Numerical Analysis of Results Simulation of Cyber-Physical Biosensor Systems

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Abstract. The article deals with the comparative analysis of the results of numerical modeling of mathematical models of cyber-physical biosensor systems on hexagonal and rectangular lattices using lattice difference equations with delay. The main attention is given to the mathematical description of the discrete population dynamics in combination with the dynamic logic of the studied models. The lattice difference equations with delay are proposed to simulate antigen-antibody interaction within hexagonal and rectangular biopixels. Appropriate spatial operators have been used to model the interaction between biopixels similar to the phenomenon of diffusion. The paper presents the results of numerical simulations in the form of phase plane images and lattice images of the probability of antigen to antibody binding in the biopixels of cyber-physical biosensor systems for antibody populations relative to antigen populations. The obtained experimental results make it possible to carry out a comparative analysis of the stability of mathematical models of cyber-physical biosensor systems on hexagonal and rectangular lattices using lattice difference equations

Keywords: cyber-physical model, biosensor systems, stability of the model, difference equations, hexagonal lattice, rectangular lattice

1 Introduction

Today, the concept of creating cyber-physical systems (CPS) for various fields of human activity is actively developing. CPS is considered as an intelligent system that integrates physical objects, external devices, processors, network equipment. The main purpose of CPS is to monitor the behavior of physical objects as components of such systems in real time. These are systems in which cybernetic tools (measuring,

computing, communication, control, executive) interact with physical processes in arbitrary objects [1].

Cyber-physical systems are identified with the manifestation of the fourth industrial revolution that takes place in the modern world [2]. Thus, there is also a physical opportunity to use technologies of "Internet of Things" [3], where it is necessary to use signals from sensors and measuring devices. Thus, more and more publications [4] appear in the literature that draw attention to the modern concepts and offer the innovative solutions. A. Platzer proposed an approach based on "dynamic logic", which describes and analyzes cyber-physical systems [5-6]. In these works, the hybrid programs (HPs) are used at the simple programming language with the simple semantics. HPs allow the programmer to refer directly to the actual values of variables that represent the real values and determine their dynamics.

With the growth of the pace of life and the need for more accurate methods for monitoring various parameters, interest in cyber-physical systems and biosensors as their components is growing in science and industry. Biosensors are an alternative to well-known measurement methods that are characterized by poor selectivity, high cost, poor stability, slow response, and can often be performed only by the highly trained personnel. This is a new generation of sensors that use biological material in a design that provides very high selectivity and allows you to quickly and simply measure [7-8].

An important stage in the design of cyber-physical biosensory systems is the development and research of their mathematical models that adequately reflect the important aspects of the spatial structure of biopixels important in terms of the research tasks. After all, the quality of the biosensor model determines the effectiveness of its processing methods in measuring systems. The design of cyber-physical biosensory systems involves the selection of parameters that would ensure their operational stability. Such a task, in particular, arises in the development of a biosensor, which includes a two- and three-dimensional array of biopixels, and which consists in finding appropriate parameters describing biological and diffusion processes. This problem can be solved by developing and studying the stability of the corresponding cyber-physical model of the biosensory system on hexagonal and rectangular lattices using difference equations [9, 10].

2 Cyber-physical Biosensory System

2.1 Development of a functional scheme of discrete dynamics CPBSS on hexagonal lattice using lattice difference equations with delay.

Cyber-physical Biosensory System (CPBSS). The definition of the term "Cyber-physical sensory system (CPSS)" is given in [6]. This definition was introduced for the industrial use of sensors. The general definition of the CPSS involves "a higher degree of combination, system sharing, the ability to use embedded systems in the field of automation and compliance with existing standards." The considered approach is used for the characterization of CPBSS, the functional scheme of which is

presented in Fig. 1 and allows to perform numerical simulation of the system under study.

According to [6], the definitions and schemes for CPBS are used to define the CPS. CPBSS converts physically measured immunological parameters into the digital information, which enables them to process signals in time using certain algorithms. There is also an interaction with their own capabilities, requirements, internal data and internal tasks in terms of distribution to the same or higher level of the hierarchy.

The concept of CPS at the basis of the CPBSS (the external rectangle in Figure 1), with the account of the features of intellectual imaging sensors is used. With the additional skills (dotted line in Figure 1), the sensor extends to CPBS, which allows to receive more diagnostic information about the object being studied.

