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Artificial Immune System Application for Solving Dynamic Optimization Problems

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***Abstract*—For the purpose of adaptation to a changing environment, immune mutation and memory mechanism in the immune system are introduced in thermodynamic genetic algorithm, which helps to prevent the diversity loss and rapidly track the optimum in dynamic environments. Experimental results on 0/1 dynamic knapsack problems demonstrate the merits of the proposed immune thermodynamic genetic algorithm (ITDGA). Compared with the existing classical primal-dual genetic algorithm (PDGA), this algorithm can maintain better diversity and be more suitable to solve 0-1 dynamic problems.**

Keywords—Artificial immune systems, diversity, immune mutation, memory mechanism, immune thermodynamic genetic algorithms, dynamic optimization.

I. INTRODUCTION

MANY real world optimization problems are actually dynamic, and optimization methods capable of continuously adapting the solution to a changing environment are needed [1], [2], [15]. However, the goal of standard genetic algorithms is eventually to converge an optimum, and consequently GAs lose their diversity and their ability to adapt to a change in the environment. In order to solve this problem, a number of techniques are proposed.

Thermodynamic genetic algorithms (TDGAs), e.g., see [3], [4], [5], simulate the competitive model between energy and entropy in annealing to harmonize the conflicts between selective pressure and population diversity in GA. In the TDGA, the selection operation is designed to minimize the free energy of the population. The free energy F is defined by $F=<E>-HT$, where $<E>$ is the mean energy of the system, H is the entropy and T is a parameter called the temperature. Minimization of the free energy can be interpreted as taking a balance between minimization of the energy function and maintenance of the diversity measured by the entropy. But high computational cost of TDGA restricts its application. In [6], [7], Ying proposes a measurement method of rating-based entropy(RE) and a component thermodynamic replacement (CTR), which remarkably improve the computational efficiency of TDGA.

In [8], Yang introduced the primal-dual genetic algorithm (PDGA) which operate on a pair of chromosomes that are primal-dual to each other in a given distance space. Within PDGA, each chromosome is defined a dual chromosome that is of maximum distance in genotype to it in a given distance space, e.g., the Hamming distance space. During the running of PDGA before iterating into next generation, a set of low fit individuals is selected to evaluate their duals and give those dual chromosomes that are superior chances to be expressed into the next generation. The Primal-Dual Mapping (PDM) between primal-dual chromosomes improves the exploration capacity of PDGA in the search space and thus its searching efficiency. In [9], a double-probability-based primal-dual genetic algorithm (DPPDGA) was proposed for 0-1 dynamic optimization problems, and the concepts of inferior-allele and superior-allele were introduced to maintain better diversity. But their repetitive calculations at all loci cause high computational cost.

Recent studies, e.g., [10], [11], [13], [14], [15], show that the dynamic learning mechanisms of biological immune system can be integrated into GAs to enhance their performance in dynamic environments. Inspired by the diversification and memory mechanism in the immune system, we introduce a immune operator in the process of TDGA. Like many other artificial immune system models, designing immune operator borrows heavily from immunological theory but is not an exact copy of the immune system's behavior. The immune mutation and memory mechanism of immune operator help individuals to explore the search space comprehensively and speed up the reaction to the moving optima when a change occurs. The immune thermodynamic genetic algorithm (ITDGA) is applied to the time-varying knapsack problems with promising results.

II. THE IMPROVED THERMODYNAMIC SELECTION RULE

There are two critical parts in TDGA: ① How to measure population diversity; ② How to design thermodynamic replacement rule. In [3], [4], and [5], Mori used a gene-based entropy and greedy thermodynamic replacement, and high computational cost restricted their applications. In this paper, we use the improved thermodynamic selection rule proposed by [6].

A. Rating-based Entropy

Rating-based entropy (RE) measure the fitness dispersal of individuals in the population by grading their fitness. Assume

u_t and l_t respectively be an upper bound and a lower bound of the individual energy at t generation, $\pi=\{R_i|0\le i\le K-1\}$ be a level partition on $[l_t, u_t]$, shown in Fig. 1.

