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Constrained Minimization Utilizing GA Based Pattern Recognition of Immune System

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Abstract

The immune system has pattern recognition capabilities based on reinforced learning, memory and affinity maturation interacting between antigens and antibodies. The paper deals with the adaptation of artificial immune system into genetic algorithm based design optimization. The present study utilizes the pattern recognition from the immune system and the evolution from genetic algorithm. The basic idea is derived from the fact that designs should be distinguished whether they are usable/feasible or infeasible and should be improved towards the optimal solution. For the expression of design solutions, binary coded strings are used to represent antigens and antibodies in artificial immune system and chromosomes in genetic algorithm. The paper discusses the procedure of constrained optimization that does not rely on any detailed mathematical formulation for constraint handling. A number of mathematical function minimization problems are examined for verification, and practical engineering optimization problems including inequality constraints are explored to support the proposed strategy.

Keywords: Design optimization; Immune system; Pattern recognition; Affinity measure; Genetic algorithm

1. Introduction

The immune system is a natural, rapid and effective defense mechanism for a given host against infections. In the biological immune system, foreign cells and molecules, denoted as antigen, are recognized and eliminated by type-specific antibodies. The antigen-antibody pair may be recognized as a lock and key combination, and an appropriate antibody must be made to fit a specific antigen. The task of recognizing antigens is formidable due to the very large number of possible antigens; it is estimated that the immune system has been able to recognize at least 10^{16} antigens (Smith et al., 1993). Such pattern recognition capabilities is impressive, given that the genome contains about 10^{5} genes, and the immune system must use segments of these to construct antibodies for all possible antigens that are likely to be encountered. In a typical mammal, there are 10^{7} to 10^{8} different antibodies. It is also important to emphasize that self-recognition must be also a part of this pattern recognition ability to prevent antibodies from attempting to eliminate other antibodies. The mechanism of the immune system has been modeled based on the clonal selection principle; the major features are immune learning and memory (de Castro et al., 2002a).

Recently, the artificial immune theory has been a promising issue in the area of computational intelligence. The biologically inspired artificial immune system has been embraced in machine learning, pattern recognition, function approximation, data clustering and optimization, etc (Coello Coello et al., 2003). There has been recent considerable attention in the application of artificial immune system (AIS) to

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design optimization; a number of remarkable issues have been focused on the constraint handling in design optimization (Hajela et al., 1996; Hajela et al., 1997), multiobjective optimization (Yoo et al., 1999a; Coello Coello et al., 2005), multi-criterion design of fuzzy systems (Yoo et al., 1999b), and coupled interactions between subsystems in multidisciplinary design optimization (Lee et al., 1997).

The present study deals with the artificial immune system and its application to genetic algorithm (GA) based constrained optimization (Lee et al., 1996; Lee et al., 2002). The formal optimization method usually finds the optimal solution which is usable and feasible in terms of objective function(s) and constraints. The present study proposes a new approach such that optimal solutions would be obtained by identifying usable/feasible and infeasible designs through AIS based pattern recognition between antibodies and antigens and further by locating better fitted designs through GA based evolution. One of advantages in the proposed strategy resides on the fact that it does not require any mathematical formulation for constraint handling. That is, the proposed optimization process works with the natural adaptation such as immune based pattern recognition and genetic evolution. In the clonal selection principle, the proliferation can reproduce high-affinity antibodies and the hypermutation can discover smart antibodies against newly created foreign antigens. Since hypermutation in the immune system is analogous to mutation operation in GA, the clonal selection algorithm is interpreted as GA without crossover (Forrest et al., 1993). The present study accommodates the fruitfulness of GA into the framework of the immune system.

The subsequent section introduces the biological immune system and its inherent pattern recognition capabilities that are analogous to computational models. Using well-known affinity measures between antigens and antibodies, GA based immune simulation discovers a generalist antibody that represents the common pattern among antigens. A method of constrained optimization based on AIS and GA is discussed in a greater detail. A number of unconstrained and constrained function minimization problems are first examined as test examples. Subsequently, a couple of constrained engineering optimization problems such as ten-bar planar truss and energy preserving flywheel are explored to support the present study.

