



ELSEVIER

Information Sciences 129 (2000) 61–79

INFORMATION
SCIENCES

AN INTERNATIONAL JOURNAL

www.elsevier.com/locate/ins

Physical model of immune inspired computing

Michail Zak *

*Jet Propulsion Laboratory, California institute of Technology, Ultracomputing Group,
4800 Oak Grove Drive, MIS 126-347, Pasadena, CA 91109-8099, USA*

Received 3 January 1999; received in revised form 10 March 2000; accepted 3 June 2000

Abstract

Artificial immune system is a rapidly growing field of information processing and computing based upon immune inspired paradigms of nonlinear dynamics. This paper introduces stochastic models which mimic the phenomenology of basic functions of immune systems such as self–nonself discrimination, self-repair, predator–prey pursuit, and reproduction. These models represent a unified formalism for building an artificial immune system for effective information processing and computing. © 2000 Elsevier Science Inc. All rights reserved.

1. Introduction

Artificial immune systems [2,6] 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.

* Tel.: +1-818-393-5351; fax: +1-818-393-5471.

E-mail address: michail.zak@jpl.nasa.gov (M. Zak).

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. That will constitute the starting point of the proposed approach. As conjectured in [9], the biological random walk must be nonlinear. Indeed, any stochastic Markov process can be described by a linear Fokker–Planck equation (or its discretized version) [5]; and only that types of processes have 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 an higher entropy. At the same time, the evolution of living systems is directed towards 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 [8] which describes 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 an increase or decrease of entropy (the decrease takes place during formation of shock waves and the increase during their dissipation). In other words, the evolution can be directed “against the second law of thermodynamics” [7] by forming patterns outside 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

$$x_{t+\tau} = x_t + h \operatorname{Sgn}[R(\pm 1) + \mu], \quad h = \text{const}, \quad \tau = \text{const}, \quad (1)$$

where h and τ are the space (along x) and time-steps, respectively, $R(\pm 1)$ a random function taking values from -1 to 1 with equal probability and μ is a control parameter with $|\mu| \leq 1/2$. (Physical implementations of this model were discussed in [9,12].)

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

$$f_{t+\tau} = pf_{x-h} + (1-p)f_{x+h}, \quad f_{t+\tau} = f(x, t + \tau), \text{ etc.}, \quad (2)$$

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 [3,5] that if the system interacts with the external world, i.e.,

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

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

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

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

From the physical viewpoint, the system (1) and (2) can be compared with the Langevin equation which is coupled with the corresponding Fokker–Planck equation such 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) calculates 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 species. 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 [9] 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–nonself discrimination, self–repair, predator–prey pursuit, multiplication, collective strategies, etc.

2. Life without intelligence: emerging self-organization

We will start the analysis of the coupled motor–mental dynamics with Eqs. (1) and (2) where

$$p = \sin^2(\alpha f + \beta), \quad \mu = \sin^2(\alpha f + \beta) - \frac{1}{2}, \quad \alpha, \beta = \text{const}, \quad (6)$$

i.e.,

$$x_{t+\tau} = x_t + h \operatorname{Sgn} \left[R(\pm 1) + \sin^2(\alpha f + \beta) - \frac{1}{2} \right], \quad (7)$$

$$f_{t+\tau} = f_{x-h} \sin^2(\alpha f + \beta) + f_{x+h} \cos^2(\alpha f + \beta). \quad (8)$$

Here, α and β are constant weights.

In order to illustrate the fundamental nonlinear effects, we will analyze the behavior of special critical points by assuming that

$$\alpha = \frac{5\pi}{12}, \quad \beta = -\frac{\pi}{6}$$

and

$$f_0 = f(t=0) = \begin{cases} f_0^{(1)} = \frac{1}{5} & \text{at } x = -\ell, \\ f_0^{(2)} = \frac{4}{5} & \text{at } x = \ell, \\ f_0^{(3)} = 0 & \text{otherwise.} \end{cases} \quad (9)$$

Then the solution to Eq. (8) will consist of two waves starting from the points $x = -\ell$ and $x = \ell$, traveling towards each other with the constant speed $v = h/\tau$, and transporting the values $f_0^{(1)}$ and $f_0^{(2)}$, respectively, i.e.,

$$f = f_0^{(1)} \left(-\ell + \frac{h}{\tau} n \right) + f_0^{(2)} \left(\ell - \frac{h}{\tau} n \right), \quad n = 0, 1, \dots, \frac{\ell}{h}, \quad (10)$$

where n is the number of time-steps.

At $n = \ell/h$, the waves confluence into one solitary wave at $x = 0$

$$f = \begin{cases} 1 & \text{at } x = 0 \\ 0 & \text{otherwise} \end{cases} \quad \text{at } t = n\tau = \frac{\ell}{h}\tau. \quad (11)$$

This process represents a discrete version of formation and confluence of shock waves, and it is characterized by a decrease of the Shannon entropy from

$$H(0) = -\frac{1}{5} \log_2 \frac{1}{5} - \frac{4}{5} \log_2 \frac{4}{5} > 0 \text{ to } H(n\tau) = 0. \quad (12)$$

However, the solitary wave (11) is not stationary. Indeed, as follows from Eq. (8), the solution at $t = (n+1)\tau$ splits into two equal values

$$f_{(n+1)\tau} = \begin{cases} 1/2 & \text{at } x = \ell \pm h, \\ 0 & \text{otherwise.} \end{cases} \quad (13)$$

The process (13) can be identified as a discrete version of diffusion during which the entropy increases again from

$$H(n\tau) = 0 \text{ to } H[(n + 1)\tau] = -\log_2 \frac{1}{2} = 1. \tag{14}$$

The further evolutionary steps $t \geq (n + 2)\tau$ will include both diffusion and wave effects, and therefore, the solution will endlessly display more and more sophisticated patterns of behavior in the probability space. The corresponding solutions to Eq. (7) represent samples of the stochastic process (8) in the form of nonlinear random walks in actual physical space.

