Multimodal Dynamic Optimization: From Evolutionary Algorithms to Artificial Immune Systems

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Abstract. Multimodal Dynamic Optimisation is a challenging problem, used in this paper as a framework for the qualitative comparison between Evolutionary Algorithms and Artificial Immune Systems. It is argued that while Evolutionary Algorithms have inherent diversity problems that do not allow them to successfully deal with multimodal dynamic optimisation, the biological immune system involves natural processes for maintaining and boosting diversity and thus serves well as a metaphor for tackling this problem. We review the basic evolutionary and immune-inspired approaches to multimodal dynamic optimisation, we identify correspondences and differences and point out essential computation elements.

1 Introduction

The domain of Artificial Immune Systems (AIS) has only recently emerged within the broader discipline of Bio-inspired Computing. There have been doubts on the necessity of yet another biologically inspired approach, especially given the perceived similarity to the well established Evolutionary Algorithms (EAs). Both use a population of simple representational units, antibodies and chromosomes respectively, that are matched/evaluated against a certain antigenic/solution space. Other than introducing a new set of theories and concepts from Immunology in Bio-inspired Computing, AIS have been treated as another algorithmic variation of Evolutionary Algorithms.

With this paper we wish to contribute to the argument stating that despite some common computational elements, AIS can be fundamentally different to EAs. We will use Multimodal Dynamic Optimisation (MDO) as a framework for comparing the two approaches at the algorithmic level to highlight their essential differences. In MDO there is no single and static optimum, but instead, a varied number of optima that continuously change their position and shape in the solution space. Changes can be both local or global, modest or radical, slow or fast, but they are not chaotic. MDO poses challenging requirements that are going to be identified and used to characterise and compare EAs and AIS.

Although life and many real world problems are inherently dynamic, research in Evolutionary Computation, focuses traditionally on optimisation of static problems, or problems treated as static, with only one global optimum. Recently

L.N. de Castro, F.J. Von Zuben, and H. Knidel (Eds.): ICARIS 2007, LNCS 4628, pp. 13–24, 2007.

there has been a growing interest for tackling non-stationary problems with rugged landscapes, where the various optima have to be found and tracked over time. It has already been recognised, that standard EAs suffer when applied to MDO, because they eventually converge to one optimum and loose the diversity necessary for covering multiple peaks and for adapting to changes in them.

The literature on Evolutionary Computation is already rife with methods for making EAs comply with the requirements of MDO. A comprehensive review of existing evolutionary approaches to MDO is outside the scope of this paper. We will concentrate on the basic techniques and will argue that these are at large ad hoc remedies without always biological foundations. It will be put forward that the drawbacks of EAs in the case of MDO derive from their fundamental algorithmic components and so existing remedies are only patches to intrinsic diversity problems. Furthermore, the proposed remedies point explicitly or implicitly towards the direction of AIS. The immune system deals with a varied and constantly changing pathogenic environment from within a developing organism. As such, it has inbuilt mechanisms for preserving and boosting the diversity of the immune repertoire. In AIS these mechanisms are translated into algorithmic processes that control a system's diversity and allow it to deal naturally with MDO. While there is some correspondence with the effects achieved with algorithmic remedies in the case of EAs, in AIS the diversity controlling mechanisms are both inherent and biologically grounded.

In the rest of this paper we first set out the requirements of MDO. We then use these requirements to critically review evolutionary (sec. 3) and immune-inspired approaches (sec. 4) to MDO. Finally we discuss their similarities and differences and point out directions for future work.

2 Requirements for Multimodal Dynamic Optimisation

A generalised MDO problem can be expressed as a multidimensional space where specific regions correspond to the current solutions, or collectively to an overall solution to a problem. The underlying problem is dynamic, but not chaotic, and hence its solutions constantly change over time. Therefore, it is at least impractical to treat the problem's solutions as points in the multidimensional space, since any point in the space only momentarily becomes a local, or global optimum. It is more appropriate to consider solution regions that change in shape, area and position due to the problem's dynamics. The latter can have different scales. At the lower level, short-term dynamics moves a solution region locally or modifies its shape. At a higher level, long-term dynamics causes new solution regions to emerge and others to disappear. In the extreme case, the space itself can have dynamics that modify its dimensions.

