Parallel Search for Multi-Modal Function Optimization with Diversity and Learning of Immune Algorithm

Toyoo Fukuda¹, Kazuyuki Mori² and Makoto Tsukiyama²

¹ School of Policy Studies
  Kwansei Gakuin University
  2-1 Gakuen, Sanda, Hyogo 669-13
  JAPAN

² Industrial Electronics & Systems Laboratory
  Mitsubishi Electric Corporation
  Amagasaki, Hyogo 661
  JAPAN

Abstract. Immune System in the higher mammal has interesting characteristics and powerful abilities from the information viewpoints, such as recognition of antigen, production of antibody and learning with memory cell. This paper proposes an optimization algorithm imitating the immune system to solve the multi-modal function optimization problem partly using a genetic algorithm. The proposed algorithm is shown to be effective for searching for a set of solutions as well as local solutions. The illustrative examples are shown for multi-modal functions such as multi-peaks function and Shubert function.

1 Introduction

The artificial immune algorithm for parallel search is shown with illustrative examples. Immune system has fundamental ability to produce new types of antibody or to find the best fitted antibody which is able to attack the antigen invading into the body. Against the unnumerable types of unknown antigen, the immune system produces a great many types of antibody by trial and error. To realize the diversity of antibody types is essential adaptability against the foreign virus and bacteria in the environment. The diversity of the immune system can be mathematically formulated as a multi-modal function optimization problem, which has multiple solutions not single solution. The proposed algorithm is aimed on how to keep the parallel search vectors for multiple solutions. The index of diversity is introduced and multiple solution vector is kept as memory cell mechanism in the immune system. The antigen can be considered as a problem to be solved and antibody as solution vector best fitted to solve the problem.
Many engineering problems can be formulated as optimization problems which optimize some objective function. Meanwhile most cases show the multi-modal function as objective function. It is not easy to solve such multi-modal function problem by the conventional optimization methods. Therefore, a method to get a set of solution is needed in the real world. Meanwhile, the immune system in a higher mammal eliminates antigens by the genetic evolution of a lymphocyte population which has capability to produce antibodies (see Figure 1). Many types of antibody are produced by combinations of gene by way of trial because the type of antigen is not known a priori. From among the varieties of antibody candidates a unique antibody is selected to destroy the antigen successfully by bio-chemically pattern matching between antigen and antibody. So the process of immune system can be considered as an optimization process. The process is to select a type of antibody from among a great many solution candidates that is the best fitted with the unknown antigen. Then the immune process is considered to be a kind of combinatorial optimization process[2].

This paper proposes an immune algorithm (IA) imitating the physiological immune system, that is based on somatic theory [1] and the network hypothesis [3]. The somatic theory describes that somatic recombination and mutation contribute to increasing the diversity of the antibodies. The network hypothesis describes that a mutual recognition network among the antibodies contributes to control of the proliferation of clones[1],[4],[6],[7]. A few numerical examples of test functions such as five-peaks function and Shubert functions are illustrated to show the abilities of immune algorithm for multi-modal function.

## 2 Immune Algorithm

### 2.1 Diversity and Affinity of Antibodies

In order to observe the diversity of antibodies produced from a lymphocyte population, it is necessary to define a measure of that diversity. A model of a lymphocyte population consisting of antibodies is shown in Figure 2.

The informative entropy of locus \( j \) in the lymphocyte population is represented by

\[
H_j(N) = \sum_{i=1}^{S} -p_{i,j} \log p_{i,j}
\]  

(1)

where \( N \) is the size of the antibodies in a lymphocyte population, \( S \) is the variety of allele and \( p_{i,j} \) means the probability that locus \( j \) is allele \( i \).