Thus, the solutions to coupled motor–mental dynamics simulate emerging self-organization which can start spontaneously. At this level of description, such an effect is triggered by instability rather than by a specific objective. In other words, the model represents a “brainless” life. However, it serves well to the global objective of each living system: the survival. Indeed, it is a well established fact in biology [1] that marginal instability makes behaviors of living system more flexible and therefore, more adaptable to changing environment.

The model (1) and (2) is easily generalizable to three-dimensional motions

$$x_{t+\tau}^{(i)} = x_t^{(i)} + h_i \text{Sgn}[R(\pm 1 + \mu_i)], \quad i = 1, 2, 3, \tag{15}$$

$$f_{t+\tau} = \sum_{i=1}^3 [p_i f_{x^{(i)}-h_i} + (1 - p_i) f_{x^{(i)}+h_i}]. \tag{16}$$

Here $x^{(1)}, x^{(2)}, x^{(3)}$ are the space coordinates, and $f = f(x^{(1)}, x^{(2)}, x^{(3)}, t)$ is the joint probability that the species occupies the point $x^{(1)}, x^{(2)}, x^{(3)}$ at the instant t .

As in the one-dimensional case, here

$$p_i = \frac{1}{2} + \mu_i, \quad i = 1, 2, 3. \tag{17}$$

In particular, one can assume that

$$p_i = \sin^2(\alpha_i f + \beta), \quad i = 1, 2, 3. \tag{18}$$

It should be noticed that the nonlinear random walks (15) in all three directions are coupled by means of the joint probability f via the control parameters μ_i .

From the mathematical viewpoint, the model of mental dynamics (8) links to the Burger’s equation in a sense that its pattern formation outside equilibrium is based upon the balance between dissipation and shock waves.

In general, this model can be enriched with the Belousov–Zhabotinskii effects by slight modification of random walk (7)

$$x_{t+\tau} = x_t + \frac{1}{2} h \{1 - \text{Sgn}[R(\pm 1) + \mu']\} \text{Sgn}[R(\pm 1) + \mu], \tag{7a}$$

which now includes the third choice for the species: to remain at rest with the probability

$$q = \frac{1}{2} + \mu', \quad (6a)$$

The corresponding version of Eq. (8) reads

$$f_{t+\tau} = qf + pf_{x-h} + (1 - q - p)f_{x+h}, \quad 0 \leq p, \quad q \leq 1. \quad (8a)$$

If $q = q(f)$ and $p = p(f)$, one arrives at the discretized version of the combined Burger–Belousov–Zhabotinskii equation which possesses a variety of new complex patterns outside equilibrium, and that increases the adaptability of species to environmental changes. One should recall that Belousov–Zhabotinskii equation was already exploited for studying pattern formation in biology [4]. However, these patterns dwell in physical space; in contradistinction to that, Eqs. (8) and (8a) simulate patterns in the probability space, i.e., in the space of the mental dynamics so that the corresponding actual motions in physical space are described by nonlinear random walks (7) and (7a), respectively. Due to that, a species is not locked up in a certain pattern of behavior: it still can perform a variety of motions, and only the statistics of these motions is constrained by this pattern. It should be emphasized that such a “twist” is based upon the concept of reflection, i.e., the existence of the self-image.

In Section 3, we will discuss motions driven by the objectives; for that purpose, we will stay with the simpler models (7) and (8), since the formation of patterns outside of equilibrium will be less important.

3. Self-identification and self-repair

One of the most remarkable properties of living systems is the ability to detect and to repair a damage to their structure, and this ability is observed at such low level as DNA. Without going into details of the biological machinery of the process, we will try to exploit the phenomenology of our artificial model of the motor–mental dynamics to simulate self-identification and self-repair. The key to that is provided by the fact of possession of the self-image. We will assume that the identity of a species is represented by the weights α_i and β_i (see Eqs. (7), (8), or (18)). Indeed, by changing these weights, one can switch from one evolutionary scenario to another.