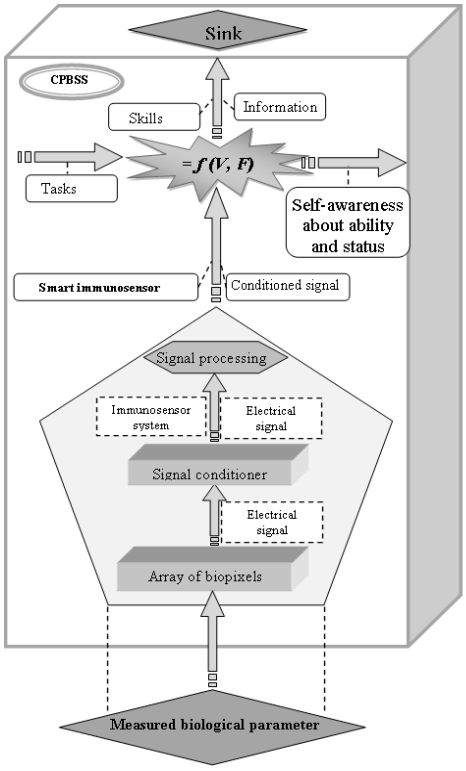


Fig. 1. Functional scheme of CPBSS.

Four main types of detection are used in biosensory devices: electrochemical (potentiometric, amperometric or conductivity (capacitive), optical and thermometric [10]). All types of sensors can be used as direct (not marked) or as indirect (marked) biosensors or immunosensors. Direct sensors are able to detect physical changes during the formation of the immune complex, while indirect use different levels of the generated signal that enable more sensible and universal detection in measuring systems.

CPBSS refers to the high-intelligence information systems. They use an affordable set of interfaces that allow you to receive fast and accurate information of the status and internal system data that should be available to other CPSs. According to [11] CPBSS as the self-organizing system requires comprehensive knowledge of its own dynamic structure and infrastructure of the general system. In order to make this, it is necessary to determine the types of biosensory devices, taking into account their functional application. For example, biosensors can be used to assess critical states in cardiovascular diseases, insulin values when measuring glucose levels in blood and to identify quantitative parameters in some pharmaceutical formulations.

In the article [11] the general structure of CPSS is proposed. While applying this scheme, in the case of biosensors, three directions can be singled out: general information about the biosensor; measurements of biological parameters and skills in relation to unit conversion and calibration; interaction with other biosensors. In this way, the certain methods are described that allow the biosensor to be described. In the study of CPBSS, the programming language R was used. Despite the great variety of programming languages used in the development of CPS (Assembly, C, C++, D, Java, JavaScript, Python, Ada, etc. [12]), the language R is widely used in many industries involved in machine learning and visualization of data.

2.2 Discrete Dynamics CPBSS on hexagonal lattice using lattice difference equations with delay.

For the CPBSS dynamics we use the mathematical description with the help of nonlinear difference equations with delay [10].

The model of the biosensor on the basis of a hexagonal lattice is considered. In this case, for the numbering of immune pixels (i, j, k), $i, j, k = \overline{-N, N}$, $i + j + k = 0$ the cubic coordinate system is used [12].

Let $V_{i,j,k}(t)$ is the concentration of antigens, $F_{i,j,k}(t)$ is the concentration of antibodies in the biopixel (i, j, k); $i, j, k = \overline{-N, N}$, $i + j + k = 0$.

The model is based on such biological assumptions for an arbitrary biopixel (i, j, k)

1. Antigens are detected, bind, and finally neutralized by antibodies with some probability velocity $\gamma > 0$.
2. It is assumed that when colonies of antibodies are absent, colonies of antigens are regulated by a logistic equation with a delay:
$$V_{i,j,k}(n+1) = (1 + \beta - \delta_{\upsilon} V_{i,j,k}(n-r)) V_{i,j,k}(n), \quad (1)$$
where β and δ_{υ} – positive numbers, and $r \geq 0$ mean latency of the negative responce of the antigens' colonies.
3. The fertility rate $\beta > 0$ for the antigen population is introduced.
4. Antigens are neutralized by antibodies at a certain probability rate $\gamma > 0$.

