HINTS FOR ADAPTIVE PROBLEM SOLVING GLEANED FROM IMMUNE NETWORKS

Hugues Bersini
Iridia - Universite Libre de Bruxelles
CP 194/6
50, Av. Franklin Roosevelt
1050 Bruxelles

Francisco J. Varela
CREA - Ecole Polytechnique
1, rue Descartes
75005 Paris

1. Introduction

There is a growing awareness of the cognitive capacities of the vertebrate immune system. These cognitive capacities are evident in its recognition and learning abilities, coupled with an amazing adaptability necessary to interact with an open and changing environment. Such capacities have began to be explained on the basis of a network approach to immune dynamics, stemming from the early proposals by N. Jerne in 1974. Neural and immune networks (IN) share many common features as basic cognitive mechanisms. However the adaptive character of immune nets goes beyond connectionist abilities to filter and to generalize their response for noisy versions of previously instructed patterns. Instead, immune systems are more like Holland's classifier system (CFS), belonging to a class of biological processes whose adaptability relies on a continuous generation of novel operators to handle an unpredictable and varying set of situations. Like CFSs, firstly INs escape the "brittleness" or "semantic closure" of other known cognitive systems including neural nets, and secondly the "problem solving" qualities belong to an evolving, adaptive and auto-organisative population of interactive small operators.

The basis for cognitive and adaptive features in IN have already been the objet of an important biological literature. In particular, an explicit network view based on an autonomous understanding of immune events has been proposed and developed by Varela et al. (1988, 1989, 1990). The learning/adaptive character of the immune system resides essentially in a recruitment mechanism which continuously generates new species. This recruitment process (also called the meta-dynamics), a basic clue to immune performance, selects for the generation of new species on the basis of the current global state of the system i.e according to the sensitivity of the immune network at these

candidate points. In the Varela et al's actual interpretation of the immune phenomenology, it is crucial to note, however, that the instance responsible for the selection of new species is not external to the system, as it is in the neo-Darwinian population genetics or in Burnetian clonal selection as the basis for an immune response to an external antigen. Rather, it is the system which "selects itself". The result is a largely unpredictable pattern of evolution more akin to "natural drift" than to a well-defined optimalisation.

However, this paper does not aim to a further description of the biological reality, but rather to a discussion on the inspiration that can be drawn from the immune dynamics analysis for adaptive problem solving in general. The position adopted here is highly pragmatic and can be compared with what have been lastly done for Genetic Algorithm (GA) and CFS which never pretend to be faithful replica of genetic and selective evolutionary mechanisms. The similarities between immune net and CFS are quite immediate and have already been remarked (Varela et al., 1989; Farmer et al., 1987; Kauffman, 1989). For our purposes here, three essential qualities can be derived from the IN comprehension and will be likened to their specific counterparts for CFS: 1) *an interesting search algorithm* - 2) *a large adaptive capacity* - 3) *an endogenous selective memory*.

The paper begins with a summarized description of the immune dynamics and meta-dynamics. We emphasize the behavioural aspects likely to be exploited in a "adaptive problem solving perspective". In this perspective, we analyse "finalist" (with an external payoff) versions of the recruitment algorithm and of the "endogenous selective memory" and we describe possible algorithmic implementations. In order to illustrate the search process intrinsic to the recruitment mechanism, some simple examples are shown more for didactic reasons than for their real performances. The last part of the paper carries on the immune/GA comparison till to attempt an immune version of the GA. Such a final investigating step will facilitate the comparison of these two systems belonging to a same family of biological adaptive processes.