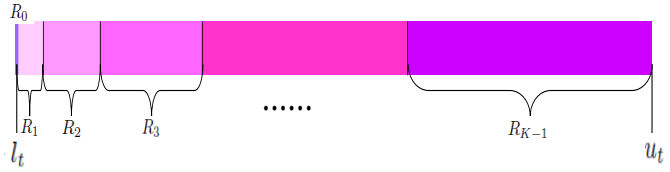

Fig.1. A level partition

Definition 1 (rating-based entropy) Let $P=(X_1,X_2,\cdots,X_N)\in S^N$ be one population of size N, $\pi=\{R_i|0\le i\le K-1\}$ be a level partition, and n_i be the number of individuals in R_i of population P. Then $H(\pi, P)$ is called the level-based entropy of P for π, where

$$H(\pi,P)=-\sum_{i=0}^{K-1}\frac{n_i}{N}\log_K\frac{n_i}{N},0\le i\le K-1. \quad (1)$$

B. Component thermodynamic replacement

Definition 2 (relative energy) Let $P=(X_1,X_2,\cdots,X_N)\in S^N$ be one population of size N, $e_u=max\{e(X_r)|X_r\in P\}$, $e_l=min\{e(X_r)|X_r\in P\}$. Then $e'(X_r)$ is called the relative energy of X_r, where

$$e'(X_r)=\frac{e_l-e(X_r)}{e_l-e_u} \quad (2)$$

Definition 3 (free energy component) Let $P=(X_1,X_2,\cdots,X_N)\in S^N$ be one population of size N, $\pi=\{R_i|0\le i\le K-1\}$ be a level partition, and n_i be the number of individuals in R_i of population P. For an individual $X_r\in P$ at level $R_i\in\pi$, $F_c(\pi,T,P,Xr)$ is called its free energy component in P at temperature T, where

$$F_c(\pi,T,P,X_r)=e'(X_r)+T\log_K\left(\frac{n_i}{N}\right). \quad (3)$$

Component thermodynamic replacement (CTR) descend the free energy of the next generation most steeply by assigning the free energy component to its individuals.

CTR algorithm

Input: e_l, e_u, T, P_t, O_t

Output: P_{t+1}

① Produce an interim population P'_t of size $N+M$ by appending M individuals in the offspring population O_t to the parent population P_t;

② Calculate the free energy component $F_c(\pi,T,P,Xr)$ for each individual $Xr\in P'_t$;

③ Pick the M individuals with the largest free energy components from P'_t, and form the next generation P_{t+1}.

III. Introducing Artificial Immune Mechanism

A. The Biological Immune Mechanism

The human body maintains a large number of immune cells, e.g. lymphocytes, which are part of the adaptive Immune System (IS). There are mainly two types of lymphocytes , the B-cells and the T-cells. The B-cells can be further decomposed into plasma B-cells and memory B-cells, and T-cells into helper T-cells and killer T-cells. The main functions of the B-cells are the production and secretion of antibodies as a response to exogenous organisms, which are activated by the helper T-cells. The B-cells replicates by a process called clonal selection: only those cells that have high affinity with an antigen proliferate. Nevertheless, during cloning some variations may occur due to a process of somatic hypermutation. This may increase the affinity between the antibody and the antigen, making the B-cell more adapted to bind to the antigen.

When an antigen invades the body for the first time, a few B-cells are activated and migrate to a lymph node, where they proliferate producing many short-lived clones through cell division. Those clones that have low affinity to the antigen will die while those with high affinity will survive and differentiate into plasma or memory B-cells. Plasma B-cells secrete antibodies that can bind to the antigen, destroying or neutralizing it.

If the same pathogens attack the body again in the future, the adapted memory B-cells can provide a second response that is much faster and more efficient than the primary response. In this sense, the immune system is said to learn to recognize specific kinds of antigens in the primary response and memorize the learned result via the memory B-cells.

B. Introducing Artificial Immune Systems

The dynamic learning mechanisms of biological immune system can be integrated into GAs to enhance their performance in dynamic environments. In ITDGA, we design an immune operator embedded in TDGA for dynamic environments. The starting point is to view the changing environment as the antigen and the changes in the environment as the appearance of different antigens.

The computational model of the immune operator of ITDGA, like many other artificial immune system models, borrows heavily from immunological theory but is not an exact copy of the immune system's behavior. The main areas of immune mechanisms exploited by ITDGA are:

- Automatic Detection: The detecting mechanism is equivalent to the role of the helper T-cells. In practice, this will be achieved when degradation in the average fitness of the population is observed;
- Diversity: The population of cells available for the immune response can be sparsely distributed covering a wide area of the antigenic space;
- Optimisation: Selection and proliferation of high affinity cells produces a rapidly increasing population of high affinity matches useful in targeting and responding to secondary infection;
- Reinforcement Learning: Repeated exposure to an antigenic stimulus can work as a method of reinforced learning. Memory cells may become increasingly more specific to that antigen and able to respond more quickly to reoccurrence.

IV. Designing Immune Operator

The ideas of clonal selection with somatic hypermutation and memory B-cells were translated and integrated into the immune operator of ITDGA to deal with dynamic environments.