5. The population of antigens tries to reach a certain limit of saturation with a speed $\delta_\upsilon > 0$.
6. The diffusion of antigens from six adjacent pixels is considered $(i+1, j, k-1)$, $(i+1, j-1, k)$, $(i, j-1, k+1)$, $(i-1, j, k+1)$, $(i-1, j+1, k)$ and $(i, j+1, k-1)$ (Fig. 2) with diffusion speed $D\Delta^{-2}$, where $D > 0$ – coefficient of diffusion; $\Delta > 0$ – distance between two adjacent pixels.
7. The constant mortality of antibodies $\mu_f > 0$ is introduced.
8. As a result of the immune response the antibody density increases with a probabilistic velocity $\eta\gamma$.
9. The antibody population is approaching a certain level of saturation with a speed $\delta_f > 0$.
10. The immune response occurs with some constant delay in a time $r > 0$.
11. Surface diffusion (motion of molecules on a solid surface for immobilized molecules) is considered.
12. The definition of a conventional diffusion operator is used in the case of surface diffusion with a diffusion imbalance coefficient $n \in (0,1]$. This means that only n portion of the pixel antigens (i, j) can be included in the diffusion process to any adjacent pixel due to surface diffusion.
13. Antigen binding to antibodies results in fluorescence in the pixel. Fluorescence intensity is assumed to be proportional to the number of contacts between antigens and antibodies, i.e. $k_{fl} V_{i,j}(n) F_{i,j}(n)$. It is also assumed that the pixel (i, j) is in fluorescence state if $k_{fl} V_{i,j}(n) F_{i,j}(n) \geq \Theta_{fl}$, where is some binding threshold at which the fluorescence phenomenon occurs.
14. The output signal $s(n)$ is proportional to the number of pixels in the fluorescence state.
15. Information on the number of biological measurements of values is calculated based on the output signal.

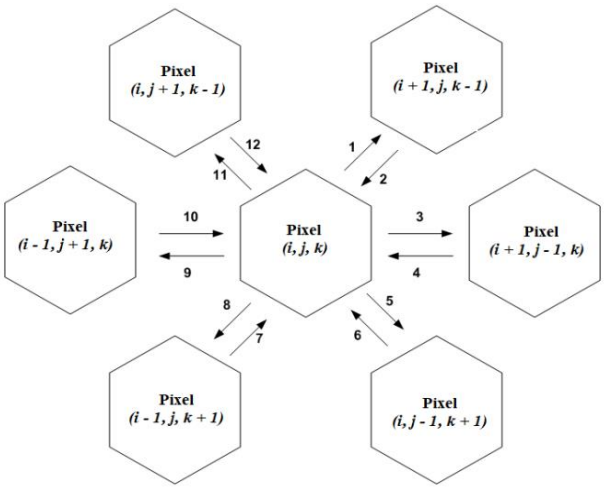


Fig. 2. Hexagonal lattice, which binds six neighboring pixels in the model of the biopixel using the cubic coordinates:

$$1, 3, 5, 8, 9, 11 - \left(\frac{D}{\Delta^2}V_{i,j,k}(t)\right);\ 2 - \left(\frac{D}{\Delta^2}V_{i+1,j,k-1}(t)\right);$$

$$4 - \left(\frac{D}{\Delta^2}V_{i+1,j-1,k}(t)\right);\ 6 - \left(\frac{D}{\Delta^2}V_{i,j-1,k+1}(t)\right);\ 7 - \left(\frac{D}{\Delta^2}V_{i-1,j,k+1}(t)\right);\ 10 - \left(\frac{D}{\Delta^2}V_{i-1,j+1,k}(t)\right);$$

$$12 - \left(\frac{D}{\Delta^2}V_{i,j+1,k-1}(t)\right).$$

On the basis of the above information, we will write the mathematical model of late-antigen-antibody interaction for a hexagonal array of biopixels based on the well-known Marchuk model [13-15] and uses the spatial operator $\hat{S}$ proposed in [16] (additional information is on page 10).

$$\begin{aligned} V_{i,j,k}(n+1) &= V_{i,j,k}(n)\exp\left\{\beta - \gamma F_{i,j,k}(n-r) - \delta_\upsilon V_{i,j,k}(n-r)\right\} + \hat{S}\left\{V_{i,j,k}(n)\right\} \\ F_{i,j,k}(n+1) &= F_{i,j,k}(n)\exp\left\{-\mu_f + \eta\gamma V_{i,j,k}(n-r) - \delta_f F_{i,j,k}(n)\right\} \end{aligned}, \qquad (2)$$

where $\hat{S}\left\{V_{i,j,k}\right\}$ is a discrete diffusion for a spatial operator $\hat{S}$.

$$\hat{S}\left\{V_{i,j,k}\right\} = \begin{cases} D\Delta^{-2}\left[V_{i+1,j,k-1} + V_{i+1,j-1,k} + V_{i,j-1,k+1} + V_{i-1,j,k+1} + V_{i-1,j+1,k} + V_{i,j+1,k-1} - 6nV_{i,j,k}\right] \\ i, j, k \in \overline{-N+1, N-1}, \quad i + j + k = 0. \end{cases} \qquad (3)$$