2. A brief description of one possible immune net modelling

The model of the immune system proposed by Varela et al (1988, 1989, 1990) comprises two major aspects. The first aspect concerns what has been called the dynamics of the system: the differential equations governing the quantitative increase or decrease of a

fixed set of lymphocyte clones and the corresponding immunoglobins (Ig). The second aspect concerns what has been called the meta-dynamics of the system: the algorithm governing the removal of certain clones from the population, and the recruitment of new clones from the pool of lymphocytes freshly produced by the bone-marrow. Regarding the dynamics, very briefly (for a deeper analysis see the references), the immune system is viewed as containing two relevant variables: the concentration of free (f_i) and bound (b_i: the lymphocytes) Ig from a same molecular clone i. Each clone type i is characterized by a specific value for several chemical and physical properties, and consequently represented by a point in a low dimensional real space R^n called the "shape space". Free Ig interact among each other by mutual binding; this binding is defined by an affinity value m_{ij} which, unlike neural nets, does not change (it only depends on the position of the two interacting clones in the shape space). At any time, the total binding to a given species i from all existing Ig indicates the sensitivity σ_i of the entire system for the molecular shape in the vicinity of i: $\sigma_i = \sum_j m_{ij} f_j$ (2.1) where $m_{ij} = m(i,j)$ with i,j being two positions in the shape space.

Today, the m function is still unknown, the only assumptions being : its symmetry ($m(i,j) = m(j,i)$) and its continuity ($m(i + di,j) = m(i,j) + dm(i,j)$). We are currently investigating possible profiles for this affinity function. The concentration of f_i decreases in proportion to the sensitivity at i, and it increases by the production coming from the corresponding bound b_i in maturing lymphocytes:

$$df_i/dt = -A_1 \sigma_i f_i + A_2 mat(\sigma_i) b_i \qquad (2.2)$$

The maturation function (mat(x)) is a smooth double-threshold function of the sensitivity at i. A_1 and A_2 are two constants allowing to vary the importance in time of the two members of the equation. The bi concentration increases through a proliferation function similar to the maturation profile, and decreases by a constant cellular death term:

$$db_i/dt = -A_3 b_i + A_4 prol(\sigma_i) b_i + recruit_i \qquad (2.3)$$

The recruit terms links to the meta-dynamics and will be discussed later.

Now, focusing on the dynamics (for a fixed number of species) and without going in great details, several results can be pointed out. For a certain range of parameter values and of initial conditions, the system becomes dissipative, presenting either a single or an oscillating attractor (Varela and Stewart, 1990; Stewart and Varela, 1990). For instance, the system of equations (2.2) alone (with bi constant) can be analytically proven to have a

single asymptotic attractor. The two systems of equations (2.2 and 2.3) together (but always neglecting the meta-dynamics: recruit = 0, and a fixed number of species) can show a cyclic behaviour (always for a certain range of parameter values and some initial conditions). Then, one can speak of pattern formation arising as a consequence of interactions with any permissible agent external to the system. The interaction can be said to leave a trace in the global state of the system, a very short term memory, until another perturbation resets the network pattern. This enlightens the "cognitive prerogatives" of the immune system.

The above description addresses the immune dynamics. The learning/adaptive character resides essentially in a recruitment mechanism ($recruit_i$), the meta-dynamics, which continuously generates new species of b_i (new points in the shape space). This recruitment process, a basic clue to immune performance, selects for the generation of new points on the basis of the current global state of the system i.e. according to the sensitivity σ_i of the network at these candidate points. This new process is fundamental because it modifies continuously the actors in presence like a neural net whose structure (the number and the nature of neurons) would change in time. Therefore, the dimension of the problem varies in time, introducing a new source of complexity in the comprehension of the system dynamics. A possible candidate point k in the shape space will be recruited if: $F(\sigma_k, p(k)) > T$ (2.4). σ_k is the sensitivity of the point k = $\sum_i m(k,i)f_i$, p(k) is a probability distribution defined on the whole space and allowing randomness (a basic clue to adaptation) to intervene in the generation of new species. F is an arbitrary function of the two variables. In the following simulation (and the one in fig.1), we use the product. T is the minimal threshold for the recruitment.

