Receptor-Based Cellular Neural Network Models

Angela Slavova
Institute of Mathematics
Bulgarian Academy of Sciences
Sofia 1113, Bulgaria
e-mail: slavova@math. bas.bg

Maya Markova
Department of Informatics
University of Russe
Russe 7000
e-mail:maya.markova@gmail.com

Abstract: In this paper receptor-based Cellular Neural Network model is considered. Dynamics and stability of such model are studied by applying describing function technique. Comparison of the obtained results with the classical ones is made as well.

Keywords:-cellular neural networks, receptor-based model, describing function method

1 Introduction

Spatial and spatio-temporal patterns occur widely in physics, chemistry and biology. In many cases, they seem to be generated spontaneously. These phenomena have motivated a great deal of mathematical modelling and the analysis of the resultant systems has led to a greater understanding of the underlaying mechanisms. Partial differential equations of diffusion type have long served as models for regulatory feedbacks and pattern formation in aggregates in living cells. In this work we proposed receptor-based models for pattern formation and regulation in multicellar biologicalm systems. The systems describing our models are composed of both diffusion-type and ordinary differential equations. Such systems cause some difficulty, since both existence and behavior of the solutions are more difficult to establish. Many aspects of qualitative behavior have to be investigated numericallly. For this purpose we apply the Cellular Neural Networks (CNN) approach for studying such models.

CNN is simply an analogue dynamic processor array, made of cells, which contain linear capacitors, linear resistors, linear and nonlinear controlled sources. Let us consider a two-dimensional grid with 3×3 neighborhood system as it is shown on Fig.1.

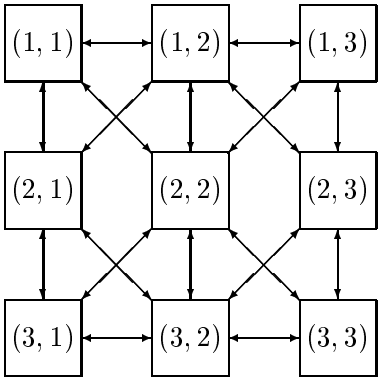

Fig.1. 3×3 neighborhood CNN.

The squares are the circuit units - cells, and the links between the cells indicate that there are interactions between linked cells. One of the key features of a CNN is that the individual cells are nonlinear dynamical systems, but that the coupling between them is linear. Roughly speaking, one could say that these arrays are nonlinear but have a linear spatial structure, which makes the use of techniques for their investigation common in engineering or physics attractive.

We will give the general definition of a CNN which follows the original one:

Definition 1 *The CNN is a*

a). 2-, 3-, or n- dimensional array of

b). mainly identical dynamical systems, called cells, which satisfies two properties:

c). most interactions are local within a finite radius r, and

d). all state variables are continuous valued signals.

Definition 2 *An $M \times M$ cellular neural network is defined mathematically by four specifications:*

1). CNN cell dynamics;

2). CNN synaptic law which represents the interactions (spatial coupling) within the neighbor cells;

3). Boundary conditions;

4). Initial conditions.

Now in terms of definition 2 we can present the dynamical systems describing CNNs. For a general CNN whose cells are made of time-invariant circuit elements, each cell $C(ij)$ is characterized by its CNN cell dynamics :

$$\dot{x}_{ij} = -g(x_{ij}, u_{ij}, I^s_{ij}), \tag{1}$$

where $x_{ij} \in \mathbf{R}^m$, u_{ij} is usually a scalar. In most cases, the interactions (spatial coupling) with the neighbor cell $C(i+k, j+l)$ are specified by a CNN synaptic law:

$$\begin{aligned} I^s_{ij} &= A_{ij,kl} x_{i+k,j+l} + \\ &+ \tilde{A}_{ij,kl} * f_{kl}(x_{ij}, x_{i+k,j+l}) + \\ &+ \tilde{B}_{ij,kl} * u_{i+k,j+l}(t). \end{aligned} \tag{2}$$

The first term $A_{ij,kl} x_{i+k,j+l}$ of (2) is simply a linear feedback of the states of the neighborhood nodes. The second term provides an arbitrary nonlinear coupling, and the third term accounts for the contributions from the external inputs of each neighbor cell that is located in the N_r neighborhood.

