한국해양공학회지 제17권 제6호, pp 38~46, 2003(ISSN 1225-0767)

Optimum Design of Sandwich Panel Using Hybrid Metaheuristics Approach

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KEY WORDS: Micro-genetic Simulated Annealing, Scatter Search, Tabu Search, Global Optimisation, Metaheuristics

ABSTRACT: *Aim of this article is to propose Micro-Genetic Simulated Annealing (μGSA) as a hybrid metaheuristics approach to find the global optimum of nonlinear optimisation problems. This approach combines the features of modern metaheuristics such as micro-genetic algorithms (μGAs) and simulated annealing (SA) with the general robustness of parallel exploration and asymptotic convergence, respectively. Therefore, μGSA approach can help in avoiding the premature convergence and can search for better global solution, because of its wide spread applicability, global perspective and inherent parallelism. For the superior performance of the μGSA, the five well-known benchmark test functions that were tested and compared with the two global optimisation approaches: scatter search (SS) and hybrid scatter genetic tabu (HSGT) approach. A practical application to structural sandwich panel is also examined by optimising the weight function. From the simulation results, it has been concluded that the proposed μGSA approach is an effective optimisation tool for solving continuous nonlinear global optimisation problems in suitable computational time frame.*

1. Introduction

The optimisation algorithms to solve the global optimisation problems can be classified into three groups: deterministic, stochastic, and stochastically combined methods. The numerous surveys of these methods were appeared in Floudas and Pardalos (1990), Rinnooy Kan and Timmer (1989), and Trafalis and Kasap (2002). In recent years, some of modern metaheuristics have been proposed such as micro-genetic algorithms (Krishnakumar, 1989; Kim et al., 2002), simulated annealing (Kirkpatrick et al., 1983; Romeijn and Smith, 1994), scatter search (Glover et al., 2003), and tabu search (Al-Sultan and Al-Fawzan, 1997).

Deterministic methods attempt to generate trajectories that eventually converge to points, which satisfy the criteria of local optimality. They are beneficial only when the starting point belongs to the region of attraction of the global optimum. This infers that any deterministic method could be attracted by the local optimum instead. On the other hand, stochastic methods attempt to reasonably cover the whole search space, so that all local and global optima are identified. That is, points that do not strictly improve the objective function can also be created and take part in the search process.

The stochastically combined (hybrid) method has been proposed to solve various search and optimisation problems. The micro-genetic algorithms (μGAs) and simulated annealing (SA) have complementary strengths and weaknesses. While the μGAs exhibit parallelism and are better suited to implementation on parallel searches, it sometimes suffers from poor convergence properties and a serial bottleneck due to global selection. By contrast, the SA has good convergence properties, but it cannot easily exploit parallelism.

With aforementioned characteristics of modern metaheuristics, a hybrid approach is suggested in this article to solve continuous nonlinear global optimisation problems. This new approach, referred to as Micro-Genetic Simulated Annealing or μGSA, was developed by extending the μGAs (Kim et al., 2002; Kim, 2002) to SA (Kim et al., 2003) by introducing the reproductive plan using metropolis selection to steer the global solution spaces more extensively.

The μGSA works with encoding populations as in the simple-genetic algorithms (SGAs), but is implemented serially using the annealing schedules in a small population. The major difference between the μGAs and μGSA is how to make a reproductive plan for better searching skill due to the selection strategy. Therefore, a metropolis selection was proposed as a new conception for the reproductive plan.

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Here, a new chromosome is accepted or rejected according to metropolis algorithm.

From the simulation results of this article, the superior performance of the μGSA is discussed with five well-known benchmark functions shown in Appendix and a practical application in engineering field mentioned in Section 5. It is shown that the μGSA implementation overcomes the poor convergence properties and searches the global optimum solution much faster than other metaheuristics methods: SS and HSGT. Consequently, it has been concluded that the proposed μGSA approach is an effective optimisation tool for solving continuous nonlinear global optimisation problems.