A. Entropy-Based Primal-Dual Mapping

Inspired by the complementarity and dominance mechanisms in nature, PDGA operates on a pair of chromosomes that are primal-dual to each other in the sense of maximum distance in genotype in a given distance space. But PDM often lose effectiveness during iteration later period or less environmental change, and its computational expense is fairly high due to selecting lower fitness chromosomes from each generation, so introducing PDM probability determined by the chromosome's rating-based entropy component is necessary.

Definition 4 (rating-based entropy component) Let $P=(X_1,X_2,\cdots,X_N) \in S^N$ be one population of size N, $\pi=\{g_i|0\leq i\leq K-1\}$ be a level partition, and n_i be the number of individuals in g_i of population P. For an individual $X_r \in P$ at level $g_i \in \pi$, $H_c(\pi,P_t,X_r)$ is called its level-based entropy component in P for π, where

$$H_c(\pi, \mathrm{P_t}, X_r) = -\log_K \frac{n_i}{N} \tag{4}$$

Definition 5 (chromosome PDM probability) Let $P=(X_1,X_2,\cdots,X_N) \in S^N$ be one population of size N, $\pi=\{g_i|0\leq i\leq K-1\}$ be a level partition, and n_i be the number of individuals in g_i of population P. For an chromosome $X_r \in P$ at level $g_d \in \pi$, $p(\pi,P_t,X_r)$ is called its PDM probability, where

$$p(\pi, \mathrm{P_t}, X_r) = K^{H_c(\pi,\mathrm{P_t},X_r)} = \frac{n_i}{N} \tag{5}$$

Therefore, the probability of primal-dual mapping in immune operator is determined by the entropy component of the population.

B. Memory-Based Scheme

The basic process of immune operator with memory scheme is described as follow:

1) Detect the change of mean best fitness. If it is more than a threshold, then demonstrate changing environment;
2) Prevenient best chromosome is saved as memory point;
3) Exploit memory. The best chromosome matched with current environment is activated and added to the intermediate population;
4) Generate a few random chromosomes and insert the intermediate population;
5) For each chromosome of intermediate population operate entropy-based PDM;
6) Obtain new population by the free energy component thermodynamical replacement (CTR);

The structure of immune thermodynamic genetic algorithm is show in Fig. 2.

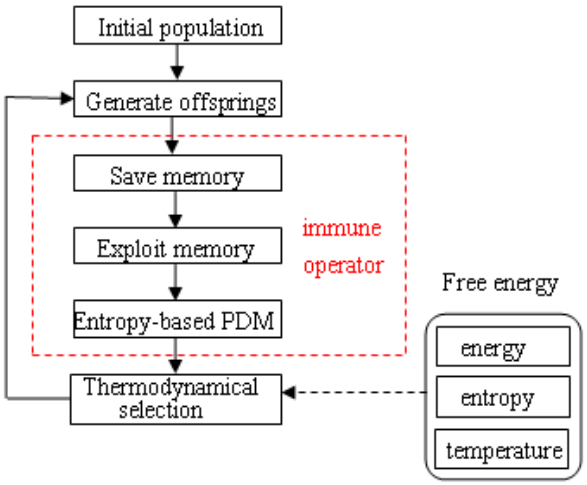

Fig.2. The structure of immune thermodynamic genetic algorithm

V. Experiments Study

A. Constructing Dynamic Test Environments

Given a set of m items and a knapsack, the 0-1 knapsack problem can be described as follows:

$$\max p(x) = \sum_{i=1}^{m} p_i x_i, \quad s.t. \sum_{i=1}^{m} w_i x_i \leq C(t) \tag{6}$$

A knapsack problem with 100 items using strongly correlated sets of randomly generated data is constructed as follows: w_i= uniformly random integer [1,50]; $p_i = w_i +$ uniformly random integer [1,5]; $C = 0.6 \times \sum_{i=1}^{100} w_i$. Given a solution x, its fitness $f(x)$ is evaluated as follows:

$$f(x) = \begin{cases} \sum_{i=1}^{100} p_i x_i, & \text{if } \sum_{i=1}^{100} w_i x_i \leq C \\ 10^{-10} \times (\sum_{i=1}^{100} w_i - \sum_{i=1}^{100} w_i x_i), & else \end{cases} \tag{7}$$

We construct dynamic test environments from above stationary knapsack problem [12]. Suppose that the environment is periodically changed every τ generations, the dynamics can be formulated as follows:

$$f(x,t)=f(x \oplus M(k)) \tag{8}$$

where $k = \left\lceil \frac{t}{\tau} \right\rceil$,

and k is the period index, t is the generation counter, $M(k)$ is the *XOR* mask for period k. And given a value for environmental change level parameter ρ, $M(k)$ can be incrementally generated as follows:

$$M(k)=M(k-1) \oplus T(k), \tag{9}$$

where $T(k)$ is an intermediate binary template randomly created for period k containing $\rho \times l$ ones. For the first period $k=1$, $M(1)$ is initialized to be a zero vector.