It is known [3,6] that some autonomous CNNs represent an excellent approximation to nonlinear partial differential equations (PDEs). In this paper we will present the receptor-based model by a reaction-diffusion CNNs. The intrinsic space distributed topology makes the CNN able to produce real-time solutions of nonlinear PDEs. Consider the following well-known PDE, generally referred to us in the literature as a reaction-diffusion equation [1]:

$$\frac{\partial u}{\partial t} = f(u) + D\nabla^2 u,$$

where $u \in \mathbf{R}^N$, $f \in \mathbf{R}^N$, D is a matrix with the diffusion coefficients, and $\nabla^2 u$ is the Laplacian operator in $\mathbf{R}^2$. There are several ways to approximate the Laplacian operator in discrete space by a CNN synaptic law with an appropriate A-template.

In Section 2 we introduce the receptor-based model. Section 3 deals with its CNN model and the dynamical behavior of the model together with numerical simulations.

2 Receptor-based models

The simplest model describing receptor-ligand is given in the form of three equations. It takes into consideration the density of free receptors, of the bound receptors and of the ligands. We use a representation of this simplest receptor-based model that is as generic as possible and based on the scheme shown in Fig.2.

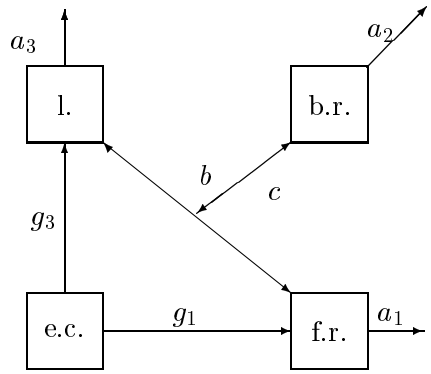

Fig.2. General scheme of the simplest receptor-based model.

We consider one-dimensional epithelial sheet of length L. We denote the concentration of ligands by $w(x,t)$, where x and t are space and time coordinates, with x increasing from 0 to L along the body column. The bound and free receptors densities are denoted by $u(,t)$ and $v(x,t)$ respectively. For simlicity we assume that all binding processes are governed by the law of mass action without saturation effects. The model is described by the following dynamical system:

$$\begin{aligned} \frac{\partial}{\partial t}u &= f_1(u,v,w) \\ \frac{\partial}{\partial t}v &= f_2(u,v,w) \\ \frac{\partial}{\partial t}w &= d\frac{\partial^2}{\partial x^2}w + f_3(u,v,w), \end{aligned} \tag{3}$$

where $u, v, w : [0,1] \times \mathbf{R}^+ \to \mathbf{R}^+$, functions $f_i, i = 1,2,3$ are nonnegative for nonnegative arguments and they have the following form:

$$f_1 = -a_1 u + g_1(u,v) - buw + cv,$$

$$f_2 = -a_2 v + buw - cv,$$

$$f_3 = -a_3 w - buw + g_3(u,v) + cv,$$

$a_i > 0, i = 1,2,3,\ b,c > 0$. We will suppoce that the functions $g_i, i = 1,3$ are of quadratic form, i.e. $g_i(u,v) = g_i u^2$. The model has biological interpretation for such functions [7].

3 CNN model and its dynamics

As we mentioned above there are several ways to approximate the Laplacian operator in discrete space by a CNN synaptic law with an appropriate A-template [2]. In our case we will take one-dimensional discretized Laplacian template:

$$A : (1, -2, 1).$$

Therefore the CNN representaion for our reseptor-based model (3) will be the following:

$$\begin{aligned} \frac{du_j}{dt} &= -a_1 u_j + g_1 u_j^2 - bu_j w_j + cv_j \\ \frac{dv_j}{dt} &= -a_2 v_j + bu_j w_j - cv_j \\ \frac{dw_j}{dt} &= -a_3 w_j + d(w_{j-1} - 2w_j + w_{j+1}) - \\ &- bu_j w_j + g_3 u_j^2 + cv_j, \end{aligned} \tag{4}$$

$1 \le j \le N$. The above equation is actualy ordinary differential equation which is identified as the state euqation of an autonomous CNN made of N cells. For the output of our CNN model we will take the standard sigmoid function [2].