2.3 Discrete Dynamics CPBSS on rectangular lattice using lattice difference equations.

Consider a simple competing antigen-antibody model for a two-dimensional biopixel array that has been proposed and investigated in [17].

$$\begin{aligned}\frac{dV_{i,j}(t)}{dt} &= (\beta - \gamma F_{i,j}(t-\tau) - \delta_{\upsilon} V_{i,j}(t-\tau))V_{i,j}(t) + \hat{S}\{V_{i,j}\} \\ \frac{dF_{i,j}(t)}{dt} &= (-\mu_f + \eta\gamma V_{i,j}(t-\tau) - \delta_f F_{i,j}(t))F_{i,j}(t)\end{aligned} \tag{4}$$

The mathematical model (4) is given by the initial functions (5):

$$\begin{aligned}&V_{i,j}(t) = V_{i,j}^0(t) \geq 0, \quad F_{i,j}(t) = F_{i,j}^0(t) \geq 0, \quad t \in [-\tau, 0), \\ &V_{i,j}(0), \quad F_{i,j}(0) > 0.\end{aligned} \tag{5}$$

Discrete diffusion is used for the rectangular array $N \times N$ for the spatial operator used in the work [18]:

$$\hat{S}\{V_{i,j}\} = \{D\Delta^{-2}[V_{i-1,j} + V_{i+1,j} + V_{i,j-1} + V_{i,j+1} - 6V_{i,j}], \quad i, j \in \overline{1, N}. \tag{6}$$

Each colony is exposed to antigens produced in four adjacent pixels, which are separated by equal distances Δ.

We use boundary condition $V_{i,j} = 0$ for array nodes $i, j = 0, N+1$.

The methods of sampling, permanence, and stability research used in the work are based on the approach developed in [19] for predator-prey systems, extensible to finite lattice diffusion models.

System (4) without diffusion is approximated by the following differential equation with piecewise constant argentations.

$$\begin{aligned}\frac{dV_{i,j}}{dt} &= (\beta - \gamma F_{i,j}([t/h]h - [t/h]h) - \delta_{\upsilon} V_{i,j}([t/h]h - [t/h]))V_{i,j}(t), \\ \frac{dF_{i,j}(t)}{dt} &= (-\mu_f + \eta\gamma V_{i,j}([t/h]h - [t/h]h) - \delta_f F_{i,j}([t/h]h))F_{i,j}(t)\end{aligned} \tag{7}$$

for $t \in [nh, (n+1)h], n \in \mathrm{N}$.

Let us denote that $[t/h] = n$, $[t/h] = r \in \mathrm{N}$.

Let's integrate the last system (7) by $[nh, t)$, where $t < (n+1)h$, then (6) can be rewritten as:

$$\begin{aligned}\frac{dV_{i,j}}{dt} &= \left(\beta - \gamma F_{i,j}(nh-rh) - \delta_\upsilon V_{i,j}(nh-rh)\right)V_{i,j}(t),\\ \frac{dF_{i,j}(t)}{dt} &= \left(-\mu_f + \eta\gamma V_{i,j}(nh-rh) - \delta_f F_{i,j}(nh)\right)F_{i,j}(t)\end{aligned} \tag{8}$$

The notation is entered $V_{i,j}(n) = V_{i,j}(nh),\ \ F_{i,j}(n) = F_{i,j}(nh),$ which results in:

$$\begin{aligned}V_{i,j}(t) &= V_{i,j}(n)\exp\left\{\beta - \gamma F_{i,j}(n-r) - \delta_\upsilon V_{i,j}(n-r)\right\},\\ F_{i,j}(t) &= F_{i,j}(n)\exp\left\{-\mu_f + \eta\gamma V_{i,j}(n-r) - \delta_f F_{i,j}(n)\right\}\end{aligned} \tag{9}$$

Considering $t \to (n+1)h$ can simplify system (9) by adding diffusion to the first equation. The result is a discrete analog continuous time system (4) in the form:

$$\begin{aligned}V_{i,j}(n+1) &= V_{i,j}(n)\exp\left\{\beta - \gamma F_{i,j,k}(n-r) - \delta_\upsilon V_{i,j}(n-r)\right\} + \hat{S}\left\{V_{i,j}(n)\right\},\\ F_{i,j}(n+1) &= F_{i,j}(n)\exp\left\{-\mu_f + \eta\gamma V_{i,j}(n-r) - \delta_f F_{i,j}(n)\right\}\end{aligned} \tag{10}$$

Addition of diffusion is performed to obtain qualitative results in the study of the persistence and stability of the model. Diffusion in a discrete space can be represented as the product of matrices, according to [7].