In this study, the environmental change speed parameter τ is set to 10(quite early searching stage),100(medium searching stage) and 200(late stage or converged). The environmental change degree parameter ρ is set to 0.05(very light shifting),

0.2, 0.4, 0.6, 0.8(medium variation), and 0.95(significant change).

Totally, we systematically construct a series of 18 dynamic problems, three values of τ combined with six values of ρ. The environmental dynamics parameter settings are summarized in TABLE Ⅰ and TABLE Ⅱ.

B. Experimental Design

For each experiment, 30 independent runs were executed with the same set of 30 random seeds. For each run of different algorithm, the best-of-generation fitness and the population entropy of generation were recorded every generation. And for each run of an algorithm on a dynamic knapsack problem, ten periods of environmental changes are allowed.

In this study, the overall performances of an algorithm are measured by the mean best-of-generation fitness and the mean population entropy of generation. More formally they are:

$$\overline{F}_{BG} = \frac{1}{G}\sum_{i=1}^{G}\left(\frac{1}{N}\sum_{j=1}^{N}F_{BG_{ij}}\right) \tag{10}$$

$$\overline{H}_{G} = \frac{1}{G}\sum_{i=1}^{G}\left(\frac{1}{N}\sum_{j=1}^{N}H_{G_{ij}}\right) \tag{11}$$

where G is the number of generations which is equivalent to ten periods of environmental changes (i.e., G=10×τ), N=30 is the total number of runs.

C. Experimental Results And Analysing

TABLE Ⅰ
MEAN BEST-OF-GENERATION FITNESS OF TDGA, PDGA, ITDGA

Index	τ	ρ	ITDGA	TDGA	PDGA
1	10	0.05	1574.6	1553.2	1552.5
2	10	0.2	1580.1	1552.6	1557.6
3	10	0.4	1573.7	1548.8	1558.2
4	10	0.6	1575.7	1547.7	1561.8
5	10	0.8	1573.5	1548.2	1564.7
6	10	0.95	1576.1	1558.4	1565.4
7	100	0.05	1601.1	1575.4	1572.5
8	100	0.2	1598.9	1568.2	1576.9
9	100	0.4	1614.2	1568.1	1578.6
10	100	0.6	1609.1	1567.7	1579.1
11	100	0.8	1596.5	1569.4	1579.7
12	100	0.95	1608.4	1564.6	1586.1
13	200	0.05	1620.2	1579.7	1581.6
14	200	0.2	1611.1	1576.8	1582.5
15	200	0.4	1610.6	1579.8	1584.4
16	200	0.6	1613.3	1573.7	1585.4
17	200	0.8	1612.4	1572.9	1585.6
18	200	0.95	1614.7	1572.9	1588.4

TABLE Ⅱ
MEAN POPULATION ENTROPY OF TDGA, PDGA, ITDGA

Index	τ	ρ	ITDGA	TDGA	PDGA
1	10	0.05	0.4575	0.4534	0.0026
2	10	0.2	0.4509	0.4465	0.0021
3	10	0.4	0.4518	0.4506	0.0013
4	10	0.6	0.4545	0.4601	0.0014
5	10	0.8	0.4491	0.4441	0.0016
6	10	0.95	0.4521	0.4563	0.0014
7	100	0.05	0.5081	0.5321	0.0013
8	100	0.2	0.4765	0.5011	0.0013
9	100	0.4	0.4698	0.4886	0.0015
10	100	0.6	0.4739	0.5017	0.0018
11	100	0.8	0.4823	0.4998	0.0016
12	100	0.95	0.4688	0.5196	0.0016
13	200	0.05	0.4845	0.5329	0.0012
14	200	0.2	0.4699	0.5024	0.0013
15	200	0.4	0.4748	0.4931	0.0011
16	200	0.6	0.4763	0.5043	0.0015
17	200	0.8	0.4761	0.5012	0.0015
18	200	0.95	0.4701	0.5207	0.0011