Borrowing Monod's famous terms, the meta-dynamics is based on an harmonious mixing of chance and necessity. By necessity, we mean that there is some "determinism" in the generation of new actors. Indeed, actors showing a high affinity with existing ones have a greater chance to be recruited. We easily see a first junction with GA. Indeed, the cross-over and mutation mechanisms can be think as the "necessity" component of the adaptive search. Quoting Goldberg (1989): "randomized search does not necessarily imply directionless search". Keeping good schema for successive generations in GA amounts to "remaining in good zones" for new operators in the immune net. This should help to glimpse the "search capability" of immune systems. But, like for GA and CFS whose adaptability relies on the presence of randomness for the mutation of bit, for the selecting of sub-string to cross-over, etc...the immune net presents some randomness in the generation of new species. Facing the uncertainty of an infinite and changing environment, randomness or chance is an essential clue to adaptability.

Fig.1 shows a simulation we performed to observe the immune model response to two different antigenic intrusions. The shape space is a discrete two-dimensional space. The affinity of each species is a gaussian centred in the position of the species. The concentration of fi is displayed. It is possible to see how the system adapts to its triggering environment and how it auto-organises, leading to an evolving emergent pattern such that harmony is always restored. In a previous publication, Varela et al. (1989) discuss the use of Aubin's viability theory as a powerful mathematical alternative for analysing the immune network dynamics and meta-dynamics in an autonomous or "intrinsic" perspective.

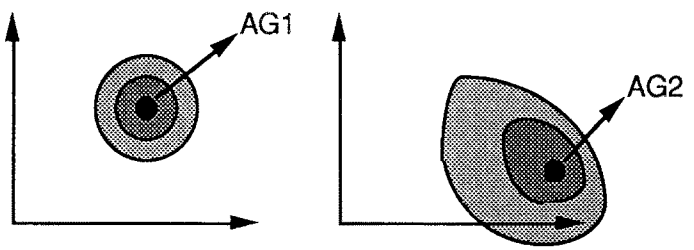

fig.1 the immune adaptability and memory

3. Hints for adaptive problem solving

Our current research follows in two parallel directions: 1) carrying on the empirical and qualitative analysis of the immune dynamics and meta-dynamics 2) investigating the ideas gleaned from this analysis in a more "engineering" perspective. In our current understanding of the immune phenomenology, three aspects may be exploited for problem solving: 1) an interesting search algorithm based on the "necessity" part of the recruitment mechanism 2) a large adaptive capacity based on the "chance" part of this mechanism 3) an endogenous selective memory based on the auto-organisative and dissipative properties of the immune dynamics. In the following, we will mainly deal with the first aspect: the search mechanism. The reasons are twofold: we already have satisfactory results for various trivial problems and an interesting comparison is possible with the GA counterpart. Regarding the last two aspects, we will restrict to speculations still to validate.

3.1 A search technic based on the immune recruitment mechanism (IRM)

Let's assume that you try to find a certain point or vector s in R^n and that you know a way of measuring the payoff of each proposal point $i : fi$. Further, suppose to interpret the IRM in this way: the fitness fi of a certain candidate boils down to be the concentration of a certain species i. Then the generation of next possible points to be tested can be defined the way indicated in (2.4) (for the time being, we neglect the randomness aspect and the adaptive needs, to focus only on the "necessary" search part). A point k will be generated i.e will be selected for being a possible solution if:
$\Sigma_j m_{kj} fj > T$ (3.1), m_{kj} is the affinity of the already tested points j with the candidate k.