An example problem that demonstrates the characteristics of MDO is Adaptive Information Filtering (AIF). AIF seeks to provide a user with information relevant to the user's multiple and changing interests. Here the user's interests define regions in a multidimensional information space. Changes in the user's interests can be short-term variations in the level of interest in certain topics,

or even more radical long-term changes like the emergence of a new topic of interest, or loss of interest in a certain topic.

To tackle MDO a system has to be able to trace, represent and track the solution regions. This is a challenging task with specific requirements. As already mentioned, both EAs and AIS use populations of simple units that are typically expressed according to the dimensions of the underlying space. *Diversity* – i.e. the presence of a wide range of variation in the qualities or attributes of the individuals involved in a population – is crucial for biological processes like evolution and immunity. Regarding MDO, diversity ensures that the population covers the various solution regions and remains spread around the space in anticipation of changes in them. The diversity problems of EAs have already been recognised and as we will further discuss in the next section, most proposed remedies focus on administering diversity into the population. There are however additional requirements for MDO that have been generally ignored.

As the number and area of solution regions varies in time the number of individuals that are required to represent them should vary accordingly. For example, in the case of AIF, whenever new topics of interest emerge additional individuals are needed to cover the new interesting areas in the information space. In contrast, when the user looses interest in a specific topic the corresponding individuals are no longer required, or it is at least inefficient to maintain them in the population. The cardinality of the population should be adjusted according to the problem characteristics.

Finally, the algorithmic processes should reflect the problem's dynamics. This implies that each individual should be able to move locally, or that the interactions and relative importance of individuals can be modified. At the global level new individuals are required to cover emerging solution regions and no longer competent individuals should be removed.

3 EAs and MDO

The insight behind EAs is that the fundamental components of biological evolution can be used to evolve solutions to problems within computers. They are stochastic search techniques that have been traditionally applied to optimisation problems. A GA starts with a problem and a *population* of random solutions. Each individual in the population, is called a *chromosome*, and is represented as a string over a finite alphabet. The population evolves through iterations, called *generations*. At each generation, each chromosome in the current population is evaluated using some appropriate *fitness function*, which measures how good the solution embodied in a chromosome is. Chromosomes are selected for reproduction according to their relative fitness. Two chromosomes mate using the *crossover* operation that combines parts of each parent chromosome to produce possibly better offspring that replace the less fit individuals in the current population. Occasionally, to randomly explore the solution space, chromosomes are slightly modified with the *mutation* operation. The evolutionary process is iterated until a certain condition is

met. In static optimisation problems for example, the iterations terminate once the observed improvements drop below a certain level.

EAs suffer in the case of MDO because they tend to converge to a single optimum. They progressively lose diversity as the optimum proliferates and spreads over the population. The remedies proposed in the literature attempt to overcome this drawback by artificially maintaining and/or injecting diversity in the population. Four types of remedies have been identified [1]:

1. explicit action is taken to increase diversity whenever changes are detected.
2. convergence is avoided by spreading out the population.
3. the GA is supplied with memory of past chromosomes that are reused whenever the optimum returns to a previous location.
4. multiple subpopulations are used to represent the solution regions and to search for new ones.

The most straightforward way for increasing the diversity of a population in EAs is through mutation, which places new offspring randomly in the solution space. Of course the effect of high mutation rates on adaptation can be unpredictable and should be controlled. One solution is to drastically increase the mutation rate only after a change in the solution space has been detected [2]. Alternatively, the range of mutation can be adjusted according to the detected changes [3].

To avoid convergence and maintain diversity in the population one has to assure that the population remains spread through out the solution space. In [4], the author describes the *random immigrants* method that in every generation replaces part of the population with randomly generated individuals, which are not the product of the genetic operations. Another solution is to take into account the similarity between individuals during selection and replacement. For example in [5], the first parent is selected based on its fitness and the second parent according to its similarity with the first. Furthermore, a method called "worst among most similar" is employed to identify the individual to be replaced by the new offspring. In [6], "direct replacement" is proposed, which avoids convergence by enforcing direct replacement of parents by their offspring after crossover.