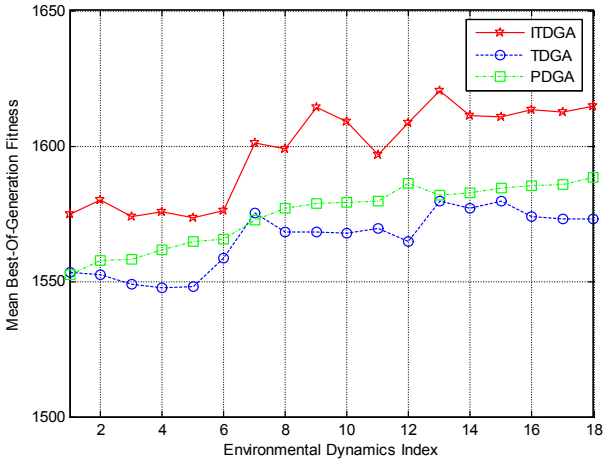

Fig. 3. Experimental results of TDGA, PDGA and ITDGA with respect to overall mean best-of-generation fitness against different environmental dynamics parameter settings

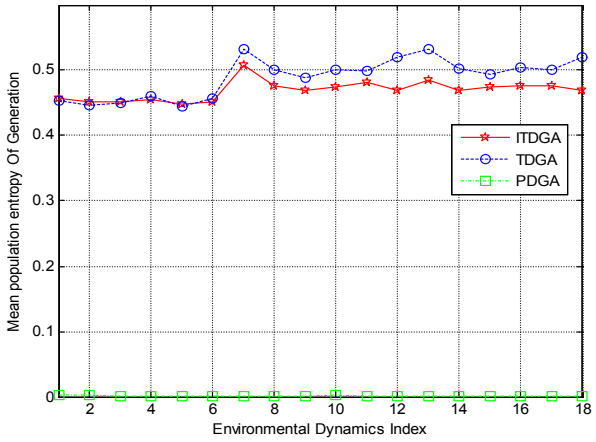

Fig. 4. Experimental results of TDGA,PDGA and ITDGA with respect to overall mean population entropy of generation against different environmental dynamics parameter settings

The experimental results on dynamic knapsack problems are summarized in TABLE Ⅰ and TABLE Ⅱ. The experimental results are also plotted in Fig. 3 and Fig. 4, where the environmental dynamics settings can be indexed according to TABLE Ⅰ. From TABLE Ⅰ, TABLE Ⅱ, Fig. 3, and Fig. 4, several results can be observed.

First, generally speaking ITDGA outperform its peers TDGA and PDGA respectively, especially when the environmental dynamics parameter τ is large and ρ is set to medium values of 0.4 and 0.6. When τ=10, the environment changes quickly and memory scheme is effective. In the case, the effect of introducing random chromosomes is not significant because convergence is not very serious. When ρ is set to medium values, an optimal solution is shifted about halfway away from its original point toward its complementary point in terms of Hamming distance, and falls into the very area represented by random chromosomes.

Second, it is easy to see that for each fixed τ PDGA outperforms other algorithms when the environment is subject to significant changes, e.g., when ρ =0.95, 0.8, even 0.6. This result confirms our expectation of introducing the PDM into ITDGA. When the environment suffers significant changes, the PDM takes effect quickly to adapt ITDGA to the changed environment.

Third, TDGA is now beaten by both PDGA and ITDGA on most dynamic problems expect when the value of ρ is small. When ρ is small, the dynamic problems are close to their corresponding stationary problems. For stationary (and nearly stationary) problems introducing extra mechanism may not be beneficial. This result confirms our expectation of introducing the change check point into ITDGA.

Fourth, from Fig. 4 it is easy to see that ITDGA and TDGA greatly outperform PDGA on all cases. The effect of introducing the thermodynamic competitive model between energy and entropy is significant. This result is consistent with our expectation of addressing diversity problem to adapt to changing environment.

VI. Conclusion

In this paper, we investigate the application of ITDGA algorithm for dynamic knapsack problems. Inspired by the immune mechanism broadly existing in nature, we propose ITDGA that introduce several artificial immune approaches in TDGA, such as detecting mechanism, PDM (i.e., immune mutation), memory scheme, random chromosomes, to maintain and add diversity measured by entropy to adapt to changing environment. Using the dynamic problem generating technique, a set of dynamic problems is generated from a typical stationary knapsack problem as the algorithm test environments. Experimental studies over these dynamic problems suggest that ITDGA can solve complex dynamic problems more efficiently than PDGA and TDGA. The experimental results show that ITDGA has strong viability and robustness in dynamic environments. We conclude that ITDGA is a good choice for dynamic problems.

The mechanisms of immune and thermodynamics in ITDGA are quite general and hence can be generalized to other optimization methods to improve their capability in non-stationary environments, which is an interesting work.

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