In this section we will introduce an approximative method for studying the dynamics of CNN model (4), based on a special Fourier transform. The idea of using Fourier expansion for finding the solutions of PDEs is well known in physics. It is used to predict what spatial frequences or modes will dominate in nonlinear PDEs. In CNN literature this approach, has been developed for analyzing the dynamics of CNNs with symmetric templates [4,5].

In this paper we investigate the dynamic behavior of a CNN model (4) by use of Harmonic Balance Method well known in control theory and in the study of electronic oscillators [5] as describing function method. The method is based on the fact that all cells in CNN are identical [2], and therefore by introducing a suitable double transform, the network can be reduced to a scalar Lur's scheme [5].

We shall study the dynamics and the stability properties of (4) by using the describing function method [5]. Applying the double Fourier transform:

$$F(s,z) = \sum_{k=-\infty}^{k=\infty} z^{-k} \int_{-\infty}^{\infty} f_k(t) exp(-st) dt,$$

to the CNN equation (4) we obtain:

$$\begin{aligned} sU &= -a_1 U + g_1 U^2 - bUW + cV \\ sV &= -a_2 V + bUW - cV \\ sW &= -a_3 W + d(z^{-1}W - 2W + zW) + \\ &+ g_3 U_b^2 UW + cV. \end{aligned} \tag{5}$$

Without loss of generality we can denote $N(U,V,W) = g_i U^2 - bUW + cV$ and then we obtain from (5):

$$\begin{aligned} U &= \frac{1}{s+a_1}N \\ V &= \frac{1}{s+a_2}N \\ W &= \frac{1}{s+a_3-d(z^{-1}-2-z)}N. \end{aligned} \tag{6}$$

In the double Fourier transform we suppose that $s = i\omega_0$, and $z = exp(i\Omega_0)$, where ω_0 is a temporal frequency, Ω_0 is a spatial frequency.

According to the describing function method, $H(s,z) = \frac{s+a_1}{s+a_3-d(z^{-1}-2+z)}$ is the transform function, which can be presented in terms of ω_0 and Ω_0, i.e. $H(s,z) = H_{\Omega_0}(\omega_0)$.

We are looking for possible periodic state solutions of system (5) of the form:

$$X_{\Omega_0}(\omega_0) = X_{m_0} sin(\omega_0 t + j\Omega_0), \qquad (7)$$

where $X = (U, V, W)$. According to the describing function method we take the first harmonics, i.e. $j = 0 \Rightarrow$

$$X_{\Omega_0}(\omega_0) = X_{m_0} sin\omega_0 t,$$

On the other side if we substitute $s = i\omega_0$ and $z = exp(i\Omega_0)$ in the transfer function $H(s,z)$ we obtain:

$$H_{\Omega_0}(\omega_0) = \frac{i\omega_0 + a_1}{i\omega_0 + a_3 - d(2cos\Omega_0 - 2)}. \qquad (8)$$

According to (8) the following constraints hold:

$$\begin{aligned} \Re(H_{\Omega_0}(\omega_0)) &= \frac{X_{m_0}}{Y_{m_0}} \qquad (9) \\ \Im(H_{\Omega_0}(\omega_0)) &= 0. \end{aligned}$$

Hence, we obtain the following constraints:

$$\begin{aligned} \omega_0 &= \frac{1}{a_3 - a_1 + d(2cos\Omega_0 - 2)} \quad (10) \\ X_{m_0} &= \frac{4}{\pi}[X_{m_0} Arcsin(\frac{1}{X_{m_0}}) + \\ &\quad \sqrt{1 - \frac{1}{X_{m_0}^2}}]. \end{aligned}$$

Suppose that our CNN model (4) is a finite circular array of N cells. For this case we have finite set of frequences:

$$\Omega_0 = \frac{2\pi k}{N}, \quad 0 \le k \le N-1. \qquad (11)$$

Thus (9), (10) and (11) give us necessary set of equations for finding the unknowns X_{m_0}, ω_0, Ω_0. As we mentioned above we are looking for a periodic wave solution of (5), therefore X_{m_0} will determine approximate amplitude of the wave, and $T_0 = \frac{2\pi}{\omega_0}$ will determine the wave speed.

