Two Models of Immunization for Time Dependent Optimization

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Abstract— **This paper investigates the relevance of the immune system metaphor to Time Dependent Optimization (TDO). At first, we review previous results underlining the over-average reactiveness and robustness featured by a *Simple Artificial Immnune System* (Sais) in comparison to well known evolutionist approaches ([GC99]). Then, we evaluate its *immunization* capability (i.e. improving robustness to previously encoutered optima) and eventually propose *Yet Another Simple Artificial Immune System* (Yasais).**

Keywords— **Immune System, Time Dependent Optimizer**

I. Introduction

A. The Biological Metaphor

In addition to non-specific defense mechanisms (*Natural Immunity*), the vertebrates also feature an *Adaptive Immunity* based on two responses to the infecting *antigens*.

The *Primary Response* reproduces the B-Cells which are best matching the infectious agents' molecular structure and therefore enables their later destruction. The *Secondary Response* improves the primary one whenever facing an already encoutered antigen. This requires to preserve (previously) useful B-Cells for long periods (*Immunization Process*). Immunologists suggested that the B-Cells can be activated by mutual matching in the absence of external stimili ([Per89]). If Each B-Cell is both activated by and activator of other B-Cells, then their presence is self-reinforced in the population.

B. Immune Systems, Diversity, Tdo and Adaptation

By exploring the space of all possible B-Cells while trying to always feature the one matching the current antigen, immune systems implicitly solve a *Pattern Matching* problem very similar to the ones used to evaluate evolutionist approaches to TDO ([PS83]). In both cases, preserving a diversified population is essential to the adaptiveness of the system which features three distinct adaptive properties:

Reactiveness: ability to recover from a transition.

Robustness: ability to reduce loss of quality of the best solution featured by a population when a transition occurs.

Immunization: ability to keep previously usefull B-Cells to improve further adaptation to similar antigens.

The next section is going to present our first model of Artificial Immune System and discuss how it relates to both biology and evolutionist approaches to TDO.

II. A Simple Artificial Immune System (Sais)

This section defines the Sais Algorithm and evaluates it comparing to well known Evolutionist TDO approaches.

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A. General Sketch

Immune Systems implicitly solve a Pattern Tracking problem for which the structure of the antigen represents the current optimum to be found and the Hamming distance stands for a measure of the matching between the antigen and the binary antibody shape of the evolved B-Cells. Sais relies on this analogy and is expected to feature both primary and secondary immune responses.

The algorithm starts with an initial random population of B-Cells, each able to recognize a given antigen specified by a λ bit long string. Then, the following three operators are repeated at each generation: Evaluation, Clonal Selection and Recruitment (cf next subsections).

A.1 Evaluation Phase

In a Pattern Tracking problem, Evaluating a binary encoded solution boils down to measure its Hamming distance to the current optimum. With Sais, we are going to refer to this fitness value as an *exogenic activation* noted $\alpha_{ex}^i = \lambda - \delta_h(B_i, O^t)$ where B_i refers to the i^{th} B-Cell of the population, O^t to the optimum at time t, and δ_h to the Hamming distance between them. The term exogenic underlines that this fitness measures the way a given B-Cell is efficient with respect to the current environment. Consequently, we are going to identify the most fitted B-Cells.

Then, we compute an *endogenic activation* for the remaining ones as follow[1]: $\alpha_{en}^i = ((1/N_s) - d_i) + 1$ where N_s is the number of different types of B-Cells in the population and d_i the density of the i^{th} B-Cell of the population. The key idea is to reproduce the B-Cells that are not related to the current optimum according to a sharing principle that will tend to keep them all equally represented and therefore mimic immunization *via* an endogenic reinforcement of their activations.

A.2 Clonal Selection Phase

In Natural Immune Systems, the Clonal Selection reproduces activated B-Cells while mutating (Somatic Hypermutation) their clones in order to explore other possible antibodies' shapes. This phase introduces an evolutionary dynamics insofar that activated (useful) elements spread exponentially in the population. Then, the Somatic Hypermutation mechanism exploits this information to search for even better solution by starting from already interesting B-Cells (similar to a local search operator).