For instance, and in order to make a comparison with GA, suppose you try to maximize the function $y = x^2$ for x an integer in the interval [0, 127] (this little problem is extracted from Goldberg's book (1989) where x is coded on 7 bits). We define the affinity function m_{ij} (here m(xi,xj)) in a linear way: $m(xi,xj) = 1 - dist(xi,xj)/scale$ (3.2), dist (xi,xj) is the distance on the R axis, in our case |xi - xj|, scale is the radius of the domain of affinity of each species

Now suppose, you always keep in your populations the N best points you already met. These N best points will constitute the basis for your selection: scale = dist (xw, xb) xw is the position of the worst of the best operators, xb is the position of the best.

$$T = \frac{\sum_{i=1}^{N} fi}{N}$$

A point k will be recruited for testing if: $\sum_{i=1}^{N} (1 - dist\ (xi, xk)/scale)\ fi > T$ (3.3)

You can see the progress of the search algorithm below:

```
97   93   66   36
122  104   97   95   93   88   70   66   63   36
        I TRY   110 With 9.683e+3   FACING THRESHOLD 8.723e+3
122  110  104   97   95   93   88   70   66   63
        I TRY   121 With 1.203e+4   FACING THRESHOLD  1.038e+4
122  121  110   104   97   95   93   88   70   66
        I TRY   114 With 1.209e+4   FACING THRESHOLD1.136e+4
122  121  114   110   104   97   95   93   88   70
        I TRY   115 With 1.265e+4   FACING THRESHOLD 1.198e+4
122  121  115   114   110   104   97   95   93   88
```

```
        I TRY   126 With 1.376e+4  FACING THRESHOLD 1.258e+4
126   122   121   115   114   110   104    97    95    93
        I TRY   120 With 1.416e+4  FACING THRESHOLD 1.395e+4
126   122   121   120   115   114   110   104    97    95
        I TRY   124 With 1.477e+4  FACING THRESHOLD 1.434e+4
126   124   122   121   120   115   114   110   104    97
        I TRY   123 With 1.492e+4  FACING THRESHOLD1.473e+4
126   124   123   122   121   120   115   114   110   104
        I TRY   127 With 1.551e+4  FACING THRESHOLD 1.505e+4
127   126   124   123   122   121   120   115   114   110
        I TRY   125 With 1.553e+4  FACING THRESHOLD 1.548e+4
127   126   125   124   123   122   121   120   115   114

After    20 tests:
The best are:  127 1.613e+4 ; 126 1.588e+4; 125 1.562e+4  ; 124 1.538e+4 ;  123 1.513e+4  ;  122 1.488e+4;
121 1.464e+4  ; 120 1.440e+4  ; 115 1.322e+4  ;  114 1.300e+4
The statistics is :  1.483e+4
```

Initially the recruitments are achieved randomly (T=0). Then progressively the number of best N to consider for the recruitment decreases with time. The search becomes more and more selective (T increases). The test for halting is this one. If following a certain pre-fixed number of random proposals, no more candidates can be recruited for testing, we assume to reach a satisfactory solution. What we can see in the example is the resulting population after 20 real tests. The population is good in average and the optimal solution (127) has been attained. Then for this trivial application, we obtain in general a better result of the Goldberg's treatment with GA (although aware that the optimizing of simple unimodal function is not a GA appealing field of application). A first explanation is immediate. The immune search, in our transposing of the recruitment mechanism, is highly selective and the last points to be tested must be very closed to the existing good points. It boils down to a kind of hill-climbing process. In counterpart, this technic is slower due to the random generation of possible candidates for recruitment. In GA the generation of a next population is immediate because straightforwardly based on a structural manipulation of the existing candidates. In our technique, the appearance of new candidates takes time because depending on a random generator.

Indeed, if this generation of new candidates were only random, resolving complicated problems in a space of large dimension might become absurd. However, this generation is oriented by the population of already present candidates. For instance, in the simple problem, we decided to generate randomly in a sub-space delimited by the N best points: [the smallest,the greatest]. Immunological empirical results tend to indicate that, in the biological reality, this generation is equally influenced by the current population of species (then in (2.4), $p(k) = p(k, \sigma)$). In the other hand, giving a geometric orientation to the domain of affinity leads to a directional search indispensable for high dimensional space.

