

AN EFFICIENT STOCHASTIC SEARCH WITH MINIMAL INITIAL POPULATION FOR STRUCTURAL OPTIMIZATION

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ABSTRACT

Genetic Algorithms are best suited for unconstrained problems; however, most of the practical cases have constraints. As a common approach, modifying initial population due to problem-specific information has not yet come to an end. This is due to the generalization challenges and also the lack of diversity and effectiveness regarding relatively narrow size of the feasible subspace of the entire search space. In this article, a new type of expanding genetic population is presented starting from its minimal size. Suitable ideas from ant colony and simulated annealing approaches are utilized for an adaptive efficient search which is also tuneable by the developed extra control parameters. Effectiveness and efficiency of the proposed method are illustrated by capturing the global optimum in a number of well-known structural size and layout optimization examples in a considerably less fitness evaluations compared to the other standard methods.

Keywords: Genetic algorithm; ant colony metaphor; simulated annealing; direct index coding; variable mutation band; topology optimization

1. INTRODUCTION

Genetic algorithm is principally a population based method to search discrete genotypic space as a mapped design space. The phenotypic information is necessarily accessed only during the fitness evaluation phase, when the genotypes are decoded to the corresponding phenotypes [1,2]. Application of the GA operators on such encoded chromosomes, rather than the phenotypic search points, is expected to provide simplicity of shifting between various islands of the design space. However, extensive sampling of the mapped design space will practically be required to capture the global optimum and its island or the genetic control parameters. The latter should be adaptively tuned to preserve proper diversity of the population during generations of the search. This is a complex task due to the unclear shape

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of the design space before its sampling. The challenge is even more crucial when dealing with the constrained spaces as the case of structural optimization problems.

It is a common practice to use randomly generated initial population of genotypes in order to increase the chance of capturing the global optimum island [2,3,4]. This can also be performed by niching and re-randomizing [4,5]. However, the efficiency of the search is often reduced as the size of such a random set increases. Consequently, some investigators have recommended the generation of suitable initial population using specific information of their own problems in order to avoid extra unnecessary computational effort [6-8].

Structural optimization is a practical and rewarding field of design problems with the following general features [9]:

There are several local optima in addition to the global optimum for the objective function. A great number of design variables and several types of constraints make the size of feasible space narrow compared to the entire design space. The latter feature affects the effectiveness and efficiency of the GA using random initial population, while it may even be filled with infeasible individuals. This problem is particularly intensified in topology optimization when sparse or instable topologies attend to fill the population because of their noticeably lower weight as a common objective to be minimized.

Two approaches have been reported to enforce the existence of feasible individuals in the population; namely, penalty functions and pull-back methods [8,9]. In the topology optimization problems, the penalty function coefficient should be determined based of several runs to preserve suitable convergence rate, while the pull-back method imposes the need to simultaneously solve another auxiliary optimization problem, e.g. by gradient-based calculations. This fact reveals an alternative idea of starting the initial population with feasible solutions. Meanwhile proper genetic operator should be employed to preserve diversity of the population in subsequent generations.

Some researchers have recommended the population size to be of order of the section variants for every member group [3]. However, this may require considerable computational cost in fitness evaluation of such a relatively large population. Some others suggested multi-stage methods with variable chromosome length [10], based on the "coarse to fine" strategy in continuum problems [10,11]. The corresponding sampling effort at each generation gradually increases as the resolution of design variables and the length of the binary chromosome increase at each new stage.

Leung and Liang [12] developed an adaptive elitist-population based genetic search method and corresponding operators aiming to increase both the effectiveness and the efficiency of GA in searching multi-modal spaces. They also employed a special selection to simulate some features of immune systems in their innovative method, and could even use two parents in test functions of analytical type. However, this required higher population size in their most complicated test problems. Such a method was based on measuring competitive individual dissimilarities by calculating their relative directions. This imposes a number of additional control parameters and extra neighborhood local search which usually require gradient estimation of the fitness function.

Alternatively, suitable integer coding in discrete structural problems reveals mutation band to be effectively controlled [13,14]. A hybrid strategy is developed to sample

competitive individuals of the population in a discrete manner. The method is based on the theory of alternate appearance of such representatives from subpopulations requiring no extra fitness evaluation cost [2].

Utilizing a variant of such an approach, this paper enables the use of minimal initial population for more efficient genetic search in structural problems. The supporting theory is reviewed in Section 2 discussing the idea for successive individuals during the search. Hybridization of an ant colony routine with the genetic search is proposed in Section 3 providing suitable analogy and the main algorithmic core. Section 4 covers extra tuning routine for mutation band and refers its basics via simulated annealing terms. After completing the methodology and the definitions of the control parameters, Section 5 applies the developed method to a number of structural benchmark sizing and layout design optimization problems to illustrate its effectiveness and efficiency of the proposed method. Section 6 contains the concluding remarks.

2. THEORY OF THE ALTERNATE ELITE APPEARANCE OF THE COMPETITIVE INDIVIDUALS

Evolution Strategies in general and the Genetic Algorithms in particular, are based on simulation of competition and survival of the fittest individuals. Many such systems may start from a small set of individuals and gradually evolve to a stabilized colony in a corporative/ competitive manner.

The competition is inspired in GA by interaction of its exploitation and exploration agents. Crossover and fitness based selection as exploitative agents tend to subdivide the initial set of individuals to a number of subpopulations. The matter is already discussed in literature and even extended to multi-objective genetic algorithms [15,16]. This type of depth-first search process on a limited set of alleles in the chromosomes of initiated population may not provide migration to any new local search island unless it is combined with an exploration agent; that is the mutation operator. Once some individuals from new islands are explored and introduced to the current population, crossover and selection provides the chance for them to compete and replace the elite individuals of the current population. In this way, alternate appearance of the fittest individuals from any new local search region in the elitist part of the population is expected until such regions covers the island of global optimum regarding fitness maximization. The idea is already introduced as theory of alternate appearance of the competitive individuals and tested for population size adjusting and providing self-adaptive diversity to overcome premature convergence [2,17].