Practically, a K-Tournament selection scheme is applied on the B-Cells featuring the best α_{ex} values in order to generate a population P_{ex}. Then, the *Somatic Hypermutation*

[1] In the following, we will differentiate exo/endo activated B-Cells.

is simulated by applying a random number of one-point mutations to each member of P_{ex}. The resulting mutants are only kept if they improve their own α_{ex} value.

The Clonal Selection is also applied to the other B-Cells in order to generate another intermediate population P_{en} but without any mutation. The purpose being this time to conserve useful information rather than exploring the search space. Under such a dynamic, the densities of previously useful B-Cells will decrease while favoring populations in which all individuals are equally represented.

A.3 Recruitment Phase

The recruitment mechanism is an essential component of the immune system's adaptiveness. It has been compared to sharing or crowding methods insofar that it also maintains stable heterogeneous populations.

At this step of the algorithm, P_{ex} and P_{en} respectively contain the offsprings of exo or endo-activated B-Cells. Then, the *recruitment* consists in reintroducing worthy B-Cells in P while discarding old or worthless ones. The mechanism varies depending on the type of B-Cell:

- B-Cells from P_{en} replace directly the endo-activated ones in P. No further selection or alteration is applied as we try to preserve an endogenic equilibrium.
- Then, the initially exo-activated B-Cells of P and their offsprings in P_{ex} undergo a selection process.

For the latter, we used a *K-Tournament* confronting each consecutive B-Cell in P to K challengers from P_{ex}.

A.4 Remarks

Sais is a minimal model designed to capture the essential mechanisms underlying the primary and secondary immune responses. Numerous choices keep Sais far away from the complexity of Natural Immune Systems. Nevertheless, we think that it is a well grounded approach to try to synthetise complex dynamics from canonical algorithms. The following subsections investigate Sais's adaptiveness *via* its ability to handle TDO ([PS83]) and discuss results in comparison with well known evolutionist approaches.

B. First Experimental Results

We are going to use a Pattern Tracking problem ([PS83]) defined on bitstrings of size $\lambda = 40$. Every 50 generations, the optimum is randomly replaced by another string located at an increasing Hamming distance[2] in order to make the *transitions* more and more difficult to adapt to ([GC97]). The figure 1 represents the value of the best fitness per generation averaged over 200 experiments for various evolutionnary approaches such as Goldberg's Simple Genetic Algorithm (Sga) with a mutation rate $\mu = 0.08$, and a Hybrid GA (Hybrid) featuring a Lamarckian Local Search with radius 40 to locally improve fitness. Then, we also evaluated a Random Immigrant GA (Riga, [CG93]) with rate 0.05, Hypermutation (Hyper, [CG93]) with rate 0.2, the μGA (Popsize 5, [Kri89]) and Giga ([Cul92]). Each

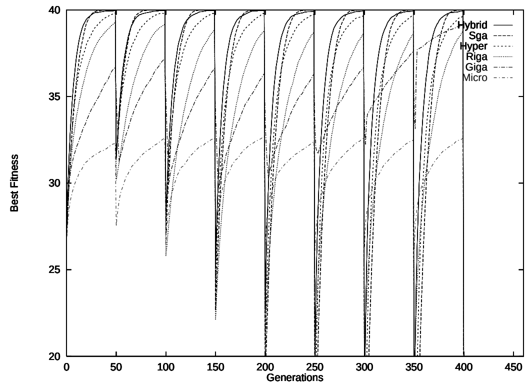


Fig. 1. Classical GAs on Pattern Tracking

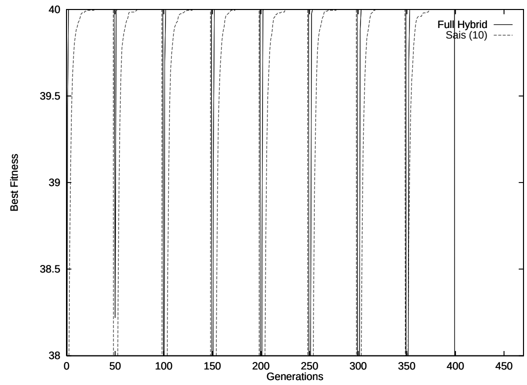


Fig. 2. Sais vs Hybrid: Reactiveness

method's parameters have been settled accordingly to authors' specification or after preliminary experiments. Non specific parameters were set as follows: Crossover rate 0.7, population size 40, Selection by K-Tournament ($K = 4$) and worst-individuals replacement scheme.

