the \mathcal{F} are called random events. P denotes the probability defined on \mathcal{F} .

If the problem is solved by the evolutionary algorithm, the vector $\mathbf{X}(\gamma)$ is called a chromosome, where $\mathbf{X}(\gamma)$, $i=1, 2, \dots, n$, are random genes. Each gene is represented by a random variable, which is a real function $X_i = X_i(\gamma)$, $\gamma \in \Gamma$, defined on a sample space Γ and measurable with respect to P : i.e., for every real number x_i , the set $\{\gamma : X_i(\gamma) < x_i\}$ is an event in \mathcal{F} .

The chromosome $\mathbf{X}(\gamma)$ is a function (measurable with respect to P) which takes every element $\gamma \in \Gamma$ into a point $\mathbf{x} \in R_n$.

The mean value of the chromosome $\mathbf{X}(\gamma)$ is given as:

$$\mathbf{m} = \mathbf{E}[\mathbf{X}(\gamma)] = [m_1, m_2, \dots, m_i, \dots, m_n] \quad (3)$$

where:

$$m_i = \mathbf{E}[X_i(\gamma)] = \int_{\Gamma} X_i(\gamma) dP(\gamma) = \int_{-\infty}^{+\infty} x_i p_i(x_i) dx_i \quad (4)$$

is the mean value of the gene $X_i(\gamma)$ and $p_i(x_i)$ is the probability density function (PDF) of this gene.

The matrix of covariance is given as:

$$\mathbf{K} = [k_{ij}] = \mathbf{E} \left[(\mathbf{X}(\gamma) - \mathbf{m})^T (\mathbf{X}(\gamma) - \mathbf{m}) \right] \quad (5)$$

The covariance between $X_i(\gamma)$ and $X_j(\gamma)$ is defined as:

$$k_{ij} = \mathbf{E} \left[(X_i(\gamma) - m_i)(X_j(\gamma) - m_j) \right] = \int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} (x_i - m_i)(x_j - m_j) p(x_i, x_j) dx_i dx_j \quad (6)$$

where $p(x_i, x_j)$ is the joint PDF of $X_i(\gamma)$ and $X_j(\gamma)$. If $i = j$, the covariance is represented by a variance.

In the present paper the random chromosome $\mathbf{X}(\gamma) = [X_1(\gamma), X_2(\gamma), \dots, X_i(\gamma), \dots, X_n(\gamma)]$ consisting of n genes has a n -dimensional Gaussian distribution function. It is assumed that random genes are independent random variables. The joint probability density function is expressed by the probability density functions of single random genes:

$$p(x_1, x_2, \dots, x_i, \dots, x_n) = p_1(x_1)p_2(x_2)\dots p_i(x_i)\dots p_n(x_n) \quad (7)$$

where:

$$p_i(x_i) = N(m_i, \sigma_i) = \frac{1}{\sigma_i \sqrt{2\pi}} \exp \left[-\frac{(x_i - m_i)^2}{2\sigma_i^2} \right] \quad (8)$$

is the probability density function of the random gene $X_i(\gamma)$, σ_i denotes the standard deviation of $X_i(\gamma)$.

If the random genes $X_i(\gamma)$, $i=1,2,\dots,n$ are independent random Gaussian variables, the PDF function can be fully described by means of two parameters: the mean value m_i and the standard deviation σ_i .

Composites are anisotropic materials. Multilayered laminates can be usually treated as thin plates made of orthotropic materials. If the plies are distributed symmetrically to the mid-plane, the laminate is called symmetrical. Main advantage of such laminates is that there does not exist a coupling between shield and bending states [8]. The single ply of the laminate, being in the plane-stress state, has 4 independent material constants: axial and transverse Young's module (E_1, E_2), axial-transverse shear modulus (G_{12}) and axial-transverse Poisson ratio (ν_{12}). It is assumed, that material constants are random variables with Gaussian PDF.

