Coevolutionary Genetic Algorithms to Simulate the Immune System's Gene Libraries Evolution

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Abstract. Two binary-encoded models describing some aspects of the coevolution between an artificial immune system and a set of antigens have been proposed and analyzed. The first model has focused on the coevolution between antibodies generating gene libraries and antigens. In the second model, the coevolution involves a new population of self molecules whose function was to establish restrictions in the evolution of libraries' population. A coevolutionary genetic algorithm (CGA) was used to form adaptive niching inspired in the Coevolutionary Shared Niching strategy. Numerical experiments and conclusions are presented.

1 Introduction

This work proposes simulations of the dynamics between antigens and antibodies' library genes, inside artificial organisms, along the evolution of a species. Coevolutionary Computation has been chosen to implement the models studied. In gene libraries populations, a genetic algorithm (GA) was used to form adaptive niching based on the ideas of Goldberg and Wang [1]. Two models are described in Sections 2 and 3, respectively, which also present numerical experiments. The paper ends with Section 4 which discusses the results of our ongoing work.

2 The First Model

2.1 The Libraries Population's GA

Each individual in this first GA's population represents a simplified library which contains only three binary encoded segment groups V, D and J. Initially, the libraries have only one segment of each group and their initialization is entirely random. One example of an individual is shown in Figure 1. The junction between one segment of each group forms the genetic code for producing an antibody.

Decoding an individual here means to produce all of its potential antibodies repertory. This is done by making recombination between the individual library segments of V, D and J kind, in this order, as shown in Figure 2. The libraries recombination operator used was a crossover in which one of the segment groups

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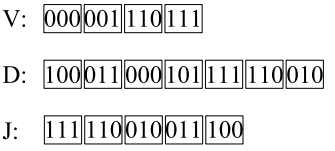

Fig. 1. A library individual

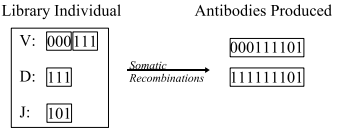

Fig. 2. Antibodies generation

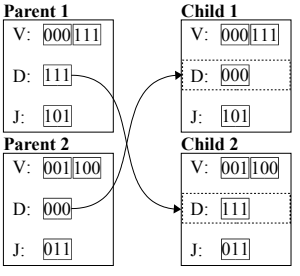

Fig. 3. Crossover operator

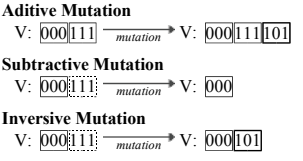

Fig. 4. Mutation operators

V, D, or J, is randomly chosen and exchanged between the parents, as shown in Figure 3. There are three kinds of mutation in the libraries GA. These mechanisms are illustrated in Figure 4.

The fitness of each library is given by its capacity of producing an antibody potential repertory capable of maximizing the neutralization of the antigens population. To neutralize an antigen, the antibody's paratope needs to bind an antigenic determinant in the pathogen's molecule. In the model, the antibody is constituted only by the paratope. The antigen can be larger than the antibody. Thus, there might be more than one region in the antigenic molecule where a set of antibodies could bind. An example is shown in Figure 5.

The capability of an antibody to neutralize an antigen is measured by means of a computational distance, known as matching function. Chromosomes are compared bitwise, and the matching value is determined by the longest complementary chain between them [2], as it can be seen in Figure 5. In the example of Figure 5, it was established that the necessary matching to consider a bind was of 100%.

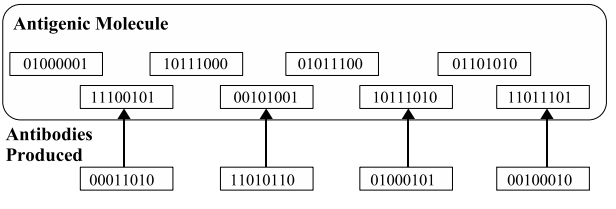

Fig. 5. An antigenic molecule and the correspondent binding antibodies

As more than one antibody could match a certain antigenic molecule, the pathogen can be seen as the owner of its complementary antibodies niche. In terms of the CSN, antigens and antibodies play the roles of the businessmen and clients, respectively. Each antibody is compared to an antigen, in order to establish which antigen is best neutralized and, consequently, which niche the antibody will belong to. The fitness of a library is measured by summing fitness from all of its produced antibodies.

