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Variable Chromosome Length Genetic Algorithm for Structural Topology Design Optimization

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This article introduces the concept of variable chromosome lengths in the context of an adaptive genetic algorithm (GA). This concept is applied to structural topology optimization with large numbers of design variables. In traditional genetic algorithms, the chromosome length is determined when the phenotype is encoded into a genotype. Subsequently, the chromosome length does not change. This approach does not effectively solve problems with large numbers of design variables and complex design spaces, e.g. structural topology optimization, because the design spaces are extremely large, and it is very difficult to explore the design spaces in their entirety with reasonable population sizes. The proposed GA starts with a short chromosome and finds an optimum solution in the simple design space. The optimum solution is then transferred to the following stages with a longer chromosome while maintaining diversity in the population. More refined solutions are obtained in subsequent stages. A strain energy filter is used in order to filter out inefficiently used cells, such as protrusions or isolated islands. The variable chromosome length genetic algorithm is applied to structural topology optimization problems of a short cantilever and a bridge problem. The performance of the method is compared with a brute-force approach GA.

Nomenclature

Ω = Design domain
ρ = Density
M_0 = Mass constraint
F^i = i th component of force vector F
z^i = i th component of displacement vector z
ρ_k^{New} = Density of the kth cell in the new stage
ρ_k^{Previous} = Density of the kth cell in the previous stage
U_k = Strain energy in the kth cell
Γ_k = Domain of the kth cell
$\boldsymbol{\varepsilon}_k$ = Strain tensor of the kth cell
$\boldsymbol{\sigma}_k$ = Stress tensor of the kth cell
$\mathbf{D}_k$ = Elasticity tensor of the kth cell

I. Introduction

Genetic algorithms (GA) have been popular in design optimization, operations research, and for general combinatorial search problems[1,2]. A key operator is the encoding step that results in a binary, real, or hexadecimal chromosome. The length of the chromosome, i.e. the number of alleles, in the genotype space is a surrogate for the amount of information describing an artifact in the phenotype space. Figure 1 shows two examples of design in the phenotype and their corresponding chromosomes in the genotype.

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Traditionally, in design optimization, the chromosome length is fixed a priori, and it cannot change with the evolution of subsequent generations. Evolution in this sense is only understood as the process of approaching an optimal instantiation of alleles given a constant phenotype-genotype mapping and a fixed chromosome length.

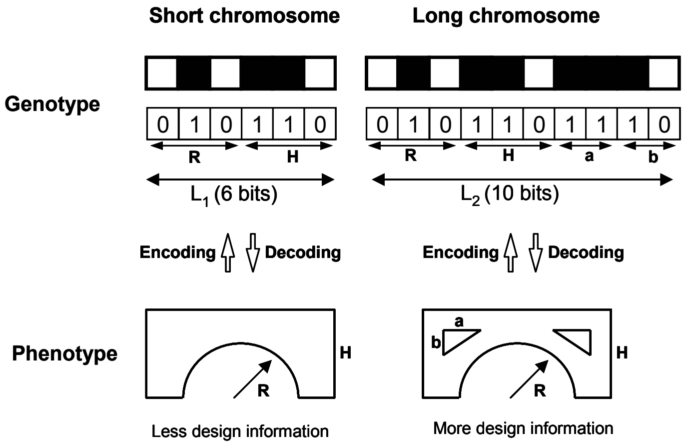


Figure 1: Examples of designs in the phenotype and corresponding chromosomes in the genotype domain.

This traditional approach has some disadvantages. The best achievable fitness is inherently limited by the chromosome length. Hence, the fitness asymptote that is typically observed in genetic optimization is as much a result of problem formulation as of the number of design variables and their resolutions. Here the problem is that we do not a priori know how long "long enough" is. If short chromosomes are used, one may not obtain good solutions due to the lack of design freedom. On the other hand, if chromosome length is excessive for a particular problem, it will cause a high computational burden without much performance benefit.

This article presents the development of an effective genetic algorithm that can change the chromosome length by implementing the design principle "from coarse to fine". It can be expected that significant fitness improvements can be achieved by gradually increasing chromosome length. This approach of increasing the design freedom by extending chromosome length allows for the reduction of the computational cost for complex problems with large numbers of design variables. The initial population features a short chromosome, and the chromosome becomes longer as evolution proceeds. The increase in chromosome length is achieved either by an increase in the resolution of the design variables or by the addition of new design variables during encoding.

A. Literature survey

For shape optimization, Cea[3], Zolesio[4], Reousselet[5], and Haug et al.[6] developed the theory for analytical sensitivity analysis based on the continuum approach. Haftka[7] and Kwak[8] reviewed structural optimization methods and shape sensitivity analysis. Michell[9] first studied structural topology optimization and obtained the analytical solution, called Michell trusses, which have infinite numbers of truss members. Bendsoe and Kikuchi[10] developed the homogenization method for topology optimization. They used the method to obtain equivalent material properties of infinitely many micro cells with voids. The method was subsequently applied to anisotropic material problems[11] and eigenvalue problems[12]. Yang and Chuang[13] proposed artificial material and used mathematical programming for topology optimization.

