IDENTIFICATION OF ELASTIC PROPERTIES OF ORTHOTROPIC MATERIALS USING EVOLUTIONARY ALGORITHMS

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ABSTRACT

The purpose of this paper is to present a numerical method to identify the linear elastic properties of orthotropic materials, as a part of a hybrid numerical-experimental model. The proposed numerical method is based on finite element analysis and evolutionary algorithms. This method, combined with full-field displacement measurement techniques, will allow the identification of all the in-plane elastic properties from one single test. The off-axis tensile test was chosen, and in order to calibrate the numerical method the wood pine lodgepole was selected. A reference displacement field generated by finite element method, using ANSYS 5.6.2 [®] package, takes the place of experimental data. An optimization algorithm based on Genetic Algorithms (GAs) was developed, which combines the reference displacement field with a search technique to find the true material properties. An initial population was randomly generated, and successive generations were created using the genetic operators (Selection, Crossover, Mutation, Elimination and Implicit Mutation). The set of elastic properties corresponding to a possible solution of the problem was used in the off-axis tensile test model and the corresponding nodal displacements were calculated using finite element analysis. An objective function was chosen in order to minimize the mean quadratic difference between the reference displacement field and that one obtained according to the proposed method.

1. INTRODUCTION

Four independent elastic properties are needed to fully describe the in-plane mechanical behaviour of an orthotropic material [Robert (1975), Tsai and Hahn (1980), Isaac and Ori (1994)]: E_1 , E_2 , v_{12} and G_{12} , where the subscripts are refered to the material axes (see fig. 1). Usually, three experimental tests to determine the in-plane elastic properties of orthotropic material are employed: two tensile tests in the material directions (directions 1 and 2) and one in-plane shear test. The tensile tests allow the identification of *Young* moduli (E_1 and E_2) and the *Poisson*'s ratio (v_{12}), while the in-plane

shear test allows the identification of the shear modulus (G_{12}) .

There are several test methods to obtain the shear moduli of an orthotropic material. Three of the commonly used tests are the off-axis tensile test [Chamis and Sinclair (1977), Pindera and Herakovich (1986), Kawai et al. (1997), Sun and Berret (1998)], the Iosipecu test [Walrath and Adams (1998), Liu (2000), (1983), Pierron Yoshihara (2001)] and the Arcan test [Hung and Liechti (1997)]. The off-axis tensile test was used in this study. In order to extract the material properties from this test, it is desired to produce a uniform state of both stress and strain throughout the specimen gauge-section. However this goal is very difficult to achieve, if not impossible. In fact, when a tensile load is applied to offaxis specimens under rigid end constraints, deformation field inhomogeneous an develops in the gauge-section due to the extension-shear coupling effect [Sun and Berret (1998)]. Such inhomogeneity generally leads to errors in the determination of shear modulus.

The inhomogeneity of the displacement field produced in off-axis tensile tests, although not desired for the purpose of shear modulus determination, gives enough information to identify all the in-plane elastic properties. To achieve this goal a measurement technique of the displacement field must be employed in combination with a suitable optimization procedure.

In recent years the devolopment of a number of optimization methods that direct towards the search of the global optimum, has been attending. These methods can be categories: classified into two main deterministic and stochastic methods. The selection of an optimization method should be done according to the characteristics of the specific problem and the results desired. This could include the nature of the design variables (discrete or continuous or a combination of both), the nature of the objective function (which can not be differentiable) and the nature of the desired result (all or several of the local minima could be required) [Potgieter and Stander Genetic algorithms (GAs) are (1998)].

stochastic methods used to solve discrete problems. An advantage of these methods compared with the gradient-based methods is that they do not require continuity or differentiability of the objective function. GAs date back about two decades to the research of De Jong (1975) and Holland (1975) in the area of genetic and adaptive systems [Potgieter and Stander (1998)]. Since then, these methods have been used in a variety of fields such as biology, computer science and social sciences. More recently, GAs were introduced in engineering design [Potgieter and Stander (1998)].