Proposition 1 *CNN model (4) of the receptor-based system (3) with circular array of N cells has periodic state solutions $x_j(t)$ with a finite set of spatial frequences $\Omega_0 = \frac{2\pi k}{N}$, $0 \le k \le N-1$.*

Remark 1 For the Turing-type instability [7], the functions describing production of free receptors (f.r.) must depend on the density of f.r. and this dependence must be a power function of the order $\alpha + 1$, where $\alpha > 0$. Hence, Turing type patterns can occur if $g_1(u) = g_1 u^{\alpha+1}, \alpha > 0$. This function can depend also on the density of bound receptors (b.r.), but also it is critical here that it depends on the density of f.r. For numerical simulations the simplest function fulfilling the above condition is used, namely $g_1(u) = g_1 u^2$. To model the production rate of ligands (l.) g_3 we also take a function of the concentration of free receptors. In numerical simulations a function similar to g_1 is used $g_3(u) = g_3 u^2$.

The following bifuraction diagrams are obtained for functions u, v, w (Fig.3,4,5).

4 Conclusions

We showed that Turing-type patterns can be obtained in a receptor-based CNN model. The Turing-type mechanism [7] is one of the simplest theories for the biological pattern formation. In models with such mechanism patterns can arrise spontaneously. The parameters must be tightly controlled to obtain the instability at the desired point in parameter space. From the simulations (Fig.3,4,5) it appears that the model (4) cannot exibit a wave bifurcation. We carry out our simulations for the following set of parameters: $a_1 = 0.2$, $a_2 = 0.02$, $a_3 = 0.2$, $b = 0.7$, $g_1 = 1.466$, $g_3 = 2$, $c = 0.02672$. In

summary, we showed that for the simplest receptor-based model consisting of 3 equations, Turing-type patterns can arrise only if there is a self-enhancement of free receptors. The final pattern strongly depends on the initial perturbation.

References

[1] Britton N.F., *Reaction-Diffusion Equations and Their Applications to Biology*, New York: Academic, 1986.

[2] Chua L.O., Yang L., Cellular Neural Network: Theory and Applications, *IEEE Trans. CAS*, vol. 35, pp. 1257-1290, Oct. 1988.

[3] Chua L.O., Hasler M., Moschytz G.S., Neirynsk J., Autonomous cellular neural networks: a unified paradigm for pattern formation and active wave propagation, *IEEE Trans. CAS-I*, vol. 42, N 10, pp. 559-577, Oct. 1995.

[4] Genesio R., Tesi A., Villoresi F., A frequency approach for analyzing and controlling chaos in nonlinear circuits, *IEEE Trans. CAS-I*, vol. 40, N 11, pp. 819-827, Nov. 1993.

[5] Mees A.I., *Dynamics of Feedback Systems*, London, England:Wiley, 1981.

[6] Roska T., Chua L.O., Wolf D., Kozek T., Tetzlaff R., Puffer F., Simulating nonlinear waves and partial differential equations via CNN- Part I: Basic techniques, *IEEE Trans. CAS-I*, vol. 42, N 10, pp. 807-815, Oct. 1995.

[7] Turing A.M., The chemical basis of morphogenesis, *Phil.Trans.Roy.Soc. B*, 237:37-72, 1952.

