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An adjacency representation for structural topology optimization using genetic algorithm

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Abstract – A new approach for continuum structural topology optimization using genetic algorithms is presented in this paper. The proposed approach is based on a representation by adjacency where the principle is founded on the concept of connectivity of finite elements, considered as cells. This principle is expressed by an adjacency matrix similar to that used in the graph theory. The encoding of the structure solutions uses this matrix by transforming it into a binary string. The research of optimal solution, i.e. the optimal material distribution, is interpreted in this approach by the determination of the connectivity of elements (cells). Using density variable, the approach has some common points with the homogenization techniques. The proposed approach is tested with simple benchmark applications.

Key words: Topology optimization; genetic algorithm; adjacency representation

1 Introduction

Genetic algorithms have proved a good efficiency to resolve complex optimization problems [1]. However, this efficiency is strongly dependent on a good choice of the algorithm parameters. The representation of solutions is the most important parameter because it must give a good formulation of the problem. Additionally, the choice of appropriate representation requires domain knowledge in order to make the search more efficient.

In topology optimization using genetic algorithm, the bit-array representation is usually used. Sandgren et al. [2] are among the first researchers to develop a genetic algorithm based approach for continuum structural topology optimization. In their work, the design domain is discretized into small elements, where each element contains material or void and thus no intermediate densities are allowed. This is a typical bit-array representation approach, in which a bit-array is used to define the design variables and can be directly mapped into the design domain discretized by a fixed regular mesh, where each of the small elements contains either material or void. Hence, the original '0-1' optimization problem was attacked directly by using a bit-array representation and a genetic algorithm. The work of Sandgren and his co-workers, using bit-array representation, has been extended by Jakiela and his co-workers [3–5], by Schoenauer and his co-workers [6, 7, 9], by Fanjoy and Crossley [8, 10], and, more recently, by Wang and Tai [11]. Although all these extensions can well prevent checkerboard patterns by exploiting a connectivity restriction, the other numerical instabilities in structural topology optimization such as mesh dependency and one-node connections still exist. More important, the issue of design connectivity analysis, which affects significantly the computational results, has not been completely solved.

The bit-array representation is founded in the intuitive concept of absence or presence of material. But structural topology optimization can be also defined as the determination of the structure elements nature and connectivity. The approach that we present in this paper is founded on this definition. We consider each finite element as a cell and then we define a representation based on the connectivity of these cells. This connectivity is expressed by a binary adjacency matrix. The encoding operation consists on transforming the matrix in one-dimensional binary string. The proposed representation seems more adequate to the topology optimization problem than the bit-array representation. Moreover, the one-dimensional string code is well matched to a genetic algorithm optimization process.

The research of optimal solution, i.e. the optimal material distribution, is interpreted in this approach by the determination of the connectivity of elements (cells). The mutation plays the most important role to accomplish this task. The operation of mutation is inspired partially from cellular automata method [12, 13]. We assign to every cell an artificial density variable whose value is altered by mutation operation. The value of the artificial density is then used for the search of the element connections associated with the mutant cell. Using density variable, the approach has some similarity to the SIMP

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techniques [14]. The proposed approach is validated with simple benchmark applications.

2 Structural optimization using GAs

Using an evolutionary, survival of the fittest optimization mechanism, genetic algorithms [1] allows designs in a population to compete against one another to serve as a parent designs. Parents then pair and mate, swapping portions of their 'chromosome' to create a generation of child designs of hopefully higher performance. After undergoing infrequent, random mutation, the child generation replaces the original generation, and the process then iterates until an optimal design is reached.

3 Problem formulation

This work is limited to linear elasticity topology optimization problems with a single objective function. The design domain is a continuous 2-D solid composed of elastic, homogeneous, isotropic material. Topology optimization consists in choosing a redistribution of material in each element according to the objective and constraint functions.