In the present work a numerical method was developed, as a part of a hybrid numerical-experimental method, in order to obtain the in-plane elastic properties of method materials. The orthotropic developed includes a genetic algorithm and a finite element analysis, performed using the commercial code ANSYS 5.6.2 [®]. This method was applied to the off-axis tensile test and the wood pine lodgepole. Α reference displacement field was also generated using the ANSYS package, which plays the role of experimental data.

2. OFF-AXIS TEST MODELLING

The orthotropic material considered in this work is the wood pine *lodgepole*, with the in-plane elastic properties presented in table 1 [FPL (1999)]. The material direction 1 is the longitudinal (L) direction along the fibres, while the material direction 2 is the radial (R) direction towards annual growth rings.

Figure 1 shows the geometry and the dimensions of the off-axis specimen, subjected to a uniaxial tensile loading in the X direction. The angle between the applied

Table 1. Elastic properties of wood pine lodgepole.

E_1 (GPa)	E_2 (GPa)	<i>v</i> ₁₂	G_{12} (GPa)
10,120	1,032	0,316	0,496

load and the L direction was chosen to be $\theta = 20^{\circ}$.

The off-axis tensile test was simulated by the finite element method, using the software *ANSYS*, in order to obtain a reference displacement field, corresponding to the elastic properties of table 1. This displacement field plays the role of experimental data used to calibrate the numerical method presented in this work.



Fig. 1 – Off-axis specimen's geometry and dimensions.

Figure 2 shows the finite element model of the off-axis specimen. The boundary conditions applied to the numerical model are in agreement with the rigid and nonrotating testing machine grips. In the right end of the specimen it was prescribed a nodal displacement u_x of 0,5 mm.



Fig. 2 – Off-axis tensile test model.

The above numerical simulation of the off-axis tensile test leads to the results shown in figure 3. As can be seen both u_x and u_y reference displacement fields are heterogeneous. It can also be observed the typical "S" deformed shape of off-axis specimen under uniaxial tensile loading.



Fig. 3 – Reference displacement field obtained by finite element method: (a) displacement field u_x and (b) displacement field u_y .

3. GENETIC ALGORITHMS

3.1 Introduction

GAs are search algorithms based on natural selection and natural genetic phenomena. Successive generations evolve more fit individuals based on Darwinian survival of the fittest. They simulate such natural evolution, where the environment is substituted by the problem that must be solved and the organisms are represented by the possible solutions of that problem [Goldberg (1989), Carroll (1999)].

A GA for a particular problem must have the following components [Michalewicz (1996)]:

- a genetic representation for potential solutions to the problem;
- a way to create an initial population of potential solutions;

- an evaluation function that plays the role of the environment, rating evolution according to their *fitness*;
- genetic operators that alter the composition of an offspring;
- parameter values to use in the genetic algorithm (population size, probability of applying genetic operators, etc.).

In GAs each individual in the population is represented by a finite string of symbols, encoding a possible solution in a given problem space. This space, referred to as the comprises search space, all possible solutions of the problem at hand. Traditional GAs deal with fixed length strings of symbols, which are called chromosomes (representation of solutions), and have the same number of individuals in successive generations. Each position in the string is associated to a gene. A set of genes, occupying a defined position in the string, represents the codification of a particular design problem (real or binary representation). As far as GAs are concerned, a gene can be any symbol, although, for both practical and theoretical convenience, the natural numbers are usually used; the binary gene {0,1} is an example. The genetic code in an algorithm is specified either by the length of a string and the genes along it or by a mapping between the strings and the possible solutions to the problem [Field (1999)].