The present study utilizes such a concept to enable starting the search with a small (minimal) initial population. The other goal is diversity expansion from the initial feasible population in structural problems to larger population as the generation size increases.

3. INCORPORATING ANT STRATEGIES IN GENETIC SEARCH TO SAMPLE THE ELITIST COMPETITIVE

On the basis of the theory of alternate elite appearance and features of the genetic algorithms in gradual fitness improvement and survival of the fittests, frequency of such appearance in the recent generations is selected as a criterion for sampling the competitive representatives for further population adjustment.

In order to fulfill this goal, the authors suggested a method of combining indirect data share strategy of *Ant Systems* [18,19] with the direct data exchange in genetic algorithms. In such a methodology, the fitness of the individuals are taken analogous to the *attractiveness*, and a *pheromone trail* process is discretely developed to extract a dynamic memory of more frequent individuals in the elitist portion of the population during recent generations [2].

Here, the main algorithm is first reviewed and then utilized for the present study adjusting its corresponding parameters. This subroutine consists of the following steps:

1. Determine the encoding method and consequently the chromosome length.
2. Nominate the initial population size as N_1 , the number of ants as N' and the pheromone deposit packet as $\Delta\tau$. Determine the value of these parameters considering $N' \leq \frac{N_1}{2}$ and $\Delta\tau \geq 2$.
3. Initiate the first population of chromosomes.
4. Perform *reproduction* including crossover, mutation and fitness based selection.
5. Sort the generated (feasible) individuals in the order of their fitness. Then let N' ants select the fitter ones as candidates for copying to the auxiliary camp of individuals.
6. For each candidate check whether the same individual (chromosome) already exists in the camp; when the answer is No, add the candidate to the camp and increase the camp size by 1 and initiate its pheromone by 0.
7. Add pheromone of the newcomer individuals by $\Delta\tau$.
8. Evaporate pheromone of all the camp individuals; i.e., decrease its value by 1.
9. Eliminate individuals with zero pheromone from the camp.
10. Go to Step 4 and repeat until algorithm stop criterion (e.g. achieving a predetermined number of generations) is satisfied.

The subroutine results in a variable-size camp of chromosomes considered as a dynamic memory of more frequent attractive individuals. It is expected to sample the representatives from various genetic islands during the search.

The present study utilizes such a routine for genetic search in structural optimization with minimal initial population. The minimum required number of parents dominated by the crossover operator is $N_1 = 2$. In this case, the number of ants should be taken as

$N' = \frac{N_1}{2} = 1$. While GA operators work in the width of population, the ant system gathers

information among generations of the search. Hence, the other parameter; $\Delta\tau$, representing the depth of the memory of the recent appeared elite individuals, is extended. As the

pheromone evaporation is discretely performed in steps of 1 unit decrease, the $\Delta\tau$ can not be taken less than 2, otherwise the pheromone is evaporated before having enough chance to be gathered. The more the $\Delta\tau$, the wider the range of the previous generations will be considered in the camp of more frequent representatives. Regarding this fact, one has the choice to decide the value of this parameter. It can be taken as 2 for more accurate sampling and more graduate increase in the population size.

For the present study, on structural optimization, such a minimal initial population consists of 2 feasible designed chromosomes as will further be described in the next section. In each generation of the main optimization algorithm, the auxiliary camp of individuals is updated by the above mentioned subroutine and is added to the population leading to the gradually widening of the *search window* (population size) as the GA progresses, Figure 1.

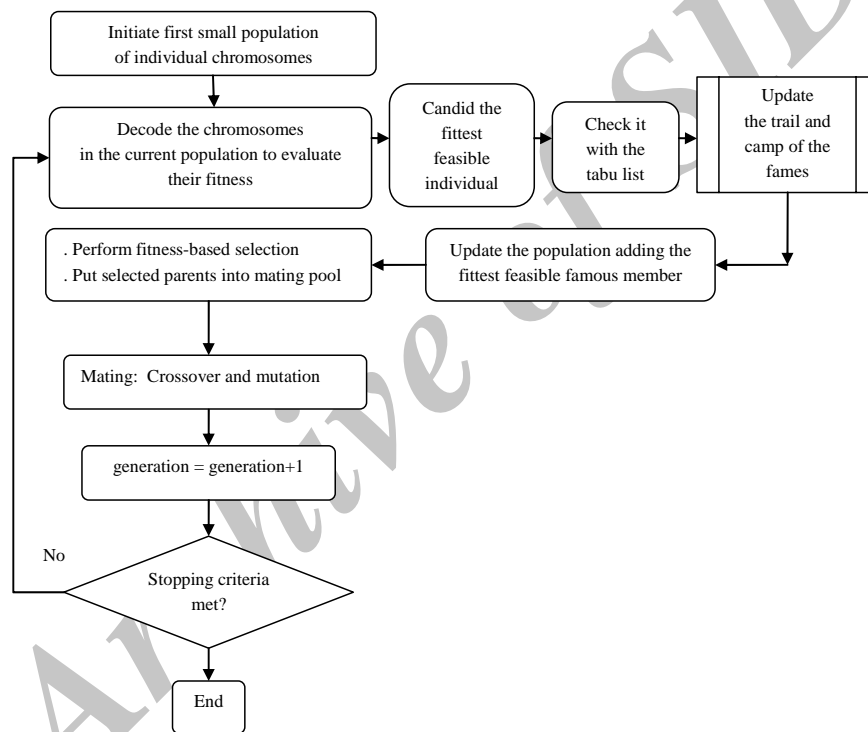


Figure 1. Flowchart of population adjusting in genetic algorithm

4. INITIATION AND SIMULATED TUNING MUTATION OPERATOR FOR DISCRETE STRUCTURAL SIZE AND TOPOLOGY OPTIMIZATION

Like many other problems with discrete limited variants for each design variable, it has already been shown that integer coding is more suitable for structural layout or size optimization [13]. In this class of problems, structural section properties are to be chosen