2. Immune system

From the viewpoint of pattern recognition in the immune system, the most important characteristics of B- and T-cells are the ability to carry surface receptor molecules capable of recognizing antigens (de Castro et al., 2002b). B-cell and T-cell receptors recognize antigens with distinct characteristics. The B-cell receptor (BCR) interacts with antigenic molecules free in solution, while the T-cell receptor (TCR) recognizes antigens processed and bound to a surface molecule so called major histocompatibility complex (MHC). The antigen B-cell receptors are bound to the cell membrane and will be secreted in the form of antibodies when the cell becomes activated. The main role of the B-cell is the production and secretion of antibodies in response to pathogenic agents. Each B-cell produces a single type of antibody, a property named monospecificity. These antibodies are capable of recognizing and binding to a determined protein. The secretion and binding of antibodies constitute a form of signaling other cells so that they can ingest, process, and/or remove the bound substance.

The clonal selection principle is the theory used to describe the basic properties of an adaptive immune response to an antigenic stimulus (de Castro et al., 2002a; de Castro et al., 2002c; White et al., 2003). Clonal expansion take place in a lymphatic gland within micro-environment called a germinal center. And it is a feature of an adaptive immune process. Clonal selection operates on both T-cell and B-cell. The main difference between B-cell/T-cell clonal expansion is that B-cells suffer somatic mutation during reproduction and B-effector cells are active antibody secreting cells. In contrast, T-cells do not undergo somatic mutation during reproduction, and T-effector cells are mainly active lymphokine secretors or T_K cells. The presence of mutational and selective events in the clonal expansion process of B-cell allows these lymphocytes to increase their repertoire diversity and also to become increasingly better in their capabilities of B-cells. Due to genetic variation, selection and adaptive abilities of B-cells, the clonal selection of the B-cell is emphasized.

Learning in the immune system involves with the raise of the population size and the affinity of those lymphocytes that have proven to be valuable during antigenic recognition phase. Therefore, the immune repertoire is biased from random base to repertoire base that more clearly reflects the actual antigenic environment. In normal course of the evolution of

immune system, an organism would be expected to encounter a given antigen repeatedly during its lifetime. The first exposure to an antigen stimulating an adaptive immune response is treated by a small number of B-cells respectively producing antibodies of different affinity. By storing some high affinity antibody to produce against first infection, it considerably improves the effectiveness of immune response to secondary encounter. This cell is called memory cell. Rather than 'starting from scratch' every time, this strategy ensure that both speed and accuracy of immune response become stronger after infection. Also, this system constantly learns through directly interacting with environment.

In a T-cell dependent immune response, the repertoire of B-cell activated by a specific antigen is basically diversified by two mechanisms; hypermutation and receptor editing. On average, the antibodies generated by secondary response have a higher affinity than those of the early primary response. This phenomenon, which is restricted to T-cell dependent responses, is referred to as the maturation of the immune response.

During clonal expansion, random changes present the V-region genes of receptor. And occasionally such changes will lead to increase affinity of antibody. These higher-affinity variants are then selected to enter the pool of memory cells. The repertoire is diversified through hypermutation, but rare B-cells with high affinity mutant receptor can be selected to dominate the response. Due to the random nature of the somatic mutation process, an amount of mutant genes become non-functional or possibly develop harmful anti-self specificities. This cells with low affinity receptor or self-activated cells must eliminate in the pool of memory cells effectively. These cells disappear through the process of cell death called apoptosis.

However, instead of the expected clonal elimination of all self-activated cells, now and then B lymphocytes were found that had undergone receptor editing: these B-cells had deleted their self-reactive receptors and developed entirely new receptors by recombination. Therefore, a high affinity clone developed by somatic mutation or receptor editing would be expected to be preferentially expanded. But some low affinity cells are allowed to enter the repertoire, thereby maintaining the population diversity.

3. GA based immune simulation

3.1 Affinity measures

The immune system model in the present study uses binary string structures to represent both the antigen and antibodies. Such representation is traditionally efficient in the GA based simulation and optimization in this context. The immune system promotes the generation of those antibodies that match several antigens simultaneously. The degree of match between an antibody and all antigens, therefore, indicates the goodness of that antibody and are interpreted as the criterion of pattern recognition. Various levels of complexity can be introduced in developing a numerical measure of the degree of match, including the number of matches on a bit-by-bit basis and the length of contiguously matches strings. The present study employs three cases of matching functions (de Castro et al., 2002b) that are analogous to affinity measurement in the biological immune system.