The evolutionary structural optimization method, in which the von Mises stress was adopted as the measure of performance of each cell, was studied by Xie and Steven[14] and Guan et. al[15]. Later the principal stress-based method was developed to deal with tension-dominant or compression-dominant material. Maute and Ramm[16] proposed an adaptive topology and shape optimization method. They performed shape optimization and topology optimization separately and mapped the results to each other. DeRose and Diaz[17] developed a meshless, wavelet-based layout optimization method. In order to overcome the problems of mesh degradation in convergence for large-scale layout optimization problem, a fictitious domain and a wavelet-Galerkin technique were used. Kim and Yoon[18] proposed a multi-resolution topology optimization based on multiscale wavelet-Galerkin technique, and later, an adaptive multiscale, wavelet-Galerkin method was developed by Kim et al.[19]

Kim and Kwak[20] proposed a generalized topology optimization formulation where the design domain enlarges in order to obtain new, better solutions that cannot be obtained by conventional methods. This work introduced the pivot phase, and the effect of new design cell addition is determined at the pivot phase using a contribution ranking based on sensitivity analysis. Diaz and Bendsoe[21] dealt with problems with multiple loading conditions, and Min et al.[22] studied multiobjective topology optimization considering static compliance and eigenvalues. Extensive reviews of topology optimization can be found in Bendsoe[23], Kirsch[24], and Rozvany et al.[25] More recent reviews can be found in Eschenauer and Olhoff[26], Kim et al.[27], and Mackerle[28].

The optimization strategies used for the above research are either gradient-based approaches or optimality criteria methods. The drawbacks of these methods are that (1) they may converge to a local optimum and that (2) often intermediate densities are obtained, which are not physically meaningful.

Genetic Algorithms can remedy these problems effectively, albeit at an additional computational expense. GA explore the entire design space and may not get trapped in local minima. Moreover, it is possible to have only binary values of density, ON (ρ=1) or OFF (ρ=0), at each cell. Jakiela et al.[29] used GA for continuum topology optimization with domain refinement. The chromosome length in this study does not change, and the domain is divided into four quadrants in every step. In order to create diversity, a high mutation rate was used. This work has been extended to several types of fitness functions[30,31].

B. Motivation

It is observed that the solutions obtained by the GA topology optimization method by Chapman et al.[29] were quite noisy. This is primarily because of the large number of design variables involved and the algorithm for filtering out bad designs. In addition, it was not possible to impose mass constraints to the optimization problem in their work.

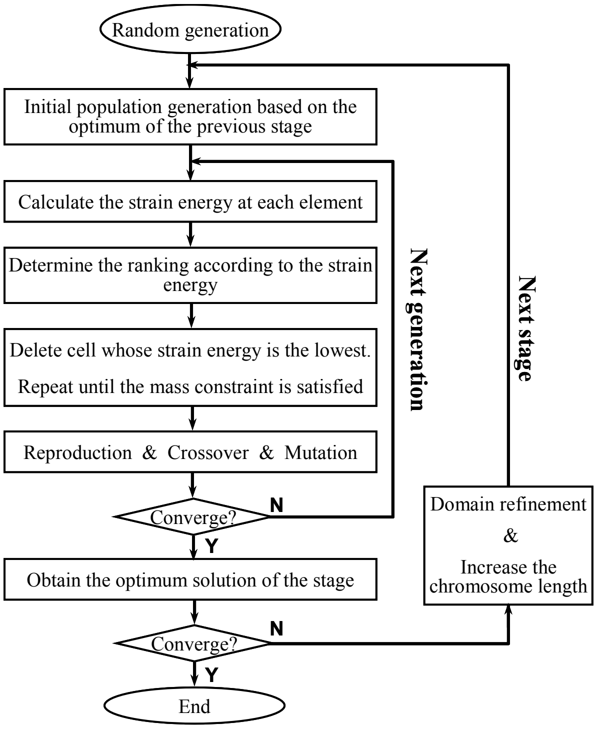


Figure 2: Flow diagram of variable length chromosome genetic algorithm.

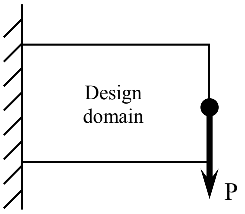


Figure 3: Short cantilever.

The design space in topology optimization is typically very large as can be seen in their work. Hence, the GA require long computing times, despite the advantages of GA mentioned above. For example, the number of design choices is as large as 2^{640} for a 2-dimensional 32×20 cell short cantilever topology optimization, which is a relatively simple problem in structural topology optimization. Among these design choices, only a very small portion is physically meaningful, and it is not efficient to explore the entire design space. One of the main difficulties is producing new designs that are meaningful and that feature no disconnected regions or material zones without a load path.

In this paper, we propose a new GA methodology for structural topology optimization. First, we develop a variable chromosome length GA that has a transition technique. This reduces the size of the design space for exploration for problems with large numbers of design variables. It also increases the likelihood of approaching the global optimum by gradually making the design space more sophisticated. This procedure allows a mass constraint imposition that gradually tightens up. Second, we adopt strain energy cell ranking as a measure for filtering out inferior designs. During the whole procedure, a Pareto front is formed, and it reveals the tradeoff between structural mass and compliance.

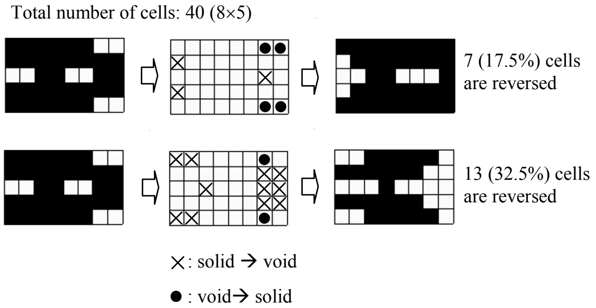


Figure 4: Sample cases of generating mutants.