2. Metaheuristics Optimisation Techniques

2.1 Simulated annealing (SA) approach

SA was motivated by an analogy to annealing in solids. Metropolis *et al.* (1953) first used the origin principle of SA to simulate on a computer the annealing process of crystals. Kirkpatrick *et al.* (1983) took the idea of the metropolis algorithm and applied it to combinatorial optimisation problems. The idea was to use simulated annealing to search for feasible solutions and converge to an optimal solution.

Consider a huge number of particles of fixed volume at some temperature T. Since the particles move, the system can be in various states. The probability that the system is in a state of certain energy E is given by the Boltzmann distribution $Prob\,(E) \approx \exp(-E/\kappa T)$. The energy state is the fluctuation of the objective cost value in the optimisation process. The quantity κ(Boltzmann's constant) is a constant of nature that relates temperature to energy. In other words, the system sometimes goes uphill as well as downhill. The simulation in the metropolis algorithm calculates the new energy of the system. If the energy has decreased then the system moves to this state. If the energy has increased then the new state is accepted using the probability returned by the above formula.

A certain number of iterations are carried out at each temperature, and then the temperature is decreased. This is repeated until the system freezes into a steady state. The SA approach is given in Fig. 1. The operators used for SA are inversion and transport operator, and will be discussed in the following Section 3.2.

2.2 Micro-genetic algorithms (μGAs) approach

The idea of μGAs was suggested by some theoretical results obtained by Goldberg (1989b), according to which a population size of 3 was sufficient to converge, regardless of the chromosomic length. The first implementation of the μGAs was reported by Krishnakumar (1989). He used a population size of 5, a crossover rate of 1, and a mutation rate of zero. For cutting path and traveling salesman problem, Kim *et al.* (2002, 2003) and Kim (2002) conducted to implement μGAs in order to achieve fast searching for better evolution and associated cost evaluation in global solution-spaces.

```
S: generate initial solution
T: initial temperature
While not yet (frozen state) do {
        perform loop L times {
                decide operators (transport or inversion)
                generate new neighbour S*
                Δ = cost(S*) - cost(S)
                if (Δ < 0.0) or (random < exp^(-Δ/κT))
                        set S = S*
        } set T = α·T (reduce temperature)
} End while
```

Fig. 1 Developed simulated annealing approach

The μGAs approach used in this article is given in Fig. 2 and described as follows: an initial population of binary chromosomes is generated using random fashion. Then, each chromosome is evaluated, and the statistics is also performed for optimised tendency. Next, the current population is shuffled for reproductive plan. The reproductive plan is accomplished by applying the genetic operators (crossover and mutation) on the current population. Each new chromosome is evaluated and performed by statistic procedure. The next job is a selection strategy, which is called airborne selection operator (Kim *et al.*, 2002). This selection strategy was developed to steer near-global optimum solution for μGAs approach by current authors. In this way, the important skill is that the information about good structure is not lost. This process is

```
initialize a population with 5 chromosomes
evaluate each chromosome and perform statistics
While not (terminating condition) do {
        shuffle current population for reproductive plan
        apply genetic operators
        evaluate new chromosomes and perform statistics
        apply airborne selection for new population
        update current iteration
} End while
```

Fig. 2 Developed micro-genetic algorithms approach repeated until the stopping criteria are satisfied. More detailed descriptions for μGAs are mentioned in Kim *et al.* (2002, 2003) and Kim (2002).

2.3 Scatter search (SS) approach

The SS approach was introduced to obtain a near-optimal solution to an integer programming problem by Glover (1977). This approach derives its foundations from earlier strategies for combining decision rules and constraints, with the goal of enabling a solution procedure based on the combined elements to yield better solutions than one based only on the original elements. That is, the approach was on the assumption that information about the relative desirability of alternative choices is captured in different forms by different rules, and that this information can be exploited more effectively when integrated by means of a combination mechanism than when treated by the standard strategy of selecting different rules one at a time, in isolation from each other.

The SS approach, which was proposed by Glover *et al.* (2003) to solve any nonlinear optimisation problems on bounded variables, was described for the comparisons of the simulation results in this article. This approach is given in Fig. 3. The procedure is sketched as follows:

Step 1: Generate a set of initial solution vectors to guarantee a critical level of diversity, and then apply heuristic processes as an attempt to improve these solutions. Designate a subset of the best vectors to be reference solutions.