Let us turn to the one-dimensional model (7) and (8) of an artificial species and assume that the nominal values of the weights α and β are

$$\alpha_0 = \frac{\pi}{2}, \quad \beta_0 = 0. \quad (19)$$

Then the artificial species can perform a calibration test starting with any initial position $x = x_0$, i.e.,

$$f = \begin{cases} 1 & \text{at } x = x_0, \\ 0 & \text{otherwise.} \end{cases} \tag{20}$$

it must move deterministically, as it follows from Eq. (7).

$$x_{t+nh} = x_0 + nh, \quad n = 1, 2, \dots, \text{etc.} \tag{21}$$

Suppose that as a result of some structural damage, the weights (19) have been changed

$$\alpha_1 = \frac{\pi}{2} + \varepsilon_1, \quad \beta_1 = \varepsilon_2, \quad |\varepsilon_1|, |\varepsilon_2| \ll 1. \tag{22}$$

Then, according to Eq. (8), the motion with the same initial conditions (20) will be represented by a random walk

$$x_0, x_1, \dots, x_n. \tag{23}$$

Now the degree of the damage can be measured by the difference between the trajectories (21) and (23) in the form of the function

$$E = \frac{1}{2} \sum_{k=0}^n (x_0 + kh - x_k)^2. \tag{24}$$

To find the correct weights (19), the species has to minimize the function (24). In order to do that, it can perform the following simple algorithm: start with the pair of arbitrary values $\alpha_1^{(1)}, \beta_1^{(1)}$ and $\alpha_1^{(2)}, \beta_1^{(2)}$, and run the system (7) and (8) subject to the initial conditions (20) twice; as a result, find the corresponding values $E^{(1)}$ and $E^{(2)}$; then use the following recurrent relationships:

$$\alpha_1^{(j+1)} = \alpha_1^{(j)} - \lambda_1^{(2)} \frac{E^{(j)} - E^{(j-1)}}{\alpha_1^{(j)} - \alpha_1^{(j-1)}}, \quad \lambda_1^2 = \text{const}, \tag{25}$$

$$\beta_1^{(j+1)} = \beta_1^{(j)} - \lambda_2^2 \frac{E^{(j)} - E^{(j-1)}}{\beta_1^{(j)} - \beta_1^{(j-1)}}, \quad \lambda_2^2 = \text{const}, \tag{26}$$

which actually implement the gradient decent of E , and therefore, the sequences $\alpha_1^{(j)}$ and $\beta_1^{(j)}$ converge

$$\lim_{j \rightarrow \infty} \alpha_1^{(j)} = \alpha'_0, \quad \lim_{j \rightarrow \infty} \beta_1^{(j)} = \beta'_0. \tag{27}$$

Strictly speaking, the limit values α'_0, β'_0 may be different from the corresponding nominal values in (19), if the functional (24) has local minima. Therefore, the species has to repeat the whole procedure several times starting from different values of $\alpha_1^{(1)}, \beta_1^{(1)}, \alpha_1^{(2)},$ and $\beta_1^{(2)}$ and then to choose those limit values in (27) which correspond to the lowest minima. It should be noticed that prior to each iteration in Eqs. (25) and (26), the system (7) and (8) have to be run in order to find the corresponding value of $E^{(j)}$

4. Self–nonself discrimination

Immunology deals with understanding how the body distinguishes between what is “self” and “nonself”. The biological machinery of this process is not well understood, but it involves cell surface molecules that are able to specifically bind and adhere to other molecules on opposing cell surfaces. However, within the formalism of the motor–mental dynamics, the only way to make the self–nonself discrimination is by observing the behavior of the potential invader, extraction of its phenomenological invariants (for instance, the weights α and β in Eqs. (7) and (8)) and by comparison with those of the self. In this section, we will propose a simple procedure for the implementation of this strategy.

Let us assume that a body cell motion is simulated by the simplest model, i.e., by the system (1) and (2), and its identity is represented by the weights α, β in Eq. (6). Suppose that the unknown agent has the same model, but different weights α', β' . What information can the body cell infer by observing the motion of the invader?

If the agent starts with a deterministic position and makes n steps, he may go via 2^n different trajectories. All these trajectories can be placed between the two extreme trajectories which are the solutions to the following versions of Eq. (2), respectively

$$f_{t+\tau} = p_1 f_{x-h} + (1 - p_1) f_{x+h}, \quad (28)$$

$$f_{t+\tau} = p_2 f_{x-h} + (1 - p_2) f_{x+h}, \quad (29)$$

where

$$p_1 = \begin{cases} p & \text{if } p \geq 1/2, \\ 1 - p & \text{if } p < 1/2, \end{cases} \quad p_2 = \begin{cases} 1 - p & \text{if } p \geq 1/2, \\ p & \text{if } p < 1/2, \end{cases} \quad (30)$$

and $p = p(f, \alpha, \beta)$ represents the identity of the body cell. The solutions to Eqs. (28) and (29) describe the most and the least probable trajectories, respectively, if the agent belongs to the same class as the self. Hence, the simplest strategy for the body cell is the following: compare the observed trajectory

$$x_0, x_1, \dots, x_n \quad (31)$$

of the agent with the extreme trajectories

$$x_0^{(1)}, x_1^{(1)}, \dots, x_n^{(1)}; \quad x_0^{(2)}, x_1^{(2)}, \dots, x_n^{(2)} \quad (32)$$

by computing the sums

$$E_1 = \frac{1}{2} \sum_{k=0}^n (x_k - x_k^{(1)})^2, \quad E_2 = \frac{1}{2} \sum_{k=0}^n (x_k - x_k^{(2)})^2. \quad (33)$$

If

$$E_1 > E_2, \tag{34}$$

then the agent is nonself, and if

$$E_1 < E_2, \tag{35}$$

then the agent is self.

Obviously the confidence of these conclusions is not high: based upon recent advances in statistical analysis of time series, discrimination can be performed much more accurately. However, time is precious for immune response: any extra-second can lead to multiplication of the invader. Therefore, the self–nonself discrimination based upon the criteria (34) and (35) can be adapted as a reasonable starting point.

