

## ARTIFICIAL IMMUNE ALGORITHMS IN LEARNING AND OPTIMIZATION

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### Summary

The term Artificial Immune Systems (AIS) refers to a class of computational algorithms that are inspired by processes apparent in the natural immune system. As such, they belong to a wider family of biologically inspired algorithms such as evolutionary algorithms, ant-colony algorithms and other swarm inspired algorithms for example. The natural immune system can in the simplest case be viewed as a body-defense system, or more generally as a body-maintenance system of which defense is a special case. From a computer science perspective, it attracted interest due to the recognition that in order to fulfill its defense role, the natural immune system utilizes a number of mechanisms that lead to useful *functionalities* such as learning and memory that are key elements in many types of problem solving activities typical in computer science. This has led to a variety of applications in domains such as optimization and machine-learning as with other biologically inspired algorithms. As such, it can be viewed as a complementary technique to many existing algorithms.

The field of AIS dates back to the late 1980s, and was popularized in the 1990s. Typically, it focuses on the derivation of computational algorithms for use in solving problems and designing engineered artifacts. Although there is no canonical definition of an AIS, the domain can be well described by the definition in (de Castro & Timmis, 2002).

*“adaptive systems, inspired by theoretical immunology and observed immune functions, principles and models, which are applied to problem solving”.*

Problem solving can be interpreted widely. The focus of this chapter however is on the application of AIS algorithms to optimization, classification and clustering problems, which typify the majority of work in the field. The interested reader should note that more recently, a diversification of the field has started to occur in which AIS is utilized as a modeling tool to develop computational simulations which explain phenomena and guide experimental work in the laboratory. This chapter however retains an engineering focus, presenting an overview of the state-of-the art in algorithms in the most commonly featured domains. It provides a practical treatment, aimed at those who wish to use the algorithms for solving optimization and classification problems.

The chapter proceeds with a brief historical perspective on the field, which is followed by a very basic guide to the immunological principles required to grasp the concepts underpinning the algorithms. It should be noted that immunology is a complex field, a complete understanding of which still remains beyond reach of experts. Therefore, in no way is this treatment an immunological primer. The chapter covers only the concepts required from an engineering perspective, in a manner that does not require anything other than high-level overview of the material. An effort is made to simplify the use of terminology so as not to blur the principles that the algorithms aim to mimic, free from immunological details that often can mask simple principles. The chapter therefore briefly describes a set of relevant immunological principles, giving an outline of the basic computational equivalent of the principle. The most commonly used AIS algorithms are then presented, separated into applications areas of optimization, anomaly detection and clustering, given that the majority of literature in AIS falls within these three domains. In each area, an outline of the basic computational algorithm that underpins the development of the field is given, followed by a discussion of the state-of-the-art algorithms that employ the principle in question. The chapter concludes with brief overviews of developing research within the AIS field, providing some insight into algorithms which although in their infancy have been shown to have promise, and further, into some of them more diverse application areas such as robotics and sensor networks to which AIS has been applied.

We begin with a brief historical background to provide some context to the discussion.

## **1. Historical Background**

The field of AIS has its roots in the mid-1980s, when a small number of people began to investigate the theoretical models to understand the basis of immune function. The seminal paper, generally accepted as the first in the field, was that of Farmer (Farmer, Packard, & Perelson, 1986) that compared networks apparent in the immune system with neural networks, and suggested the immune system might be viewed as a computational system. Around about the same time, Varela et al, proposed that the immune system could be viewed as a cognitive system (Varela, Coutinho, Dupire, & Nelson, 1988). The start of the 1990s saw the first translation of these early ideas to practical problems, with a number of influential papers (Bersini, Varela, Schwefel, & Männer, 1991; Ishida, 1993). These papers marked the true crossing of the divide from theoretical immunology to problem solving, with the ideas rapidly taken up and developed by Stephanie Forrest et al., (Forrest, Perelson, Allen, & Cherukuri, 1994). Her influential work adopted perhaps the most instinctive interpretation of natural

immunology, that of the immune system playing the role of defense, and was therefore focused on computer security, in particular, anomaly detection within a computer.

In the mid 1990s, the field rapidly diversified, with immune algorithms being commonplace in applications within the domains of both optimization and classification. The field had matured sufficiently by 2000 that an international conference, ICARIS, was established to support researchers in the field. The proceedings of this established conference remain an excellent resource for those interested in the field. A number of textbooks also exist which provide both background material and state-of-the-art reviews of the field, (Das Gupta, 1998; de Castro & Timmis, 2002) In recent years, following an explosion of publications reporting both applications and modifications to the basic algorithms, a more reflective approach is now apparent in the literature, with a slowly growing body of theoretical work that both provides insights into existing algorithms and underpins new developments in the field e.g. (Timmis, Andrews, Owens, & Clark, 2008; Timmis, Hone, Stibor, & Clark, 2008).