It should be noted that the behaviour of system (10) may not coincide with the differential equations (4). The equivalence of differential difference equations obtained by direct Euler transform, Euler inverse transform or central difference schemes can only be used for sufficiently small sampling intervals [20].

2.4 Dynamic logical simulation of CPBSS on hexagonal lattice using lattice difference equations with delay.

In order to simulate the dynamic logic of CPBSS, we use the syntax proposed by A. Platser for the general CPS [5]. The CPS uses the HP, which has more features than difference equations. The first level of HP is a dynamic program that is defined by the following grammar

$$\begin{aligned}a ::= V_{i,j,k}(n+1) &= V_{i,j,k}(n)\exp\left\{\beta - \gamma F_{i,j,k}(n-r) - \delta_\upsilon V_{i,j,k}(n-r)\right\} + \hat{S}\left\{V_{i,j,k}(n)\right\},\\ F_{i,j,k}(n+1) &= F_{i,j,k}(n)\exp\left\{-\mu_f + \eta\gamma V_{i,j,k}(n-r) - \delta_f F_{i,j,k}(n)\right\} \,\&\, \Phi_t\end{aligned} \tag{11}$$

where Φ_t is an evolutionary domain constraint in the form of a formula for the logic of the first order of real arithmetic

$$\begin{aligned}&\Phi_t \overset{def}{\equiv} V^{\min} \le V_{i,j,k}(n) \le V^{\max}\\ &\wedge F^{\min} \le F_{i,j,k}(n) \le F^{\max} \wedge i, j, k = \overline{-N, N} \wedge n > 0, i + j + k = 0\end{aligned} \tag{12}$$

The functioning of the biopixel (i, j, k) is determined by two states, with respect to fluorescence. Namely, s_{fl} is a state of fluorescence and $s_{non\,fl}$ is one of the non-fluorescence states. The use of the first order of semantics of logic and the satisfaction ratio $s \models L$ for the first-order formula L of real arithmetic and state s can be determined for some pixels (i, j, k); $i, j, k = \overline{-N, N}$, $i + j + k = 0$ states s_{fl} and $s_{non\,fl}$ as

$$\begin{aligned} s_{fl} &\models k_{fl} V_{i,j,k}(n) F_{i,j,k}(n) \geq \theta_{fl}, \\ s_{nonfl} &\models k_{fl} V_{i,j,k}(n) F_{i,j,k}(n) < \theta_{fl} \end{aligned} \tag{13}$$

Discrete changes occur in computer programs when they accept new values for variables. This situation occurs when a fluorescence phenomenon occurs in a pixel (i, j, k); $i, j, k = \overline{-N, N}$, $i + j + k = 0$. The state $s_{fl,i,j,k} := 1$ is assigned a value of 1 to the variable $s_{fl,i,j,k}$. This leads to a discrete, jump-like change, as the value $s_{fl,i,j,k}$ does not change smoothly, but rapidly when it suddenly changes from 1 to $s_{fl,i,j,k}$, causing a discrete jump of values $s_{fl,i,j,k}$. In this way, we obtain a discrete model of change $s_{fl,i,j,k} := 1$, except for the model of change (13).

2.5 Investigation of stability model of CPBSS on hexagonal lattice. Constant states.

In general, the state of equilibrium $\varepsilon_{i,j,k} \equiv \left(V_{i,j,k}, F_{i,j,k}\right)$, $i, j, k = \overline{-N, N}$, $i + j + k = 0$ for the system (2) can be found as a solution of an algebraic system:

$$\begin{aligned} V_{i,j,k} &= V_{i,j,k} \exp\left\{\beta - \gamma F_{i,j,k} - \delta_\upsilon V_{i,j,k}\right\} + \hat{S}\left\{V_{i,j,k}\right\} \\ F_{i,j,k} &= F_{i,j,k} \exp\left\{-\mu_f + \eta\gamma V_{i,j,k} - \delta_f F_{i,j,k}\right\}. \end{aligned} \tag{14}$$

Considering $\left(V_{i,j,k}, F_{i,j,k}\right)$, $i, j, k = \overline{-N, N}$, $i + j + k = 0$, we have the following cases.

Stable state without antigens and antibodies $\varepsilon_{i,j,k}^{0,0} \equiv \varepsilon^{0,0} = (0, 0)$, $i, j, k = \overline{-N, N}$, $i + j + k = 0$.