from a discrete list of available profiles meanwhile the topology of each member is to be altered in an integrated manner. Thus the authors developed the *direct index coding*, DIC, as the most suitable encoding method for this problem [13]. According to DIC, each j^{th} gene in the chromosome is assigned an alphabet of $[1, 2, \dots, n_j]$ characters to address the section profiles for the corresponding member group. In cases where the topological and profile member groups coincide with each other, a zero index is added to such an alphabet to indicate the elimination of that group during layout (simultaneous topology and size) optimization. Otherwise, the ratio of mutation probability threshold in the topological bits to the sizing part of optimization is limited based on such a concept [13]. In every stage of optimization, the permissible number of neighbor indices for the current allele to mutate plus one, is known as its *mutation band* [14].

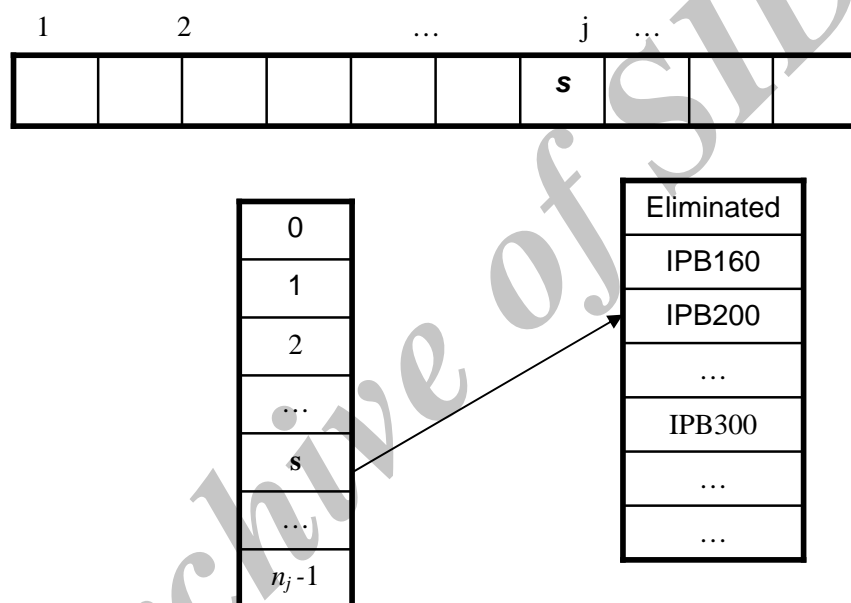


Figure 2. Example of a direct index coded chromosome and the structural section associated to the j^{th} gene

Figure 2 shows a sample direct index coded chromosome in which the value of the j^{th} gene can vary between 0 to n_j-1 ; i.e. n_j choices. While 0 index means the elimination of that member group, the other indices address the structural sections to be associated with it as depicted, correspondingly.

Definition of 1-point, 2-point and uniform crossover operator for DIC is similar to those of the binary coding, with the only difference that DIC crossover acts on genes which can have integer values other than 0 and 1. As an example, in a direct uniform crossover, a mask bit-string is first generated. Then for each zero mask bits, the value of corresponding genes in the direct index parent chromosomes are exchanged to produce 2 children. Figure 3 shows an example of a direct crossover.

11	0	5	0	9	0	11	7	17	1	19	0
Parent 1						Child 1					
34	7	17	1	14	1	34	0	5	0	14	1
Parent 2						Child 2					
1	0	0	0	1	1	Mask					
Allele variation											
1~42	0~7	1~42	0~1	1~20	0~1						

Figure 3. Example of two-point crossover applied to 2 sample direct index coded parents. Pre-assigned range of allele variation is also given. Values of the genes in places of zero mask bits are exchanged. Note that in this 2-point crossover there are only 2 change sites in the corresponding mask string

The crossover operator in DIC can be employed similar to the case of the binary encoding. However, special mutation operators previously developed by the authors should be utilized [13,14]. It should be noted that the sensitivity of GA convergence to the mutation probability or band in the early generations of the proposed method with small population size is less than those in the subsequent generations. Therefore, it is desirable to initialize such thresholds with higher values and then gradually decrease them to a lower pre-determined limit. One way to tune the mutation band or the probability between these thresholds among generations of the search is to implement the following envelope function developed based on fast simulated annealing approaches [14]:

$$P = e^{\frac{-\Delta E}{C_b T(k)}} \tag{1}$$

$$f_e(k) = \begin{cases} 1, & \text{for } k = 1 \\ e^{\frac{-1}{C_b T}}, & \text{whereas } T = \frac{N}{k-1} - 1.0, \text{ for } k > 1 \end{cases} \tag{2}$$

$$R_j(k) = \max(2, \text{round}(f_e(k) \times n_j)) \tag{3}$$

Where N is the maximum generation number in the GA search, T denotes the cooling temperature with P and C_b indicating the Boltzman Probability and its pre-determined coefficient for the artificial energy difference, ΔE is taken as unity. $R_j(k)$ is the index range for the j^{th} gene in k^{th} generation. The resulted curves with $C_b \leq 0.5$, shown in Figure 4, are similar to those reported as the result of explicit parameter tuning techniques, with the difference that the proposed method is designed for single-stage runs and do not require excessive multiple runs in an auxiliary hyper-level optimization [20].

Despite the mutation probability, such upper and lower limits for the mutation band are

quite clear according to Eq. (3) without the need to further tuning trials. Thus, the variation of mutation band is preferred in this article. The resulting method is called *Annealed Variable Band Mutation*, AVBM [14].