### **1.1. AIS in the Context of Other Paradigms**

Comparison of immune algorithms to other biologically inspired paradigms is inevitable. Similarities between immune inspired algorithms and evolutionary algorithms are apparent within the field of optimization while inevitable comparisons have been made with classification immune algorithms to existing machine learning techniques. More recently, comparisons have also been drawn to the swarm intelligence field (Timmis, Andrews, & Hart, 2010). Other recent publications highlight the inter-disciplinary nature of AIS research, stressing that better interactions with both immunologists and mathematicians will advance the development of novel AIS algorithms applied to computational problems – it is worthy of note that in contrast to other biological paradigms such as evolutionary computing where the biological basis is well established, immunology remains a developing field in the laboratory with new advances continually being made, thereby offering scope for the development of further novel computational algorithms.

From a practical perspective, the algorithms described in this chapter provide a useful addition to the armoury of the computer scientist, whether in the field of machine learning, optimization classification or anomaly detection.

## **2. Basics of Immunology**

The natural immune system plays a major role in protecting our bodies against attack from external microorganisms, providing both maintenance and repair. As a whole, the body employs several lines of defense, which become increasingly more complex:

1. Skin, presenting a physical barrier to organisms.
2. Physiological factors, for example increasing body temperature.
3. The innate immune system, which provides a rapid but non-specific response to potential pathogenic material.
4. The adaptive immune system, which learns to recognize and eliminate pathogens over the lifetime of the host.

The final two components, the innate and adaptive immune systems, are of most interest from a computer science perspective, with the majority of attention paid to the latter. Both of these systems comprise of large families of cells, which collectively and collaboratively constitute the immune response. For the computer scientist, it is unnecessary to delve into detail in order to understand how these mechanisms inspire computational algorithms. Therefore, in the remainder of the chapter we restrict the use of immunological terminology to the following general terms:

- **Dendritic Cell:** a cell belonging to the innate immune system.
- **Antigen:** a foreign agent which initiates a response from the immune system.
- **Lymphocyte:** a broad term covering a range of cells, generally belonging to the adaptive immune system and responsible for the recognition and elimination of foreign agents.
- **Affinity:** the strength of binding between an antigen and a lymphocyte: the extent to which an antigen is recognized by a lymphocyte

In particular, we note that the term lymphocyte covers a broad class of immune cells such as B-Cells, T-Cells and antibodies. Often, these terms are used loosely within AIS literature, without strict adherence to their biological counterparts. In terms of functionality, for the purpose of most immune algorithms it is sufficient to assume that the term lymphocyte refers to a cell that adapts during the course of the algorithm, without having to understand specific details regarding the precise mechanisms within the natural immune system by which this adaptation takes places.

The main processes that occur within the innate and adaptive immune systems that have inspired computational algorithms are now briefly described at a high level, with the aim of providing sufficient understanding of the *computational* analogies of the mechanisms apparent in the natural system.

## 2.1. Antigen Presentation

Cells from the innate immune system are known to play a key role in initiating the adaptive immune response. Computationally, research has focused on a single type of cell termed the dendritic cells (an example of a broad class of cells termed macrophages). These cells circulate through the body tissues where they collect debris located in the tissue (which includes potential antigenic material) and display it on their surface. In addition, they further collect signals from the environment in which the material is found, which indicate the context in which the material was collected. Certain signals indicate potential danger (for example tissue damage), while others may indicate normal functioning. The accumulated signal eventually causes maturation of the cell into one of two types, semi-mature and mature, depending on the relative proportions of the signals collected. Matured cells of both types traffic to the lymph organs where they present collected material to the cells of the adaptive immune system. Semi-mature cells present information with signals that indicate a safe context, and do not trigger a response. Matured cells on the other hand trigger a response, by presenting information in a danger context.

Computationally, the dendritic cell performs data collection and a mechanism for determining context; it can also be considered to perform data-fusion, processing a range of signals that when fused indicate the presence of an anomaly within the system, conversely that the system is behaving ‘normally’. A key idea is that the dendritic cells react to changes within the tissue, therefore recognizing the *effect* of an intrusion rather than the intrusion itself. This is accomplished by collecting potential *suspects* from the tissue whilst, at the same time, reacting to the *effect* of the intrusion which, from a computational perspective, offers a mechanism for correlating cause with effect.