II. Variable Chromosome Length Genetic Algorithm

Figure 2 shows the overall procedure of topology design optimization using the variable chromosome length GA. The inner loop is the typical topology optimization by GA. Strain energy ranking is used to ensure the connectivity

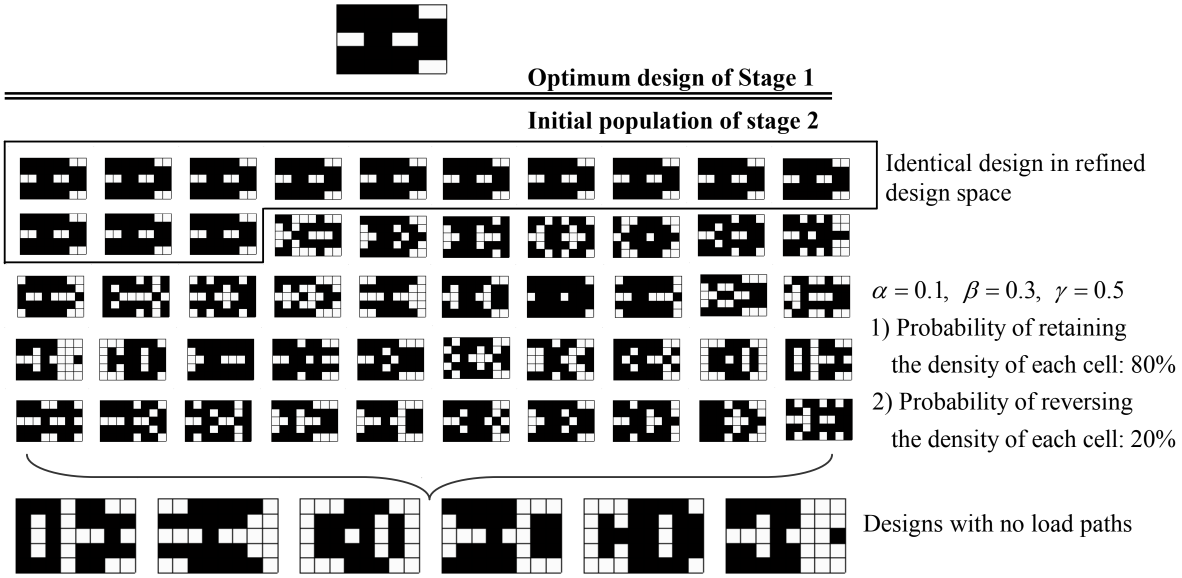


Figure 5: Initial population of the second stage. Six designs do not have load paths.

of structural elements and to specify the mass constraint. Optimization starts from a short chromosome representation, and when it converges, it transitions to the next stage of longer chromosomes or higher refinement.

Convergence within the inner loop is achieved when the progress from one generation to the next, as measured by the average population fitness, falls below a numerical tolerance. Convergence of the outer loop is a more difficult question since this relates to the desirable fineness of design resolution. The final mass constraint or the final chromosome length is a typical termination criterion for the outer loop.

A sample example of topology optimization in this paper is illustrated in Fig. 3. It is a short cantilever whose left side is clamped and that is subject to a concentrated loading at the mid-point of the right side. The design domain is discretized into rectangular cells; then the normalized density of each cell becomes the design variable. The binary encoding is used, and the density is either zero (void) or one (solid), which leads to a binary 0-1 choice for each cell. In the computational implementation, the elasticity of a void cell is set to a very low value. The objective function to be minimized is the compliance of the structure. The optimization problem statement is

$$\begin{aligned} &\textit{Minimize} \quad \int_{\Omega} F^i z^i \, d\Omega, \\ &\textit{Subject to} \quad \int_{\Omega} \rho \, d\Omega \le M_0, \\ &\quad 0 \le \rho \le 1 \end{aligned} \tag{1}$$

where F^i is i th component of force vector F, z^i is i th component of displacement vector z, Ω is the design domain, ρ is the normalized density of each cell, and M_0 is the maximum allowable mass which is often expressed as a percentage of the design domain volume. The design variables in this optimization are the densities of the cells.

In the proposed adaptive genetic algorithm, the design domain is initially discretized into coarse design cells, which are represented by short chromosomes in the early stages of design evolution. The optimal solution of this stage is transferred to a next stage that has more refined design cells or longer chromosomes. In this transition, the optimal solution is used to generate the initial population of the next stage. Some individuals of the next population are made by the exact mapping of the previous-stage optimum (elitism), and other members of

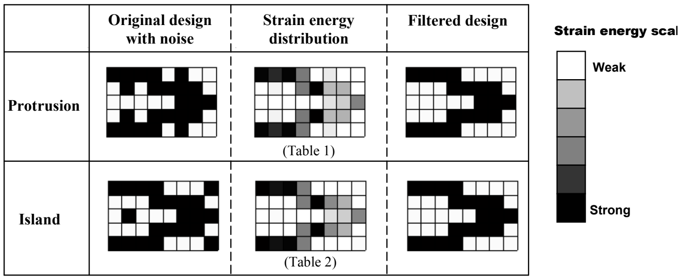


Figure 6: Strain energy filter for removing protrusions and islands.

the population are mutated variants stemming from the optimum. This seeding of the initial populations in progressively finer stages is the main mechanism by which information is transferred between stages. This allows us to keep the number of generations and population sizes small compared to a brute-force approach, in which topology optimization would start at the finest resolution level with a random initial population. This brute-force approach is later used as a reference for comparison.