Stable state without antibodies $\varepsilon_{i,j,k}^{*,0} \equiv \varepsilon^{*,0} = \left(\dfrac{\beta}{\delta_\upsilon}, 0\right)$, $i, j, k = \overline{-N, N}$, $i + j + k = 0$

Identical endemic steady state. In the case if $V_{i,j,k} \equiv V^{ident} > 0$, $i, j, k = \overline{-N, N}$, $i + j + k = 0$, $\left(\hat{S}\left\{V_{i,j,k}\right\} \equiv 0\right)$, we receive the stable state $\varepsilon_{i,j,k} \equiv \varepsilon^{ident} = \left(V^{ident}, F^{ident}\right)$, where

$$V^{ident} = \frac{\beta\delta_f + \gamma\mu_f}{\eta\gamma^2 + \delta_\upsilon\delta_f},\ F^{ident} = \frac{-\mu_f\delta_\upsilon + \eta\gamma\beta}{\eta\gamma^2 + \delta_\upsilon\delta_f}.$$

So, if $-\mu_f\delta_\upsilon + \eta\gamma\beta > 0$, then ε^{ident} is an endemic state.

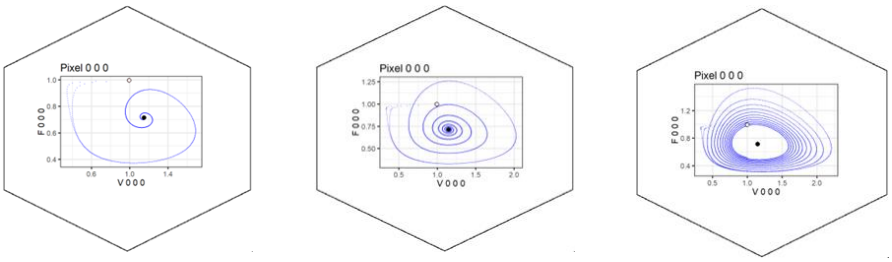
Non-identical endemic steady state. In the general case, we need to solve the algebraic system (14) and find an endemic stable state, which will be called non-identical stationary state $\varepsilon^{non-ident} = (V_{i,j,k}^{non-ident}, F_{i,j,k}^{non-ident})$, $i, j, k = \overline{-N, N}$, $i + j + k = 0$. In case all $(V_{i,j,k}^{non-ident}, F_{i,j,k}^{non-ident}) > 0$, then $\varepsilon^{non-ident}$ is an endemic state. Values V^{ident} and F^{ident} can be used as the initial approximations for numerical methods for solving a nonlinear algebraic system (14).

3 Numerical Simulation Cyber-physical Biosensory System

3.1 Results of numerical simulation of mathematical model of CPBSS on hexagonal lattice using lattice difference equations with delay.

Model (2) is considered at $h = 0.01^2$; $\beta = 2h$; $\gamma = 2h$; $\mu_f = h$; $\eta = 0.01184/\gamma$; $\delta_\upsilon = 0.5h$; $\delta_f = 0.5h$; $D/\Delta^2 = 2.22\sqrt{h}$; $N = 4$.

Similar to the model based on the differential equations [17], in a system with the discrete time when the delay time value is changed r we observe the qualitative changes in the behavior of biopixels and the model under study as a whole. Numerical modeling is performed at the values of the parameters given above. In this case, the long-term behavior of the system (2), which describes a hexagonal array of biopixels at $N = 4$ for $r = 5$; $r = 17$; $r = 22$. Phase diagrams of antibody and antigen populations for pixel and adjacent pixels at different values are shown in fig. 3–5.



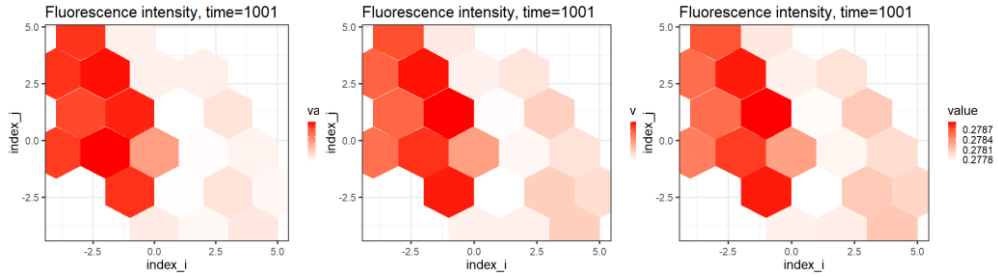
a) b) c)

Fig. 3. Results of numerical modeling of the system (2) at $r = 5$ (a), $r = 17$ (b), $r = 22$ (c). The image of the phase planes in coordinates $(V_{i,j,k}, F_{i,j,k})$ for the pixel $(0,0,0)$. Designation: ○ – identical stable state, ● – non-identical steady state

Thus at $r \le 16$ there are trajectories that correspond to a stable focus for all pixels (Fig. 3(a)). At a value $r = 17$ Hopf bifurcation occurs – the following trajectories

correspond to stable ellipsoidal boundary cycles for all pixels (Fig. 3(b)). The results of numerical modeling are consistent with the theoretical results on the basis of the theorem on the Hopf bifurcation [21], which confirms the appearance of small invariant cycles of the radius $O(\sqrt{h})$. Fig. 3(c) for $r = 22$ shows the phase diagrams, which are the limit cycles with two extremums (one local maximum and one local minimum).