The principle of the genetic algorithms is a search of the fittest individual (global optimum solution) in the population. If the optimization problem is to maximize the objective function then the fitness function for evaluation of each individual is the same as the objective function. For the minimization problem, the fitness function is defined as the reciprocal objective function. The optimal solution should satisfy some constraints of inequality type. Finally, the optimization problem is stated in the following form

$$\begin{aligned} &\text{Maximize:} \quad Fitness\,(x) = \frac{1}{f(x)} \\ &\text{Subject to:} \quad g_i(x) \geqslant 0 \quad i = 1, K, n \end{aligned} \tag{1}$$

where, x is the solution vector, $f(x)$ is the objective function to be minimized, $g_i(x)$ is the i-th inequality constraint function, n is the number of inequality constraint functions.

Although genetic algorithms were initially developed to solve unconstrained optimization problems, during the last decade several methods have been proposed for handling constrained optimization problems as well [15]. The methods based on the use of penalty functions are employed in majority of cases for treating constraint optimization problems with GA. In this study, an efficient constraint handling method proposed by Deb [16], witch is also based on penalty function approach, is further used. Using the Deb penalty method the fitness function of constrained problem (1) is transformed into the following form

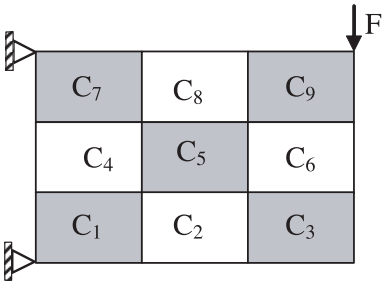

Fig. 1. Principle of adjacency representation.

$$\text{Max:}\, Fitness(x) = \begin{cases} \frac{1}{f(x)} & if\ x \in \Omega^F \\ \frac{1}{f_{\max} \times (1 + \sum_{i=1}^{n} \max[0,\, -g_i(x)])} & \text{otherwise} \end{cases} \tag{2}$$

where, Ω^F is the feasible region of design domain, $f_{\max}$ is the objective function value of the worst feasible solution in the population.

4 Adjacency representation approach

4.1 Principle

The principle of this new representation is based on the adjacency or neighborhood's concept. Each finite element is considered as a cell (Fig. 1). By considering the gray finite elements as cells, the white finite elements which connect these cells between them are considered as connection elements. The remove of a connection element involves the elimination of the material which occupied the finite element geometrical domain. On the other hand, the search of optimal material distribution can be done by adding or removing element connections. Practically, the finite element considered as cell in the present generation will be considered as connection in the next generation, and vice versa for an element connection type. Thus, each finite element alternates, as cell or connection type, from one generation to another. This alternation makes possible to explore the solution research space. That can not be possible if elements remain fixed in a particular role.

A particular case concerns the element cells which are on boundary condition surfaces. For these elements, we add virtual cells which represent the boundary condition surfaces (Fig. 2). The cells C_1, C_7 and C_9 have the virtual neighborhood cells C_{1f}, C_{7f} and C_{9f} respectively. The virtual cells are considered empty spaces without physical or mechanical properties.

4.2 Chromosome representation

The cell elements neighborhood relative to Figure 2 can be expressed by a binary adjacency matrix as follows.

The structure representation is only the gray part of the adjacency matrix (Fig. 3) which explains the element

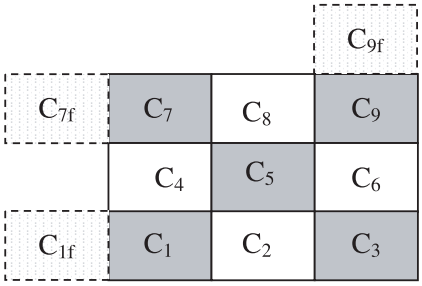

Fig. 2. Virtual cells on boundary condition surfaces.

	C1	C3	C5	C7	C9
C2	0	1	1	-	-
C4	1	-	1	1	-
C6	-	1	1	-	1
C8	-	-	1	0	1
C1f	1	-	-	-	-
C7f	-	-	-	1	
C9f	-	-	-	-	1

Fig. 3. Representation through adjacency matrix.

connectivity. This part, indicated by the gray color, is that which we use to build the chromosome, i.e. encoding operation.

4.3 Chromosome encoding

The encoding operation consists to transform the adjacency matrix, given in Figure 3, into one-dimensional binary string in order to facilitate genetic operations. The column, corresponding to an element cell in the adjacency matrix, represents the element cell associated gene and the element connection associated gene is corresponding to a line in the adjacency matrix. The encoding operation consists to place these genes one beside other in order to forming one-dimensional string. The resulting chromosome is given in Figure 4.