Case 1: Hamming distance

Hamming distance between antigen and antibody is simply computed by counting the number of matched bits using Eq. (1).

$$D = \sum_{k=1}^{L} d_k \tag{1}$$

$d_k = 1$ for a matched bit

$d_k = 0$ for a unmatched bit

where, L is the string-length of antigen or antibody. The typical illustration of Hamming distance is shown in Table 1, wherein there are seven bit-matches between antigen and antibody.

Case 2: Multiple contiguous bit rule

Shape-space that measures the number of *r*-contiguous complementary symbols, named *r*-contiguous bit rule, is considered. Extensive complementary

Table 1. Affinity measures.

antigen	11001 00101 10100 11010
antibody	00110 10101 00101 00101
similarity	00000 01111 01110 00000
Case 1: Eqn. (1)	D = 1+1+1+1+1+1+1 = 7
Case 2: Eqn. (2)	$D = D_H(=7) + 2^4 + 2^3 = 31$
Case 3: Eqn. (3)	D = 0 + (8+4+2+1) + (4+2+1) + 0 = 22

regions might be interesting for the detection of similar characteristics in symmetric portions of the molecules and can be useful to perform specific tasks such as pattern recognition. Assuming that there are a total of R contiguous sub-strings where a number of bits are matched between antigen and antibody, multiple contiguous bit rule is expressed as follows:

$$D = D_H + \sum_{r=1}^{R} 2^{D_r} \tag{2}$$

where, D_H is Hamming distance obtained from Eqn.(1), and D_r is the total number of matched bits in the r-th contiguous sub-string. The example of multiple contiguous bit rule is shown in Table 1. In this case of 2 contiguous sub-strings, note that D = 7 + (2^4 + 2^3) = 31.

Case 3: Weighted distance

Weighted distance is quite similar to multiple contiguous bit rule, but this considers binary weight for matched bits as shown in Eqn.(3).

$$D = \sum_{r=1}^{R} \sum_{k=1}^{D_r} 2^{(k-1)} \tag{3}$$

Table 1 demonstrated its results such that D = (8+4+2+1) + (4+2+1) = 22.

3.2 Pattern recognition

Consider a pool of antigens, half of which are the type 1111111111 and the other half are of the type 0000000000. If the both types of antigens are exposed to the prospective pool of antibodies with the same frequency, than, if the antibody pool is large enough, compliments of both these antigen types will be developed and maintained in the immune simulation. A second example would be an antigen pool that contains antigens of the type 000, 110 and 011. Again, specialist antibodies that are complimentary to these antigens can be developed of the antibody pool is large enough to maintain stable populations of these antibodies. It is also possible to develop a generalist antibody that is minimally different from each of these antigens. An antibody of the type 101 has two complimentary bits from each of three antigens, i.e., it is different from each antigen in exactly two bits. The discovery of such a generalist antibody demonstrates the ability of the immune simulation to identify common patterns among antigens.

The present study conducts the GA based simulation to discover common antigens using generalist search algorithm whose process is shown in Fig. 1. Assume that antigens are presented as follows:

```
50%   11...11**...**
50%   **...**11...11
```

where, * means don't care. Now construct four antigens of the above type whose 8-bit values are fixed to 1.

```
1111111100101010
1111111100100100
1001010111111111
0011001011111111
```

From Fig. 1, take 'antigen selection parameter' as ρ=3 with a total of 50 antibodies in a population. It should be noted that the antibody population is initially generated at random. In GA based simulation, aforementioned three cases of affinity measures are tested with crossover and mutation probabilities of 0.6 and 0.05, respectively. After a number of GA generations as shown in Fig. 2, the average fitness for all three affinity measures converges to one, which implies that antibodies successfully discover the common antigens.

4. Proposed strategy

The process is a novel approach towards the optimal

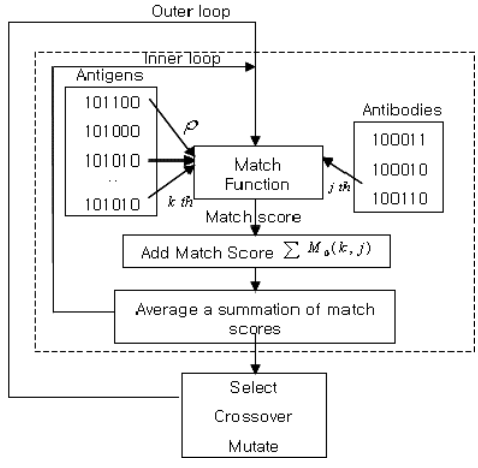


Fig. 1. Discovery of generalist antibody from antigens.