When making the mutants, the density of each cell is determined by the following equation:

$$\rho_k^{\text{New}} = \text{round}(\alpha + \beta\rho_k^{\text{Previous}} + \gamma\,\text{random}(0,1)) \tag{2}$$

where ρ_k^{New} is the density of the kth cell in the new stage, ρ_k^{Previous} is the density of the kth cell in the previous stage, "random(0,1)" is the uniform probability density function between 0 and 1, and "round( )" is the function that rounds off to the nearest integer. In this research, the values of the parameters, α, β, and γ, are 0.1, 0.3 and 0.5, respectively. With these values, the probability of retaining the density of the previous stage in an individual cell is 80%, and the probability of reversing it is 20%. By adjusting the three parameters, the degree of diversity generated can be controlled, depending on the characteristics of a problem. Figure 4 shows two sample cases of generating mutants, in which 17.5 % and 32.5 % of the cells are reversed, respectively. This mechanism makes it possible to transfer the overall layout to a stage with a different chromosome length, maintaining diversity in the population.

Table 1: Strain energy and the ranking (protrusion).

Element	Strain energy	Ranking	Feature
1	9.4419	3	
2	8.0666	4	
3	9.4815	2	
4	4.9600	6	
5	3.3997e-017	18	*Void*
6	6.1725e-001	12	**Protrusion**
7	1.2187e-018	24	*Void*
8	6.4800e-018	21	*Void*
9	2.0019e-017	20	*Void*
10	3.8160e-001	13	**Protrusion**
11	2.8523e-017	19	*Void*
12	5.0708	5	
13	9.8526	1	
14	2.5776	9	
15	2.8597	8	
16	3.7503e-017	17	*Void*
17	6.9412e-017	16	*Void*
18	8.9555e-017	15	*Void*
19	9.5157e-017	14	*Void*
20	2.6762e-018	23	*Void*
21	4.7923e-018	22	*Void*
22	1.0727	11	
23	1.7719	10	
24	4.6901	7	

Element number

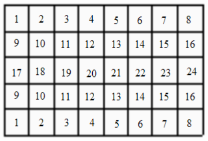


Table 2: Strain energy and the ranking (island).

Element	Strain energy	Ranking	Feature
1	1.0049e+001	2	
2	9.3191	4	
3	9.784	3	
4	4.9424	6	
5	3.3772e-017	14	*Void*
6	1.8232e-017	16	*Void*
7	2.2150e-018	23	*Void*
8	1.2859e-005	12	**Protrusion**
9	1.2928e-017	19	*Void*
10	1.4381e-017	18	*Void*
11	1.5363e-017	17	*Void*
12	4.9748	5	
13	1.0109e+001	1	
14	4.4807	8	
15	2.9549	9	
16	2.8325e-017	15	*Void*
17	7.1200e-018	21	*Void*
18	6.0905e-006	13	**Island**
19	8.8569e-018	20	*Void*
20	1.5533e-018	24	*Void*
21	3.7276e-018	22	*Void*
22	1.1345	11	
23	1.8450	10	
24	4.6690	7	

Figure 5 represents an example of an optimum of the first stage and 50 individuals of the initial population of the more refined stage that follows. The optimum design in the first stage is transferred to the second stage by elitism and by the mutant equation. The first 13 designs are exactly the same, but they are mapped to a more refined design domain. Another feature of this transition is that designs with no load paths may be generated. In this example, six designs do not have load paths. They are not feasible designs because theoretically the compliance is infinite. They serve only as diversity-generating seeds in the process of crossover, and later they are rejected from populations because of their low fitness values. In this algorithm, the elitism GA replaces the worst designs with no load paths with the best design at the end of each generation.