5. Predator–prey pursuit

The final act of the immune response is to kill the invaders. Within the phenomenological formalism of the motor–mental dynamic, this can be translated into a predator–prey pursuit. We will assume that both the predator and prey possess not only the image of the self, but the image of the adversary as well. In terms of the three-dimensional model (15) and (16), the pursuit can be formulated as follows:

$$x_{t+\tau}^{(i)} = x_t^{(i)} + h_i \text{Sgn}\left(R + \mu_i^{(1)}\right), \quad i = 1, 2, 3, \tag{36}$$

$$f_{t+\tau, x^i}^{(i)} = p_i f_{t, x^{(i)}-h_i}^{(i)} + (1 - p_i) f_{t, x^{(i)}-h_i}^{(i)}, \quad i = 1, 2, 3, \tag{37}$$

$$\tilde{f}_{t+\tau}^{(i)} = \tilde{q}_i \tilde{f}_{y^{(i)}-h_i}^{(i)} + (1 - \tilde{q}_i) \tilde{f}_{y^{(i)}+h_i}^{(i)}, \quad i = 1, 2, 3, \tag{38}$$

$$y_{t+\tau}^{(i)} = y_t^{(i)} + h_i \text{Sgn}\left(R + \mu_i^{(2)}\right), \quad i = 1, 2, 3, \tag{39}$$

$$\varphi_{t+\tau}^{(i)} = q_i \varphi_{y^{(i)}-h_i}^{(i)} + (1 - q_i) \varphi_{y^{(i)}+h_i}^{(i)}, \quad i = 1, 2, 3, \tag{40}$$

$$\tilde{\varphi}_{t+\tau}^{(i)} = \tilde{p}_i \tilde{\varphi}_{x^{(i)}-h_i}^{(i)} + (1 - \tilde{p}_i) \tilde{\varphi}_{x^{(i)}+h_i}^{(i)}. \tag{41}$$

Here, Eq. (36) simulates the motor dynamics of the predator, i.e., a random walk in three-dimensional space. Eq. (37) describes the predator’s mental dynamics, i.e., evolution of the probability $f(x^{(1)}, x^{(2)}, x^{(3)}, t) = f^{(1)} f^{(2)} f^{(3)}$, where $x^{(i)}$ denote the predator’s position, p_1, p_2 and p_3 are the transition probabilities

$$p_i = \frac{1}{2} + \mu_i^{(1)} = \sin^2 \left(\alpha_{i(1)} f^{(1)} + \beta_{i(1)} \right). \quad (42)$$

Eqs. (39) and (40) simulate the motor–mental dynamics of the prey, where $y^{(i)}$ denote the prey’s positions in space, and $\varphi(y^{(1)}, y^{(2)}, y^{(3)}, t) = \varphi^{(1)} \varphi^{(2)} \varphi^{(3)}$ is the corresponding probability; q_1, q_2 and q_3 are the transition probabilities

$$q_i = \frac{1}{2} + \mu_i^{(2)} = \sin^2 \left(\alpha_{i(2)} \varphi^{(i)} + \beta_{i(2)} \right). \quad (43)$$

Finally, Eqs. (38) and (41) simulate mental images of the adversaries: $\tilde{f}(\tilde{y}^{(1)}, \tilde{y}^{(2)}, \tilde{y}^{(3)}, t) = \tilde{f}^{(1)} \tilde{f}^{(2)} \tilde{f}^{(3)}$, and \tilde{q}_i represent the prey’s images in the “mind” of the predator, and $\tilde{\varphi}(\tilde{x}^{(1)}, \tilde{x}^{(2)}, \tilde{x}^{(3)}, t) = \tilde{\varphi}^{(1)} \tilde{\varphi}^{(2)} \tilde{\varphi}^{(3)}$ and \tilde{p}_i represent the predator’s images in the mind of the prey.

If the predator and the prey never met before, the best strategy for them is to assume that

$$\tilde{q}_i = (1 - p_i), \quad \tilde{p}_i = (1 - q_i), \quad (44)$$

i.e., to consider the adversary as an extreme opposite to the self.

At this point, Eqs. (36), (37), (39), (40) are coupled only in pairs, while Eqs. (38) and (41) are decoupled.

Now we will introduce the objectives of the pursuit: the predator objective is to minimize the distance between the prey and himself during the next n steps, and the prey’s objective is to maximize the same distance.

The distance after k steps is expressed as:

$$E = \sum_{i=1}^3 \left(x_k^{(i)} - y_k^{(i)} \right)^2. \quad (45)$$

The only way to optimize it is to manipulate by the weights $\alpha_{i(1)}, \beta_{i(1)}, \alpha_{i(2)}$ and $\beta_{i(2)}$ in Eqs. (42) and (43) using the strategy of the gradient descent approach (see Eqs. (25) and (26)). However, here this strategy cannot be applied in a direct way since neither the predator, nor the prey know their actual future positions $x^{(i)}$ and $y^{(i)}$. Therefore, these positions have to be predicted based upon their images. The images can be represented by expectations, modes or medians of the corresponding probability distributions. For instance, in case of expectations, the distance (45) is replaced by:

$$\tilde{E} = \sum_{i=1}^3 \left(\hat{x}_k^{(i)} - \hat{y}_k^{(i)} \right)^2, \quad (46)$$

where

$$\hat{x}_k^{(i)} = \sum x^{(i)} f_k^{(i)}, \quad \hat{y}_k^{(i)} = \sum y^{(i)} \varphi_k^{(i)}. \quad (47)$$