GAs start with a population of individuals called the initial population, randomly generated. By applying the genetic operators (Selection, Crossover and Mutation), a combinatory process is done. Each individual belonging to the initial population is decoded, and evaluated according to some defined quality criterion, referred to as fitness function. Ranking of such individuals is done afterwards. Then, pairs of strings, among these initial solutions, are randomly Selected and each of them subjected to Crossover and Mutation, producing offsprings that will be decoded and their fitness calculated. After that, a new Ranking of solutions is performed and the fittest individuals will constitute the new

population. The process will continue until the convergence of the algorithm is achieved. When the stopping criterion is verified, the global optimum is supposed to be the solution that is decoded from the chromosome of the fittest solution [Field (1999), Sipper (2000)].

3.2 Problem formulation in the GA context

In the context of GAs, each solution for a problem, is defined by a set c of design variables, a_i , which identify the sequence A of real numbers [Galante (1996)]:

$$A = a_1 \times a_2 \times \ldots \times a_c = \prod_{i=1}^c a_i \quad , a_i \in \mathrm{IR} \; . \tag{1}$$

The number of solutions available for each a_i is defined, limiting the size of their search space. Afterwards the encoding of each a_i in a binary string is established, and the length of the binary string, l_{ci} , reserved for the variable a_i , is determined according to the equation [Jenkins (1993)]:

$$l_i = 2^{l_{c_i}}$$
, (2)

where l_i represents the total number of positions on the binary string corresponding to the variable a_i . For each binary representation of a solution a_i , corresponds, after decoding, a position p_i . This position allows the calculation of the real value of that solution belonging to the respective domain:

$$a_i = \underline{a}_i + \frac{\overline{a}_i - \underline{a}_i}{l_i - 1} \times p_i \quad . \tag{3}$$

In this equation \underline{a}_i and \overline{a}_i are, respectively, the lower and upper limits of the values assumed by the design variable a_i .

Encoding each a_i to binary code turns the phenotype structure into a string of bits, called chromosomes [Galante (1996)]:

$$A(t) = \prod_{i=1}^{c} a_i = \prod_{i=1}^{c} \left(e: a_i \longrightarrow \{0, 1\} \right)$$
(4)

An evolutionary process (t = 0, 1, 2, ...)should be able to modify the population of solutions, A(t), in order to achieve better performance in an interation with the environment conditions, E.

GAs, as Evolutionary Theories preconize, need to receive information, I(t), about the adaptation of the population, A(t), to its environment E (see fig. 4). By this way GAs successively modify the population, achieving a progressively better adaptation to the surrounding environment. In general terms, GAs can be formulated as [Galante (1996)]:

$$GA: A(t) \times I(t) \longrightarrow A(t+1).$$
(5)

The initialization process consists on the creation of an initial population of chromosomes randomly generated. Each chromosome is then evaluated according to the defined objective function, y(A), showing its adaptability to the environment in which it is inserted, E. Since GAs seek to increase *fitness* while it operates, a *fitness* function, f(A), was defined as [Jenkins (1993)]:

$$f(A) = k - y(A), \tag{6}$$

k being an arbitrarily large positive value that ensures that *fitness* f(A) never becomes negative.

Figure 4 resumes the GA process. After the creation of an initial population of potential solutions, randomly generated, the algorithm proceeds evaluating its *fitness* and creating a new population of equal size. Individuals of the new population will be elaborated from those of the proceeding one after subjecting them to the set of genetic operators. Offsprings *fitness* evaluation is done and the results are compared with reference values. The algorithm stops when a solution value is close enough to the reference value.



Fig. 4 – Genetic Algorithm process scheme.

4. IDENTIFICATION OF ELASTIC PROPERTIES USING GAS

4.1 Problem formulation

When a body is loaded, a material point that initially occupies the space point Q_i , will displace to another space point Q_i , and the associated displacement vector is represented by $\overline{u}(Q_i)$ (see fig. 5). Considering the off-axis tensile test examined in this work, the experimental displacement field was replaced by the nodal displacement values numerically determined using *ANSYS* (see fig. 3 *a* and *b*):

$$\vec{u}_i = \vec{u}_i(x_i, y_i)$$
 $i = 1, ..., N$, (7)

where N represents the total number of nodes on the XY plane of the off-axis specimen (see fig. 2).