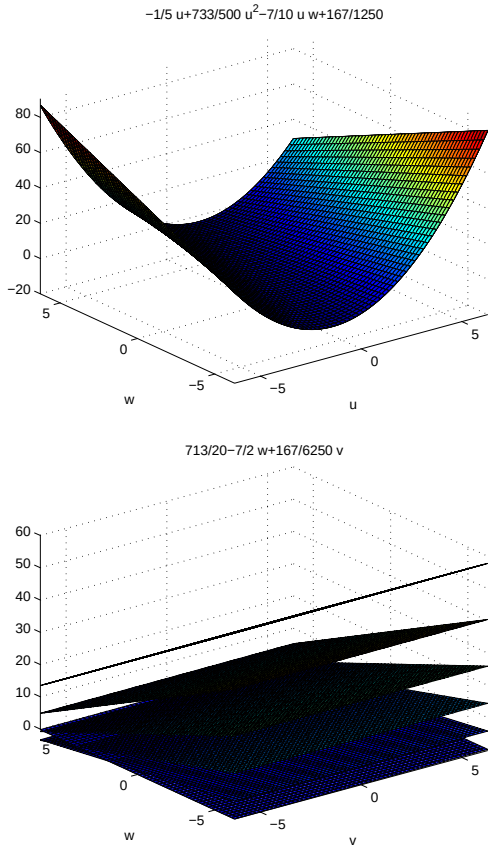

Fig. 3. The bifurcation diagrams for the first equation of the CNN model (4).

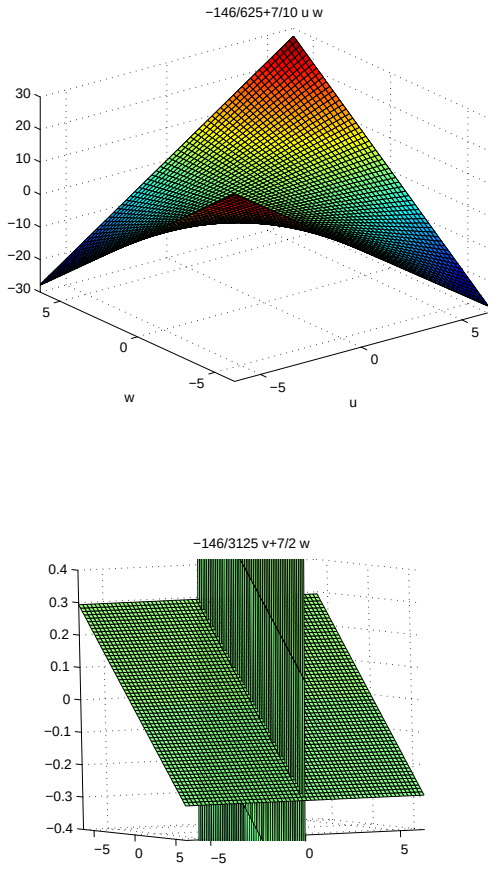

Fig. 4. The bifurcation diagrams for the second equation of the CNN model (4).

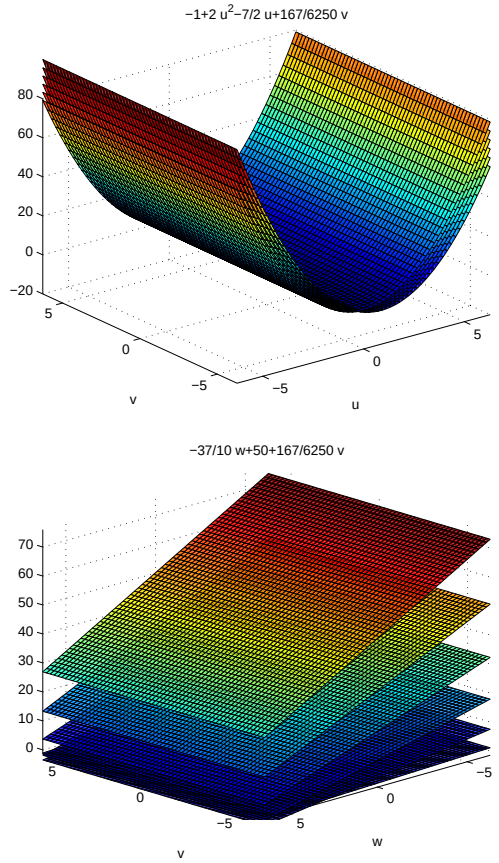

Fig. 5. The bifurcation diagrams for the third equation of the CNN model (4).