2.2 The Antigens Population's GA

The GA operates in the antigens' population by making mutations on the individual's chromosome. If the mutation increases the antigen fitness, this change on the genetic material is kept. The antigen fitness is given by its capacity of aggression inside the organism. A mutation in the antigen's chromosome is made by randomly selecting and inverting a bit. The fitness calculation is similar to the one done for libraries. The difference is that the antibodies have to maximize matching in the niche, while antigens need to minimize it.

In our experiment, the parameters used for the libraries population GA were: 120 generations per epoch, 10 individuals in the population, elitism of 1 individual, 4 bits per gene segment and 85% of probability of crossover and mutation. The probabilities of application assigned to the additive, subtractive, and inversive mutations were, respectively, 20%, 10%, and 70%. The group of segments V, D, and J had the same chances of selection for mutation. The antigens GA used 400 generations, 200 individuals, 64 bits per chromosome and 85% of mutation probability. The number of recognized antigens along the generations is shown in the graphic of Figure 6.

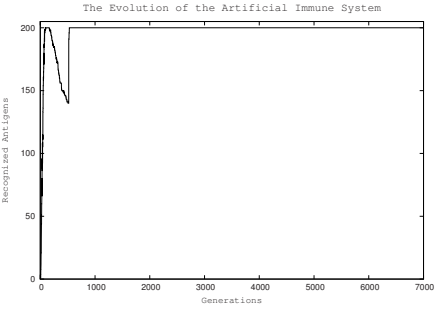

Fig. 6. First Model: The evolution of the IS

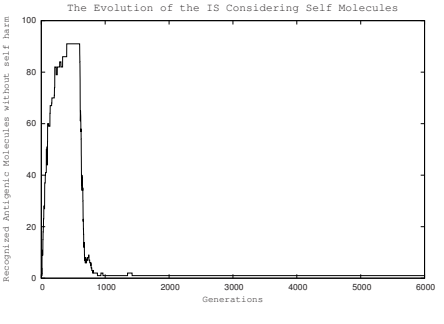

Fig. 7. Second Model: The evolution of the IS

3 The Second Model

This second model simulates IS tolerance by adding a new population representing self. Now, the libraries' population has to evolve maximizing the coverage

of the antigens population and minimizing the attack of self molecules. To implement this new requirement, a penalization for those individuals that produce self-reactive antibodies is introduced. Such penalization is computed by dividing the antibodies fitness sum by the number of self molecules attacked. For the experiment, the libraries' GA used 600 generations per epoch. The other parameters assumed the same values used in the first model. The antigens' GA used 1500 generations per epoch, 100 individuals with chromosomes of 120 bits and mutation probability of 85%. The self population had size 50 and its molecules were represented by chromosomes of 12 bits. The results can be seen in Figure 7.

4 Conclusions

This paper has proposed two models describing some aspects of the evolution in an artificial immune system with some characteristics similar to the real biological systems. The first model has focused on the coevolution between an antibodies producing gene libraries population and a set of antigens. Results of this experiment showed that, as evolution proceeded, antibodies became much more adapted to the environment presented, being able to recognize any new mutated antigen that would appear in the population. Also, the real immune systems coverage stability was reached and an artificial system able to adapt and recognize any given binary segment has been created. In addition, the necessity and ability of a fast changing genetic mechanism to provide robustness to a biological species antibodies' genotype has been demonstrated. The improvement of the first model produced a second one with characteristics more similar to real immune systems. Now the evolution has involved a new group of strings that represented molecules belonging to the organism and against who the immune system could not activate defense mechanisms. The results obtained have shown that the antigens' evolution proceeded towards imitating self molecules bits sequences. As a result, antigens became invisible to the antibodies defense mechanisms pointing to the necessity of other means of protection. In real immune systems, these other means are constituted by T-cells.

References

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