Fig. 5 – Reference displacement $\vec{u}(Q_i)$ of a generic material point Q_i , and displacement $\vec{u}(Q_i^j)$ calculated for the *j* solution generated by the GA.

The mechanical properties of wood pine lodgepole (see table 1) establish the relationship between the load applied to the off-axis specimen and the displacement field. These properties are the design variables in the numerical identification method developed in this study. The in-plane elastic properties are represented, in the present GA, by the sequence:

$$A = \prod_{i=1}^{4} a_i = E_1 \times E_2 \times v_{12} \times G_{12} \quad , a_i \in \text{IR} .$$
(8)

The domain of each variable was specified as follows:

$$\begin{split} E_1 &\in [9020, 15070] \times 10^6 \ (Pa), \ E_1 \in \mathrm{IN} \\ E_2 &\in [867, 1537] \times 10^6 \ (Pa), \ E_2 \in \mathrm{IN} \\ v_{12} &\in [280, 392] \times 10^{-3}, \ v_{12} \in \mathrm{IN} \\ G_{12} &\in [400, 1351] \times 10^6 \ (Pa), \ G_{12} \in \mathrm{IN} \ . \end{split}$$

The lower and upper limits for each variable were chosen according to the values of the elastic properties of *pinus* species [FPL (1999)]. Thus, each domain is representative of the corresponding design variable for such species.

According to equation (2), the length of the binary string reserved for each variable is:

$$E_1 \rightarrow l_{c1} = 13$$
, $E_2 \rightarrow l_{c2} = 10$,
 $v_{12} \rightarrow l_{c3} = 7$, $G_{12} \rightarrow l_{c4} = 10$.

A number of individuals in each generation are chosen. These individuals represent possible solutions to the problem, *i.e.*, a set of elastic properties available for the orthotropic material.

Possible solutions obtained by the GA are decoded, originating a set of in-plane properties: $P^{j} = \left\{ E_{1}^{j}, E_{2}^{j}, v_{12}^{j}, G_{12}^{j} \right\}, \quad j=1, 2, 3, \ldots$ For each set of properties the off-axis tensile test model was again analysed in the *ANSYS* finite element package, and their nodal displacement field $\vec{u}(Q_{i}^{j})$ was calculated (see fig. 5).

The objective function to be minimized was the quadratic mean difference between the reference displacement field, $\vec{u}_i(x_i, y_i)$, and the displacement field obtained for the *j* solution generated by the GA, $\vec{u}_i^j(x_i, y_i)$:

$$y(A) = \frac{1}{N} \left\{ \sum_{i=1}^{N} \left\| \vec{u}_{i}^{j} - \vec{u}_{i} \right\|^{2} \right\}.$$
(9)

* 1× 1

The *fitness* value of each solution is evaluated and registered during the evolution process, according to equation (6). The process is interrupted when the stopping criterion is verified. The global optimum represents the best solution found in the last generation. Figure 6 shows a schematic drawing of the developed numerical method.



Fig. 6 – Schematic drawing of the numerical method.

4.2 Genetic operators

GAs are under evolution and researchers are trying to improve them in a way that enables increasingly efficiency, better adaptation to different types of optimization problems and more easily convergent [Kallassy and Marcelin (1997)]. Having this in mind, some improvements have been made in the set of classic elastic operators, which will be exposed on the sequence.

4.2.1 Selection

After the Ranking of the solutions, according to their objective function values, the total number, n, of solutions from the population are divided in three sub-groups composed by an even number of solutions: n_T , n_M and n_B (see fig. 7).



Fig. 7 –Order of the Solutions after Ranking.