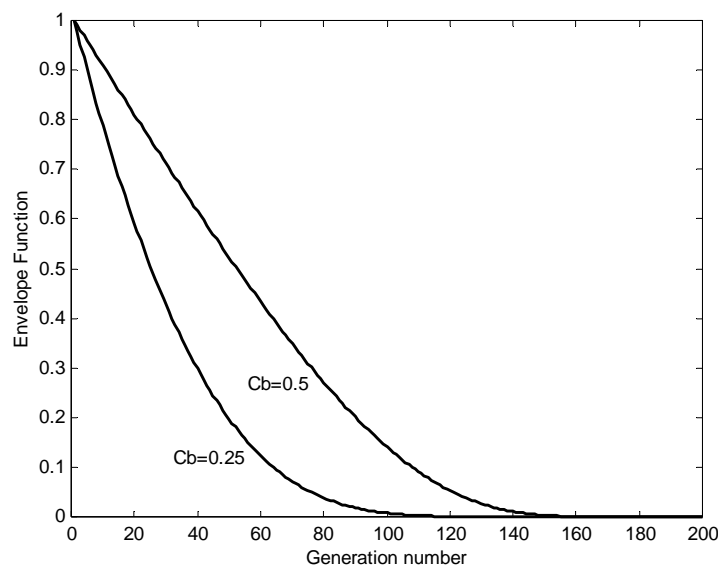


Figure 4. Envelope function curves for sample Boltzman coefficients

In the most popular class of structural optimization problems, a component property can be found which has a direct relation to the resulted objective function. For example, the total structural weight as an objective is dependent on the cross-sectional area of its members. In such cases, the corresponding profile list can be sorted in terms of that property so that initiating each gene of the 1st population chromosomes with its maximum index preserves the feasible and the strongest designs. Such a technique is also employed to initiate the minimal population of 2 chromosomes in this article rather than excessive sampling of the search space to find feasible initial individuals. This can somehow be considered similar to the strategy of “coarse to fine” in continuum problems. Since the number of population individuals in early generations as grand parents of the future larger populations is relatively small, the effectiveness of the mutation operator in these generations is expected to be higher, maintaining the diversity of the population in subsequent generations.

5. ILLUSTRATIVE EXAMPLES

The proposed hybrid method is applied to the following examples from the literature benchmarks with minimal starting population. The *tournament selection* is preferred to be employed because it does not eliminate the chance of the least fit but probably good individuals as parents of the subsequent generation. The fittest individual of every previous

generation is put into the current mating pool as the elitist chromosome. The structural optimization problem is formulated as follows:

Minimize:

$$w = \rho \cdot \sum_{i=1}^M A_i \cdot L_i \quad (4)$$

Subjected to:

$$KU = P \quad (5)$$

$$g_j^d = \left| \frac{\Delta^j}{\Delta^{j,a}} \right| - 1 \leq 0 \quad (6)$$

$$g_i^s = \left| \frac{\sigma_i}{\sigma^a} \right| - 1 \leq 0 \quad (7)$$

for: $i = 1, \dots, ne$, $j = 1, \dots, nDOF$

Where K , U and P are the stiffness matrix, nodal displacement, and force vectors, respectively; ρ is the material density; and L_i and A_i denote the length and the cross-section area of the i^{th} member, respectively. Δ^j and σ_i are the nodal displacement and axial member stress response, while the number of elements and the degrees of freedom in the problem are denoted by ne and $nDOF$, respectively.

The fitness function is considered as:

$$F = F_0 - w * (1 + K_p \cdot V) \quad (8)$$

$$V = \sum_{nLC} (\max(g^d, 0) + \max(g^s, 0)) \quad (9)$$

Where K_p is the penalty constant and V denotes the total constraints' violation regarding all nLC loading conditions. F_0 is taken 0 in the case of tournament selection scheme. Initial smallest population, consists of 2 parents whose genes are assigned their maximum available indices to start the search in the following examples. The static equilibrium constraint (5) is satisfied when deriving stress and displacement responses.

5.1 Parameter setting

Among the control parameters of the present method, K_p is taken 10 for this class of treated examples [21] and the number of ants is set to 1. The pheromone packet is taken its minimal value 2 unless otherwise mentioned. Other required parameters are summarized in Table 1 and determined for each case.

Since the present method includes floating-point control variables, the number of possible parameter combinations is infinite. Thus for practical purposes, only some finite number of

combinations are tested for parameter setting as illustrated in the following example. One may follow the same way for her/his own case, however for theoretical purposes hyper tuning is still an active field of research [20] which has not come to an end yet.

Table 1: Parameter sets considered to study for the proposed methods in Example 1

Parameter : set number	Mutation probability	Mutation type	C_b	Crossover type	Crossover probability	Pheromone packet	Initial population size	Number of generations (NG)
1	0.10	AVBM	1	2-point	0.90	2	2	200
2	0.10	AVBM	0.5	2-point	0.90	2	2	200
3	0.10	AVBM	0.25	2-point	0.90	2	2	200
4	0.10	AVBM	1	1-point	0.90	2	2	200
5	0.10	AVBM	0.5	1-point	0.90	2	2	200
6	0.10	AVBM	0.25	1-point	0.90	2	2	200
7	0.10	DIM	-	1-point	0.90	2	2	200
8	0.15	DIM	-	1-point	0.90	2	2	200
9	0.20	DIM	-	1-point	0.90	2	2	200
10	0.10	DIM	-	1-point	0.90	0	30	200
11	0.15	DIM	-	1-point	0.90	0	30	200
12	0.20	DIM	-	1-point	0.90	0	30	200
13	0.15	AVBM	0.5	2-point	0.90	2	2	200
14	0.15	AVBM	0.5	1-point	0.90	2	2	200
15	0.15	AVBM	0.25	2-point	0.90	2	2	200
16	0.15	AVBM	0.5	2-point	0.90	4	2	200
17	0.15	AVBM	0.5	2-point	0.90	2	8	200
18	0.15	AVBM	0.5	2-point	0.80	2	2	200
19	0.15	AVBM	0.5	2-point	0.90	2	2	400
20	0.15	AVBM	0.5	2-point	0.90	2	2	100

The results for every such set in Table 1 are summarized in Table 4. Statistical results are extracted based on the same number of trails for each parameter set. A total number of 200 trial runs is selected for this study, while each run itself takes thousands of fitness evaluations; i.e., structural model regenerations and analyses.