Step 2: Create new solutions consisting of structured combinations of subsets of the current reference solutions.

Step 3: Apply the heuristic processes used in Step 1 to improve the solutions created in Step 2. These heuristic processes must be able to operate on infeasible solutions and may or may not yield feasible solutions.

```
generate a set of initial solution vectors
improve these solutions by heuristic processes
designate reference solutions
While not (specified iteration limit) do {
        create new solutions
        improve these solutions by heuristic processes
        extract improved best solutions
        add these solutions to reference set
} End while
```

Fig. 3 Scatter search approach (Glover *et al.*, 2003)

Step 4: Extract a collection of the improved best solutions from Step 3 and add them to the reference set.

Step 5: Repeat Steps 2, 3 and 4 until the reference set does not change. Diversify the reference set by re-starting from Step 1. Stop when reaching a specified iteration limit.

2.4 Hybrid scatter genetic tabu (HSGT) approach

The HSGT approach was suggested by Trafalis and Kasap (2002) to solve an unconstrained continuous nonlinear global optimisation problem. This approach combined the features of the following metaheuristics: scatter search, genetic algorithms, and tabu search. The HSGT approach starts with a randomly generated initial point and search directions to construct a collection of solutions. Then, it computes the weighted centre of gravity using these solutions and the weight assigned to each solution. Next, a new weighted centre of gravity is accepted or rejected according to its tabu status. Subsequently, a new set of search directions using the old search directions are generated either randomly or using the genetic operators. If the new centre of gravity is tabu, then the new directions are randomly generated. Otherwise, the genetic operators are used to construct the new search directions. At this stage, a complete iteration of the HSGT approach is performed, and the final weighted centre of gravity is the solution to the problem. The procedure is repeated until the stopping criterion is satisfied. The HSGT approach is given in Fig. 4.

```
Step 1: generate initial solution, S^k and set S^best = S^k
Step 2: generate reference points
Step 3: evaluate objective function for each of reference points
Step 4: assign weight to each of reference points
Step 5: compute new solution, S^k+1
Step 6: if cost(S^k+1) < cost(S^best) then go to Step 8
Step 7: check tabu status. If S^k+1 satisfies tabu conditions then
        do not accept S^k+1 as solution, go to Step 2 to generate
        new reference points
Step 8: S^best = S^k+1, update search directions by genetic operators
Step 9: go to Step 2 and repeat until stopping criterion satisfy
```

Fig. 4 Hybrid scatter genetic tabu approach (Trafalis and Kasap, 2002)

3. Micro-Genetic Simulated Annealing (μGAs) Approach

The μGAs and SA have complementary strengths and weaknesses. While the μGAs exhibit parallelism and are better suited to implementation on parallel explorations, it sometimes suffers from poor convergence properties and a serial bottleneck due to global selection. The SA, by contrast, has good convergence properties, but it cannot easily exploit parallelism. With above characteristics of modern metaheuristics (μGAs and SA), a hybrid approach is suggested to solve continuous nonlinear global optimisation problems in this article.

This new approach, referred to as Micro-Genetic Simulated Annealing or μGSA, has been shown to overcome the poor convergence properties and perform better than other approaches alone with five benchmark functions in Appendix. Specifically, the current authors extend the μGAs (Kim *et al.*, 2002; Kim, 2002) to SA (Kim *et al.*, 2003) by introducing the reproductive plan using metropolis selection to steer the global solution spaces more extensively.

The μGSA approach explores in a small population with some genetic operators to find the global optimum solution. The μGSA works with encoding populations as in the simple-genetic algorithms (SGAs), but is implemented serially using the annealing schedules. The main skeleton of the μGSA is illustrated in the Fig. 5.