The identification of the material constants can be treated as the minimization of the objective function F with respect to the vector of the design variables \mathbf{x} :

$$\min_{\mathbf{x}} (F), \quad \text{where: } F = \sum_{j=1}^N (q_j - \hat{q}_j)^2. \quad (9)$$

The functional F depends on N measured \hat{q}_j and N calculated q_j values of the state fields. It is assumed, that measured and calculated values of the state fields have stochastic character.

The identification results strongly depend on the number of measurement data. To reduce the number of sensors, the dynamic properties of laminates can be taken into account and the modal analysis methods can be employed. The eigenfrequencies are used as the measurement data [11]. The numbers of plies, their thicknesses, fibres orientation and the number of layers made of each material are assumed to be known.

3 Evolutionary Algorithm for Stochastic Problems

The application of evolutionary algorithms to solve stochastic optimization problems requires some modifications of the classical evolutionary approaches. The main reason is that chromosomes consist of random genes $X_i(\gamma)$, $i=1, 2, \dots, n$. As the results the genes are described by the moments, e.g. by the mean value m_i and the standard deviation σ_i (in the case of Gaussian independent random genes).

The main idea of presented Evolutionary Algorithm is analogous to the deterministic evolutionary algorithm [2], but all steps of the algorithm require some modifications due to the stochastic character of the data. Each individual (chromosome) in employed EA expresses a stochastic solution of the optimization problem. The fitness function value for each individual is evaluated and a stochastic value of the fitness function is obtained as the result of calculations. To calculate the stochastic fitness function value the Stochastic Finite Element Method (SFEM) is employed [9].

The original stochastic problem can be reduced to the deterministic one. Random chromosome $X_i(\gamma)$ can be replaced by a deterministic chromosome $ch^j(\mathbf{x})$ in which each gene x_i is a stochastic variable represented by 2 values: mean value and standard deviation: $x_i=(m_i, \sigma_i)$, $i=1, 2, \dots, n$ corresponding to the random variable $X_i(\gamma)$:

$$ch^j(\mathbf{x}) = [x_1; x_2; \dots; x_i; \dots; x_n] = [(m_1, \sigma_1); (m_2, \sigma_2); \dots; (m_i, \sigma_i); \dots; (m_n, \sigma_n)] \quad (10)$$

Two kinds of constraints are imposed for each chromosome $x_i=(m_i, \sigma_i)$, $i=1, 2, \dots, n$:

$$m_i^{\min} \leq m_i \leq m_i^{\max} \quad (11)$$

$$\sigma_i^{\min} \leq \sigma_i \leq \sigma_i^{\max} \quad (12)$$

where: *min* and *max* indices denote the maximum and minimum values of m and σ .

The selection method is based on the classical tournament selection. The minimization problem is taken into account. Consider the fitness functions for two different random chromosomes: $F_1(\gamma) = F(\mathbf{X}_1(\gamma))$ and $F_2(\gamma) = F(\mathbf{X}_2(\gamma))$. The random values $F_1(\gamma)$ and $F_2(\gamma)$ are described by the moments: $F_1(\gamma) \rightarrow (m_{F_1}, \sigma_{F_1})$ and $F_2(\gamma) \rightarrow (m_{F_2}, \sigma_{F_2})$, respectively. The parameters β_1 and β_2 , which decide about the probability of the survival of chromosomes: $\mathbf{X}_1(\gamma)$ and $\mathbf{X}_2(\gamma)$, respectively, are introduced. At the beginning of the parameters β_1 and β_2 are equal to β_0 (in considered case $\beta_0=0.1$). In the next step, the conditions:

$$m_{F_1} < m_{F_2} \quad (13)$$

$$\sigma_{F_1} < \sigma_{F_2} \quad (14)$$

are checked. If the conditions (12) and (13) are fulfilled, the probability of the survival of the first chromosome is increased by $\Delta\beta_m$ and $\Delta\beta_\sigma$, respectively (in present paper $\Delta\beta_m=0.7$, $\Delta\beta_\sigma=0.3$). In the contrary cases the probability of the survival of the second chromosome is increased by $\Delta\beta_m$ and $\Delta\beta_\sigma$, respectively. If the both stochastic values of the fitness functions are identical, the probabilities of the survival of both individuals are the same. Finally, the survived individual is sampled with respect to the survival parameters β_1 and β_2 .