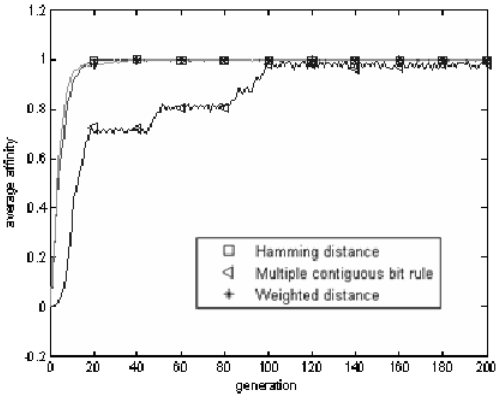


Fig. 2. Average affinity in GA based simulation.

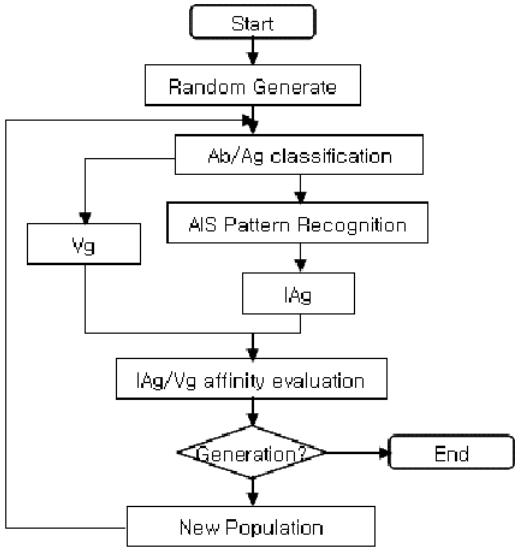


Fig. 3. Procedure for AIS based constrained optimization.

design utilizing a concept of artificial immune system. Function based optimization methods such as genetic algorithm and simulated annealing tradionally employ the penalty function technique to accom-modate constraint functions. However, such technique necessitates the proper selection of penalty functions and their corresponding penalty parameters. The proposed strategy adapts GA based evolution and AIS based pattern recognition in design optimization, hence the approach does not require any mathematical formulation in constrained optimization problems.

The procedural steps as shown in Fig. 3 are explained as follows:

(1) Given a constrained optimization problem, generate the design population at random.

(2) Rank the design population based on the fitness value. For unconstrained optimization problems, the design individuals are sorted in terms of the objective function value only. Constrained problems consider both the objective and constraint function values. For infeasible designs, one can impose the large value (e.g., five to ten times the objective function value) to the objective function value. The present study uses the factor of 'five'. Even though this concept is much similar to the use of penalty parameters, the present study dose not employ the detailed formulation for constraint handling.

(3) Assign the first half of the ranked population to the antibodies (Ab), and the second half to the antigens (Ag).

(4) Also store such antigens into a virus group (Vg).

(5) Perform the GA based immune simulation between antibodies and antigens (Fig. 1).

(6) After the generalist pattern recognition with genetic evolution, antigens have been immunized and are denoted as IAg.

(7) Compare Vg and IAg using a proper affinity measure as well. Exclude individuals of IAg that are quite similar to those of Vg. After the affinity measurement, such excluded designs are also stored into Vg.

(8) Add individuals of IAg that are different from those of Vg to antibodies, Ab. If the population size is not sufficient, generate remaining designs at random.

(9) Redo from the step (2) until the user specified convergence.

The initial stage assigns relatively better designs as antibodies and relatively worse designs as antigens. Using the GA based pattern recognition process between antibodies and antigens, antigens are immunized to accommodate the generalist of antibodies. This is an evolutionary process to find better designs by creating antibodies with more fit. The proposed algorithm generates the cells which internally include the characteristics of the evolving antibodies through the GA based immune simulation. A design with the higher fitness continuously evolves during the immune process and such appearance is referred to as reinforced learning in terms of biological immune system. Participating antibodies are also said to be memory cells since they maintain the relatively high affinities over the generations.