Resulting curves are plotted by order of efficiency (cf Fig. 1) which is evaluated both by the level of fitness achieved and inversely to the depth of the drop off at each transition. The Hybrid GA revealed to be the most reactive but only Giga reduced the depth of the fitness drop off.

The following subsections are going to evaluate Sais' reactiveness and robusteness respectively in respect to an improved Hybrid approach and Giga.

C. Reactiveness: Sais vs Local Search

The previous results revealed that the Hybrid approach is the most reactive one. Sais also relies on a Local Search mechanism (Somatic Hypermutation) which applies up to 40 mutations to each of the 10 clones produced from a given B-Cell. To conduct fair comparison with the Hybrid approach we kept the exploration radius identical in both cases and allowed the Hybrid to keep each of the 40 possible mutations only if it improves the overall fitness. From a Computational point of view, both methods are expansive as they require respectively 10 and 40 evaluations for each B-Cell undergoing Local Search. The experimental results (fig. 2) reveal that Sais makes a better use of its computational ressources: it is very close to the Hybrid's results,

[2] This distance is 5 for the first transition, then 10, 15, ... until λ. Consequently, each run lasts 400 generations.

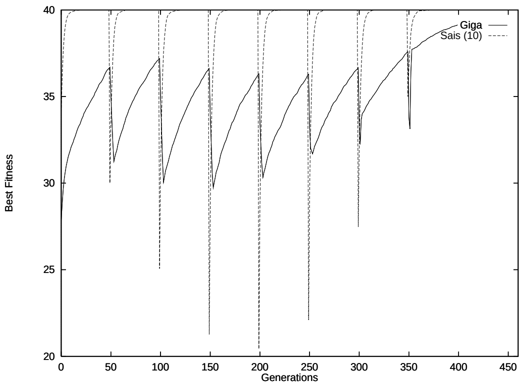


Fig. 3. Sais vs Giga : Memory Effect

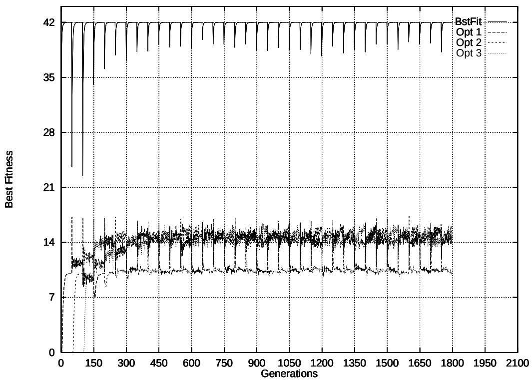


Fig. 4. Sais on a Cyclic Pattern Tracking Problem (CPT)

but uses only a quarter of its evaluations.

D. Robustness: Sais vs. Giga

From the robustness standpoint, Giga revealed in previous experiments that it could maintain a sufficient diversity in the population to improve significantly its robustness to arbitrary transitions. The Figure 3 compares Culberson's Giga to Sais in order to evaluate the latter's robustness. It appears that sais realizes a tradeoff between diversity preservation and convergence (i.e. between robustness and reactiveness) as it simultaneously features both a higher fitness level and a lower diversity than Giga. This can be interpreted as a sign that diversity is due to the past experiences of the system rather than randomness. In fact, as T_r increases we are more about to encounter a new optimum close to a previous one. In such a context, a good robustness can equally indicates an over average ability to preserve a diversified population, or to remember previously encountered optima. In order to clarify whether Sais is able of such an immunization process, we are going to use a Cyclic Pattern Tracking (CPT) environment.

E. Immunization: Experimental Study

E.1 Pointing Out the Immunization Phenomenon

We experiment with a CPT featuring 42 bit long strings and 3 successive optima: 100, 010 and 001 (1 digit = 14 bits) cycling over 150 generations (other parameters being identical). We plotted the best fitness value per generation as well as the densities of each optimum in the lower part of the graph. On single runs (not plotted here), Sais revealed to be able to keep previously encountered optima for long times thus featuring a perfect transition robustness when they were faced again. On the other hand, the Figure 4 (averaged results) underlines that the densities of the memorised optima undergo a rocky dynamics leading to "catastrophic forgetting" phenomena despite of the global robustness improvement.