Then the predator’s and the prey’s images of the same objective are, respectively,

$$\tilde{E}_1 = \sum_{i=1}^3 \left(\sum x^{(i)} f_k^{(i)} - \sum \tilde{y}^{(i)} \tilde{\varphi}_k^{(i)} \right)^2, \tag{48}$$

$$\tilde{E}_2 = \sum_{i=1}^3 \left(\sum \tilde{x}^{(i)} \tilde{f}_k^{(i)} - \sum y^{(i)} \varphi_k^{(i)} \right)^2. \tag{49}$$

These images are different since neither the predator, nor the prey knows the actual probabilities $f_k^{(i)}$ and $\varphi_k^{(i)}$ of their adversaries, and they replace them by the images $\tilde{f}_k^{(i)}$ and $\tilde{\varphi}_k^{(i)}$, respectively (see Eqs. (42)–(44)). Now the strategy of the predator follows from the gradient descent minimization:

$$\alpha_{i(1)}^{(j+1)} = \alpha_{i(1)}^{(j)} - \lambda_1^2 \frac{\tilde{E}_1^{(j)} - \tilde{E}_1^{(j-1)}}{\alpha_{i(1)}^{(j)} - \alpha_{i(1)}^{(j-1)}}, \quad \lambda_1 = \text{const}, \tag{50}$$

$$\beta_{i(1)}^{(j+1)} = \beta_{i(1)}^{(j)} - \lambda_1^2 \frac{\tilde{E}_1^{(j)} - \tilde{E}_1^{(j-1)}}{\beta_{i(1)}^{(j)} - \beta_{i(1)}^{(j-1)}}, \quad \lambda_1 = \text{const}. \tag{51}$$

Similarly, the strategy of the prey follows from the gradient descent maximization:

$$\alpha_{i(2)}^{(j+1)} = \alpha_{i(2)}^{(j)} + \lambda_2^2 \frac{\tilde{E}_2^{(j)} - \tilde{E}_2^{(j-1)}}{\alpha_{i(2)}^{(j)} - \alpha_{i(2)}^{(j-1)}}, \quad \lambda_2 = \text{const}, \tag{52}$$

$$\beta_{i(2)}^{(j+1)} = \beta_{i(2)}^{(j)} + \lambda_2^2 \frac{\tilde{E}_2^{(j)} - \tilde{E}_2^{(j-1)}}{\beta_{i(2)}^{(j)} - \beta_{i(2)}^{(j-1)}}. \tag{53}$$

Thus, prior to each move, the predator and prey find the optimal weights α_i and β_i from Eqs. (50)–(53), plug them into Eqs. (36)–(41) via Eq. (42), and then make the next (“optimal”) step.

There are four comments to be made concerning the model pursuit. First of all, the system Eqs. (36)–(41) is now fully interconnected via the objectives (48) and (49) by means of Eqs. (50)–(53) and (42) and (43). In particular, that means that the stochastic process (37) and (40) are correlated. But it does not necessarily mean that there exists a joint probability function $\tilde{f}(\{x\}, \{y\})$ for which $f^{(1)}$ and $f^{(2)}$ are the conditional probabilities. Indeed, as shown in [10,11], special compatibility constraints should be imposed upon the transition probabilities p and q in order to guarantee the existence of \tilde{f} . Hence, applying the terminology introduced in [10], the stochastic processes (37) and (38) are entangled in a sense that there is no such transformation of coordinates $\{x\}, \{y\}$ which would decouple them.

Secondly, each species exploits the probabilistic images of the self and its adversary to predict future positions, and therefore, to make the best available move, and this remarkable property is a privilege of the living systems.

Thirdly, success of the pursuit depends upon the degree of superiority of the predator's mental capacity over those of the prey if the mental capacity is measured by the speed of learning, i.e., by finding the correct values, the weights α and β from the gradient descent (50) and (51).

Finally, in the pursuit model, each species demonstrates intelligence since its activity is not spontaneous any more, but it is rather controlled by the objective.

6. Innate and acquired immunity

In this section, we will propose a biological interpretation of the pursuit model introduced above. As follows from that model, the successful defense against an invader can be associated with the catching of a prey by the predator, and that depends upon how well the predator predicts the prey's moves. The power to predict starts with Eq. (44) when the predator selects the transition probabilities for his image of the prey. The ability to make this simple and universal choice mimics the so called innate immunity conferred by all those elements with which the species was born. However, the choice (44), in general, may be not good enough: it does not include the specific characteristic of the prey. That is why the very first "acquaintance" between the adversaries may end in a failure on the part of the predator. But suppose that the predator managed to catch the prey, then he can "record" the values of the actual objective (45) and its image (48). Therefore, the difference

$$|\Delta E_1| = |E - \tilde{E}_1| \quad (54)$$

will serve as a measure of the mismatch between the image and reality. Based upon this difference, the predator can correct his prey's image by appropriate change of \tilde{q}_i in Eq. (44). Actually, he should minimize the difference (54) as a function of $\tilde{\alpha}_{i(2)}$ and $\tilde{\beta}_{i(2)}$, where