In the features of artificial immune system (de Castro et al., 2002a), the *basic component* is an artifi-

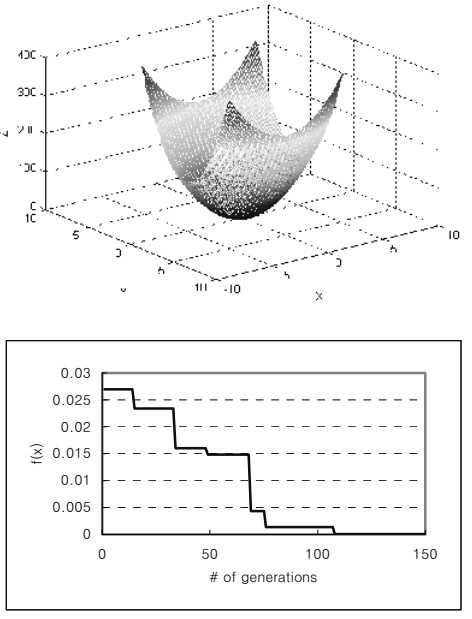


Fig. 4. Moved axis parallel hyper-ellipsoid function.

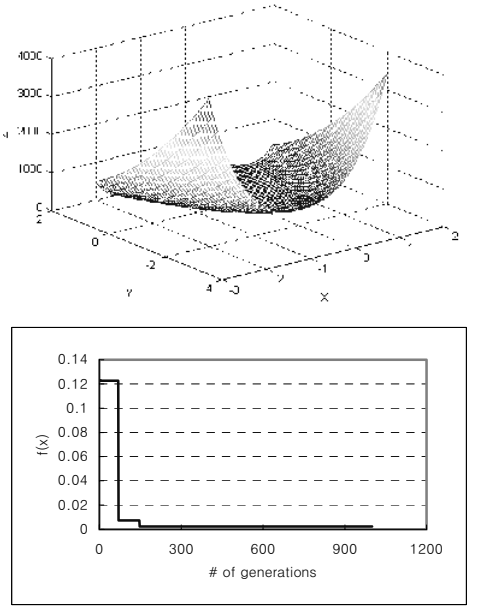


Fig. 5. Rosenbrock's valley function.

cial cell, which is antibody or antigen. The *shape-space model* is represented by a binary string type, and the *structure* is a population of artificial cell, which corresponds to Ab, Ag, IAg or Vg in the present study. The *dynamics* means the change of binary data (step 5) and *meta-dynamics* implies the elimination of poor components and the influx of new components (step 7).

5. Illustrative examples

A number of unconstrained and constrained mathematical functions are explored to find the optimal solution using the proposed strategy. Unconstrained function problems are first explored to see the adaptation of better solution towards the optimum. Each function minimization problem uses ρ=10 with a total of NPOP=100 design populations. As a method of affinity measure, a case of multiple contiguous bit rule is considered.

5.1 Moved axis parallel hyper-ellipsoid function

$$\text{Minimize } f(x) = \sum_{i=1}^{2} 5i \cdot x_i^2 \qquad (4)$$

$$\text{where,} \quad -5.12 \le x_i \le 5.12$$

This function is derived from the axis parallel hyper-ellipsoid and is more elliptic than the original function. The function contour and optimization history are shown in Fig. 4. The optimal solution obtained from the present study is $f(x_1^*, x_2^*) = f(0.00500, -0.01501) = 0.00238$, while the global optimum is located at $f(x_1^*, x_2^*) = f(0, 0) = 0.0$.

5.2 Rosenbrock's valley

$$\text{Minimize } f(x) = 100(x_2 - x_1)^2 + (1 - x_1)^2 \qquad (5)$$

$$\text{where,} \quad -2.048 \le x_i \le 2.048$$

Rosenbrock's valley is a well-known benchmarking problem for optimization. To find the global optimum is very difficult since it is located inside a long, narrow and parabolic shaped flat valley. From the present study, $f(x_1^*, x_2^*) = f(1.00447, 1.00847) = 4.38\text{E-}5$, while the global optimum is located at $f(x_1^*, x_2^*) = f(1, 1) = 0.0$. The function contour and convergence history during the optimization process are shown in Fig. 5.