The first three sets include variation of Boltzman Coefficient C_b when 2-point crossover is applied. In the next 3 sets, the 1-point crossover is used instead. Another set with no

mutation band control is also tested for comparison.

Table 2: Lists of profile properties and their associated indices

Profile index	S ₁	S ₂	S ₃	S ₄
	Section area (10 ⁻⁴ m ²)	Section area (10 ⁻⁴ m ²)	Section area (10 ⁻⁴ m ²)	Section area (10 ⁻⁴ m ²)
1	10.45	10.45	6.45	0.774
2	11.61	11.61	19.35	1.255
3	12.84	15.35	32.26	2.142
4	13.74	16.90	51.61	3.348
5	15.35	18.58	64.51	4.065
6	16.90	19.94	67.74	4.632
7	16.97	20.19	77.42	6.542
8	18.58	21.81	96.77	7.742
9	18.90	23.42	109.68	9.032
10	19.93	24.77	141.94	10.839
11	20.19	24.97	154.84	12.671
12	21.81	26.97	167.74	14.581
13	22.39	28.97	180.64	21.483
14	22.90	30.97	187.10	34.839
15	23.42	32.06	200.00	44.516
16	24.77	33.03	225.81	52.903
17	24.97	37.03	-	60.258
18	25.03	46.58	-	65.226
19	26.97	51.42	-	-
20	27.23	74.19	-	-
21	28.97	87.10	-	-
22	29.61	89.68	-	-
23	30.97	91.61	-	-
24	32.06	100.00	-	-
25	33.03	103.23	-	-
26	37.03	121.29	-	-
27	46.58	128.39	-	-
28	51.42	141.94	-	-
29	74.19	147.74	-	-
30	87.10	170.97	-	-
31	89.68	193.55	-	-
32	91.61	216.13	-	-
33	100.00	-	-	-
34	103.23	-	-	-
35	109.03	-	-	-
36	121.29	-	-	-
37	128.39	-	-	-
38	141.93	-	-	-
39	147.74	-	-	-
40	170.97	-	-	-
41	193.55	-	-	-
42	216.13	-	-	-

Table 3: Optimal indices for sizing optimization of the 10-bar truss [13,21,22], Figure 5

Member ID	1	2	3	4	5	6	7	8	9	10	Structural Weight (N)
Profile Index in List S_1	42	1	39	32	1	1	28	39	38	1	24428

Table 4: Parameter study results for the 10-bar truss example

Parameter set number	Ratio of global optimum capture within NG. generations (%)	Best structural weight (N)	Average structural weight (N)	Average number of generations up to the last improvement	Average number of fitness evaluations up to the last improvement	Ratio of standard deviation to average weight (%)
1	10	24428	25310.7	188	3103	5.6
2	20	24428	25303.4	183	3132	5.4
3	0	24878	26368.6	197	4010	7.0
4	10	24428	25487.6	184	2794	6.4
5	20	24428	26433.6	189	3018	9.5
6	0	24469	25727.1	196	4090	6.8
7	0	24808	26146.0	179	2423	4.5
8	0	24820	26046.3	172	2168	3.2
9	0	25913	27161.8	172	1706	5.3
10	0	24793	25582.9	164	4929	2.4
11	0	25270	25703.6	238	7155	8.5
12	0	25351	25916.1	147	4401	2.0
13	20	24428	26006.6	195	3485	7.4
14	10	24428	25388.7	185	2733	6.4
15	10	24428	25333.1	188	3326	2.8
16	0	24590	25846.1	192	1601	6.2
17	30	24428	24613.4	179	3669	1.5
18	20	24428	25394.7	194	2939	4.8
19	80	24428	25015.6	332	7699	8.0
20	0	24934	26576.8	98	1138	6.8

As shown in Table 4, using the 2nd set with C_b of 0.5, 20 percent of trials captured the global optimum while this measure is 10% and 0 for other tested C_b 's. The 1-point crossover revealed the same conclusion but led to more average structural weight than the 2-point crossover. The ratio of standard deviation to the average of structural weight computed over

trials of each set is 5.4% for 2-point crossover and less than 9.5 for 1-point case. The 7th set in which the mutation band is fixed to its maximum, could not achieve the global optimum within 200 generations. This shows superiority of 2-point crossover with C_b of 0.5 among these sets.

Variation of mutation rate, as another important parameter, is studied through further parameter sets. In the next three sets 10, 11, 12, the population size is kept fixed as 30, i.e.; slightly greater than average PopSize of the previous ones. Among the mutation rates of 10%, 15% and 20%, the 2nd had better results in the case of variable PopSize while the 1st was best for the case of traditional fixed size population. This shows the capability of the proposed method in working with higher mutation rates. Thus the AVBM with 15% mutation rate and variable mutation band according to relations (1) to (3) with C_b of 0.5 is chosen for the parameter Set-13. Every next set has only one parameter varied with respect to this parameter set.

Changing the crossover type to the 1-point in Set-14, resulted in less percentage of capturing the global optimum. Altering the C_b from 0.5 in Set-13 to 0.25 in Set-15, led to identical results.