Initiating a preliminary comparison with GA, we can say that a mutation corresponds in our case to a recruitment in the neighbouring of a good point, and a cross-over corresponds to a recruitment in the intersection of two good zones (with a gaussian affinity, we see that the best place to recruit is really the centre of the zones intersection). Then, roughly, the notion of zone in the shape space seems to replace the GA notion of schema.

3.2 The adaptability and memory

The previous chapter only focused on the search part of the immune meta-dynamics. However, imagine that in our previous example the goal is no more to maximize $y=x^2$ but to minimize it. Restricting the search only in the neighbouring of the best points will prevent the system to adapt to this new situation. On the contrary, allowing continuously some randomness in the recruitment of new points will allow the system to re-localize its good zones of interest. The high affinity zones will smoothly and slowly move making the system reacting to this change. This adaptive process shares some resemblance with the biological reality sketched in the fig.1. It relies on a continuous random production of points in the shape space.

Like CFS the immune system can selectively memorize its good behaviours to the detriment of bad ones. But unlike CFS, this learning does not result from a supervising procedure which separates good from bad operators and which preserves the good ones for successive generations. It results from an endogenous interaction amongst the operators whose global tendency is to sustain and stabilize, without the need for a central control, a limited set of good operators homogeneously distributed in the shape space i.e realizing the memory of the system history. Indeed, we speculate that the immune dynamics, making the points interacting together in the shape space, realize this system memory and is essential for various reasons:

1) It gets rid of wrong points but also of redundant good points that might complicate the search progress. For example, during the function approximation, only a minimal set of good points could be kept for each zone of action. An inhibitory mechanism for neighbouring points could be responsible for that.

2) It tries to keep an ideal balancing between economy and performance in conserving a minimal but sufficient memory of the past. This compromise could be the result of an auto-organisative process which just keeps what's sufficient for reacting adequately and faster to a next encounter of a same situation. If a specific behaviour of the environment has to repeat, the system will be prompter to react. Obviously, like for any implementation of cumulative learning, the strength and the efficiency of the trace must be function of the frequency of the situations and of a forgetting decay.

4. A preliminary comparison between GA and IRM

Previously, we stressed the adaptive/cognitive capacities of immune network. Practically we limited our investigation to IRM, the "search" component of the immune function. A complete comparison between CFS and Immune net should cover the whole cognitive domain: search, adaptability, memory and learning. Nevertheless and considering that the major use of GA is reduced to a search alternative technique, the comparison will only concern the search processes deriving from these two biological systems.

We already initiated a comparison between GA and IRM for searching a point in R^n. This kind of problem is recurrent in AI, from the Samuel's chess player to the today research of synaptic values for connectionist systems. We believe that for this particular class of application, IRM offers precious advantages beyond GA and in spite of its slowness due to the random generator. The convergence is certainly faster i.e requiring a less number of trials, but with the risky side-effects (characterizing any hill-climbing technique) of local minima. We are currently investigating this challenging prolem and we suppose that a parallel search could be implemented by reducing the domains of affinity of the points, creating then a multitude of "niches" for local search.

However, the GA field of application is larger than the quest for numerical values, It includes all kind of combinatorial analysis. This last field of application amounts to the search for good structures, when the user knows an adequate way to represent the possible candidates in strings capable of meaningful structural manipulations. For instance, since Holland's works (1986), binary string has been largely exploited by the GA users even if GA is not limited to this type of coding.

Has IRM anything to tell for this class of problem solving: the quest for a good structure? The answer is yes as far as it is possible to define a metric in the space of candidates. In a numerical space this metric is obvious but for structural representation it is not. However in the case of binary string composing a great part of GA applications, an immediate choice is Hamming's metric: Dh. IRM can be re-exploited leading to define an immune version of GA. A candidate string k will be recruited if: $\sum_j m(j,k)\, fj > T$ (4.1) with $m(j,k) = F(Dh(j,k))$. For example with the linear function: $m(j,k) = 1 - Dh(j,k)/scale$

Initially, we can take for the scale value: L the length of the strings. Then, mutation boils down to a recruitment in the zone of hamming distance 1 and the cross-over to a recruitment in the intersection of two zones.