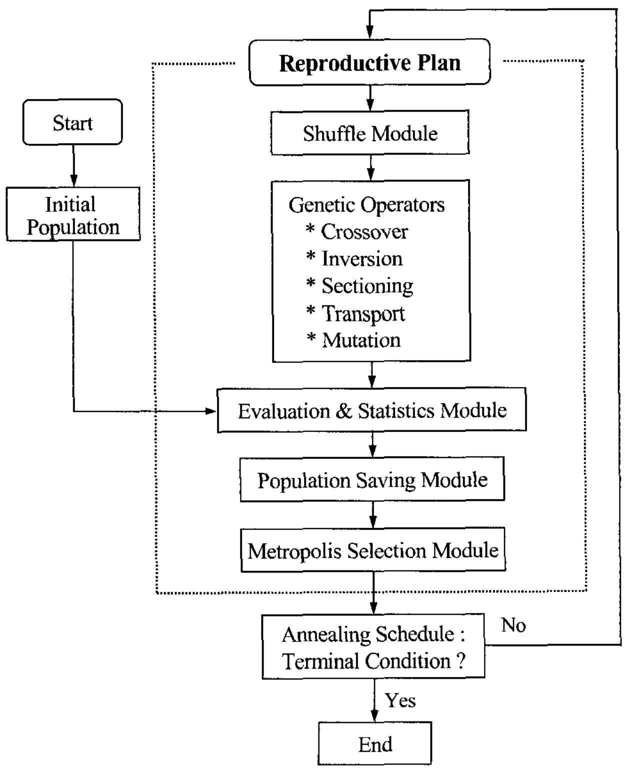

Fig. 5 Main skeleton of the μGSA

3.1 Reproductive plan by metropolis selection

An initial population, consisting of five chromosomes, is generated by random fashion to serve as a starting solution-space with binary coding. The population serves as a reservoir of information about the environment and as a basis for generating new trials. At each temperature step, the fitter chromosomes are selected to produce offspring, which inherit the best characteristics from the parents, for the next annealing schedule. After many annealing schedules of selection for the fitted chromosomes, the result is hopefully a population that is substantially fitter than the original.

Reproductive plan is to represent a legal domain-solution to the problem described by a string of genes that can take on some value from a specified finite range. With the structure designed and built, the five main operators are adopted for evolution process of the μGSA in global nonlinear optimisation problems. These genetic operators are crossover, inversion, sectioning, transport, and mutation. The metropolis selection is proposed as a new conception for the reproductive plan of the μGSA to steer global optimum solution. The metropolis selection is the process of choosing chromosomes for the next iteration by the metropolis algorithm from chromosomes of the previous and current iteration. By exploiting the metropolis selection strategy, the processing bottleneck of global selection is eliminated.

Since the μGSA has evolved in a dual solution-spaces (previous and current solution-spaces) to generate new solution-spaces as a parallel process, the μGSA approach can help in avoiding the premature convergence and always look for better global solution. Although this metropolis selection is based on sampling space of the SGAs, it is reasonable to implement this selection strategy on enlarged sampling space, as illustrated in Fig. 6.

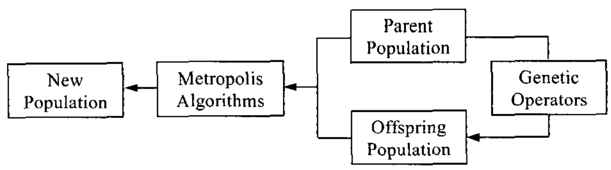

Fig. 6 Metropolis selection strategy

3.2 Genetic operators

The μGSA is composed of five genetic operators such as crossover, inversion, sectioning, transport, and mutation. These genetic operators allow the exploration of new solution spaces in the global domain space. That is, these operators play different roles at different stages of the evolutionary process. The following five operators are suggested as the essential contributors for each approach that was mentioned in Section 2.

3.2.1 Crossover operator

Once a pair of chromosomes has been selected, crossover can take place to produce offspring. Crossover exchanges alleles among adjacent pairs of chromosomes in the new population. The contribution of the crossover is times derived in which the crossover ratio crosses population size. Since the μGSA only use the crossover one time in the current population, this crossover rate is not used in the μ GSA approach.

Crossover might be implemented in a variety of ways, but there are theoretical advantages in treating the chromosome as a ring, choosing two crossover points, and exchanging the segment between these points (Goldberg, 1989a). In this concept of exchanging partial information, two different crossover points are chosen at random. This will divide the chromosome into three segments. The crossover operation is completed by exchanging the middle segment between the crossover points. If, after crossover, the offspring are different from the parents, then the offspring replace the parents, and are measured by an evaluation and statistic procedure later on.