E.2 Influence of the Number of Optima

To evaluate the magnitude of the catastrophic forgetting phenomenon, we applied Sais to a 40 bits CPT in which we have been varying the number of optima while still keeping the same other parameters. The cycles are also composed of a serie of optima designed by shifting to the right at each transition a block of '1' which length is λ/n (n being the number of optima and $\lambda = 40$).

We experimented with 2, 4, 5, 8, 10 and 20 optima. The results, which have been averaged over 200 runs, are presented in the Figure 5. For each problem, we plotted in the upper part of the graph the best fitness value at each generation and in the lower part, the densities of the optima expected to be tracked. For the problems involving a large number of successive optima, only some were plotted.

As the number of optima n increases, the memorisation capacity deteriorates even if the plotting of the best fitness still displays drop off which magnitude decreases. Basically, consecutive optima only differ on two blocs (i.e. λ/n bits). Increasing n decreases their relative distance and helps in reducing the drop off phenomena but A closer look at the densities of the optima reveals that Sais looses every optimum when they are numerous. This limits seriously its use as a black box optimization tool.

F. Synthesis

We have illustrated Sais' improved reactiveness and robustness in comparison with evolutionist approaches to TDO. Besides that, Sais also succeeded in improving its robustness to previously encountered optima but only on average. The system remembers previously encountered optima but catastrophic forgettings can occur. In such cases, the forgotten structure has to be searched for again. Plotting the densities of the optima over time makes apparent the instability of the immunization dynamics. In the following, we are going to consider alternative approaches to model the immunization process in order to reach a stable memorization of previously encountered optima.

III. Yet Another Sais

This section proposes to reduce the instability of optima's densities by introducing sets of B-Cells (*Gatherings*).

A. Using Gatherings with Sais

This section defines the YaSais algorithm. Our idea is to use explicit sub-populations which are going to group B-Cells into separated set. Like the Idiotypic Cycles these

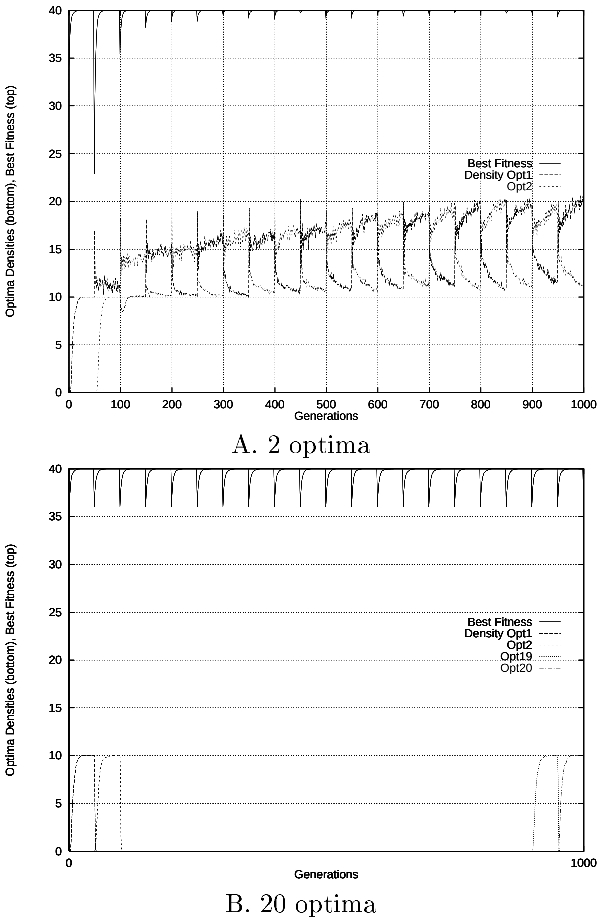


Fig. 5. Sais's immunization ability vs nb of optima

groups of B-Cells are going to be used to preserve previously usefull elements. In the following, we will refer to these as *gatherings* and note their numberd $\mathcal{G}$.

In YaSais, ExoActivation only concerns a certain amount of B-Cells *per gathering*. In our experiments, we started by exoactivating only one B-Cell per Gathering. We expect a population featuring gatherings of size g to be able to ideally memorize in each of them g encountered optima. We are going to see that this vision was somewhat optimistic.