According to the technique used by the Selection operator (see fig. 7), n_T solutions from S_T subgroup may couple together or with the ones belonging to S_M , following a random logic and resulting in a number of couples equal to the number of solutions of S_T subgroup. Bigamy can occur within this group of solutions. S_M subgroup if then half divided resulting two sets of n_{MS} and n_{MI} solutions. n_{MS} solutions are coupled with the n_{MI} . This set of couples are also randomly arranged, but, unlike the previous set, run without the occurrence of bigamy. S_B subgroup is not coupled.

4.2.2 Crossover

Crossover operator is responsible for the elaboration of the genetic material of a new generation of solutions, created from the set of chromosomes, which belong to a list of mating pairs, randomly generated mentioned in 4.4.1. This operator starts generating a random number, r_i , within the range of the length of the design string (see fig. 8). This number is used to indicate the position of the cross-site in both mating strings. Then, all the gene values from one mating element are copied to the child element till r_i . The remaining sub-string is copied from the other mating element. Offspring generation enhances the design space exploration, in a way such that corresponds to a continuous seeking of the global optimum.



Fig. 8 – Crossover scheme representation.

4.2.3 Mutation

Mutation operator is carried out by randomly flipping one gene in a chromosome of a recently generated solution. Mutation operates with a predefined probability, p_m . Figure 9 exhibits the Mutation process.

Fig. 9 – Flipping genes in a chromosome.

Thus Mutation operator allows the reposition of some information eventually lost in Crossover, and enables the search of solutions, which also belong to the search space. This operator is although of secondary importance so it has been attributed a small probability to occur.

4.2.4 Elimination

Once Selection, Crossover and Mutation process has been concluded, *fitness* of new solutions (offspring) is evaluated. This appreciation enables the accomplishment of a new Ranking of solutions, verifying the inclusion of a greater number of positions and a new order (see fig. 10). The ascension of a new solution to a top position in this Ranking, will not allow their elimination by . "natural selection".

Consecutively, all the solutions that occupy the half inferior positions from the list represented in figure 10 (b), are eliminated. This operation simulates the natural selection of individuals, acting as a natural agent for the exclusion of the less fit individuals [Dourado (2000)].



Fig.10 – Solutions arrangement: (a) before Ranking and (b) after Ranking.

4.2.5 Implicit mutation

The observation that migration streams in biological systems constitute a catalyze agent on genetic diversity of an amphitryon population, provide a model to the elaboration of a strategy of a population genetic diversity reinforcement. This undertaking reinforcement effort consisted in the restitution of the original population size, n, generating a set of $n - (n_T + n_M)$ solutions randomly generated.

4.3 Stopping criterion

The stopping criterion was established in terms of the relative error calculated for each elastic property and a maximum number of generations with constant *fitness* value. The convergence of the algorithm is reached when the obtained values of relative error were less then 22% (the value of the coefficient of variation of each elastic properties [FPL (1999)]) and accounted 15 generations without any *fitness* value changing.

4.4 Algorithm synthesis

Figure 11 resumes all the steps previously described.

5. RESULTS AND DISCUSSION

During the convergence of the genetic search, the minimum value of the objective function in each generation is registered. When the stopping criterion is satisfied, the global optimum is supposed to be the decoded solution that occupies the first position in the ranking of solutions. In this study a total of 115 generations were obtained, and the evolution of fitness of the best solution in each generation can be appreciated in figure 12. Table 2 shows the elastic property found by the optimization algorithm. For each elastic properties the relative error between its true value and the value found by the GA was less than 22 %, that is, less than the coefficient of variation associated to the experimental identification of elastic properties of wood species [FPL (1999)].