Now using this mechanism for the generation of new strings, we compare GA performance with IRM again for the Goldberg's example: the maximizing of x^2 by a seven bit string. The result is indicated below. There again IRM seems to converge faster (i.e less trials) but slower in time due to the random generator.

********** GA POPULATION REPORT **********

****GENERATION 9 *********				********* GENERATION 10 ******			
1) 1101111	1.110e+2	12321.0000	I	1) (2, 7) 7	1111011	1.230e+2	15129.0000
2) 1111011	1.230e+2	15129.0000	I	2) (2, 7) 7	1111111	1.270e+2	16129.0000
3) 1101111	1.110e+2	12321.0000	I	3) (5, 2) 5	1111011	1.230e+2	15129.0000
4) 1101111	1.110e+2	12321.0000	I	4) (5, 2) 5	1111011	1.230e+2	15129.0000
5) 1111011	1.230e+2	15129.0000	I	5) (2, 2) 3	1111011	1.230e+2	15129.0000
6) 1101111	1.110e+2	12321.0000	I	6) (2, 2) 3	1111011	1.230e+2	15129.0000
7) 1101111	1.110e+2	12321.0000	I	7) (1, 3) 3	1101111	1.110e+2	12321.0000

Note: generation 10 & Accumulated Statistics: max= 16129.0000, min= 12321.0000,
avg= 14870.7139, sum= 104095.0000, nmutation= 15, ncross= 23

**********IRM POPULATION REPORT **********

**** GENERATION 8 ****				******* GENERATION 9 ******			
1) 1111111	1.270e+2	1.613e+4	I	1) (0, 0) 0	1111111	1.270e+2	1.613e+4
2) 1111111	1.270e+2	1.613e+4	I	2) (0, 0) 0	1111111	1.270e+2	1.613e+4
3) 1111111	1.270e+2	1.613e+4	I	3) (0, 0) 0	1111111	1.270e+2	1.613e+4
4) 1111111	1.270e+2	1.613e+4	I	4) (0, 0) 0	1111111	1.270e+2	1.613e+4
5) 1111111	1.270e+2	1.613e+4	I	5) (0, 0) 0	1111111	1.270e+2	1.613e+4
6) 1111111	1.270e+2	1.613e+4	I	6) (0, 0) 0	1111111	1.270e+2	1.613e+4
7) 1111110	1.260e+2	1.588e+4	I	7) (0, 0) 0	1111111	1.270e+2	1.613e+4

Note: generation 9 & Accumulated Statistics: max= 16129.0000, min= 16129.0000,
avg= 16129.0000, sum= 112903.0000, nmutation= 0, ncross= 0

We know that in GA the more a schema is short and member of good strings, the greater its chance to remain in subsequent generations. Using the mechanism (4.1) and supposing a schema s of length ls, IRM will keep it in successive populations if:

$$\sum_j l_s\, fj > T \text{ for strings j containing s.}$$

Then large schemas already present in good strings have a greater chance to remain in subsequent generations. To illustrate what we said, let's imagine some trivial cases, for instance two strings: s1 = 111000 and s2 = 000111, with fitness f1 and f2. The cross-over can generate a large numbers of new strings mixing homogeneously s1 and s2. Now using the linear affinity function, it is easy to verify that with the threshold :

$T = (f1 + f2)/2$, a string sk will be recruited if: $(f1 - f2)(1/2 - Dh(sk,s1)/L) > 0$

with Dh(sk,s1) being the hamming distance between the string sk and s1.