The dedicated stochastic versions of mutation and crossover operators are also applied. Two types of the Gaussian mutation are introduced. In the first type of mutation the mean value m_i of the random gene $X_i(\gamma)$ is modified. In the second type of the mutation the standard deviation σ_i of the random gene $X_i(\gamma)$ is modified. A dedicated arithmetic crossover operator creating two offspring chromosomes from two parents is proposed for the stochastic evolutionary algo-

rithm. The evolutionary operators applied in presented EA are more comprehensively described in [7].

In considered case chromosomes have one of the following forms (the densities of materials also have to be identified in the case of hybrid laminates):

1. For simple laminates:

$$ch^i(\mathbf{x}) = (E_1, E_2, G_{12}, \nu_{12}) \quad (15)$$

2. For hybrid laminates (superscripts specify the material number):

$$ch^i(\mathbf{x}) = (E^1_1, E^1_2, G^1_{12}, \nu^1_{12}, \rho^1, E^2_1, E^2_2, G^2_{12}, \nu^2_{12}, \rho^2) \quad (16)$$

where ρ^i - the density of the i -th material.

4 Numerical Examples

4.1 Identification of the simple laminate

A rectangular simple laminate plate made of the glass-epoxy is considered (Figure 2a). Each ply of the symmetrical laminate has the same thickness $h_i=0.002\text{m}$. The stacking sequence of the laminate is: (0/45/90/-45/0/90/0/90)s. To solve the direct problem the plate is divided into 200 4-node plane finite elements. The first 10 eigenfrequencies ω_i of the plate are taken into account as the measurement data.

It is assumed, that measurement are random variables with the Gaussian distribution. The measurements were repeated 200 times to collect data. Each chromosome $ch_j(\mathbf{x})$ in population consists of 4 genes. Each gene x_i in chromosome $ch_j(\mathbf{x})$ is a random number represented by 2 moments: mean value m_i and standard deviation σ_i .

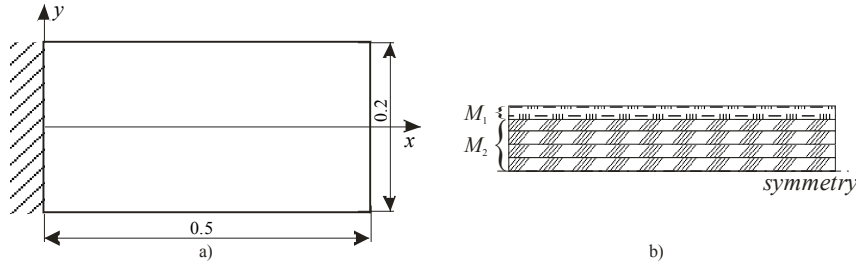


Figure 2. a) The laminate plate a) shape and dimensions; b) materials location in hybrid laminate.

The parameters of the EA (experimentally selected) are:

- the number of chromosomes $pop\ size = 200$;
- the number of generations $gen_num = 400$;
- the arithmetic crossover probability $p_{ac} = 0.2$;
- the gaussian mutation probability: $p_{gm} = 0.4$.

The variable ranges, actual values and identification results are collected in Table 1.

Table 1. Identification results for the simple laminate.

	E_1 [Pa]		E_2 [Pa]		ν_{12}		G_{12} [Pa]	
	m	σ	m	σ	m	σ	m	σ
Min	2.00E10	0.00E9	4.00E9	0.00E9	0.00	0.00	2.00E9	0.10E8
Max	6.00E10	0.30E9	9.00E9	0.30E9	0.50	0.10	6.00E9	0.70E8
Actual	3.86E10	0.12E9	8.28E9	0.20E9	0.26	0.02	4.14E9	0.50E8
Found	3.92E10	0.11E9	8.14E9	0.17E9	0.27	0.04	4.07E9	0.22E8

All material parameters, represented by mean value and standard deviation, have been found with satisfactory precision.