Set-16 with more pheromone packet, $\Delta\tau$, resulted in less average structural weight; however, it could not capture the global optimum within 1 trials and 200 generations.

In Set-17, variable population size was started from 8 instead of its minimum value of 2. Consequently, the capture ratio to the global optimum was increased.

The effect of crossover rate variation from 0.9 to 0.8 in the Set-18 resulted in the same capture ratio and similar number of required iterations to achieve the global optimum.

For the proposed method, the maximum generation number is altered to 400 and 100 (i.e. 2 and half times the current value) in the sets number 19 and 20, respectively. As expected, the results were improved in more generations and suffered in fewer. The capture ratio of the global optimum in Set-19 increased to 80% while decreased to 0 in Set-20. The latter with half the population size of 200, has led to the most structural weight among the entire tested sets in Tables 1 and 4.

The best run of the best parameter set; i.e., Set-13, is chosen here as a sample run called Present Work-1 to illustrate further information. The corresponding computational cost is then given in Table 5. The variation history of population size during such an optimization is depicted in Figure 6 while Figure 7 shows the history of mutation band for maximum index of 42 in this example. Similarly, the information for the next examples are given for their corresponding sample runs.

Table 5: Computational effort in sizing optimization of the 10-bar truss (with the search space cardinality of 42^{10})

Method	Final population size	Number of fitness evaluations to achieve optimum	Number of generations to achieve optimum
Present Work 1	29	3694	183

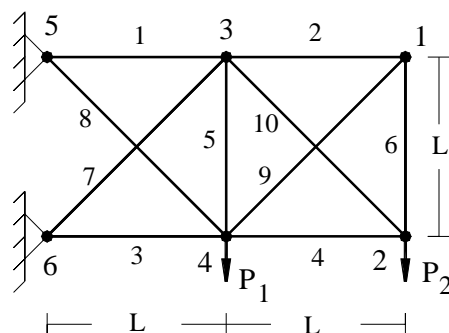


Figure 5. Boundary conditions, dimensions and loading of the 6-node truss: $L=9.14m$,
 $P_1=P_2=445.4\text{ kN}$

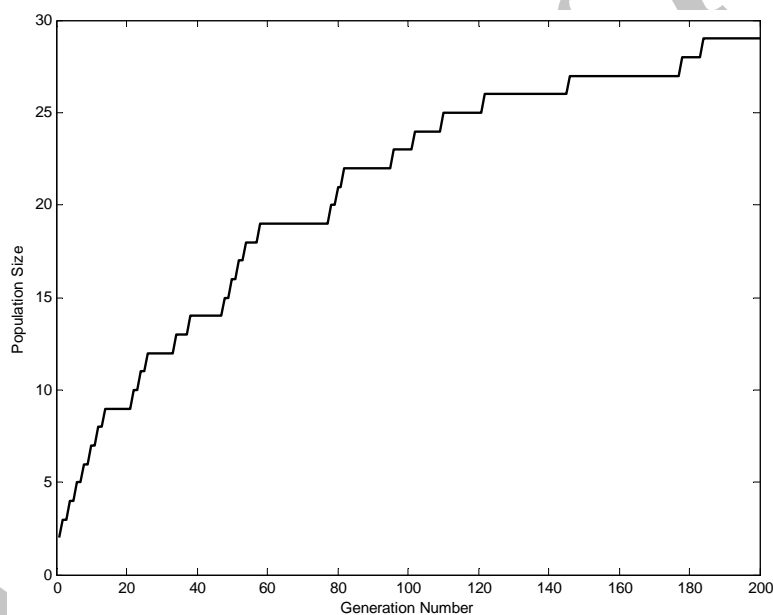


Figure 6. Variation history of the population size in the Present Work 1

5.2 Layout optimization of the 6-node planar truss

Here, the truss of Figure 5 under the same loading condition is considered for simultaneous topology and size optimization. For topological part of optimization, the protomorph structure [23] of Figure 5 is used as a planar graph [24]. Cross sectional areas are to be selected from 32 profiles from the list S_2 of Table 2.

For the set of control parameters provided in Table 6, the proposed method again could capture the global optimum as reported in literature [7,13], and shown in Table 7. Mutation band tuning in this example did not violate the necessary diversity of the population to achieve the global optimum with corresponding computational cost (see Table 8). Thus, the

gradual procedure of adjusting and qualifying population allowed the mutation probability of 0.15 to be employed.

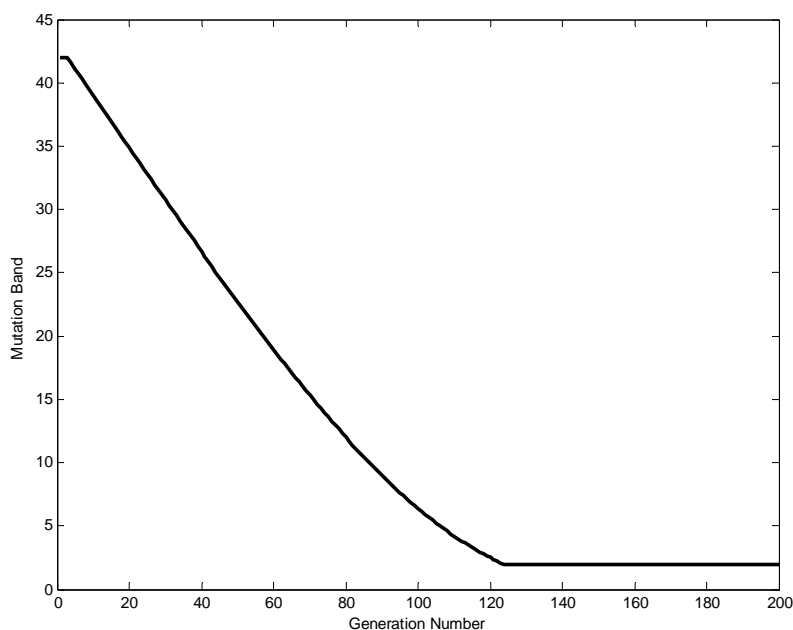


Figure 7. Variation history of the mutation band in the Present Work 1

Table 6: Genetic parameters applied to the 6-node truss layout optimization example; Sec.5.2