Unlike in the encoding based on the 'bit-array' representation, where each finite element is represented by one bit, in the adjacency approach each element is represented by a gene. Each gene associated to an element cell is composed by some bits where each bit corresponds to an element connection. Practically, each finite element is a cell surrounded by connection elements. Thus, cell elements and connection elements can divide some bits between them.

4.4 Evaluation

The evaluation needs structural analysis by finite element method. However, in the present approach we use the physical properties relaxation technique as it used by SIMP method (Bendsøe et al. [14]). The elastic modulus of each element, E_{ie}, is modeled as a function of the relative density, ρ_{ie}, using the power law. This can be expressed as

$$E(ie) = \rho_{ie}^{p} E_0 \qquad (p > 1) \tag{3}$$

where E_0 is the elastic modulus of the solid material and p is a coefficient used to penalize intermediate relative density values and drive the design to black and white structure. The relative density ρ_{ie} of each cell is expressed as

$$\rho(ie) = \frac{\sum_{j=1}^{Nbits(ie)} bit_j(ie)}{Nbits(ie)} \tag{4}$$

where $Nbits(ie)$ is the length of the gene associated to the ie element cell.

Expression (4) gives the density of the element cell ie according to the average of the associated gene bits values. Knowing that these values are binary, the density value is equal 0 if all the bits values are zeros or equal 1 if all the bits values are equal 1. Practically, in order to avoid the singularity of the stiffness matrix we affect a low value of about 10^{-4} to the empty element cells. Then the global stiffness matrix is calculated as follows

$$K_G = \sum_{ie=1}^{nelt} \rho_{ie}^{p} k(ie) \tag{5}$$

where K_G is the global stiffness matrix, $k(ie)$ is the elementary matrix associated to ie element and $nelt$ is the total number of finite elements.

4.5 Mutation

The mutation operation consists to alter one or some genetic information of an individual arbitrary chosen. Once the chromosome chosen, the mutation consists to modify the information of some genes. Practically, in our approach we use the cell densities as variables. The number of the element connections is proportional to the density of the associated element cell (expression (4)). Thus, the modification of the density of the mutate cell leads to the modification of the configuration and the number of the associated element connections. The proposed technique is based on the adaptation of each cell with its neighborhood (Tatting et al. [12], Tovar et al. [13]).

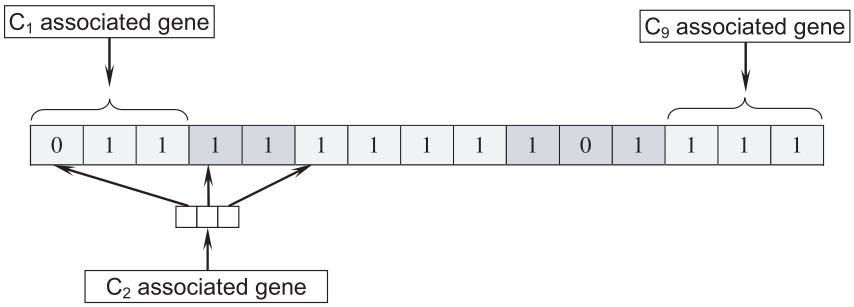

Fig. 4. Chromosome storage.

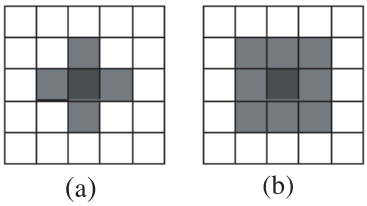

Fig. 5. Cell neighborhoods (a) Von Neumann (b) Moor.

The principle consists in interpolating the density of the mutate cell according to the adjacent cells layout. The most commonly used are the von Neumann layout that includes four neighboring cells ($N = 4$) (Fig. 5a) and the Moore layout that includes eight neighboring cells ($N = 8$) (Fig. 5b).