Supplying a GA with memory has been suggested as a way of dealing with dynamic environments, especially in those cases where there is a fixed number of optima, or the optima tend to return to the same positions in the solution space. Memory can be either explicit or implicit. In the first case, individuals from past generations are externally stored and reused whenever it is deemed necessary. *Elitist strategies* that periodically store the best individuals in the population for future use belong to this category. For instance, [7] extends the random immigrants approach described above using an elitist strategy. The best individuals from past generations are stored and used to generate the immigrants. A similar approach to the open shop scheduling problem is described in [8]. How to best store and reuse individuals has not been yet clarified. [9] compares various strategies for storing and retrieving individuals from the external memory and his experiments indicate that memory is only advantageous when the optimum repeatedly returns to the exact previous location and not to a slightly different one.

Rather than being external, implicit memory is encoded in the genotype itself. Diploidy is a characteristic example of implicit memory. Each individual has a pair of chromosomes and a separation exists between genotype and phenotype. During evaluation an individual's diploid genotype is first mapped into a haploid phenotype by some dominance mechanism. The dominance mechanism can be modified in response to changes in the environment, e.g. by reversing the dominance relation [10]. Nevertheless, experiments show that a simple haploid GA with an appropriate mutation rate performs comparably to the diploidy approach. More importantly, the diploid mechanism is able to learn a problem with two changing optima, but fails completely in the case of more that two optima.

Instead of memory that becomes obsolete if the environment does not change in such a way that specific solution regions are revisited, another remedy is to maintain subpopulations that cover the solution regions and track their changes. In [11] the "self-organising-scouts" approach is described, which divides the search space into regions and assigns a small scout subpopulation whenever a new promising region is detected. Similarly, the "multinational" GA structures the population into subpopulations ("nations") based on a method for detecting valleys in the solution space [3, 12]. Selection is performed at both national and global level and in the latter case special care is taken so that nations can not easily go extinct. The algorithm also includes processes for migration to new promising regions and for merging nations that converge to the same region. A similar approach, called the "shifting balance GA", which maintains a "core" population and "colonies" exploring different regions in the environment is described in [13].

The above is only a sample of the techniques that appear in the literature for tackling MDO with EAs. For a more comprehensive review see [1] and the proceedings of the workshop on Evolutionary Algorithms for Dynamic Optimization. MDO is clearly a significant problem that has attracted a lot of interest, yet, the proposed techniques are to a great extent ad hoc remedies without clear biological correspondence. To our knowledge there is no biological evidence showing that mutation rate can vary based on changes in the environment[1], or that it can be encoded in the genome itself. It is also unclear how evolution could produce individuals at specific, non random, phylogenetic regions. The lack of biological correspondence is further reflected in the terminology used to describe these techniques, which adopts concepts from sociology and politics, but without being firmly grounded in some specific theory. Of course, from an engineering point of view, moving away from biological metaphors is not necessarily inadequate, but nevertheless it hinders the constructive interplay between computing and biology. Research in evolutionary computation should look more thoroughly into the biological evolutionary processes that produce extremely diverse species.

Moreover, we argue that the problems EAs face in the case of MDO are intrinsic in nature and the suggested remedies are treating the symptoms rather than the source of the problem. In particular, we believe that the diversity problems of EAs derive from the way the principle of the "survival of the fittest" is implemented. According to evolutionary theory the fittest an organism is, the higher

[1] Other than changes in radiation levels.