Method	Crossover type	Crossover probability	Mutation type	Boltzman coefficient	Mutation probability	Initial pop size	Number of generations
Present Work 2	2-point	0.90	AVBM	0.5	0.15	2	200

Table 7: Optimal layout for the 6-node truss in the 6-node truss [7,13]

Member ID	1	2	3	4	5	6	7	8	9	10	Structural weight (N)
Profile index in the list S_2	31	0	27	24	0	0	18	28	28	0	22058

5.3 Layout optimization of the 6-node planar truss - multiple loading conditions

For this example, P_1 and P_2 in Figure 5 are applied as 2 distinct loading conditions. Sixteen

profiles of the list S_3 of Table 2 are to be selected for the sizing part of optimization. Since the elimination of members is also addressed with a zero index in the minimal length direct indexed chromosome, the corresponding search space size is 17^{10} . Material properties and stress and displacement constraints are the same as those of the previous examples.

Table 8: Computational effort in layout optimization of the 6-node truss (with the search space cardinality of 33^{10})

Method	Final population size	Number of fitness evaluations to achieve optimum	Number of generations to achieve optimum
Present Work 2	58	4395	180

The effectiveness of the proposed method was again shown by achieving the global optimum layout of Table 9, which has ever been found in literature [13]. The method was successful in finding true optimum even with relatively high mutation rate of 0.20 and simple 1-point crossover. The first run starts with minimal population of two chromosomes with index number of 16 assigned to its gene alleles. During the simultaneous optimization and tuning process, such a population size reached to 29 and then the optimal layout was obtained.

Table 9: Optimal layout for the 6-node truss under two loading conditions [13].

Member ID	1	2	3	4	5	6	7	8	9	10	Structural weight (N)
Profile index in the list S_3	13	0	8	8	2	0	2	9	10	0	19267

Maximum index range in this example is only 17 indices. Subsequently, more trials were considered to compare the efficiency of the algorithm and the population initiation method in this structural problem. Control parameters of these sample runs are given in Table 10 except that the 1st population of chromosomes in the Present Work 5 is formed in a different way; that is random generation of allele indices within their index range.

Table 10: Genetic parameters applied to the 6-node truss under two loading conditions; Section 5.3

Method	Crossover type	Crossover probability	Mutation type	Boltzman coefficient	Mutation probability	Initial pop size	Number of generations
Present Work 3	1-point	0.90	AVBM	0.25	0.20	2	200
Present Works 4,5	1-point	0.90	AVBM	0.25	0.20	30	200

These trials could achieve the problem optimum in less than 200 generations. Therefore, the number used to set the temperature cooling for simulated annealed mutation band tuning. However, as shown in Table 11, the computational cost and even the generation number of optimum capturing were less for variable population size tuning than the other 2 methods. Such a cost is measured by number of fitness function evaluations, its most value belonged to the GA implementation with fixed randomly initiated population.

Table 11: Computational effort in layout optimization of the 6-node truss under two loading conditions (with the search space cardinality of 17^{10})

Method	Final population Size	Number of fitness evaluations to achieve optimum	Number of generations to achieve optimum	Percentage of unstable topologies
Present Work 3	29	1171	70	1.8
Present Work 4	30	2357	80	1.8
Present Work 5	30	2912	100	2.9

Taking to account the last column of Table 11, it may be concluded that such a difference in required computational effort is related to the overall percentage of unstable topologies generated in each of the methods. The percentage of such irregular light-weight layouts which tend to disturb the population and decrease the convergence rate, is more when the initial population is generated randomly compared to the allele initiation with the index of the strongest structural section.

The history of computational effort to achieve the optimum employing these 3 methods is shown in Figure 8. As can be realized, fixed population size causes almost linear increase in the number of fitness function evaluations vs. generation while the nonlinear curve of simultaneous population tuning in optimization falls well below it.

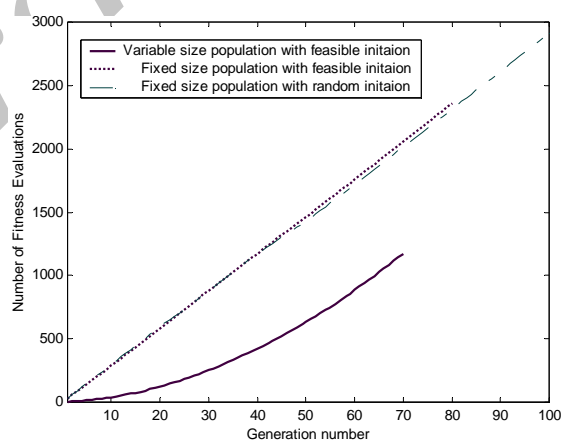


Figure 8. Comparison of computational cost to achieve global optimum in the Present Works 3, 4 and 5