Lattice graphs were used for numerical modeling of the cyber-physical model of the biosensor. Firstly, the corresponding graphs were constructed, where the probability of antigen-antibody contact was given for each pixel, and as $V_{i,j,k} \times F_{i,j,k}$ at $r = 5$, $r = 17$, $r = 22$, are shown at Fig. 4 (a-c).



a) b) c)

Fig. 4. Lattice images of the probability of antibody bonds with antibodies in pixels of the system (2) at $r = 5$ (a), $r = 17$ (b), $r = 22$ (c).

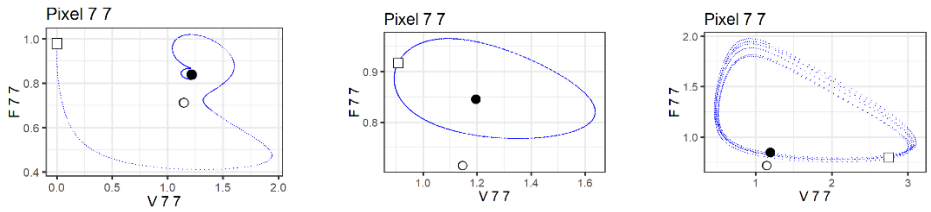
As it was shown by the numerical analysis fluorescing states in biopixels are changed according to the laws of discrete dynamics. Analyzing the obtained results, it was concluded that when changing the values of r, the behavior of pixels and CPBSS changes qualitatively.

3.2 Results of numerical simulation of mathematical model of CFBSS on rectangular lattice using lattice difference equations with delay.

Consider model (10) for: $N = 16$, $\beta = 2\,\text{min}^{-1}$, $\gamma = 2\frac{mL}{\text{min}\cdot\mu g}$, $\mu_f = 1\text{min}^{-1}$,

$\eta = 0.8/\gamma$, $\delta_\upsilon = 0.5\frac{mL}{\text{min}\cdot\mu g}$, $\delta_f = 0.5\frac{mL}{\text{min}\cdot\mu g}$ $D = 0.2\frac{nm^2}{\text{min}}$, $\cdot\Delta = 0.3\,nm$.

The results of numerical simulations were implemented for different values r of time delay (Fig. 5(a-c)).



a) b) c)

Fig. 5. Image of phase planes of system (10) for antibody $F_{i,j}$, populations relative to antigen populations $V_{i,j}$, as a result of numerical simulation at $r=8$ (a), $r=12$ (b), $r=16$ (c). Designation: □ - initial state, ○ - identical steady state, ● - non-identical steady state.

The results of the numerical simulations presented in Figures 7(a-c) were constructed for $n\in[0,5000]$. As Figure 5(a) shows, the solution converges to a non-identical steady state, which is a stable focus.

In Figure 5(b), the solution converges to a stable boundary cycle with two local extrema in the cycle.

Figure 5 (a) for $r\in[0,12)$ shows trajectories corresponding to a steady focus for all pixels. Hopf bifurcation [21] occurs for values $r=12$ and the following trajectories correspond to stable boundary cycles of the ellipsoidal shape for all pixels.

Phase diagrams for $r=12$ show that the solution is a boundary cycle with two local extrema (one local maximum and one local minimum per cycle). Chaotic behaviour is observed for $r=16$ (Figure 5 (c)), i.e. no periodic behaviour over a large time interval. Initial conditions were disturbed to test the sensitivity of the system to verify that the solution is chaotic for $r=16$. Comparisons of solutions for the population of antigens $V_{1,3}$ with the initial conditions $V_{1,3}(t)=1$, $V_{1,3}(t)=1.001, n\in[-r,0]$ and all other identical initial conditions, show chaotic behaviour. Namely, at the initial time, the two solutions appear to be the same, but with the increase of time there is a difference between the solutions, which confirms the conclusion that the behaviour of the system is chaotic at $r=16$.