$$\tilde{q}_i^1 = \sin^2 \left(\tilde{\alpha}_{i(2)} \tilde{f}^{(2)} + \tilde{\beta}_{i(2)} \right), \quad i = 1, 2, 3, \quad (55)$$

i.e.,

$$\tilde{\alpha}_{i(2)}^{(j+1)} = \tilde{\alpha}_{i(2)}^{(j)} - \lambda_1^2 \frac{|\Delta E_1^{(j)}| - |\Delta E_1^{(j-1)}|}{\tilde{\alpha}_{i(2)}^{(j)} - \tilde{\alpha}_{i(2)}^{(j-1)}}, \quad \lambda = \text{const}, \quad (56)$$

$$\tilde{\beta}_{i(2)}^{(j+1)} = \tilde{\beta}_{i(2)}^{(j)} - \lambda_1^2 \frac{|\Delta E_1^{(j)}| - |\Delta E_1^{(j-1)}|}{\tilde{\beta}_{i(2)}^{(j)} - \tilde{\beta}_{i(2)}^{(j-1)}}. \quad (57)$$

It should be noted that the predator cannot rerun the actual trajectory after the pursuit has been ended: he can change $|\Delta E|$ only by rerunning the image of this trajectory, i.e., by simulating the solutions to Eqs. (36)–(38).

Eventually,

$$\lim_{j \rightarrow \infty} \tilde{\alpha}_{i(2)}^{(j)} = \alpha_{i(2)}, \quad \lim_{j \rightarrow \infty} \tilde{\beta}_{i(2)}^{(j)} = \beta_{i(2)}, \quad (58)$$

i.e., the predator’s image of the prey coincides with the prey’s self-image.

Thus, if Eq. (44) is associated with the innate immunity, Eq. (55) can be associated with an acquired immunity.

Obviously, the invader learns from the same experience, and as a result, he can acquire some resistance by correcting his image of the predator, i.e., by departing from Eq. (44) to the following:

$$\tilde{p}_i^1 = \sin^2 \left(\tilde{\alpha}_{i(1)} \tilde{f}^{(1)} + \tilde{\beta}_{i(1)} \right), \quad i = 1, 2, 3, \quad (59)$$

where the weights $\tilde{\alpha}$ and $\tilde{\beta}$ are adjusted by means of minimizing the difference

$$|\Delta E_2| = |E - \tilde{E}_2|. \quad (60)$$

7. Viral DNA integration

The pursuit is not the only model of the body cell–invader interaction. In this section, we will discuss simulation of the process of destruction of the species’s self-image (cell transformation) by the invader’s intrusion (virus recombination).

Let us assume that the body cell’s behavior is described by Eqs. (7) and (8), and suppose that the invader (virus) wants to copy the cell’s mental image. Then, following the learning paradigm described by Eqs. (46)–(53), the virus can reorganize its own image in such a way that its mental evolution will be described by the same equation, i.e., by Eq. (8). Now, as a result of intrusion into the cell, the virus can change the cell’s transition probability Eq. (6) as follows:

$$p = \sin^2[\alpha(f - f') + \beta], \quad (61)$$

where f' is the acquired virus’ probability distribution.

If $f = f'$, then

$$p = \sin^2 \beta = \text{const.} \quad (62)$$

Thus, the cell has lost its “free will” since it behaves now as an inanimate physical particle performing a Brownian motion.

This effect can be associated with the virus DNA integration.

8. Self-reproduction

Self-reproduction is one of the privileges of living systems. In order to simulate it within the framework of our phenomenological formalism, we have to make the following assumption: all the species of the same genotype have the same probabilistic invariants of their behaviors. In other words, their trajectories are different samples of the same stochastic process, i.e., they are different on the level of deterministic details, but are identical on the level of statistics. Then the self-production process can be simulated by throwing into the “battlefield” new samples of the same stochastic process (for instance, the one described by Eq. (8)). The rate of reproduction has to be governed by the logistic equation

$$N_{j+1} = N_j - \gamma N_j(1 - N_j), \quad (63)$$

where N is the population density and γ is the coefficient describing effects of food availability and death rate.

Thus, again we arrive at two different types of descriptions: the global picture is still expressed by Eq. (8), i.e., by the mental dynamics in the probability space; the local picture, or motor dynamics represented by a set of nonlinear random walks (7) whose density (in physical space) is expressed by Eq. (61).

If several genotypes occupy the same physical space (for instance, the body cells and the invaders), then the global picture (in the mental space) is represented by Eqs. (37), (38), (40), and (41), while the motor dynamics is described by a two set of random walks (36) and (39) whose densities are expressed by the corresponding versions of Eq. (63).

9. Collective performance

In this section, we will briefly describe collective phenomena in the proposed model of artificial immune systems which combine the paradigms discussed above (on the level of individual or pairs of species) with the effects of swarms of species having variable population density.

(a) *Collaboration.* Suppose that there are several different, but “friendly” swarms of species having the probability distributions

$$f_j = f_j(\{x_j^{(1)}\}, \{x_j^{(2)}\}, \{x_j^{(3)}\}, t); \quad j = 1, 2, \dots, s, \quad (64)$$

where $\{x_j^{(1)}\}$, $\{x_j^{(2)}\}$ and $\{x_j^{(3)}\}$ are sets of space coordinates occupied by the species of the j th swarm.