4.2 Identification of the hybrid laminate

A rectangular hybrid laminate plate of shape and dimensions presented in Figure 2a) is considered. Each ply of the laminate has thickness $h_i = 0.002\text{m}$. The symmetrical laminate plate consists of 10 plies of the stacking sequence: (0/15/-15/45/-45)_s. The external plies of the laminate are made of material M_1 , the internal laminas are made of the material M_2 (Figure 2b). The plate FEM model consists of 200 4-node plane finite elements. The first 10 eigenfrequencies of the plate are considered.

It is assumed, that measurement data have stochastic nature and they are described by the normal distribution. The measurements were repeated 200 times to collect data. Each of 10 genes x_i in chromosome $ch_i(\mathbf{x})$ is a random number represented by 2 moments: mean value m_i and standard deviation σ_i .

The parameters of the EA (experimentally selected) are:

- the number of chromosomes $pop\ size = 400$;
- the number of generations $gen_num = 1200$;
- the arithmetic crossover probability $p_{ac} = 0.2$;
- the gaussian mutation probability: $p_{gm} = 0.4$.

The variable ranges, actual values and identification results are collected in Table 2 for material M_1 and in Table 3 for material M_2 .

Table 2. Identification results for the hybrid laminate – material M_1 .

	E_1 [Pa]		E_2 [Pa]		ν_{12}		G_{12} [Pa]		ρ [kg/m ³]	
	m	σ	m	σ	m	σ	m	σ	m	σ
Min	2.00E10	0.00E9	4.00E9	0.00E9	0.00	0.00	2.00E9	0.10E8	1.00E3	0.00E2
Max	6.00E10	0.30E9	9.00E9	0.30E9	0.50	0.10	6.00E9	0.70E8	3.00E3	0.50E2
Actual	3.86E10	0.12E9	8.28E9	0.20E9	0.26	0.02	4.14E9	0.50E8	1.80E3	0.20E2
Found	3.75E10	0.04E9	8.12E9	0.28E9	0.25	0.04	4.21E9	0.61E8	1.81E3	0.17E2

Table 3. Identification results for the hybrid laminate – material M_2 .

	E_1 [Pa]		E_2 [Pa]		ν_{12}		G_{12} [Pa]		ρ [kg/m ³]	
	m	σ	m	σ	m	σ	m	σ	m	σ
Min	1.20E11	0.00E10	0.80E10	0.00E10	0.00	0.00	2.00E9	0.10E8	1.00E3	0.00E2
Max	2.50E11	0.30E10	2.00E10	0.30E10	0.50	0.10	9.00E9	0.70E8	3.00E3	0.50E2
Actual	1.80E11	0.12E10	1.00E10	0.20E10	0.28	0.02	7.10E9	0.50E8	1.60E3	0.20E2
Found	2.01E11	0.18E10	0.89E10	0.18E10	0.31	0.01	6.89E9	0.52E8	1.63E3	0.19E2

All material parameters for both materials (M_1 and M_2) of hybrid laminate have been found with acceptable precision.

5 Final Conclusions

An efficient identification method based on the stochastic representation of the identified parameters has been presented. A global optimization method in the form of the Evolutionary Algorithm has been employed to solve the identification task for simple and hybrid laminates. Presented EA works on the stochastic genes converted to deterministic ones by representing stochastic variables by two moments: the mean value and the standard deviation. Positive identification results have been obtained for simple as well as for hybrid laminates.

The future work is to combine global optimization methods with local ones. To reduce inconveniences connected with the necessity of the fitness function gradient calculations, it is possible to employ Artificial Neural Network (ANN). This attitude was successfully tested on the fuzzy and interval representation of the identified parameters [5]. The EA is used in the first step; afterwards the local optimization method supported by ANN is employed to finish the computations. The ANN is used to approximate the fitness function and the fitness function gradient.

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