5.3 Rastrigin's function

$$\text{Minimize } f(x) = 20 + x_1^2 + x_2^2 - 10\cos(2\pi x_1) - 10\cos(2\pi x_2) \qquad (6)$$

$$\text{where,} \quad -5.12 \le x_i \le 5.12$$

Rastrigin's function is composed of a polynomial

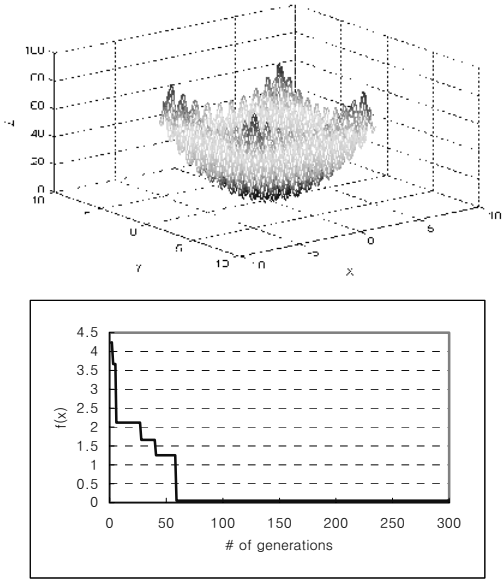


Fig. 6. Rastrigin's function.

Table 2: Results of a constrained function minimization.

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	OBJ
global	2.250	1.956	-0.500	4.375	-0.612	1.094	1.531	680.762
AIS	2.385	2.006	-0.890	4.050	0.000	0.811	1.811	689.838
	1.893	2.142	-0.473	3.728	0.079	0.344	1.362	698.355
	2.442	1.758	0.037	4.705	-0.555	-0.133	1.804	699.352
	1.860	1.796	0.377	4.783	-0.775	-0.220	1.221	701.094
	1.825	1.846	-0.383	4.592	0.127	-0.002	1.536	698.868
	Average value of OBJ (AIS)							697.501
	Standard deviation of OBJ (AIS)							3.941
GA	0.000	2.070	0.000	4.219	0.000	1.250	1.485	714.945
	2.490	2.129	0.000	3.745	-0.625	1.429	2.500	706.867
	2.109	1.987	0.000	4.219	0.001	1.431	2.500	706.266
	0.000	1.719	0.000	5.000	0.000	1.250	1.484	720.517
	1.229	1.871	-0.241	4.726	-0.384	1.133	1.465	691.891
	Average value of OBJ (GA)							708.097
	Standard deviation of OBJ (GA)							9.681

and cosine modulation to produce multiple local minima, thus, the function is highly multimodal. Fig. 6 shows the function contour and optimization history from which the optimal solution is $f(x_1^*, x_2^*) = f(0.0, 0.0) = 0.0004$. Note that the global optimum is also located at $f(x_1^*, x_2^*) = f(0, 0) = 0.0$.

5.4 Constrained function minimization

This problem has seven design variables with four inequality constraints whose optimization statement is written as follows (Parsopoulos et al., 2002):

$$\begin{aligned}
\text{Minimize} \quad & f(x) = (x_1 - 10)^2 + 5(x_2 - 12)^2 \\
& + x_3^4 + 3(x_4 - 11)^2 + 10x_5^6 \\
& + 7x_6^2 + x_7^4 - 4x_6x_6 - 10x_6 - 8x_7 \\
\text{subject to} \quad & 2x_1^2 + 3x_2^4 + x_3 + 4x_4^2 + 5x_5 - 127 \le 0 \\
& 7x_1 + 3x_2 + 10x_3^2 + x_4 - x_5 - 282 \le 0 \\
& 23x_1 + x_2^2 + 6x_6^2 - 8x_7 - 196 \le 0 \\
& 4x_1^2 + x_2^3 + 3x_1x_2 + 2x_3^2 + 5x_6 - 11x_7 \le 0 \\
\text{where,} \quad & -10.0 \le x_i \le 10.0
\end{aligned} \tag{7}$$

AIS based pattern recognition and GA based evolution strategy are conducted to find their results of the optimal solution. A total of 10 trials with different random seeds in a population are performed for AIS and GA, and 5 best solutions are presented in Table 2. For both AIS and GA, the population size is 300, and the number of generation is 10000. In AIS, ρ is taken as 7. GA considers probabilities of crossover and mutation as 0.8 and 0.05, respectively. It is shown that AIS provides better design solutions in terms of mean and standard deviation of optimized objective function values. Note that numerical values are properly truncated to appear.

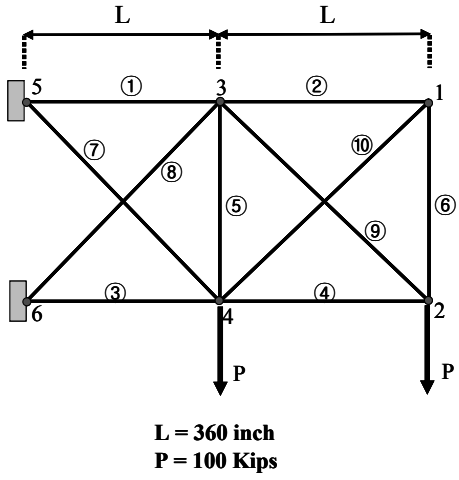


Fig. 7. Ten-bar planar truss.