The average cell density is then altered according to the following expression

$$x_{ie} = \hat{x}_{ie} + \Delta x_{ie} \tag{6}$$

$$\text{where} \quad \hat{x}_{ie} = \frac{\rho_{ie} + \sum_{je=1}^{Nc} \rho_{je}}{Nc + 1} \tag{7}$$

$$\text{and} \quad \Delta x_{ie} = rand \cdot (-1)^{round(rand)} \tag{8}$$

where x_{ie} is density variable, $\hat{x}_{ie}$ is the ie element density computed using the expression 7 and Δx_{ie} is real value randomly generated using expression (8).

The new density value done by the expression (6) should be always positive and less than one.

$$x_{ie} = \begin{cases} 0 & \text{if } x_{ie} < 0, \\ 1 & \text{if } x_{ie} > 1, \\ x_{ie} & \text{if } 0 < x_{ie} < 1. \end{cases} \tag{9}$$

Consequently, if the density value decreases that leads to material elimination and, on the contrary, it leads to material addition if the density value increases.

The corrected density (expression (9)) is then used to find the new element connection number:

$$Nbr = round(x_{ie} \times Nbit) \tag{10}$$

where *Nbit* is the mutate element gene length corresponding to the number of associated connection elements.

4.6 Selection method

Selection operator is applied to the current population to create an intermediate one. The so-called "Stochastic Universal Sampling" method is used in this paper. The probability of selection of each individual is proportional to the performance calculated in function of its rank in the population. According to a linear version of this method proposed by Baker [17] a selection pressure encloses to two is applied in genetic algorithm. The artificial performance of an individual of rank r_i is calculated in the following way

$$Fit_{Rk}(r_i) = -\frac{2 \times (r_i - N)}{N - 1} \tag{11}$$

where, $Fit_{Rk}(r_i)$ is the artificial fitness function value of the i-th individual, N is the population size, r_i is the rank of the i-th individual (the rank number one designates the best individual).

5 Numerical implementation

The algorithm of the method developed in this paper has been implemented in MATLAB programming language [18]. The computer code includes also a finite element solver for isotropic linear elasticity with plane stress elements. Figure 6 shows the flow chart of the proposed approach.

The employed strategy involves also the transfer of best individual of each population into the next generation without transformations. This individual replaces the best of the current generation if this last one is worst. If the best individual remainders the same during fifty successive generations, the optimization process is halted. This is the first stopping criteria we are using in our approach. The second one, often used, is based on a prefixed maximum number of generations.

5.1 Application

The proposed approach is tested using standard benchmarks of structural topology optimization problems. One of these benchmarks involves a rectangular structure supported at the lower corners, with a downward force of

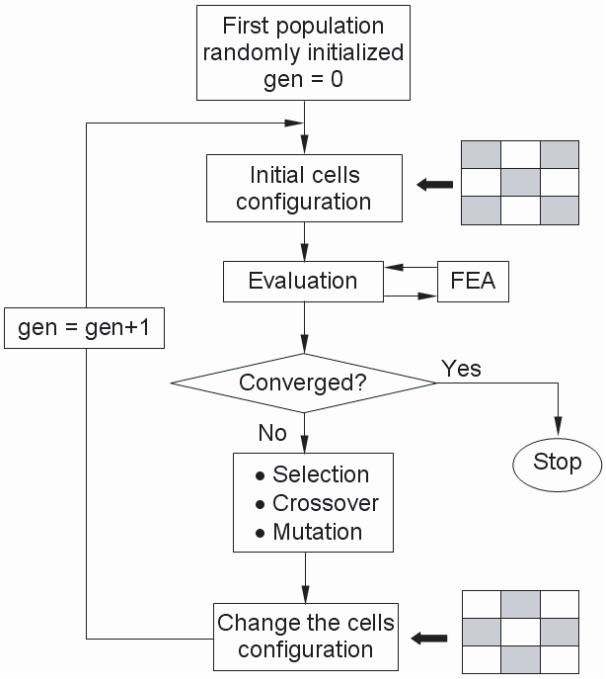

Fig. 6. Flow chart of the proposed approach.

