

1 Artificial Immune Systems

Artificial Immune Systems (AIS) are adaptive systems inspired by abstracted aspects of vertebrate immune systems and applied to problem solving [3]. This is different from the field of computational immunology that is concerned with modeling exact immune systems to increase knowledge and understanding of the immune system [7]. In Garrett's survey [7] he divides AIS into three categories. These categories are artificial negative (and positive) selection, artificial clonal selection and hypermutation (ACSH), and artificial immune network models (AINM) [7]. The remainder of this paper describes each category's relation to the immune system, some details of the algorithm, lists applications, and mentions variations on the algorithms.

The vertebrate immune system is a complex system that provides a defense against unwanted bacteria, viruses, fungi, and other pathogenic agents [9]. These unwanted substances are known as foreign antigens. Antigens are substances that can be recognized by the immune system [4]. Lymphocytes cells in the immune system that recognize, interact with, and remove antigens. For the immune system to perform properly lymphocytes must distinguish between foreign antigens (nonself) and antigens belonging to the organism (self). Negative selection is an immune process that variations of lymphocytes, eliminating all lymphocytes that attack self antigens. Cells that weakly or do not respond to self antigens are released into the immune system [7].

Forrest et al. [6] introduced the first artificial negative selection system. This system creates a set of equal sized binary strings to represent self antigens. A large, random set of strings representing lymphocytes is also created. The two sets are tested against each other and random strings that do not strongly match any self strings are retained. The strength of matches is determined by the largest number of matching contiguous bits. The retained strings are called detectors and foreign objects are identified by matches with detectors. Closely related to negative selection are positive detection systems that use detectors that identify self rather than the nonself objects [7].

Negative and positive selection algorithms have been applied to detection of viruses in machine code, tool breakage detection, hardware fault-tolerant systems, encryption, and for detecting network intrusion [7]. Recent works on these algorithms have addressed scalability to large problems, use of other matching functions, methods to increase detection of foreign objects, variable sizes for detector strings, and combining positive and negative selection[7].

ACSH is a technique that focuses on how B and T cell lymphocytes adapt and match to destroy foreign objects. One of the simplest ACSH methods, described by de Castro and Von Zuben [2] proceeds as follows: In the first step a random population of binary strings equivalent to antibodies is produced. Antibodies are proteins secreted by B cell lymphocytes that bind to and kill antigens [4]. A fitness function is then used to select a subset of the best antibodies. These antibodies are copied and mutated at a rate inversely proportional to the antibody's fitness. The mutated clones and the non-mutated antibodies are then assessed for fitness. Unfit antibodies are culled until the population of antibodies is reduced to its original size. These selection, mutation, and culling operations are continued until a problem dependent termination condition is met [7].

ACSH algorithms have been applied to optimization, determining centers of radial basis functions, pattern recognition, graph coloring, character recognition, automated scheduling, and document classification [7]. Recent works have hybridized the algorithm with immune networks, used information theory to provide termination conditions, and used data structures that reduce calculation and memory usage [7]. In Garrett's survey [7] he notes that in ACSH algorithms mutation rates are functionally related to fitness, differentiating ACSH from genetic algorithms.

AINM are concerned with modeling the interactions between antibodies and antigens in the immune systems. Jerne's [8] immune network model theory labels the areas of an antibody that can bind to antigens as paratopes. The areas of antigens that become bound are known as epitopes. Antibodies also have epitopes that can be bound by other antibodies [8]. Lastly this theory states that all entities with bound epitopes become eliminated or repressed and antibodies with a bound paratope is proliferated. This immune network yields a system of increasing and decreasing antibody/antigen concentrations triggered by these stimulatory and suppressive interactions [7].

Farmer et al. [5] created the Farmer-Packard-Pereson (FPP) model that abstracts and mimics this process. With epitopes and paratopes modeled as binary strings the FPP models describes a matching affinity function between any two antibodies or an antibody and antigen. A dynamic differential equation incorporating this matching function is used to model the changing concentrations of antibodies and antigens [5].

Detection of gene promoter sequences, data mining, diagnosis, and cluster analysis are demonstrated applications of AINM [7]. Other AINM have avoided use of derivatives through using replicator equations or cellular automata, limited the effects of antigens to k-nearest neighbors, and have limited the size of the antibody/antigen populations to decrease the computation time and memory space[7].

2 Reference Justification

The majority of this paper is based upon Garret's 2005 survey of AIS techniques [7]. This work is a useful survey appears to cover all AIS material and it discusses the applications as well as the originals of the AIS techniques. Similarly de Castro and Von Zuben's survey on basic AIS theory is also useful [4]. A particularly helpful attribute of this second survey is the included comprehensive glossary of immune system terminology. De Castro and Timmis' book [3] as well as Dasgupta's book [1] also provide a comprehensive overview of the AIS systems and applications.

Perelson and Weisbuch [9] provide an overview of immunological theories in a manner comprehensible for non-immunologists. They also discuss several applications of physical and mathematical models to understanding immune systems.

Forrest et al.'s work [6] is important as it introduces the first negative selection abstraction.

De Castro and Von Zuben's system [2] is important because it seemed to be the most easily understood ACSH systems.

Jerne's immune network model theory, although abstract and now partially believed to be incorrect [7], provides a model leading to AINMs that produce useful systems. The most well known of these systems [7] is Farmer et al.'s [5] FPP model.

Lastly the starting point Wikipedia [10] entry on artificial immune systems provides a concise summary of AIS and links to a great deal of useful content.

References

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