## 2.2. Clonal Selection

Clonal selection was proposed by Burnet in (Burnet, 1959) to explain the basic properties of an adaptive immune response in response to an antigenic stimulus. It can be described simply as follows:

- Lymphocytes that contain receptors that can bind to the antigen begin to proliferate, producing copies or *clones* of themselves
- During the cloning procedure, some lymphocytes will undergo *mutation* which may increase the binding capacity or *affinity* of the clone for the antigen
- Clones effectively undergo *selection*; clones which bind more strongly to the antigen proliferate more rapidly; those which do not bind do not proliferate
- Some of the cloned population differentiates into *memory-cells*; they do not proliferate further but remain in circulation over long-periods of time thereby providing *memory* of the antigen that stimulated the response.

The proliferation, selection and refinement through the mutation process described is akin to natural evolution, albeit on a much faster timescale. From a computational perspective, this accomplishes a rapid *search* of the space of possible receptors, resulting in lymphocytes with very high affinity for the antigen.

## 2.3. Negative Selection

Recognition of body cells (*self*) by lymphocytes as explained above would result in the destruction of self. Therefore, a mechanism must exist which prevents activation of lymphocytes that recognize self-material in the body. This mechanism is known as negative-selection and occurs within the thymus (a small organ located just behind the sternum). Lymphocytes newly generated from the bone marrow pass through the thymus before moving into free circulation within the body. Here, they are exposed to self-cells; those that bind to any self-cells are eliminated within the thymus, leaving only those which have failed to recognize any self-cells to pass into free circulation. Once in circulation, if a lymphocyte binds to any cell, the cell must therefore be antigenic (non-self).

From a computational perspective, negative selection can be considered as a one-class classification algorithm: having been trained on a set of examples from a single class (self) it is able to classify objects from a second class of which it has no previous knowledge.

## 2.4. Idiotypic Networks

According to the clonal selection theory, lymphocytes produced by the bone marrow that are not stimulated by antigen undergo a natural cell death. In 1974 Jerne proposed an alternative view however, which proposes that the immune system sustains a dynamic, regulated network of immune cells, even in the absence of antigenic stimuli. Immune cells recognize each other, creating complex positive and negative feedback loops that result in a network that reaches a dynamic steady state (Jerne, 1974). The network offers an explanation for immune memory, in that it sustains certain cells that have participated in immune response. Meta-dynamic processes allow for recruitment of new cells into the network as well as enabling pruning of existing cells from the network. Furthermore, it is proposed that the topology of the network determines whether a new cell will be recruited into the network or rejected, thereby providing a dynamic definition of self.

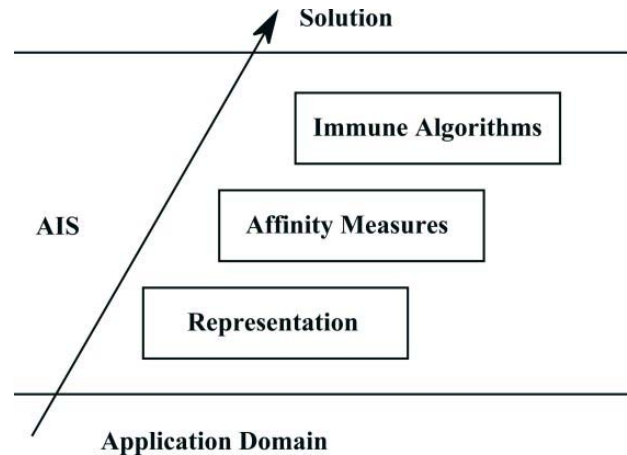
Computationally, an idiotypic network can be viewed as the internal representation of a system, encapsulating memory and providing an explanation for emergent properties such as learning, self-tolerance, size control and diversity of cell populations.

## 3. Abstraction into Computing

As should now be clear from the previous section, the immune system exhibits a number of properties that are attractive from a computational perspective and are thought to give rise to systems that are scalable, robust and maintain homeostasis. In order to translate these properties into algorithms which can solve engineering problems, a method is needed to map the entities of the natural immune system – cells which interact through electrostatic and chemical binding – into entities that can be exploited within a computer program. Research in AIS has been greatly facilitated by a concept originally introduced in order to undertake computational studies of the immune system (Perelson & Oster, 1979) known as shape-space. The concept enables the representation of cells in a low-dimensional space in which properties such as mutual affinity and similarity of cells could be derived from the relative positions of points in the space. A cell is represented as a set of  $N$  parameters, describing physical properties such as molecular shape or molecular charge etc. These  $N$  parameters can be represented as an  $N$ -dimensional vector space known as shape-space  $S$ , and affinity between two cells can be measured by any suitable metric within  $S$ .