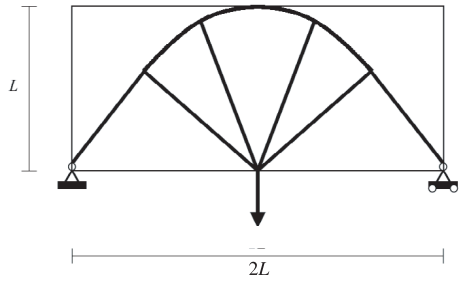

Fig. 7. Ideal solution of the Michell truss.

magnitude 4×10^3 N applied at the centre of the bottom edge (see Fig. 6). The design domain dimensions are $1 \times 0.5\ \mathrm{m}^2$. The material is elastic isotropic and he have the following physical properties: $E = 100$ GPa and $\nu = 0.3$.

This problem roughly corresponds to the Mitchell truss, a classical topology optimization problem. The ideal solution is shown in Figure 7.

The GA algorithm is applied on a population composed of 80 individuals randomly generated at the beginning of the algorithm. The domain conception is meshed on a 36×18 cells (finite elements) mesh modeling a half of the domain by using symmetry. The optimization problem consists to minimize de compliance subject to 50% initial structure volume limitation. The minimum compliance optimal topology design problem can be expressed as

$$\text{Minimize: } F^T U \tag{12a}$$

$$\text{Subject to: } V(x) - V_{\lim} \leqslant 0 \tag{12b}$$

where F is the applied force, U is the displacement array, V is the volume and $V_{\lim}$ the imposed volume limitation.

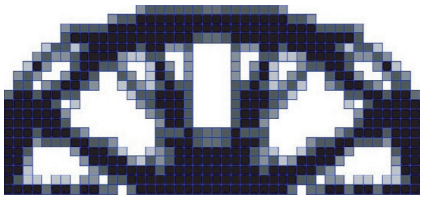

Fig. 8. Optimal solution by GA.

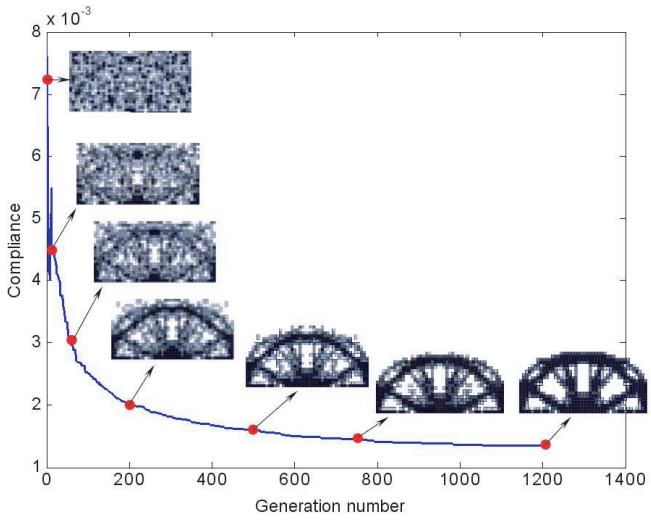

Fig. 9. Best solution and its objective value histories.

The optimal topology solution reached after 1201 generations is shown in Figure 8. The optimal solution topology tends to the ideal solution.

Figure 8 shows the best solution and its objective function history at each generation. The solution converges to the optimal topology by searching of the material distribution in each finite element. As it shown in Figure 9, the float elements are eliminated automatically without need to using the connectivity analysis technique [5].

6 Conclusions

This paper presents a topology optimization approach for 2-D structures using genetic algorithm and a new representation by adjacency. The proposed approach uses the finite element connectivity to encoding the structure solutions. The element connectivity is coded by binary adjacency matrix. By using the connectivity principle, our approach seems more compatible with the topology optimization problem than the Bit-array representation based approach.

The approach shears some concepts with the Cellular Automata Method, and uses, also the SIMP density penalization technique. Indeed, the material interpolation technique it used to analyze the structural solution using the finite element method. The density variable it also used by the mutation operator to search to the optimal distribution material. It is an efficient technique which plays an important role to eliminate checkerboards

and floating elements. In other words, the technique consists in automatically correcting the possible connectivity problems.

Finally, using an appropriate chromosome representation, GA overcome the use of connectivity repair techniques which are expensive and often leads to chromosome degeneracy.

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