the probability of reproduction. This is typically translated into an algorithmic process for choosing parents to mate according to their **relative** fitness. For example, in [14] a fixed percentage of the fittest individuals is selected. To more accurately reflect natural evolution, one may use *roulette wheel* selection that assigns to each individual reproduction probability proportional to its fitness [15]. As a consequence of selection based on relative fitness, individuals covering the region of the space that corresponds to the best current solution are more likely to mate and reproduce. Crossover, combines the parent chromosomes to produce offspring with genotypes made out of genes inherited from the parents. The offspring are thus bound to regions in proximity to their parents. Since a developmental process capable of inducing large phenotypic differences out of small genotypic differences is typically excluded, the crossover operation can not generate diversified offspring. It is up to mutation, which randomly introduces diversity in the genotype of offspring, to produce radical new solutions in new previously unexplored space regions. Even so, in multidimensional spaces, only mutation with a high rate affecting multiple loci in the genotype, could generate diversified enough offspring. Last but not least, the offspring replace the less fit individuals in the population. In other words, it is typically assumed that the population has a certain fixed capacity, predefined as a system parameter. Combined with selection based on relative fitness, this leads to the spread of the best individuals in the population, and the progressive loss of diversity. Individuals covering the best current solution region multiply at the cost of individuals covering other, possibly promising or even essential, solution regions. A fixed population capacity, does not comply with the requirements of the MDO problem. The population's cardinality should reflect the current problem needs: in spaces with a few solution regions less individuals are required[2] and more individuals are necessary for spaces with multiple solution regions. There is a lack in EAs of a mechanism that controls the size of the population in response to changes in the environment.

Overall, diversity problems in EAs derive from their basic algorithmic processes and their interaction. Selection based on relative fitness causes the fittest individuals to proliferate, creating similar offspring that can only be diversified with intense mutation, and which replace the least fit, but possibly important individuals in the population. The reviewed remedies are external processes that treat the effects of the intrinsic diversity problems of EAs. They unnecessarily increase the parameters involved. For example in the Multinational GA [12], the parameters involved include in addition to the population size, mutation probability and crossover probabilities, the ratio between global and national selection, and mutation variance for individuals close to and distant from the nation's centroid. In dynamic environments however, the number of system parameters should be minimised because it is difficult to tune them as they most likely change along with the landscape. How to best control the parameters of EAs during adaptation and according to the problem is a research question in its own right [16]. One solution is to encode the additional parameters in the

[2] Or can be sustained.

genome, but experimental results show that this causes a lag in the algorithms ability to keep up with changes in the environment [12].

4 AIS and MDO

AIS are not meant to be accurate models of the biological immune system, but use relevant processes and concepts. Common components of AIS include: a *representation* of the cell (e.g. antibody) structure, a measure of the *affinity* between cells and an *algorithm* that simulates immune processes such as negative selection, clonal selection and idiotypic effects. Currently, various AIS exist with many and diverse applications[3].

The biological immune system serves well as a computational metaphor for tackling MDO, due to its ability to maintain and boost diversity. This is achieved in two ways: with *heterostasis*, the preservation of diversity and *heterogenesis*, the introduction of diversity. On one hand, the diversity of the immune repertoire is preserved due to the way immune cells (lymphocytes in particular) are triggered to clone. According to *clonal selection*, a lymphocyte is triggered to clone when its antibodies recognise an antigen. The cloning rate is analogous to the affinity between antibody and antigen and is usually high. This is a local selection scheme that chooses cells to proliferate not according to their relative fitness, but rather according to the absolute value of their affinity to an invading antigen. So even lymphocytes that have not been successful so far in recognising antigens can be triggered to clone when the antigenic environment changes and new matching antigens invade the organism. In addition, long-lived memory cells that have been successful in the past and idiotypic effects [19], due to the ability of antibodies to recognise each other and form chains of suppression and reinforcement, contribute further to heterostasis.

Heterogenesis on the other hand is achieved in two ways. When a lymphocyte is triggered to clone the cloning process is not perfect, but is subjected to intense mutation, called *somatic hypermutation*, that results in slightly different lymphocytes and hence antibodies, which can be a better match to the invading antigen. Further diversity is introduced with the recruitment of new lymphocytes manufactured in the bone marrow. Hypermutation and cell recruitment cause new antibody types to be added to the immune repertoire, and play the role of local and global search respectively. Finally, it should be noted that the clones and the recruited cells do not necessarily replace existing immune cells. Individual cells die through natural decay processes (like *apoptosis*), independently of how successful they have been in recognising antigens. Hence, the size of the immune repertoire is not fixed. This implies that some mechanism exists for controlling repertoire size. For example, in *self-assertion* models of the immune antibody network, *endogenous selection*, according to which the network itself selects which recruited cells are going to survive in the repertoire, plays this role. Using a computational self-assertion model, De Boer and Perelson have shown that the immune system can control both its size and connectivity [20].

[3] Textbooks in AIS include [17, 18].