Once ExoActivated B-Cells have been selected, they undergo Clonal Selection and Somatic Hypermutation as previously described for Sais. Unlike Sais, there are no EndoActivated B-Cells. All the remaining B-Cells are just preserved in the population in their respective gatherings. This dynamics is considerably simpler than Sais' endodynamic and should spare us to have to deal with instability.

Indeed, this approach can be compared to the recessiveness approaches which central principle is to preserve from the selective pressure a part of the genetic material in order to preserve the global diversity of the population. In each gathering, a certain number of B-Cells only is going to be exoactivated depending on their fitness value. If we consider gatherings as macro individuals, a strong parallel can be established with methods such as Dasgupta's Structured Genetic Algorithm ([DM92]) and Levenick's Swappers Introns. In these models, different phenotypes can be expressed from a given genotype on the basis of a special encoding. YaSais uses instead a fitness driven decision rule to choose among the components of its macro individuals.

In our implementation, a fixed number of B-Cells can be exoactivated ($\mathcal{G}$ to start off with) in the population. After this selection, permutations in the population ensure that only one B-Cell per gathering will be exo-activated.

The next subsections are going to investigate YaSais' reactiveness and robustness in comparison to Sais. Then, we will focus on the influence of the number of gatherings on the immunization capabilities of the system.

B. First Experimental Results

In this section, we investigate the effect of the number of gatherings on YaSais' efficiency. For that purpose, we used the same 50 bits, 5 optima, Cyclic Pattern Tracking problem than in the previous section.

B.1 The Influence of the $\mathcal{G}$ parameter

The Figure 6 sums up the results of the experiments conducted on YaSais by varying the number $\mathcal{G}$ of gatherings in the population. For each gathering, we still only allowed one B-Cell to be exoactivated per generation. Consequently, $\mathcal{G}$ also represents the search potential in the population. This comes to light in the curves by the fact that the maximal density of any optima is bounded by this value.

As the problem features 5 optima, we expected the best setting to be $\mathcal{G} = 8$. Indeed, this would correspond to gatherings of size 5 perfectly suited to end up containing the whole set of optima of the environment. From this perspective, YaSais also evolves macro individuals getting progressively immunized against all optima. The experimental results revealed that as $\mathcal{G}$ increases, the immunization deteriorates (cf Fig. 6).

B.2 Comparison with Sais

We are going now to compare the best results obtained with YaSais to the ones provided by Sais. The Figure 7 confirms that our new approach has some advantages over Sais. The reactivity is globally equivalent, being slightly inferior when using two gatherings only. On the other hand, the robustness has been clearly improved.

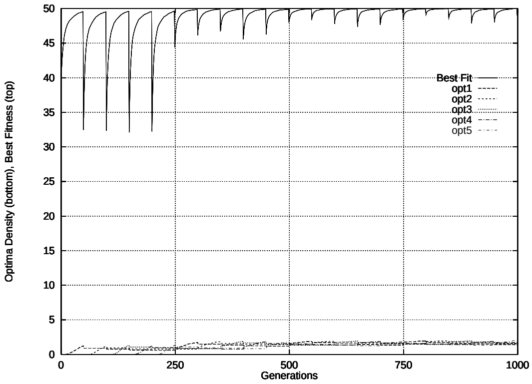
Nevertheless, it is not yet understood why the number of gatherings is such a sensitive parameter in respect with the memorization ability whereas it should be only relevant to reactive aspects. Even if on non epistasic problems the Somatic Hypermutation takes care of most of the exploration effort, this still does not explain the unability to use efficiently numerous gatherings.

C. Taking a closer look to the Immunization Process

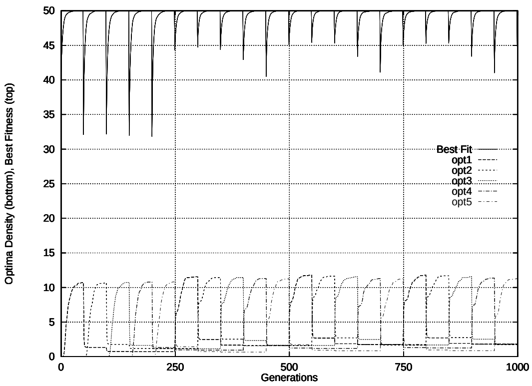
Why is the immunization still suboptimal despite of the improved robustness ? The answer is in the influence of the number of optima on the effect of $\mathcal{G}$ on YaSais's efficiency.