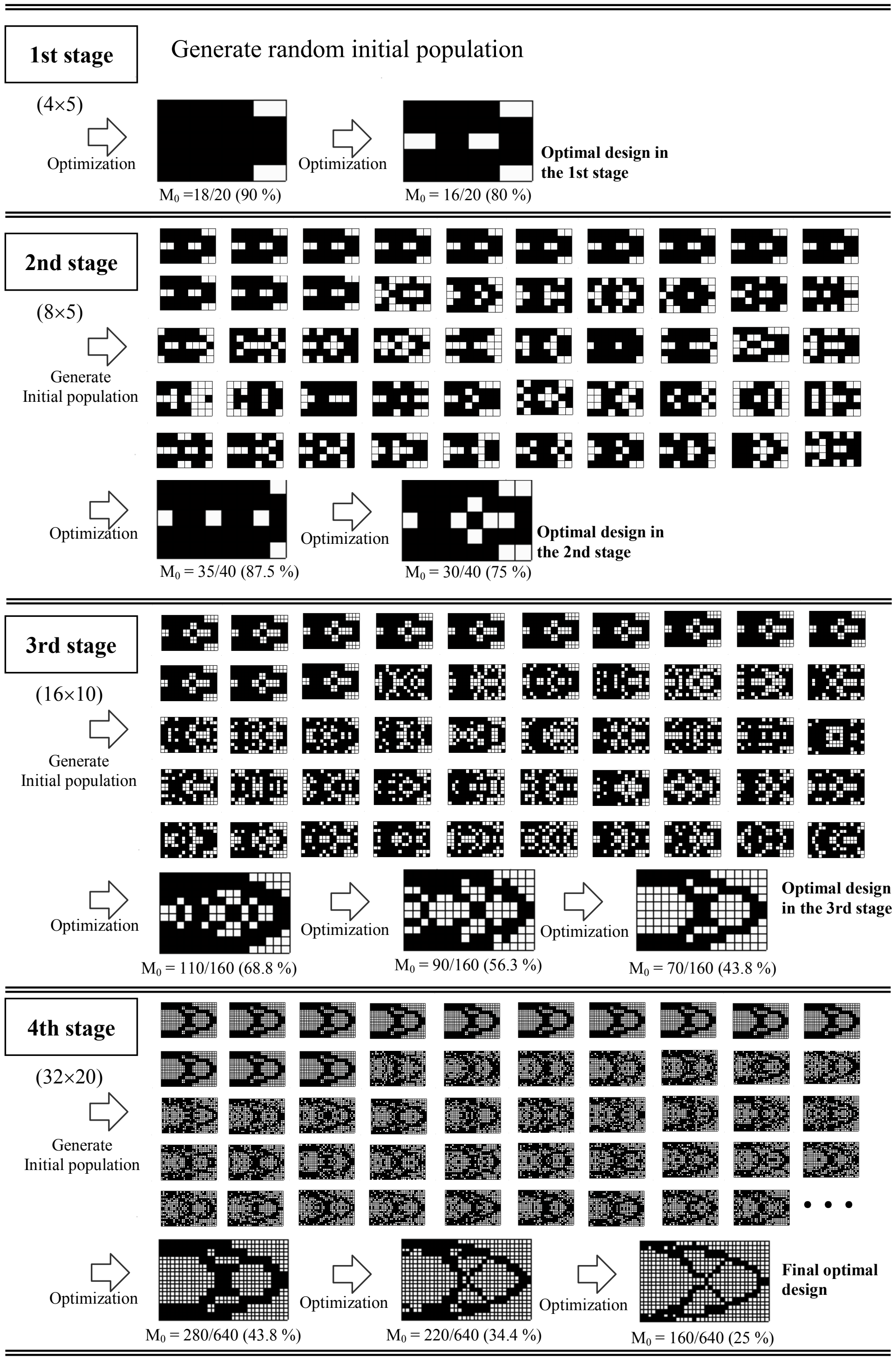


Figure 7: Optimum solution history for the short cantilever problem.

III. Strain Energy Filter

One of the difficulties in applying GA to structural topology optimization is that often noisy designs are produced. In particular, designs with protrusions or islands are inferior solutions because these protrusions or islands contribute very little or nothing to the strength of a structure. A technique of filtering out protrusions was considered in previous research[30]. However, it was applicable only for a protrusion with a corner point connection, and a protrusion with an edge connection or an island was not dealt with.

In this work, we use strain energy as the contribution measure of each cell for GA-based topology optimization.

$$\text{Strain energy: } U_k = \frac{1}{2}\int_{\Gamma_k} \boldsymbol{\varepsilon}_k \, \boldsymbol{\sigma}_k \, d\Gamma = \frac{1}{2}\int_{\Gamma_k} \boldsymbol{\varepsilon}_k{}^T \mathbf{D}_k \boldsymbol{\varepsilon}_k \, d\Gamma \tag{3}$$

U_k is the strain energy in the kth cell, Γ_k is the domain of the kth cell, $\boldsymbol{\varepsilon}_k$ is the strain tensor of the kth cell, $\boldsymbol{\sigma}_k$ is the stress tensor of the kth cell, and $\mathbf{D}_k$ is the elasticity tensor of the kth cell. In each step, the strain energy of each cell is computed, and then the ranking of the cells in terms of their strain energy is determined. Figure 6 demonstrates the filtering procedure for noisy designs with protrusions and islands in the short cantilever example. The figures in the second column show the strain energy distribution in each case. Table 1 and Table 2 present the strain energy values and the ranking for each case. Void cells have strain energies that are almost zero, and cells whose strain energies are relatively low are protrusions or isolated islands to be deleted by the filter. This method determines the ranking of the cells according to their strain energy and then rejects one by one beginning from the last one until the mass constraint is met.

This scheme enables the mass constraint imposition of an arbitrary level in any stage. However, it has been our experience that the method performs better when the mass constraint is imposed gradually, reducing the allowable amount of mass with each subsequent stage of refinement until the ultimate mass constraint has been reached. The reason is that a tightened mass constraint produces slender, fine structures, which are difficult to be represented by large, coarse cells in the initial stages. Therefore, starting optimization with a tightened mass constraint from the beginning is not a good strategy.

IV. Numerical Examples

A. Short cantilever optimized by the adaptive chromosome length GA

Figure 7 shows the results of the short cantilever topology optimization by variable chromosome length GA. The evolution starts with a domain refinement of 4×5. As the generation proceeds, the domain is discretized, and more refined solutions are obtained. The final domain is discretized into 32×20. M_0 in the figure denotes the maximum allowable mass in Eq. (1). Only half of the domain is modeled and optimized by the symmetric condition for the actual analysis. A population size of 50 is used for the first three stages, and the population size of the last stage is 150. The mutation rate is 1%, and the crossover probability is 100%. Because good solutions are often destroyed by mating with bad designs, the elitism scheme is used where the best individual replaces the worst 30% of individuals in each generation. The mass constraint gradually decreases from 90% mass of the total design domain to 25%. IMOS[32] is used for the finite element analysis. It is well known that checkerboards can be restricted to some extent if

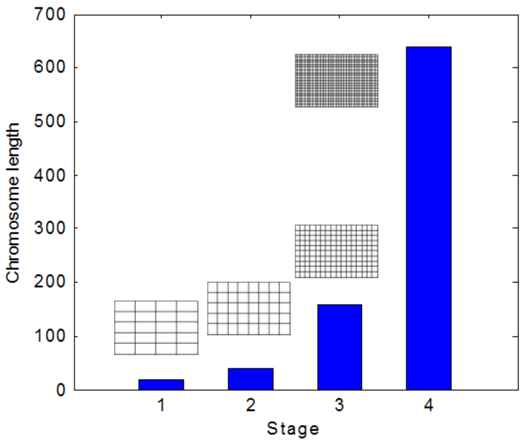


Figure 8: Chromosome length change for the short cantilever problem.