As can be seen in table 2, a good approximation was reached for E_1 , E_2 and G_{12} . However a great relative error for v_{12} was found. This result is probably related to the information content in the reference displacement field. Indeed, the contribution of the Poisson ratio to the response of the test specimen can be less decisive than the contribution of other elastic properties. In order to check this idea, the influence on the value of the objective function of each inplane elastic property was study. The objective function was calculated for four sets of elastic properties (see table 3), each of them differing from the optimum solution only in one elastic property, which assumes its upper limit value. It was concluded that the objective function is significantly

influenced by E_1 , E_2 and G_{12} , and slightly influenced by v_{12} (see table 3). This can explain the smaller convergence of the method for v_{12} .



Fig. 11 – Scheme of the genetic algorithm developed.

 Table 2 –Elastic properties obtained according to the numerical method.

Design variables	Elastic properties: (pine lodgepole)	Elastic properties (numerical method)	Relative error [%]
E_1 [<i>GPa</i>]	10,120	10,455	3,31
E_2 [GPa]	1,032	1,030	0,19
<i>V</i> ₁₂	0,316	0,372	17,72
<i>G</i> ₁₂ [<i>GPa</i>]	0,496	0,519	4,64

Individuals belonging to the last generations indicate two different groups of in-plane elastic properties with minimum objective functions, where, one of each converges to the true values and the other one has a set of properties not desired. This observation can indicate the presence of local minima.

According to result obtained, the solution of the problem is not probably sufficiently matured.

Table 3 –	Variation	of the	objective	function	with
	each o	design	variable.		

E_1 [<i>GPa</i>]	E_2 [GPa]	<i>v</i> ₁₂	G ₁₂ [GPa]	Objective function
10,455	1,030	0,372	0,519	4,399×10 ⁻⁶
15,070 ¹	1,030	0,372	0,519	1,288×10 ⁻⁴
10,455	1,537 ¹	0,372	0,519	4,515×10 ⁻⁵
10,455	1,030	0,392 ¹	0,519	6,845×10 ⁻⁶
10,455	1,030	0,372	1,351 ¹	3,093×10 ⁻⁴

¹ Upper limit of the domain associated with the design variable

6. CONCLUSIONS

work numerical In the present a identification method of the in-plane elastic properties of orthotropic materials was developed, to be included in a hybrid numerical-experimental technique. The purposed method relies on the off-axis tensile test, and includes the finite element method and genetic algorithms. In order to calibrate the method the wood pine lodgepole was selected and a reference displacement field was obtained simulating the off-axis tensile test in the ANSYS finite element package.



Fig. 12 – Fitness evolution of the best solution.

A genetic algorithm was implemented in Each possible solution FORTRAN 77. generated by this algorithm represents admissible in-plane elastic properties of the wood pine lodgepole in the LR plane. For each set of properties the nodal displacement field was evaluated using the ANSYS This displacement field was package. compared with the reference displacement field through an objective function. The selected objective function to be minimized evaluates the mean quadratic difference between the reference displacement field and that one obtained by the optimization method.

The convergence of the presented method led to good approximation of E_1 , E_2 and G_{12} . Relatively to v_{12} , a great relative error was found, although even less than the 22% of the coefficient of variation associated to the experimental identification of the elastic properties of wood species.

Further developments should be done in order to improve the method presented above. Some aspects are:

- development of other schemes of Crossover, in order to accelerate the convergence;
- implementation of a different off-axis tensile test in order to extract more information from the displacement field;

- evaluation of alternative objective functions that are more equally sensible to all elastic properties;
- analysis of the numerical method sensibility to experimental errors.

Although the reference displacement field was numerically obtained, in the future fullfield displacement measurement techniques should be used.

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APPENDIX

Pseudo-Algorithm

The implementation of the current GA is given below. The symbols are defined as follows: Integer counters, *iteri*, *i*, *j*, *k*, n_l , n_{li} , n_T , n_i and i_l ; length of the design vector string, *l*; random number, $ran \in [0,1]$; objective function, y(A); population size, *n*; number of elitist solutions, n_T ; number of solutions belonging to group S_B , n_B (see fig. 7); chromosome matrix, **pop**[*i*, *j*]; required information, *inf*; state variables vector, **s**; solutions *fitness* vector **fit**(*i*); number of couples, n_S (see fig. 7); couples matrix, **par**[*i*, *j*]; probability of mutation, p_m ; maximum number of generations

with constant *fitness* value, n; gene identifier within the chromosome, al; relative error calculated to each found elastic property, rel; maximum percentage allowed for the relative error, *per*.