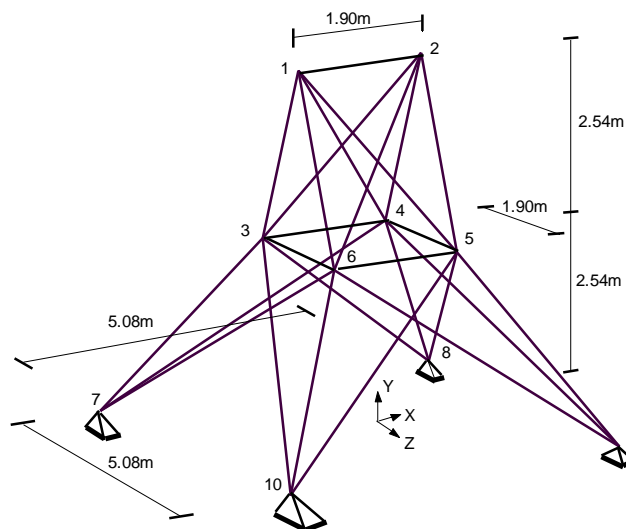


Figure 9. Boundary conditions and dimensions of the 10-node space truss example

5.4 Layout optimization of the 10-node space truss

This example is selected in order to test the capability of the proposed method in structural layout optimization in three dimensional problems and for grouped members, Figure 9. The loading state is given in Table 12. Material properties are taken as $E = 68.95GN/m^2$, $\rho = 27.1KN/m^3$ while the constraint on nodal displacements is $|\Delta^a| \leq 0.0089m$. Allowable stresses are given in Table 13. Since the topological groups are taken identical to the 8 profile groups (Table 14), the minimal length chromosome with 8 direct indexed genes can be employed in this example. The section list S_4 of Table 2 with 18 profile indices together with one 0 index, are considered as the character alphabet for every gene.

Table 12: Loading state applied to the 10-node space truss; Sec.5.4

Loading condition	Node number	Px (kN)	Py (kN)	Pz (kN)
1	1	4.45	-22.25	44.5
1	2	0	-22.25	44.5
1	3	2.225	0	0
1	6	2.225	0	0
2	1	0	-22.25	89
2	2	0	-22.25	-89

Table 13: Allowable tension and compression stresses for profile groups of the 10-node space truss

Profile group	1	2	3	4	5	6	7	8
Allowable tensile stress (MPa)	275.90	275.90	275.90	275.90	275.90	275.90	275.90	275.90
Allowable compression stress (MPa)	242.04	79.94	119.36	242.04	242.04	46.62	46.62	76.64

Table 14: Member list of the protomorph used for the 10-node space truss and corresponding member groups

Member ID	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
Node-1	1	1	2	1	2	2	2	1	1	3	4	3	5	3	6	4	5	3	4	6	5	3	4	5	6
Node-2	2	4	3	5	6	5	4	3	6	6	5	4	6	10	7	9	8	8	7	9	10	7	8	9	10
Profile Group	1	2	2	2	2	3	3	3	3	4	4	5	5	6	6	6	6	7	7	7	7	8	8	8	8
Topology Group	1	2	2	2	2	3	3	3	3	4	4	5	5	6	6	6	6	7	7	7	7	8	8	8	8

The proposed method of variable population size from initial parents of only two chromosomes is compared with the greater but fixed size population. Other parameters are kept the same for the sake of comparison.

In this example, another set of control parameters such as uniform crossover is used, Table 15. Individuals of the initial population in both runs consist of alleles with their maximum available index.

Table 15: Genetic parameters applied to the 10-node space truss

Method	Crossover type	Crossover probability	Mutation type	Boltzman coefficient	Mutation probability	Initial pop size	Number of generations
Present Works 6	Uniform (50%)	0.85	AVBM	0.25	0.10	2	200
Present Works 7	Uniform (50%)	0.85	AVBM	0.25	0.10	24	200

The layout of the achieved global optimum is listed in Table 16, as previously reported in literature [6,13]. The proposed method compared to the fixed population-size, requires less computational cost as shown in Table 17. It also generated more percentage of unstable truss

topologies as a measure of inefficiency for such a fixed population-size run.

Table 16: Optimal layout of member groups for the 10-node truss in the 10-node space truss [7,13]

Member group	1	2	3	4	5	6	7	8	Structural weight (N)
Profile index in the list S_4	0	10	13	0	0	7	11	12	2517

Table 17: Computational effort for optimizing the 10-node space truss with the search space cardinality of 19^8

Method	Final population size	Number of fitness evaluations to achieve optimum	Number of generations to achieve optimum	Percentage of unstable topologies
Present Work 6	24	1059	69	0.1
Present Work 7	24	1531	64	0.3

6. CONCLUDING REMARKS

In this article, the possibility of using minimal initial population for structural weight minimization is shown, introducing a suitable method for simultaneous tuning of the population size/quality together with a simplified mutation band control.

In order to improve the population quality, more frequent representatives of local search islands are sampled by the developed hybrid ant strategy and genetic search method in the light of the theory of alternate elite competitive appearance. Structural problem-specific information is also used to initiate minimal population of only one pair of feasible good parents and the results were quite satisfactory.

The employed direct index coding is suitable for size and layout optimization problems of structures and enables the mutation band control in a minimal fixed length chromosome as a compromise to other methods of encoding with variable chromosome length. A previously adopted simulated annealing approach is also utilized and combined with the presented work to improve the efficiency of the search meanwhile preserving its effectiveness as shown by the comparison curves.

The method is then applied to a number of structural examples and could successfully capture the global optimum for literature benchmarks. A variety of genetic parameter sets are used in the treated examples to test the stability and the effectiveness of the proposed method. The capability of the method to work with higher mutation rates is shown which can be related to less sensitivity of the small feasible initial population to such a threshold,

as well as qualifying the newcomer individuals, while limiting the mutation band in subsequent generations.

Considering the treated examples, it is shown that the developed method of population tuning can provide more computational efficiency than the traditional methods with fixed population size. Such an achievement stood stable for either feasible or randomly generated initial fixed-size population of chromosomes.

In the case of size or layout optimization, where the feasible region constitutes a relatively small portion of the search space, using randomly initiated population is generally less efficient than a population of maximal strength feasible designs. This is confirmed by studying the effect of more unstable topologies generated during the GA search in the first case, which tend to disturb and dominate the population due to their less weight as a common structural minimization objective. In this view, the unified proposed method is preferred for such problems, providing not only the efficiency but also the simplicity of the implementation.

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