6. Engineering optimization

6.1 Ten-bar truss

The proposed strategy is applied to a constrained structural optimization problem. The design objective is to determine the optimal cross sectional areas by

minimizing the total weight of a statically loaded ten-bar planar truss subjected to stress constraint on each truss member. The schematic is shown in Fig. 7 and the mathematical statement of this optimization problem and its problem parameters are presented at Reference (Haftka et al., 1993).

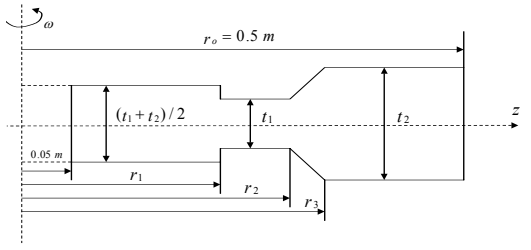
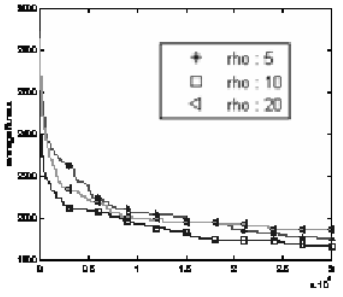
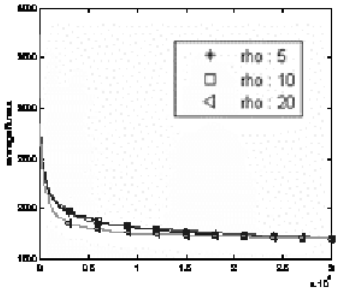


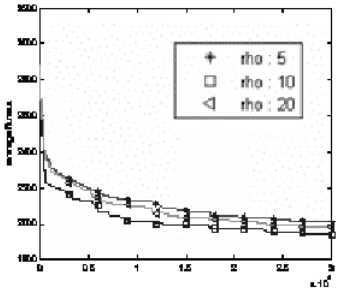
Fig. 8. Rotating disk of flywheel.



(a) Hamming distance



(b) Multiple contiguous bit rule



(c) Weighted distance

Fig. 9. Average fitness for truss problem.

6.2 Rotating disk

For a flywheel design as shown in Fig. 8, the objective is to determine radius and thickness variables by maximizing the kinetic energy (*KE*) subjected to weight and yield stresses. The optimization problem (Mistree et al., 1994) is stated as follows:

$$\begin{aligned} &\text{Minimize} && \frac{1}{KE(r_1,r_2,r_3,t_1)} \\ &\text{subject to} && \sigma_R \le \sigma_Y \\ & && \sigma_T \le \sigma_Y \\ & && W \le 0.9W_o \\ & && t_1 \le t_2 \ \ \& \ \ 0.01 \le t_1 \le 0.1 \ \ \text{(unit: m)} \\ & && 0.05 \le r_1, r_2, r_3 \le 0.5\ . \end{aligned} \tag{8}$$

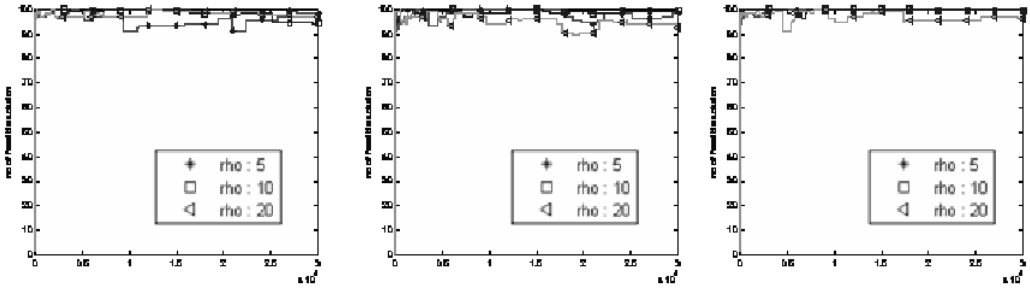
In the above problem, σ_R and σ_T are denoted as radial and tangential stresses, respectively, and are limited by the yield stress, σ_Y. For a volume restriction, the designed weight W should be less than 90% of the baseline design, W_o. Problem parameters include-ing material properties are summarized in Table 3.