The model of the biosensor was analyzed using a lattice graph representing the probability of binding of antigens to antibodies in the pixels of system (10) (Figure 6). It was accepted $\Theta_{fl}=1{,}5$.

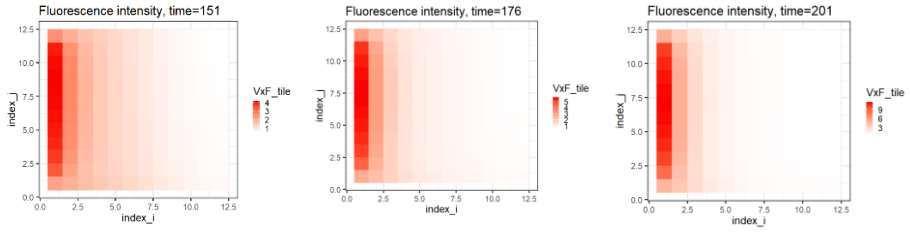


Fig. 6. Lattice images of the probability of binding of antigens to antibodies in pixels of system (10) at $r = 8$.

The study of phase diagrams and lattice images of the binding of antigens to antibodies in the pixels of system (10) is completely consistent with previous studies [9-10] regarding the stability of the array of biopixels in CPBSS.

3.3 Comparative analysis of results of numerical modeling of mathematical models of cyber-physical biosensor systems on hexagonal and rectangular lattices using lattice difference equations

The results of comparative analysis of numerical modeling of the studied mathematical models of CPBSS in the form of phase diagrams of populations of antigens, antibodies (Fig. 3a, 5a) and lattice images of the binding of antigens to antibodies from biopixels of the studied systems (Figs. 4a, 6a) that for $r = 5$ (hexagonal lattice) and $r = 8$ (rectangular lattice) the solutions of the respective systems (2) and (10) tend to non-identical endemic states, which in this case are stable focuses. A similar dependence was observed for all biopixels of the CPBSS model on the hexagonal lattice for $r \in [0, 17)$ (Fig. 3a, 4a), and in the case of using a rectangular lattice a non-identical endemic state was observed for $r \in [0, 12)$ (Figs. 5a, 6).

According to the results of the phase diagrams of antigen populations, antibodies and lattice images, the probability of antigen to antibody binding in CPBSS biopixels, we can conclude that for $r = 17$ (in the case of hexagonal lattice (Figs. 3b, 4b)) and $r = 12$ (in the case of a rectangular lattice (5b)) Hopf bifurcation occurs and all subsequent trajectories correspond to stable boundary cycles for all pixels (Figs. 3c, 4c, 5c).

The results of numerical analysis, the probability of binding of antigens to antibodies in the biopixels of the studied models, change according to the laws of discrete dynamics. Analyzing the results, it is concluded that for r the behavior of the biopixels and CPBSS changes qualitatively.

4 Conclusions

In the work a comparative analysis of CPBSS models was performed on hexagonal and rectangular lattices using difference equations. The general scheme of the cyber-physical sensor system proposed in [11] was used. The basic model has been modified to take into account the features of biosensors. Lattice images in biopixels are modified according to the laws of discrete dynamics. The developed models take into account the interaction of biopixels with each other by antigen diffusion.

The mathematical description of the CPBSS contains discrete population dynamics, which is combined with the dynamic logic used for discrete events. The paper uses a class of time-lattice difference equations that model the interaction of antigens and antibodies in biopixels. Spatial operators model the interaction of diffusion type between biopixels. Dynamic mathematical modeling is insufficient to simulate discrete dynamics in the systems under study. To address this drawback, we used the dynamic logic syntax proposed for Platzer cyber-physical systems to describe the discrete states of a biopixel as a result of fluorescence.

In the paper represents the results of numerical simulations in the form of phase plane images and lattice images of the probability of antigen to antibody binding in the biopixels of cyber-physical biosensor systems for antibody populations relative to antigen populations. The obtained experimental results make it possible to carry out a comparative analysis of the stability of mathematical models of cyber-physical biosensor systems on hexagonal and rectangular lattices. We can conclude that for $r = 17$ (in the case of hexagonal lattice) and $r = 12$ (in the case of a rectangular lattice) Hopf bifurcation occurs and all subsequent trajectories correspond to stable boundary cycles for all pixels.

The numerical simulation results obtained in the paper make it possible to carry out stability analysis and comparisons of the studied models, taking into account the time delay. Future research plans to study cyber-physical biosensor systems using fast dynamic wireless networks [22]. Also, as records are accumulated in the systems under study, it is planned to analyze them in order to optimize the distributed database structure, according to [23].

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