C.1 Where do the previous optima go ?

Previous optima are not kept until the next cycle of the environment despite the fact that YaSais' selective pressure

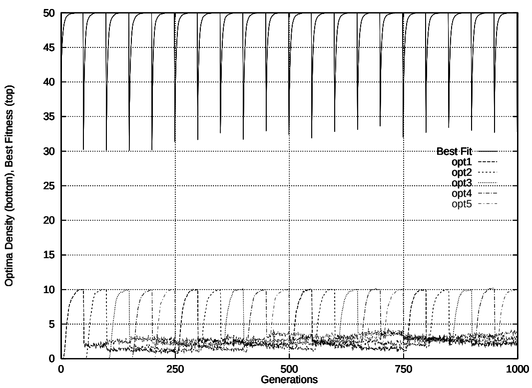


A. $\mathcal{G} = 2$

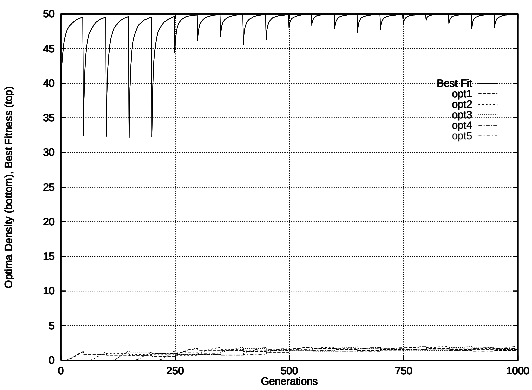


B. $\mathcal{G} = 20$

Fig. 6. Varying $\mathcal{G}$ with YaSais



A. Sais



B. YaSais ($\mathcal{G} = 2$)

Fig. 7. Comparing YaSais to Sais

is particular and tends to preserve most of the population from generation to generation while only exo-activating a small proportion. Consequently, chances are that the problem may come from the exoactivation mechanism which is coherent with the fact that $\mathcal{G}$ is also the number of exoactivated B-Cells. We considered a single run of YaSais with 5 gatherings containing 8 B-Cells each in the same environment than previously. The Figure 8 plots only the density of the second optimum of the cycle. It is conspicuous that, as soon as the optimum 2 is replaced by the third one in the environment, its density in the population decreases abruptly. Moreover, the decrease continues during the following transitions. This can be interpreted as the participation of the B-Cells encoding the 2nd optimum in the exploration when further transitions occur. In other terms, instead of being preserved in the population those B-Cells that revealed to be usefull during the period of the second optimum are discarded or, more probably, re-used via local search to explore the environment toward the new optima. According to the way we apply the local search, this means that these B-Cells are a good starting point for reaching new optima. Their distance to it is small enough to enable the local search to reach it quicker than if it was applied to another individual of the population.

At the generation 1000, the evolution of optima's densities is worth a closer examination (cf Fig. 8): 6 B-Cells that should have been preserved have been lost while the number of B-Cells encoding the new optimum increased from 2 to 8. In other terms, the system used previous optima to reach the new opimum whereas it should have used the rest of the population to respect the immunization.

The previous optima are interesting starting points for finding new ones because of the distance that separates any optimum from the others. The n optima are determined by shifting of λ/n positions from left to right a block of λ/n '1'. Consequently, each optimum is only two blocks away from the others. With $n = 5$ and $\lambda = 50$, this means that they are at a Hamming distance of 20 from each other.

In this context, YaSais systematically exoactivates in priority B-Cells which are located at this distance (or below) from the new optimum. The question that arises now is to know what is the probability for a non previously optimal B-Cell to be located that close to an arbitrary new optimum. At the Transition of the generation 1000, we can count 17 individuals which are or were optimal. How many of the remaining 23 B-Cells are potentially interesting ? Assuming these are random, the probability for one of them to be within a Hamming distance of 20 from the new optimum is: $P = \sum_{d=0}^{20} 0.5^{50}.C_{\lambda}^{d}$ On average, only 3 individuals (P=10% here) on average may be more interesting as a starting point than the B-Cells encoding a previous optimum. As we are going to exoactivate 8 individuals (one per gathering), even if these 3 ones are selected, 5 B-Cells encoding a previous optimum will be used to reconverge toward the new one. This is coherent with the fact that 6 B-Cells were used that way in our experiment.