Perelson's "shape-space formalism" has become the de facto representational abstraction in AIS: a vector representing a point in a data-set symbolizes an antigen. Vectors are similarly used to represent lymphocytes, and affinity between the two entities can be calculated using an appropriate metric for the vector. Possible representations can include binary strings, vectors of real numbers or even symbolic spaces. In each case, having defined a representational space within which to operate, an appropriate metric can be defined to quantify affinity between two entities. With binary representations for example, a Hamming distance metric may be suitable whereas when dealing with a vector space Euclidean distance is often used. A more detailed discussion of both representations and metrics is given later in this chapter in the context of negative selection.

Shape-spaces facilitate the mapping of entities in a biological system to those in an engineered system. A framework by which this mapping can then be used to develop an algorithm is proposed in (de Castro & Timmis, 2002) and is shown in the following:



The framework identifies three important steps. In the first, a suitable representation is chosen, which specifies the shape-space. Given the representation, an affinity metric can be defined. From these two definitions, it is then possible to define an algorithm which utilizes the representation and affinity metric to model immune processes such as learning and adaptation. In (Freitas & Timmis, 2003) the authors discuss the need for care in the choice of representation and affinity function, advocating that it must be tailored to both the type of data and the application that one is dealing with.

#### 4. Optimization

A family of AIS algorithms have been developed that can be applied to typical optimization problems, in which given a function  $f : A$  the goal is to find an element  $x_0$  such that for all  $x$  in  $A$  in the case of minimization or for all  $x$  in  $A$  in the case of maximization. Typically,  $A$  is a subset of the Euclidean space  $\mathbf{R}^n$ , and often specified by a set of constraints that all members of  $A$  have to satisfy. Optimization problems are common in a range of real-world domains such as scheduling, routing, and packing, as well as occurring in function optimization applications in engineering and mathematics. Biologically-inspired approaches to solving optimization problems are common in the literature, with a plethora of algorithms developed in the Evolutionary Computing and Swarm Intelligence domains. AIS algorithms can be viewed as complementary to both of these approaches.

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### **Biographical Sketches**

**Emma Hart** received a BA(Hons) in Chemistry from the University of Oxford in 1990, followed by an MSC in Knowledge Based Systems from the University of Edinburgh (1996). Following a period of working as a researcher in the Department of Artificial Intelligence at the University of Edinburgh in the domain of evolutionary algorithms and optimization, she received a PhD from this institution in 2002, the subject of which was Immunology as an Inspiration for Computing: Fact or Fiction ?. She moved to Edinburgh Napier University as a lecturer in 2000, where she pursued her interests in the rapidly developing field of AIS, and was promoted to Reader and then Professor in 2008. Her research in the AIS field is recognized internationally: she has twice chaired the International Conference on Artificial Immune Systems (ICARIS); she was co-organiser of a Dagstuhl seminar on AIS in 2010; she has chaired numerous conference workshops in the domain at major international conferences and examined a number of AIS related PhDs both in the UK and abroad. Her research interests cover a broad range of topics, ranging from computational modeling of immune systems to practical applications. From an application perspective, she has developed novel immune algorithms for optimization in the scheduling and packing domains, for use within wireless sensor network applications for system monitoring, and within the field of document classification. She is particularly interested in the use of computational modeling as a precursor to algorithm development, and in the potential benefits that computational modeling techniques from software engineering can bring to the field of immunology.

**Kevin Sim** received a BSc(HONS) in Software Technology from the then named Napier University in 2009 before completing an MSc in Advanced Software Engineering at the renamed Edinburgh Napier University the following year. Since completing his MSc, Kevin has been studying towards a PhD at the same institution under the supervision of Professors Emma Hart and Ben Paechter in the field of optimization. More specifically concentrating on Hyper-heuristics; an emerging field which incorporates many of the existing biologically inspired methodologies used for optimization, in which the objective is to search for, or to generate, a suitable procedure for the problem being addressed rather than searching directly for a solution as with other more established biologically inspired approaches. Kevin has been involved in the EvoStar conference for the past two years and has been appointed as co-chair of the EvoIndustry workshop and as web designer for the upcoming 2013 conference.