6.2 Results and discussion

For a ten-bar planar truss problem, design results are demonstrated according to 'antigen selection parameter' ρ and affinity measures. The truss design problem uses a total of NPOP=200 design populations in GA based immune simulation and optimization. Convergence histories for each of three affinity measures with different values of ρ are shown in Figs. 9 and 10. The final solutions with each method are also summarized in Table 4. It is expected that multiple contiguous bit rule is the most efficient among three cases of affinity measures, and the best choice of 'antigen selection parameter' is ρ=10. In Figs. 10, the number of antibodies which is deemed to be better or usable/feasible solutions goes up aroud

Table 3. Problem parameters for rotating disk problem.

parameter	Value
Yield stress, σ_Y	1.48E9 N/m^2
Rotating speed, ω	2000 rad/sec
Poisson ratio, ν	0.3
Material density, ρ	7830 kg/m^3
Initial weight, W_o	2171.35 kg



(a) Hamming distance (b) Multiple contiguous bit rule (c) Weighted distance

Fig. 10. The number of feasible designs for truss problem.

Table 4. Results of ten-bar truss problem.

			X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	weight
AIS	case 1	ρ=5	8.05	0.90	8.73	5.17	0.46	1.07	6.41	6.19	4.48	0.95	1797.67
		ρ=10	7.83	1.29	8.94	3.66	0.77	1.22	6.81	7.11	2.97	1.40	1787.26
		ρ=20	7.38	3.23	9.20	3.54	1.01	2.06	7.37	4.56	3.40	2.59	1865.45
	case 2	ρ=5	8.17	0.54	8.64	4.33	0.21	0.48	6.29	5.28	4.81	0.47	1665.28
		ρ=10	8.23	0.20	8.20	4.14	0.47	0.25	5.88	5.89	5.31	0.27	1658.47
		ρ=20	7.99	0.46	8.62	4.25	0.50	0.66	6.46	5.51	4.46	0.67	1680.81
	case 3	ρ=5	9.18	1.25	8.70	4.97	1.73	0.91	7.23	5.43	5.12	1.09	1925.72
		ρ=10	8.26	1.50	9.02	4.11	1.27	2.84	7.01	5.42	3.17	2.17	1878.85
		ρ=20	7.96	2.11	9.18	3.13	0.94	2.02	7.58	5.19	4.26	1.76	1871.29

100 at the early stage of the optimization process, and is maintained at that value. In this study, the number of antigens and antibodies turns out to be almost the same. The distinction between antigens (worse or infeasible designs) and antibodies (better or usable/ feasible designs) are examined based on affinity measures, and much better solutions of antibodies are discovered via GA based immune simulation for locating the final optimal design.

A rotating disk problem is further explored with the best choices of parameters and method as used in the truss design problem; ρ=10, NPOP=200 with multiple contiguous bit rule as affinity measure. The convergence history for rotating disk problem is shown in Fig. 11, wherein the feasible design solution rapidly reduces its objective function value at the early stage of the optimization process. The optimized design solution and its performances are as follows: $\{r_1^*, r_2^*, r_3^*, t_1^*\} = \{0.663, 0.720, 0.116, 0.086\}$ with KE^* = 51.6MJ starting with an initial design of $\{r_1^0, r_2^0, r_3^0, t_1^0\} = \{0.165, 0.275, 0.525, 0.055\}$.

7. Closing remarks

The paper proposes a novel algorithm for constrained optimization utilizing artificial immune system and genetic algorithm. Design solutions are expressed by binary coded strings to represent antigens and antibodies in artificial immune system and chromosomes in genetic algorithm. For designs in a population, worse, infeasible designs are considered as antigens whereas better, usable/feasible designs are denoted as antibodies. Affinity measures are used to recognize how much antigens and antibodies are similar and GA based immune simulation is conducted to discover generalist antibodies that represent the common pattern among antigens. Such newly generated antibodies would have more fit and consist of new design populations with higher possibility of locating the optimal solution. It is emphasized that the present study utilizes the pattern recognition capability from immune system and the evolution process from genetic algorithm. It is a method of natural adaptation

such that any detailed mathematical formulation for constrained minimization process is not required. However, there still needs to be more investigation on how efficiently 'antigen selection parameter' is handled, what type of affinity measure is useful, etc.

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