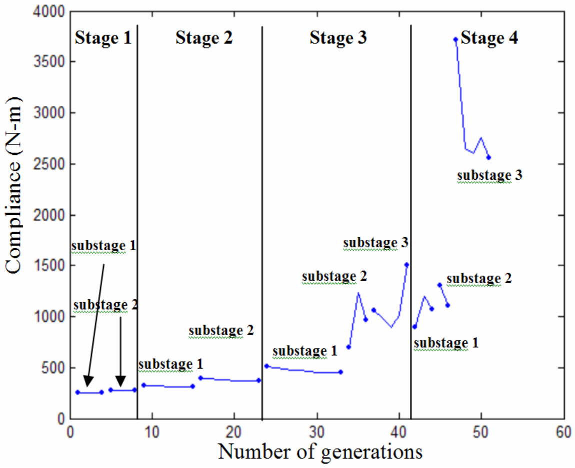


Figure 9: Compliance history for the short cantilever problem.

quadratic finite elements are used. Because IMOS does not have quadratic elements, four linear elements are used to represent one design cell. The total CPU time for the analysis is 2.21×10^5 sec (61.38 hours) on a 3.05 GHz Pentium 4 computer.

The first stage starts with a randomly generated population, and then the optimum solution of the stage is transferred to the following generations by means of the diversity-generating scheme in Eq. (2). From the second generation on, the initial population design share a similarity among themselves, because they are generated based on the optimum solution of the previous stage. Because the allowable mass decreases gradually, the structure becomes more slender with increasing number of stages.

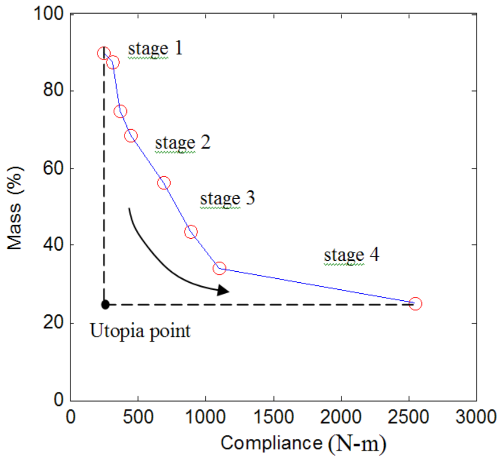
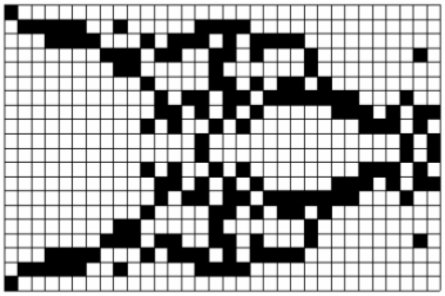


Figure 10: Multiobjective optimization with mass and compliance as objective functions for the cantilever problem.

Figure 8 shows the chromosome length change over stages. The length in the first stage is 20, and it increases to 640 in the last stage (More information is required to describe the more refined designs). The history of the objective function, compliance, is shown in Fig. 9. The first stage and second stage have two substages each, and the third stage and fourth stage have three substages each. The compliance shows a monotonous decrease within most substages, but there are a few substages whose compliance do not converge, but fluctuates. The overall compliance increases as the stages proceeds; this is because the mass constraint becomes tighter with each stage.

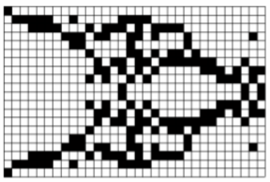
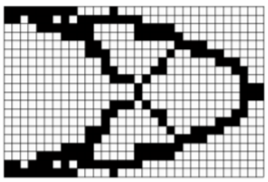


Design domain: 32×20

Figure 11: Optimum solution by the brute-force genetic algorithm.

Another interesting aspect is that a Pareto front naturally emerges from the solutions obtained during the whole analysis. The Pareto front explores the tradeoff between mass and compliance, as shown in Fig. 10. Tightening the mass constraint does not increase the compliance severely in early stages. However, as the total mass approaches 20%, the mass reduction is achieved by sacrificing strength considerably. When most of the design domain is used for structure (early stages), some part of the structure can be removed without affecting the compliance much. When the mass portion is low (later stages), on the

Table 3: Performance comparison of the brute-force method and the variable chromosome length GA.

	Brute-force GA	VCL GA
Domain refinement resolution	32×20	32×20 (final resolution)
CPU time ($\times10^5$ sec)	2.37	2.21
Compliance (N-m)	4780	2500
Result	 islands & protrusions checkerboards	 clearly X-shaped structure

other hand, most of the structure is used very efficiently. Even a small removal decreases the structural strength significantly.