We will postulate that within the framework of our formalism, the “friendliness” is equivalent to the existence of the joint probability

$$f = f\left(\{x_1^{(1)}\}, \dots, \{x_s^{(3)}\}\right), \tag{65}$$

so that f_1 in (64) are interpreted as the conditional probabilities

$$f_j = f_{\{j\}|\Omega}\left(\{x_1^{(1)}\}, \dots, \{x_s^{(3)}\}\right). \tag{66}$$

As shown in [10,11], this imposes upon f_j the following constraints:

$$\frac{\partial^2}{\partial x_j \partial x_k} \ln \frac{f_j}{f_k} = 0; \quad j, k = 1, 2, \dots, s; \quad j \neq k. \tag{67}$$

If these constraints are satisfied, one can describe the joint evolution of all the s swarms by only one equation:

$$f_{t+\tau} = \prod_{j=1}^s \prod_{i=1}^3 \left[p_j^i f_{\{x\}_j^i - \{h\}_j^i} + (1 - p_j^i) f_{\{x\}_j^i + \{h\}_j^i} \right], \tag{68}$$

which represents the evolution of the image of the whole set of species in the probability space. This evolution as a collective brain [10] controls motor dynamics of each species

$$x_{t+\tau}^{(j)} = x_t^{(j)} + h_j \text{Sgn}(R + \mu_j), \quad j = 1, \dots, 3s \tag{69}$$

in a centralized way.

The simplest version of the dependence $p_j(f)$ is

$$p_j = \sin^2(\alpha_j f + \beta_j), \quad \mu_j = p_j - \frac{1}{2}, \tag{70}$$

which is similar to Eq. (6) for a single species. However, here the coefficients α_j and β_j may depend upon the population density N , i.e.,

$$\alpha_j = \alpha_j(N), \quad \beta_j = \beta_j(N). \tag{71}$$

At the same time, the coefficient γ in Eq. (63) is likely to depend upon the probability f , i.e.,

$$\gamma = \gamma(f). \tag{72}$$

As a result, Eqs. (71) and (72) couple the motor–mental dynamics (69) and (70) with the dynamics of the population density (63).

Hence, in addition to multi-dimensional version of the nonlinear effects discussed for a single species, such as the spontaneous self-organization, one can expect phenomena associated with a many-body problem: aggregation, formation of new alliances, explosions of the population densities, etc.

(b) *Competition*. Suppose the swarms described by the probabilities (64) are “hostile”. In terms of our formalism, it means that the constraints (67) are not satisfied, and therefore, a joint probability (65) does not exist. In

other words, the hostile swarms cannot be controlled by a unified “collective brain” as in the previous case. However, they can be entangled in a more sophisticated way. Indeed, here instead of Eq. (65), one arrives at a set of s coupled equations:

$$f_{t+\tau}^{(j)} = \prod_1^3 \left[p_j^i f_{\{x\}_j^i - \{h\}_j^i}^{(j)} + (1 - p_j^i) f_{\{x\}_j^i + \{h\}_j^i}^{(j)} \right], \quad j = 1, 2, \dots, s, \quad (73)$$

where

$$p_i^{(j)} = p_i^{(j)}(f^{(1)}, \dots, f^{(s)}). \quad (74)$$

Each of these equations represent the evolution of the image of the corresponding swarm; however, these evolutions are coupled via Eq. (74).

In order to emphasize the fundamental difference between the unified evolution Eq. (68), i.e., the collective brain, and the coupled evolutions (73), one has to recall that in physics, the violation of compatibility conditions are usually associated with fundamentally new concepts or a new physical phenomenon. For instance, incompatibility of velocities in a fluid, i.e., non-existence of a velocity potential

$$\text{curl } v \neq 0 \quad (75)$$

introduces vorticity and rotational flows. In the same way, the violations of Eq. (67), i.e., nonexistence of a joint probability (68), leads to coupled evolution of the stochastic processes (73), while the degree of the incompatibility

$$\text{ink}(f^{(j)}, f^{(k)}) = \frac{\partial^2}{\partial x_j \partial x_k} \ln \frac{f^{(j)}}{f^{(k)}} \quad (76)$$

can be interpreted as a some sort of “vorticity” in the probability space.

As mentioned earlier, the vorticity makes impossible to find such a transformation of the coordinates x_j which would decouple the stochastic processes (73), i.e., these processes are entangled.

Thus, the vorticity (76) brings a new dimension in the complexity of the motor–mental dynamics (69): it makes the control of the motor dynamics of each species less centralized and more distributed. In addition to that, as shown in [10], the information capacity of a set of entangled stochastic processes (73) is greater than that of the processes having the joint probability (68).

In the same way, as it was described for a simple species, the evolutions (68) and (73) can be driven not only by nonlinear instability, but by the objective as well, and that includes learning, self–nonself discrimination (on the level of swarms), calibration, etc.

10. Minimum-free-will principle

In our previous discussion, for the proof of concept, the nonlinear function $p(f)$ has been chosen in the simplest form (6). However, the only restriction imposed upon this function is the condition

$$0 \leq p \leq 1. \quad (77)$$

Therefore, in general, it can be sought in the form

$$p = \sin^2[\varphi(f)], \quad (78)$$

where $\varphi(f)$ is an arbitrary function.