Overall, by combining heterostatis with heterogenesis, and more specifically, through *affinity maturation* (i.e. the combined effect of clonal selection and hypermutation), memory, idiotypic effects, cell death and recruitment, the immune system succeeds in maintaining and boosting its diversity. Compared with EAs, this is a significant property that invites the application of AIS to MDO. AIS have already been applied to optimisation problems (see [21] for a survery). Here we concentrate on immune-inspired approaches to MDO in particular.

The ability of immune processes to maintain and boost diversity has been recognised by researchers in evolutionary computation. Many hybrid algorithms that introduce immune inspired elements in EAs have been proposed. In [22], the authors describe the Immunity based Genetic Algorithm, which incorporates in addition to genetic operations, clonal selection and idiotypic effects. [23] proposed another hybrid that includes clonal selection and somatic hypermutation performed using gene libraries. A secondary memory population stores individuals that have proved successful in the past and redeploys them whenever a degradation in performance is detected. These hybrids are only partial, engineered solutions that do not fully exploit the computational capabilities of the immune system. They typically exclude a local selection schema and use a fixed population size.

The Simple Artificial Immune System (SAIS) [24] was one of the first attempts to fully exploit immunity as a metaphor for tackling dynamic optimisation. SAIS encodes cells as binary strings, and comprises clonal selection, cell decay, recruitment and idiotypic effects. Although K-tournament selection on the best than average cells is adopted rather than a local selection schema, the repertoire size is not fixed, but is controlled through recruitment, idiotypic effects and cell decay. In comparative experiments on changing environments with a single optimum, SAIS demonstrated improved reactiveness and robustness in comparison with EAs. However, SAIS performed worse than a GA with Lamarckian local search and had unstable dynamics. This latter finding is representative of the difficulty involved in devising a mechanism for appropriately controlling the number of immune cells in an adaptive manner. To deal with this issue, in [25] the authors simplify the system's dynamics by dropping idiotypic effects and instead grouping cells into a predefined number of gatherings that play the role of diversity preserving memory. They found however, that the system became sensitive to the number of gatherings.

opt-aiNet is a multimodal function optimisation algorithm that exhibits dynamic allocation of repertoire size [26]. It comprises affinity maturation, recruitment of new random cells and idiotypic effects that cause similar cells to be removed. A modified version, called dopt-aiNet, that deals with dynamic environments is described in [27]. It extends opt-aiNet with a separate memory population, a search procedure for controlling decay, new mutation operators and a different measure of affinity. It also includes a maximum population size for avoiding the unnecessary escalation in the number of cells in opt-aiNet, when multiple optima have to be captured. According to the authors these additions

improve opt-aiNet's ability to quickly find optimal solutions and to maintain diversity when dealing with dynamic environments.

Nootropia is an immune-inspired model applied to adaptive information filtering [28, 29]. It is a self-assertion model that follows Varela's autopoietic view of the immune system [30]. Rather than being antigen driven it uses a self-organising network of antibodies to define and preserve the organism's identity, which in the case of adaptive information filtering corresponds to a user's multiple interests. Antibodies correspond to features describing information items and the affinity between antibodies is statistically measured. It has been argued and supported experimentally that the nonlinearity that results from the interaction of antibodies is beneficiary for capturing multiple regions of interest in the information space [31]. Adaptation is achieved through a process of self-organisation that renders the system open to its environment. New antibody types produced by the bone marrow are recruited and incompetent antibodies are eventually removed from the repertoire. The combination of dynamics that reinforces and suppresses existing antibody types and metadynamics that controls recruitment and removal of cells, allow the system to drift, constantly following changes in user interests. Experiments have demonstrated Nootropia's ability to adapt to a variety of interest changes [29], while yet unpublished results show that, in accordance with [20], the system can control both its size and connectivity.