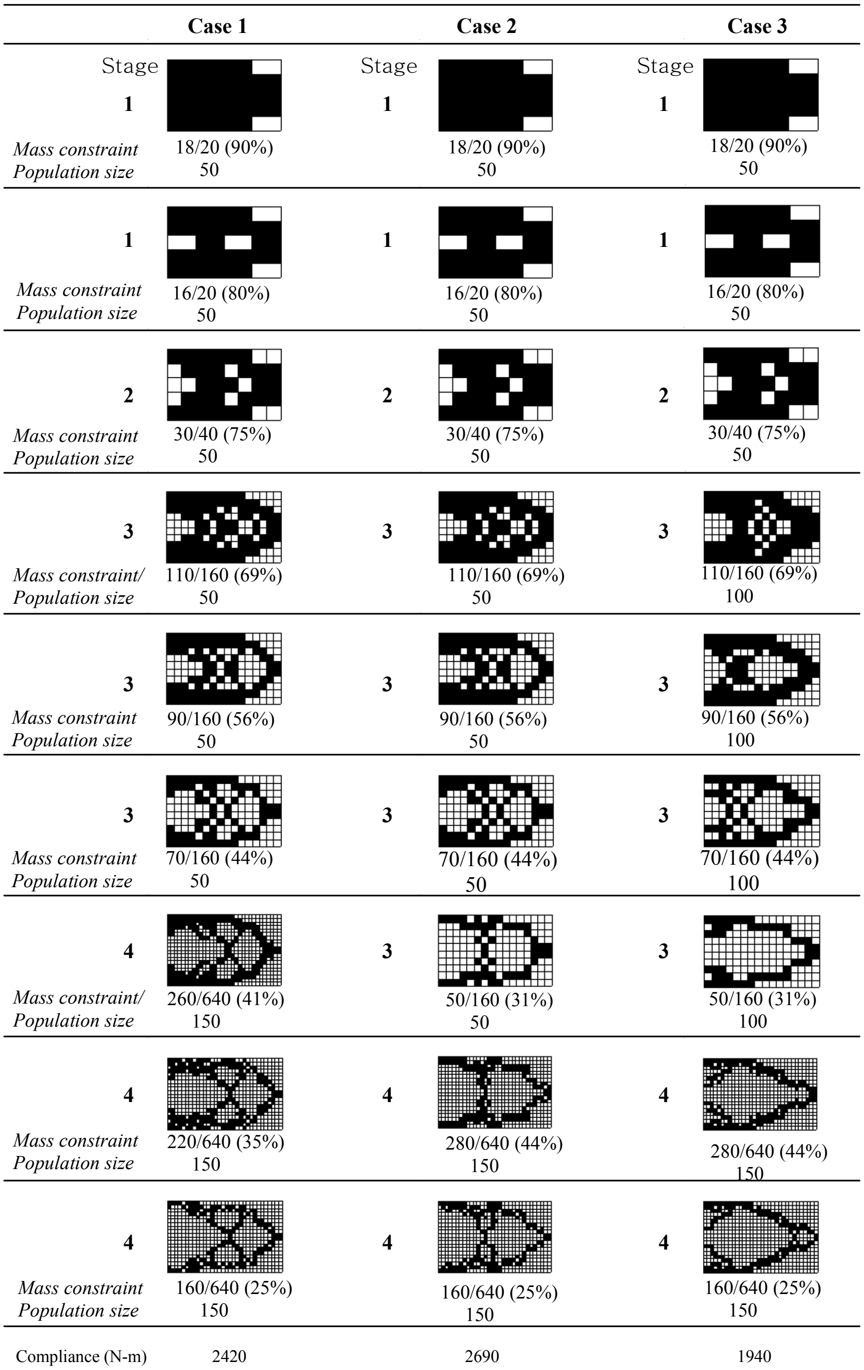


Figure 12: Different solutions for various settings of parameters.

B. Short cantilever obtained by a brute-force approach

It may be argued that the same optimum solution can be obtained by an ordinary GA in the finest design domain setting and that the seemingly complicated adaptive method does not provide a measurable benefit. Figure 11 shows the solution of the brute-force approach with the same computational effort. The same strain energy filter is used to restrain protrusions and islands. The mass constraint is 25%, which is the same for the constraint for the last stage in Fig. 7. The filter does remove some islands and protrusions, but still there are some islands and protrusions left because the original solution before filtering is very noisy. Some checkerboards are also observed. While the solution obtained by this brute-force approach does not have a clear structure, the variable chromosome length GA produces a more distinct solution with one X-shaped support in the structure. Table 3 compares the performance of the brute-force method and the variable chromosome length GA. With the same computational cost, the objective function value (compliance) by the variable chromosome length GA is lower than that by the one-time approach.

The proposed method has two advantages over the brute-force method, which assumes the finest resolution level from the start with a large random initial population. First, the brute-force approach may not find a design as good as the variable chromosome length method can, because the design space for exploration is extremely large and it is very difficult to explore the entire design space with reasonable population sizes. Second, the variable chromosome length method determines rough optimum designs in the early stages when computational cost is inexpensive, and these designs are used as starting points in the following stages. Therefore, even when the one-time approach can find a fairly good solution, its computational cost is far more expensive than that of the variable length approach.

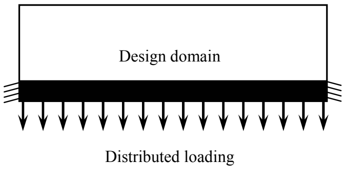


Figure 13: Bridge problem.