3.2.2 Inversion operator

The origin of this strategy was used in the Lin-Kernighan (1973) heuristic for the travelling salesman problem. Let $(s_1, s_2, \cdots, s_n)$ be the structure of the current chromosome. There is a bond between s_1 and s_2, s_2 and s_3, $\cdots$, s_{n-1} and s_n, and s_n and s_1 in the current chromosome. In the two bonds exchange perturbation strategy, two bonds are selected at random and broken. These are replaced by the two unique bonds required to rejoin the chromosome and create a new one. For example, if the bonds (s_i, s_{i+1}) and (s_j, s_{j+1}) are broken, for $i < j < n$, the new bonds are (s_i, s_j) and (s_{i+1}, s_{j+1}).

The net result is that the segment between s_{i+1} and s_j is inverted. As illustrated in Fig. 7, the perturbed chromosome is $(s_1, \cdots, s_i, s_j, s_{j-1}, \cdots, s_{i+1}, s_{j+1}, \cdots, s_n)$.

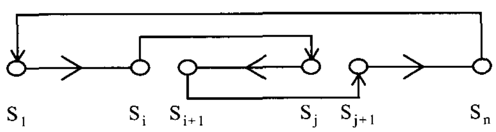

Fig. 7 Inversion strategy with two bonds

3.2.3 Sectioning operator

This strategy has three bonds between (s_i, s_{i+1}), (s_j, s_{j+1}) and (s_k, s_{k+1}), $i < j < k < n$. These bonds are broken in the current chromosome. Therefore, this chromosome has four continuous segments. This sectioning strategy selects two continuous segments, (s_{i+1}, s_j) and (s_{j+1}, s_k), and a target point, s_i. The target point is randomly chosen as a pivoting point for moving these segments. That is, the segments are swapped at the front of the target point to generate a new offspring.

Fig. 8 shows the perturbed chromosome, $(s_1, \cdots, s_{i-1}, s_{j+1}, \cdots, s_k, s_{i+1}, \cdots, s_j, s_i, s_{k+1}, \cdots, s_n)$.

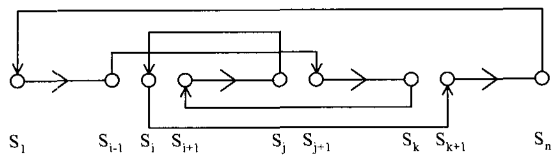

Fig. 8 Sectioning strategy with three bonds

3.2.4 Transport operator

This strategy has two bonds between (s_i, s_{i+1}) and (s_j, s_{j+1}), $i < j < n$. These bonds are selected at random and broken in the current chromosome. This strategy consists of determining whether any segment in the current chromosome can be inserted between two segments so as to decrease the fitness. A segment (s_{j+1}, s_n) is removed and then replaced in between a bond (s_i, s_{i+1}) on another, randomly selected, part of the chromosome. The perturbed chromosome is $(s_1, \cdots, s_i, s_{j+1}, \cdots, s_n, s_{i+1}, \cdots, s_j)$, as illustrated in Fig. 9.

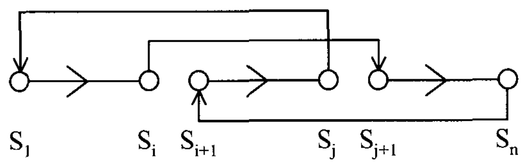

Fig. 9 Transport strategy with two bonds

3.2.5 Mutation operator

Once the new population has been done by genetic operators (crossover, inversion, sectioning, and transport), a mutation is applied to each chromosome in the new population. The mutation is usually used as a background in the μGSA. It helps to prevent premature loss of alleles and enables the algorithm to explore the domains containing potentially better chromosomes. Therefore, this operator leads independently the possibility to explore the whole search space from the specific initial population.

In binary coding, the mutation operator that attempts to introduce some random alteration of the genes, e.g., 0 becomes 1 and viceversa. Each position of the chromosome is given a chance (mutation ratio) of undergoing mutation. This is implemented by computing an interarrival interval between mutations, assuming a mutation rate.