5 Discussion and Future Directions

MDO is a challenging problem and how to best deal with it remains an open research question. It has already been recognised that EAs face diversity problems when dealing with MDO and various ad hoc remedies for artificially maintaining or injecting diversity have been proposed in the literature. However, we put forward that the diversity problem's of EAs are intrinsic in nature. They are mainly due to the combined effect of selecting parents for reproduction based on their relative fitness and using a fixed population size, which implies that offspring replace existing individuals and typically the less fit. On the contrary, the biological immune system involves natural processes for maintaining and boosting diversity. It exhibits both dynamics at the level of individual cell concentration and metadynamics at the level of antibody types. These control the repertoire's diversity, but also its size, and allow the immune system to adapt both locally and globally to changes in the antigenic space. Immune-inspired algorithmic elements have been used to hybridise EAs for MDO, but there are also fully fledged AIS for tackling the MDO problem.

There is clearly a plenitude of approaches, but no agreement yet on which one is the best and why. There have been experiments showing the benefits of maintaining and boosting diversity for MDO, but they don't compare the different mechanisms for doing so. Furthermore, the terminology used is either just descriptive (e.g. "random immigrants"), or reflects the biological phenomenon being modelled (e.g. "fitness" and "affinity"), rather than the underlying computational elements, thus obscuring essential similarities or differences. As already proposed in [32], a

common computational framework for making correspondences and transferring mathematical results across disciplinary boundaries is required. Before any performance comparisons between different approaches to MDO, common computational elements should be distilled. For example, there appears to be a correspondence between the remedies used to overcome the diversity problems of EAs (section 3) and immune processes for maintaining and boosting diversity (section 4). Introducing diversity by increasing the rate of mutation in EAs, is achieved with hypermutation in AIS. Adding random individuals ("immigrants") is analogous to the generation of new lymphocytes by the bone marrow based on gene libraries. Suppression of similar individuals, which is accomplished in EAs with ad hoc methods like replacing the "worst among most similar", is the effect of idiotypic interactions between antibodies in AIS. Memory in AIS is either achieved explicitly with long-lived cells, or implicitly due to idiotypic effects. Subpopulations ("nations") of cells can also emerge in AIS due to interactions between antibodies. Without doubt there are common computational elements despite differences in describing them, but there are also essential differences in the way these elements are implemented and combined.

A local selection schema, rather than selection based on relative fitness, was deemed essential for maintaining diversity. Interactions between individuals function as another diversity controlling mechanism through suppression and excitation. In self-assertion models they also affect the recruitment and removal of individuals. Furthermore, they give rise to non-linear (developmental) processes that can be crucial for adaptation. A dynamically controlled population/repertoire size that reflects the environment's characteristics is also essential, but has only been adopted by a fraction of the reviewed approaches. Dynamically controlling the size of the population/repertoire is still an open research question. It is also yet unclear how to best track changes in the environment, which requires an appropriate combination of dynamics for local and metadynamics for global adaptation. To tackle these issues, we should pursue an abstraction of the various approaches according to these fundamental computational elements and a mapping from computational elements to the requirements of MDO. We will then be able to draw justifiable conclusions about the behaviour of different systems and how it is affected by their elementary processes. We further expect that such an analysis will raise questions about the underlying biological processes like: What is the role of development in evolution? Is evolution really a competitive process of "survival of the fittest", or the result of the ongoing interaction between adaptive individuals in changing environments?

Finally, we believe that existing experimental settings do not fully reflect the requirements of MDO (section 2). The common practice is to use simulated experiments like pattern tracking [24], dynamic gaussian [4] and dynamic knapsack problems [23]. These experiments have the advantage of being controlled and reproducible, but in most cases they lack in complexity, since they are based on low dimensional spaces. More importantly, changes in the environment are simulated by periodically relocating one or more optima. Changes are thus discrete rather than continuous and the evaluated systems have to be able to re-converge to the

new positions of the optima, instead of being required to constantly track changes in time. MDO is simplified to the task of reinitialising the convergence process every time the environment changes, starting with a population that is hopefully better than random. There is a need for controlled and reproducible experimental settings that simulate continuous changes in multidimensional spaces. These could be based on real world data like the genomics data of the Text Retrieval Conference (TREC)[4] and the data for the International Challenge to create and train computationally intelligent algorithms on clinical free-text[5]. The experimental methodology described in [29] is a first step towards this direction. MDO can form the experimental test bed for the comprehensive analysis of EAs, AIS and possibly other biologically-inspired algorithms and for further constructive interaction between biology and computing.

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