Then if f1 > f2, the only possible new strings must have more in common with f1 than with f2. In GA terms, in the cross-over, the f1's schema must be larger than the f2's one. sk = 111011 is possible, but not sk = 110111 which are both possible with GA. The immune versions of GA seems to be an interesting alternative to the GA classical mechanisms. Indeed, the search needs less trials due to a most selective cross-over and also because more than two strings can be considered for a next generation. The speed of IRM to find a solution (with the risk of local minima perhaps preferable to a longer search in the immunological context) is due to an implicit hill-climbing. Let's imagine this last trivial case: three strings with equal fitness f1 = f2 = f3 and s1 = 110000, s2 = 001100, s3 = 000011. With GA, obtaining sk = 111111 needs two generations. That's not the case for IRM. Indeed, the immune generation of potential candidates amounts to a multi-crossover (for schema of any strengths) for multi-parents. For biological concerns, this is realistic since the great variety of antibodies result from a similar genetic mixing mechanism. At last, it is easy to understand that IRM does not exhibit the weakness of GA in performing fine-tuned local search.

But the most interesting aspect is certainly the unification of GA and IRM by a same formalism, allowing each technique to benefit knowledge drawn from the other one. Indeed, we are carrying on the analysis of the cognitive/adaptive capabilities of both the immune system and the CFS to extend the comparison on the whole cognitive domain. For instance, the bucket-brigade algorithm could have a immune counterpart easily coded by a mutual influence of points in the shape space. This could be immediately integrated in the immune dynamics.

5. Conclusions

Biology gives us numerous examples of self-assertional systems whose essence does not precede their existence but is rather revealed through it. Immune system is one of them. The fact of behaving in order not only to satisfy external constraints as a pre-fixed set of possible environments and objectives, but also to satisfy internal "viability" constraints justifies a sharper focus. Adaptability, creativity and memory are certainly interesting "side-effects" of such a tendency for self-consistency. However in this paper, we adopted a largely pragmatic attitude attempting to find the best hybridizing between the biological lessons and the engineering needs. The great difficulty, also shared by neural net and GA users, remains the precise localisation of the frontier where the biological reality must give way to a directed design.

ACKNOWLEDGMENT : This work would have not been possible without the financial and intellectual support of Shell Recherche SA France. We acknowledge John Stewart and our colleagues from the Unité d'immubiologie at the Pasteur Institute, Paris, for their essential collaboration.

REFERENCES

Doyne Farmer, J., A. Packard and A. Perelson (1987): The immune system, adaptation and machine learning. *Physica 22D.*

Kauffman, S.A. (1989): Principles of Adaptation in Complex Systems, in D. Stein (Ed), *Lectures in the Sciences of Complexity*, SFI Series on the Science of Complexity, Addisson Wesley.

Goldberg, D.E. (1989): *Genetic Algorithms in search, optimization and machine learning*. Addison-Wesley Publishing Company, Inc.

Holland, J.H., Holyoak, K.J., Nisbett, R.E. & Thagard, P.R. (1986): *Induction: Processes of inference, learning and discovery*. Cambridge: MIT Press.

Stewart, J. and F. Varela (1990): Dynamics of a class of immune networks. II) Oscillatory activity of cellular and humoral component. *J. theoret. Biol.* Vol. 144 pp. 103 - 115

Varela, F., A. Coutinho, B. Dupire and N. Vaz (1988): Cognitive networks: Immune, neural and otherwise, in A. Perelson (Ed.), *Theoretical Immunology, Vol.2* SFI Series on the Science of Complexity, Addisson Wesley, New Jersey.

Varela, F., V. Sanchez and A. Coutinho (1989): Adaptive strategies gleaned from immune networks, in B. Goodwin and P. Saunders (Eds.), *Evolutionary and epigenetic order from complex systems: A Waddington Memorial Volume*. Edinburgh U. Press

Varela, F. and Stewart, J. (1990): Dynamics of a class of immune networks. I) Global behaviour. *J. theoret. Biol.* Vol. 144: pp. 93 - 101