If this function is parametrized, for instance, as

$$\varphi(f, \alpha) = \sum_{k=0}^q \alpha_k f^k, \quad (79)$$

then the weights α_k can be found from the objective by minimization of the corresponding functional (see Eqs. (46)–(53)).

But suppose that there are several different ways in which the same objective can be achieved, i.e., the function (79) includes a set of weights β

$$\varphi = \varphi(f, \alpha, \beta), \quad (80)$$

which do not affect the objective. How should the species solve such a redundancy problem?

Let us assume that the physical (i.e., the passive) component of the species motion is a symmetric random walk which is a discretized version of the Brownian motion.

Then the transitional probability p in Eq. (78) can be decomposed as

$$p = \sin^2 \left[\hat{\varphi}(f) + \frac{\pi}{4} \right], \text{ i.e., } p = \frac{1}{2} \text{ if } \hat{\varphi}(f) \equiv 0. \quad (81)$$

In this form, the nonlinear component of p , i.e., the function $\hat{\varphi}(f)$ represents the deviation from the passive motion, i.e., the free will.

Now we will make the following statement: if a species can achieve its objective by several different ways, it will choose one which minimizes the deviation from the passive motion, i.e., it will minimize its free-will component. In other words, if a species is offered a “free ride” by physics, it should take it. This minimum-free-will principle can be associated with the Gaussian minimum constraints principle according to which the motion of a constrained system minimizes the deviation from the corresponding free motion. However, in contradistinction to that, the minimum-free-will principle is not required by physics, but it is rather imposed by biology. Indeed, a “crazy” species can move against the minimum-free-will principle, but it will waste its energy and “intellectual” effort, and as a result, its chances for survival will be decreased.

A natural measure of deviation from the passive motion is the difference

$$|\Delta H| = |H_0 - H|, \quad (82)$$

where H_0 and H are the entropies of the passive and the actual motions, respectively.

Now we can give the mathematical formulation of the minimum-free-will principle: if the species objective is defined in the time interval $0 \leq t \leq T$, its motion will minimize the free-will measure

$$F_w = \sum_{t=0}^T |H_0 - H|_t \quad (83)$$

subject to the objective. In other words, if the weights α in Eq. (80) are defined by the objective, then the redundant weights β^* must be found from the condition

$$F_w(\beta^*) = \inf F(\beta). \quad (84)$$

One should recall that

$$H = - \sum_{x=0}^L f_x \log_2 f_x, \quad 0 \leq x \leq L \quad (85)$$

and f is found from Eq. (2) where $p = \sin^2[\varphi(f, \beta)]$.

11. Discussion and conclusion

The natural immune system is a subject of great research interest because it provides an excellent model of adaptive processes operating at the local level and of useful behavior emerging at the global level; therefore, it inspires new powerful paradigms for information processing and computing.

However, since the biological machinery of the immune system is poorly understood, the only alternative is to mimic the phenomenology of its performance using some equivalent physical models. Such a model which simulates the main immune functions based upon dynamics of behavior of “body cells” and “invaders” is developed in this paper.

In contradistinction to existing stochastic models (multi-agent nets, colored petri net) [2], the proposed model is based upon the concept of reflection, i.e., the human ability to take the position of an observer in relation to one’s own thoughts, and that makes it more adaptable to the world of biological and social evolutionary processes.

The model consists of a generator of stochastic processes which represents the motor dynamics in the form of nonlinear random walks, and a simulator of

the nonlinear version of the Fokker–Planck equation which represents the mental dynamics.

It has been demonstrated that coupled motor–mental dynamics can simulate such processes as emerging self-organization, self-identification and repair, self–nonself discrimination, formation of acquired immunity, etc. Therefore, the proposed model can serve as a starting point for a unified approach to immune inspired information processing and computing.

Acknowledgements

The research described in this paper was performed by the Jet Propulsion Laboratory, California Institute of Technology, under contract with the National Aeronautic and Space Administration. The effort was sponsored by the NASA Astrobiology Institute.

References

- [1] E. Bonabeau, Marginally stable swarms, *J. Phys. I* 6 (1996) 309–324.
- [2] D. Dasgupta, *Artificial Immune Systems*, Springer, Berlin, 1998.
- [3] W. Feller, *An Introduction to Probability Theory*, vol. I, Wiley, New York, 1957, pp. 358, 391.
- [4] A.S. Mickhailov, *Foundations of Synergetics*, Springer, Berlin, 1990.
- [5] H. Risken, *The Fokker–Planck Equation*, Springer, Berlin, 1989.
- [6] A.S. Perelson, *Theoretical Immunology*, Addison-Wesley, Reading, MA, 1988.
- [7] E. Schrödinger, *What is Life?* Cambridge University Press, Cambridge, 1944.
- [8] G. Whitham, *Linear and Nonlinear Waves*, Wiley, New York, 1976, p. 96.
- [9] M. Zak, Physical invariants of biosignatures, *Phys. Lett. A* (1999).
- [10] M. Zak, Dynamical simulations of probabilities, *Chaos, Solitons, Fractals* 8 (5) (1997).
- [11] M. Zak, Incompatible stochastic processes, *Phys. Lett. A* 238 (1998) 1–7.
- [12] M. Zak, Creative dynamics approach to neural intelligence, *Biol. Cybernetics* 64 (1990) 15–23.