4. Benchmark Results

With general definition of global optimisation, a series of computational benchmark was performed using five well-known test functions, which were taken from the specialized literature to compare our approach. The mathematical representations of these test functions are fully explained in the Appendix.

The proposed μGSA approach was coded in C language on a personal computer with 500-MHz Pentium CPU and 192 MB RAM. In order to compare the effectiveness of the proposed μGSA approach, two more global optimisation techniques shown in Table 1 were tested and compared on benchmark test functions. HSGT approach developed by Trafalis and Kasap (2002), and SS approach developed by Glover *et al.* (2003) are also tested to optimise the same test functions. The coding of SS approach downloaded from the Martis website (2003).

The probability of obtaining the global minimum for the μ GSA approache is measured by running the 100,000 independent trial iterations for each of the benchmark test functions. The compared HSGT and SS approaches are measured by running 100 independent runs and 20 iterations, respectively. The parameters used in μGSA are population size (100) and mutation rate (0.06). In the HSGT approach, the optimum results of the test functions are taken from the research of Trafalis and Kasap (2002). Moreover, the optimum results in the SS approach are obtained from the computational simulations. The quality of solutions obtained by each approach in this article was measured by the number of best trials, gap from the global minimum, and CPU time as shown in Tables 2-6 for each of test functions.

The "number of best trials" and "gap from the global minimum" are the numerical parameters based on the fitness of the objective function. That is, the "number of best trials" is an iteration number (or generation number) that a best fitness is found in trial iterations during annealing schedule. The "gap from the global minimum" is a distance between the best fitness of the μGSA and the objective function value of the benchmark test functions at the "number of best trials". These parameters are important factors to demonstrate the superior performance of the proposed μ GSA.

From the global optimum results (Tables 2~6), it can be obviously seen that the μGSA approach finds the global optimum solution, because of its wide spread applicability, global perspective and inherent parallelism. This implies that the results of the μGSA approach can converge to the global optimum solution better than those of the other approaches (HSGT and SS) for continuous nonlinear optimisation problems.

Table 1 Definition of global optimisation approaches

Method	Full Name	Reference
μGSA	Micro-Genetic Simulated Annealing	Kim *et al.* (this paper)
HSGT	Hybrid Scatter Genetic Tabu	Trafalis and Kasap (2002)
SS	Scatter Search	Glover *et al.* (2003)

Table 2 Results for Goldstein and Price's function

Method	CPU time (seconds)	Number of best trials	Gap from global minimum
μGSA	1.271	80,307	0.000001
HSGT	2.39	100	0.0001
SS	1.041	None	0.00001

Table 3 Results for 6-Hump Camelback function

Method	CPU time (seconds)	Number of best trials	Gap from global minimum
μGSA	1.952	76,201	0.0
HSGT	3.72	100	0.0
SS	1.271	None	0.000002

Table 4 Results for Shubert function

Method	CPU time (seconds)	Number of best trials	Gap from global minimum
μGSA	1.642	3,107	0.000001
HSGT	4.45	100	0.5617
SS	2.213	None	0.003561

Table 5 Results for Himmelblau's function

Method	CPU time (seconds)	Number of best trials	Gap from global minimum
μGSA	1.351	78,289	0.0
HSGT	1.9	100	0.0
SS	15.812	None	0.0

Table 6 Results for Branin's function

Method	CPU time (seconds)	Number of best trials	Gap from global minimum
μGSA	1.472	55,456	0.0
HSGT	4.34	100	0.0
SS	1.301	None	0.000005

5. Optimum Design of Sandwich Panel

Now, we show one application of μGSA to sandwich panel structure shown in Fig. 10. This structure consists of two thin skins (or faces) of thickness t, each separated by a thick layer (or core) of low density material of thickness c. All three layers are firmly bonded together and the face material is much stiffer than the core material. It is assumed that the face and core materials are both isotropic.