The flaws of the immunization seem caused by the peculiar nature of our problem. When optima are close enough

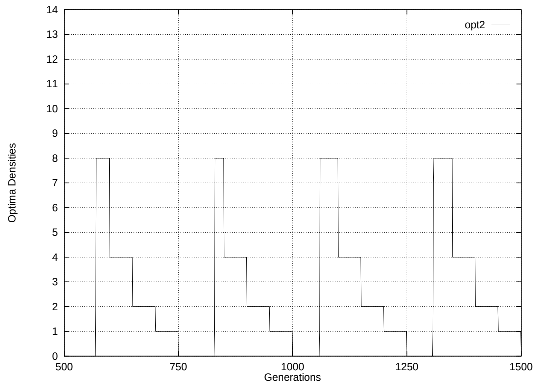


Fig. 8. YaSais ($\mathcal{G} = 8$, 1 run, Density of 2^{nd} optimum)

from each other, they serve as starting points for further explorations. Moreover, their relative distance being small, the fitness drop off is reduced. On the other hand, if distances are big, consequences could be harmfull but then the immunization process works fine.

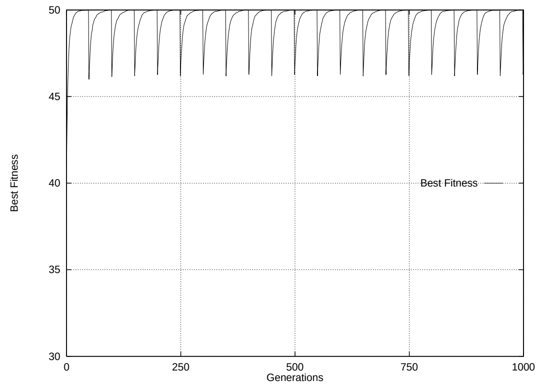
C.2 Influence of the Distance between Optima

In order to check this hypothesis, we used a Cyclic Pattern Tracking problem and varied the distance between its two consecutive optima. This should enable us to conclude that the Hamming distance between optima is responsible for the immunization difficulties we encountered.

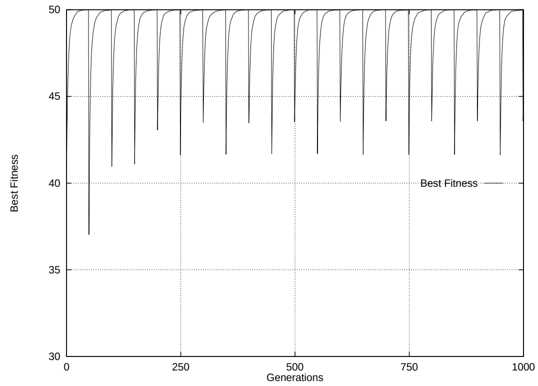
The experimental results (cf Figure 9) confirm this hypothesis: the immunization gets more and more flawless as the distance increases. When observing the best fitness per generation one must be careful to remember that a high fitness level does not always implies an efficient robustness. In fact, the closer are successive optima to each other, the smaller will be the fitness drop off when transition occurs idependently of any robustness property. Our conclusions have been confirmed by taking a closer look to the optima densities. They reveal that for low distances the system systematically looses track of the optima to be tracked. On the other hand, when optima are chosen far enough appart, their densities are maintained over time which is the external sign of an ongoing immunization dynamics. The experiments also revealed that for a distance superior to 16 the immunization was fully effective when dealing with two optima. We think that this limit value characterises the domain of efficiency of the immunization mechanism proposed in this paper.

IV. Conclusion

This paper investigated two simple models of artificial immune systems on TDO. Both revealed to be robust, reactive and efficient optimization tools, the later even featuring a quasi-optimalimmunization capability: For easy transitions, the diversity of the population ensures the robustness while the system exploits presence of previous optima to face difficult transitions. Further work will be concerned with exploring the limits of YaSais.



A. Distance 2



B. Distance 14

Fig. 9. Influence of the Distance btwn Optima on Immunization

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