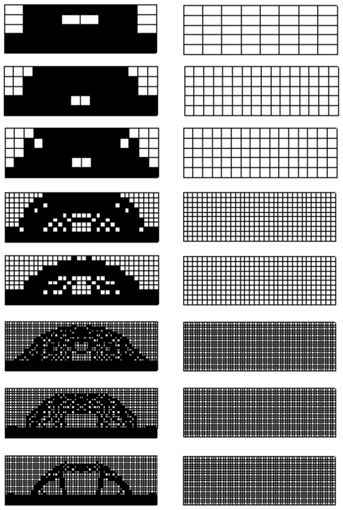


Figure 14: Optimum solution history for the bridge problem.

C. Short cantilever with various settings

The previous optimum solution (Fig. 7) is obtained for a specific case of mass reduction history and population size. In this section, three different settings are investigated, as shown in Fig. 12. The final mass constraint is 25%, which is the same for all three cases. Case 2 has a different mass reduction history from Case 1 for the last three substages. They have the same design evolution until the third stage, and in the fourth stage, they start to evolve into different solutions. Case 2 and Case 3 have the same mass constraint throughout the whole analysis, but the population size in the third stage is different. This leads to somewhat different solutions. The final solution is somewhat dependent on the parameters chosen and the evolution path of the variable chromosome length. This might be seen as a disadvantage, but it also enables one to find several different "concepts" by changing the parameters.

D. Bridge Problem

In Figure 13, a bridge problem is investigated using the proposed method. There is a rigid roadway domain whose normalized density is always one in the bottom of the design domain. A distributed loading is applied downwards underneath the domain, and both ends of the rigid domain are clamped. The domain discretization starts with 8×4 and then is refined into 16×4, 32×8, and 64×16. Symmetry is utilized for analysis in this example, as above. As in the previous example, 30% elitism and a 1% mutation rate are used.

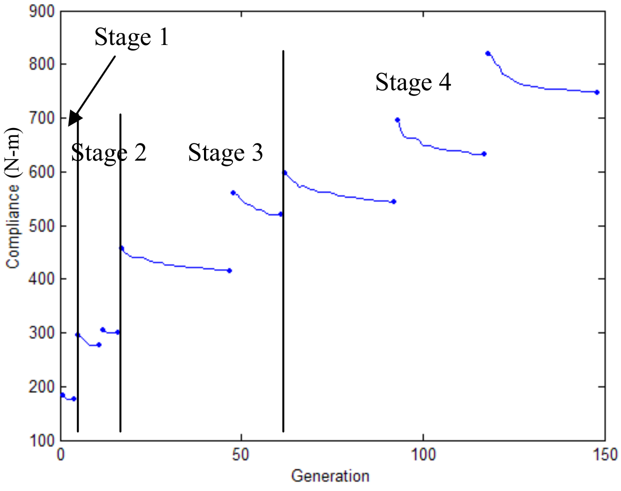


Figure 15: Compliance history for the bridge problem.

The solution history is shown in Fig. 14. The overall layout is found quickly in the first stage, and in the following stages, the solution becomes more and more refined. In this example, some checkerboards are observed, and finally an arch bridge is obtained. It is observed that the ends of the arch do not meet with the ends of the rigid roadway. This is because the rigid roadway is quite thick, and only the middle region of the bridge needs additional support by the arch. The compliance converges in each substage (Fig. 15), but the overall compliance increases as the stages progress due to the gradual imposition of the mass constraint. This gradual change in mass naturally generates a Pareto front that shows the tradeoff between the mass and compliance, as shown in Fig. 16.

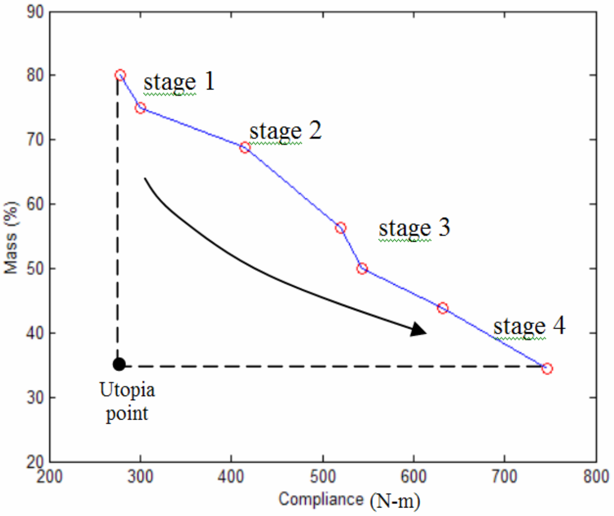


Figure 16: Multiobjective optimization with mass and compliance as objective functions for the bridge problem.

V. Conclusions and Future Work

A novel GA method in which the length of a chromosome evolves is developed for structural topology optimization. The design domain is refined gradually in stages. The proposed method is applied to two typical structural optimization problems: a short cantilever and a bridge problem. The algorithm increases the likelihood of approaching higher levels of fitness, allows the solution of problems with large numbers of design variables, and broadens the notion of design evolution to include gradually increasing levels of complexity. The solution is compared with the one-time brute force approach, and it is demonstrated that the variable chromosome length GA finds a better solution with less computational cost. This approach is inspired by the gradual progression of biological systems from single cell organisms to higher life forms. In a similar fashion, design progresses from coarse stages to gradually higher levels of refinement.

An adaptive chromosome length GA, in which chromosome length changes adaptively according to the characteristics of problems, will be developed as future work. Efficiency of each optimization method will be assessed based on complexity theory or information theory[33]. Several convergence criteria for outer loop convergence will also be developed and tested.

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