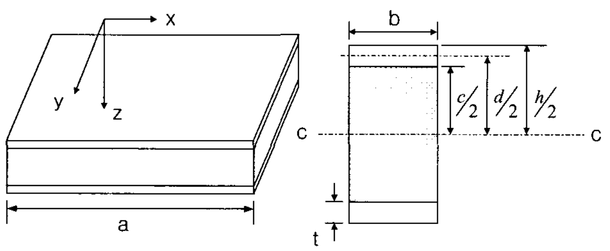

Fig. 10 Dimensions of sandwich panel

The objective is to find a feasible combination of design variables so that the weight function is minimised. The design variables in this model are the thickness of faces (t) and core (c). For notational convenience we redefine these two variables in terms of the design vector X:

$$X = [x_1, x_2]^T = [t, c]^T \tag{1}$$

The optimum design of this model is the combined minimum weight of the faces and core (per unit area). The objective function is

$$F(x) = 10(2\mu_f \cdot x_1 + \mu_c \cdot x_2) \tag{2}$$

The μ_f and μ_c are the densities of the faces and core materials respectively. The faces are assumed to be very thin; it is therefore in order to take c as the core thickness and to neglect the local bending stiffnesses of the faces. The E-glass Woven Roving and Divinycell (H100) are adopted for faces and core material in this design model, respectively. Table 7 is the mechanical properties of these two materials. The length and width of sandwich panel are 690cm and 230cm, respectively. The allowable deflection (w_{all}) in z-direction is set at 2.3cm.

There are several functional relationships between the design variables which delimit the region of feasibility. These relationships, expressed in the form of inequalities, represent the design model. The inequality constraints are,

$$\begin{aligned} g_1(x) &= x_1 - 0.0125 \\ g_2(x) &= \frac{x_1}{x_2} - 0.01 \\ g_3(x) &= 0.0143 - \frac{x_1}{x_2} \\ g_4(x) &= \frac{w_{all}}{w} - 1.0 \\ g_5(x) &= \frac{\sigma_{all}}{\sigma_y} - 1.0 \\ g_6(x) &= \frac{\tau_{all}}{\tau_{yz}} - 1.0 \end{aligned} \tag{3}$$

where,

w : Maximum deflection in z-direction (cm)

σ_{all} : Allowable bending stress of faces (kg/cm^2)

σ_y : Bending stress in y-direction of faces (kg/cm^2)

τ_{all} : Allowable shear stress of core (kg/cm^2)

τ_{yz} : Shear stress in yz-plane of core (kg/cm^2)

The structural analysis and design of sandwich panel is fully described in Allen (1969) and Kim *et al.* (1991). Kim *et al.* (1991) solved this problem using SUMTNM (SUMT with Nedler and Mead simplex search method) to minimise weight function. The same parameters are adopted for the proposed μGSA to compare the optimal simulation results. The simulation results between the μGSA and SUMTNM are listed in Table 8.

In computations of the μGSA, the total number of trial iterations is 1.0×10^5. The μGSA implementation has better improvement of about 0.12 % than SUMTNM approach in optimal weight. Fig. 11 shows the evolution process as the best-so-far fitness of the weight function. As can be seen in

Fig. 11, the μGSA approach performed a rapid convergence tendency to global optimum solution-space.

Table 7 Mechanical properties of faces and core material

Face : E-glass Woven Roving				
σ_{all}	E_f	density	Poisson's ratio	
884.0	183600.0	2.6	0.13	
Core : Divinycell (H100)				
τ_{all}	E_c	density	Poisson's ratio	G_c
5.086	1008.526	0.1	0.1	458.421

E_f, E_c; the modulus of elasticity of faces and core, G_c; is the shear modulus of core.

