

Reflexive Biodynamics for Immune Inspired Computing

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Extended Abstract

Artificial Immune Systems ^(A.S. Perelson, 1988; D. Dasgupto, 1998) is a rapidly growing field of information processing based upon immune inspired paradigms of nonlinear dynamics. Although it has many features in common with neural networks, there are some differences: the immune system is more complex, more diverse, and it performs many different functions simultaneously. In contradistinction to neural networks, the immune system, from the viewpoint of nonlinear dynamics, can be considered as a multi-body system (with "bodies" represented by cells) which is interconnected via information flows. Since these flows as well as responses to them may be distorted, delayed, or incomplete, the motion of each cell becomes stochastic, and it can be simulated by a controlled random walk.

One of the main challenges in modeling living systems is to distinguish a random walk of physical origin (for instance, Brownian motions) from those of biological origin and that will constitute the starting point of the proposed approach. As conjectured in ^[3], the biological random walk must be nonlinear. Indeed, any stochastic Markov process can be described by linear Fokker-Planck equation (or its discretized version) ^[4], only that types of processes has been observed in the inanimate world. However, all such processes always converge to a stable (ergodic or periodic) state, i.e., to the states of a lower complexity and higher entropy. At the same time, the evolution of living systems is directed toward a higher level of complexity if complexity is associated with a number of structural variations. The simplest way to mimic such a tendency is to incorporate a nonlinearity into the random walk; then the probability evolution will attain the features of the Burgers equation ^[5]: the formation and dissipation of shock waves initiated by small shallow wave disturbances. As a result, the evolution never "dies": it produces new different configurations which are accompanied by increase or decrease of entropy (the decrease takes place during formation of shock waves, the increase-during their equation

such dissipation). In other words, the evolution can be directed “against the second law of thermodynamics”^[6] by forming patterns outside of equilibrium.

In order to elucidate both the physical and the biological aspects of the proposed model, let us start with a one-dimensional random walk:

$$x_{t+\tau} = x_t + h R(\mu), \quad h = \text{Const}, \tau = \text{Const}, \quad (1)$$

where h and τ are the space (along x) and time steps respectively; $R(\mu)$ is a random function taking values -1 or 1 with the probability $\frac{1}{2} \pm \mu$; μ is a control parameter while $|\mu| \leq 1/2$. (Physical implementations of this model were discussed in^[3]).

Eq. (1) describes motion in actual physical space. But since this motion is irregular, it is more convenient to turn to the probability space:

$$f_{t+\tau} = p f_{x-h} + (1-p) f_{x+h} \quad (2)$$

where $f(x, t)$ is the probability that the moving particle occupies the point x at the instant t , and the transition probability

$$p = \frac{1}{2} + \mu, \quad 0 \leq p \leq 1 \quad (3)$$

It is well known^[4,7] that if the system interacts with the external world, i.e.,

$$\mu = \mu(x), \quad \text{and therefore, } p = p(x) \quad (4)$$

then the solution to Eq. (2) subject to the reflecting boundary conditions converges to a stable stochastic attractor. However, if

$$\mu = \mu(f), \quad \text{and therefore, } p = p(f), \quad (5)$$

Eq. (2) becomes nonlinear, and Eq. (1) is coupled with Eq. (3) via the feedback (3).

From the physical viewpoint, the system (1), (2) can be compared with the Langevin equation which is coupled with the corresponding Fokker-Planck that the stochastic force is fully defined by the current probability distributions, while the diffusion

coefficient is fully defined by the stochastic force. The process described by this system is Markovian since future still depends only upon present, but not past. However, now present includes not only values of the state variable, but also its probability distribution, and that leads to nonlinear evolution of random walk.

From the mathematical viewpoint, Eq. (1) simulates probabilities while Eq. (2) manipulates by their values. The connection between these equations is the following: if Eq. (1) is run independently many times and a statistical analysis of these solutions is performed, then the calculated probability will evolve according to Eq. (2).

From the biological viewpoint, Eqs. (1) and (2) represent the same subject: a living specie. Eq. (1) simulates its motor dynamics, i.e., actual motion in physical space, while Eq. (2) can be associated with mental dynamics describing information flows in the probability space. Such an interpretation ^[3] was evoked by the concept of reflection in psychology. Reflection is traditionally understood as the human ability to take the position of an observer in relation to one's own thoughts. In other words, the reflection is a self-awareness via the interaction with the "image of the self." In terms of the phenomenological formalism proposed above, Eq. (3) represents the probabilistic "image" of the dynamical system (1). If this system "possesses" its own image, then it can predict, for instance, future expected values of its parameters, and, by interacting with the image, change the expectations if they are not consistent with the objective. In this context, Eq (1) simulates acting, and Eq (2) simulates "thinking." Their interaction can be implemented by incorporating probabilities, its functions and functionals into the control parameter μ (see Eq. (5)).

The objective of this paper is to exploit the coupled motor-mental dynamics approach to simulate the phenomenology of basic tasks performed by immune systems such as: self-nonsel self discrimination, self repair, predator-prey pursuit, multiplication, collective strategies, etc.

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