Step 1: Start Program. *iteri* = 1

- Step 2: Read GA control parameters and problem related data.
- Step 3: Initialise **first population** randomly (binary code as a chromosome).

For (i=1 to n)

For
$$(j=1 \ to \ l)$$

Set each design variable at index [i, j] in **pop**[i, j] matrix.

End

Step 4: Start of evolution process For (*iteri*=1 to $+\infty$). Do Step 5 to 13 with: $n_{li} = 1$ and $n_r = n$ End Step 5: Reproduction process. For $(n_l = n_{li} to n_l)$ Step 5.a: Design variables decoding from **pop** [i, j]. ANSYS data file generation Step 5.b: for each design vector in the population. Step 5.c: ANSYS analysis. Step 5.d: Objective function, y(A), evaluation for each design vector. Step 5.e: Fitness evaluation for each design vector. End Step 5.f: **pop**[i, j] ranking according to fitness evaluation. Step 5.g: Selection process For $(i=1 to n_T)$ par[i,1] = iChoose vector pairs randomly from $pop[(1 \ to \ n), j]$ except i, with i=1 to lCopy *i* to par[i,2]End For $(i = n_T + 1 \quad to \quad n)$ par |i,1| = iChoose vector pairs randomly from **pop** $[(i \ to \ n), j]$ except *i*, with j=1 to lCopy *i* to par[i,2]End Step 6: Crossover process For $(i = 1 to (n_T + n_S))$ Generate a random integer $r_i \in [1, l-1]$ progl = par[i, 1]prog2 = par[i, 2]For $(j=1 \ to \ r_i)$ pop[prog1, j] = pop[i + n, j]End For $(j = r_i + 1 \ to \ l)$ $\operatorname{pop}[\operatorname{prog}2, j] = \operatorname{pop}[i+n, j]$ End Step 7: Mutation process



according to p_m : For $(i=n+1 \ to \ (n_T+n+n_S))$ Generate a random number $ran \in [0,1]$ If $(ran \le p_m)$ generate an integer number $r_i \in [1, l]$ If $(pop[i, r_i] = 1)$, $pop[i, r_i] = 0$ Else $, pop[i, r_i] = 1$ End Step 8: Offspring vectors *fitness* evaluation

For $(i=1 \ to \ n_s)$ do Step 5 considering

$$n_l = n+1, n_t = n+n_S+n_T$$

Step 9: $pop[(n_T + n + n_S), j]$ ranking according to

fitness evaluation.

Step 10: Elimination of the half-inferior vectors belonging to $pop[(n_T + n + n_S), j]$ matrix.

Step 11: Randomly generation of n_T solutions (binary code).

Step 12: Best solution *fitness* registration, fit (i).

Step 13: Check for convergence according to the **stopping criterion** (see 4.2.6). Evaluate maximum relative error value of found best set of elastic properties, *rel*.

> If $(n_i = n \text{ and } rel < per)$ do Step 14 Else *iteri* = *iteri* + 1 Do Step 5 End

Step 14: Data decoding from $pop[1, j] \rightarrow \{E_1\}$

 E_2, v_{12}, G_{12}

Step 15: Stop program.

GENETIC PARAMETRES

Table 4 shows the genetic parameters considered on the occasion of the development of this GA model.

Table 4 –	Values	attributed	to the	genetic	parameters
				, Morrocro	parametero

Parameter	Value
n	10
n _T	2
n _M	6
n _B	2
p _m	0,5 %
n _i	10