Table 8 Simulation results between μGSA and SUMTNM

	x1	x2	F(x)
μGSA	0.1573	16.6821	24.8811
SUMTNM	0.1639	16.388	24.9104

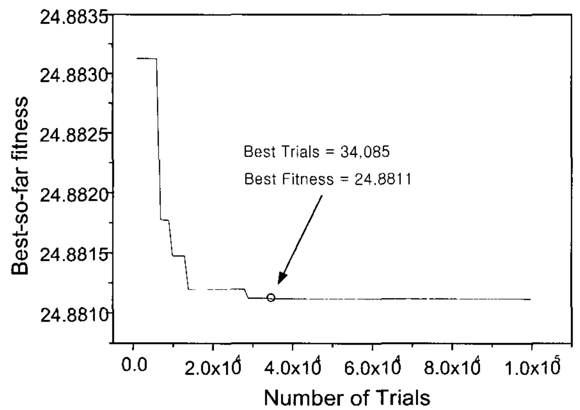

Fig. 11 Evolution process as the best-so-far fitness

6. Concluding Remarks

A new approach to solve continuous nonlinear optimisation problems is proposed and developed with the help of some of metaheuristics introduced in this article. The μGSA approach is an abstraction of natural genetics and theoretical physics and is aimed to search global optimum solution space in global optimisation problems. Therefore, μGSA approach can help in avoiding the premature convergence and search for better global solution, because of its wide spread applicability, global perspective, and inherent parallelism.

From the simulation results of Tables 2-6, it was shown that the μGSA implementation performed a rapid convergence tendency than the other approaches, and reached the global optimum solution for all test functions. That is, the μGSA achieved near-zero gap from the global minimum for all benchmark functions. This implies that the μGSA has a higher probability of obtaining the global optimum. Moreover, the results of the μGSA approach also converged to global optimum solution with a marvellous explorability in application of structural sandwich panel. Therefore, it is concluded that the proposed μGSA is both efficient and effective in identifying a global optimum solution.

Consequently, the new approach, using micro-genetic algorithms and simulated annealing, can be suggested as useful tool for solving nonlinear global optimisation problems.

Acknowledgements

This research was financially supported by the RRC, which is an affiliated organisation of korea Ministry of Science and Technology, Factory Automation Research center for Parts of Vehicles, Chosun University, KOREA in 2003.

Appendix: Benchmark Test Functions

In order to compare the various approaches, the following five test functions are selected from the specialised literature (Trafalis and Kasap, 2002) for benchmark test.

Function 1 (Two-dimensional): Goldstein and Price's function with a search domain, $X_i \in [\pm 2, \pm 2] \forall i$. The global objective function value is equal to 3.0 and the minimum point is (0.0, -1.0). There are four local minima in the solution-space.

$$f(x) = \{1 + (x_1 + x_2 + 1)^2 \cdot (19 - 14x_1 + 3x_1^2 - 14x_2 + 6x_1x_2 + 3x_2^2)\} \cdot \{30 + (2x_1 - 3x_2)^2 \cdot (18 - 32x_1 + 12x_1^2 + 48x_2 - 36x_1x_2 + 27x_2^2)\}$$

Function 2 (Two-dimensional): 6-Hump Camelback function with a search domain, $X_i \in [\pm 5, \pm 5] \forall i$. The global objective function value is equal to -1.031628 at (-0.0899, 0.7128) or (0.0899, -0.7128). This function has 6 local minima and 2 global minima in the solution-space.

$$f(x) = (4 - 2.1x_1^2 + \frac{x_1^4}{3})x_1^2 + x_1x_2 - 4(1 - x_2^2)x_2^2$$

Function 3 (Two-dimensional): Shubert function with a search domain, $X_i \in [\pm 20, \pm 20] \forall i$. This function has more than 760 local minima and more than 18 global minima with an objective function value of -186.7309.

$$f(x)=\left\{\sum_{i=1}^{5} i\cdot\cos[(i+1)x_1+i]\right\}\cdot\left\{\sum_{i=1}^{5} i\cdot\cos[(i+1)x_2+i]\right\}$$

Function 4 (Two-dimensional): Himmelblau's function with a search domain, $X_i \in [\pm 6, \pm 6]\forall i$. There are four global minima with an objective function value of 0.

$$f(x)=(x_1^2+x_2-11)^2+(x_1+x_2^2-7)^2$$

Function 5 (Four-dimensional): Branin's function with a search domain, $X_i \in [\pm 20, \pm 20]\forall i$. This function has more than 3 local and global minima with an objective function value of 0.397887.

$$f(x)=(x_2-\frac{5.1x_1^2}{4\pi^2}+\frac{5x_1}{\pi}-6)^2+10(1-\frac{1}{8\pi})\cos x_1+10$$

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2003년 10월 2일 원고 접수
2003년 10월 28일 최종 수정본 채택