Synchronization properties in networks of Hindmarsh-Rose neurons and their PWL approximations with linear symmetric coupling

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Abstract—In this paper we analyze the collective behaviors of networks of Hindmarsh-Rose (HR) neurons and compare them with the behaviors of networks of piecewise-linear (PWL) approximations of the HR neurons. In all cases, the neurons are assumed to be symmetrically and diffusively coupled, with different topologies. The analysis is based on the Master Stability Function (MSF) approach. The obtained results are verified by numerical time domain simulations of networks of 100 neurons. The synchronization properties of the PWL networks turn out to be very similar to those of the HR networks, as well as the dynamical properties of the single neurons (analyzed elsewhere).

I. INTRODUCTION

This paper is concerned with a particular aspect of the general problem of studying the behavior of relatively large networks (e.g., millions) of neurons and modeling/emulating such networks. To this end, a significant common effort is necessary, which involves several disciplines such as biology, neuroscience, physics, mathematics, computer science, and electronics. In this kind of research activity, it is necessary to combine experimental studies of animal and human nervous systems with numerical simulation of mathematical models. From a biophysical-mathematical point of view, to model the electrical behavior of a biological neuron is one of the main problems. In developing such models, a compromise must be found between two seemingly mutually exclusive requirements: The model for a single neuron must be computationally simple and, at the same time, capable of mimicking almost all the behaviors exhibited by real biological neurons (in particular the rich firing patterns). Up to now, the simulation of large networks of accurate neural models is generally unrealistic if not hardware implemented. On the other hand, the actual circuit implementations of neurons (see, e.g., [1], [2] and references therein) exhibit behaviors only partially similar to those of the real neurons.

In the last few years, a piecewise-linear (PWL) approximation/synthesis technique has been applied towards the implementation of nonlinear dynamical systems [3], [4] and in particular the Hindmarsh-Rose (HR) neuron model [5], [6]. The dynamics of the single PWL model has been verified to be qualitatively and quantitatively very similar to those of the

HR model. The circuit implementation of a single neuron is in progress and the next step would be the circuit implementation of a neuron network. Of course, there is no guarantee that the collective behaviors of networks of PWL models will be similar to those of networks of HR models. With this caveat in mind, in this paper we analyze the synchronization properties of networks composed of neurons described by either the original HR model or its PWL approximation [6]. To this end, we use the Master Stability Function (MSF) approach [7]. It requires some restrictive assumptions (all nodes must be identical and the coupling has to satisfy certain constraints), but it has a straightforward application and can be a valid benchmark for future improvement and testing. If even under such tight hypotheses the PWL approximation did not fit the real model, then some changes would be needed for a better identification.

The obtained results, even if preliminary, show that the synchronization properties of the HR networks are preserved in the corresponding PWL networks. In particular, in Section II a brief description of the MSF approach is given. In Sections III and IV we evaluate the MSF for both the HR neuron and its PWL approximation and compute the critical parameter values for synchronization. We find that HR networks and their PWL approximation synchronize for almost the same values of the coupling strength. These results are validated through extensive software simulations. Finally, in Section V we draw some conclusions and propose future developments of this research.

II. THE MASTER STABILITY FUNCTION APPROACH

We consider a network of N identical systems, whose state is $\xi_i \in \mathbb{R}^Q$ (i = 1, ..., N). The evolution of the global system is described by the following set of equations:

$$\dot{\xi}_i = f(\xi_i) + g_s \sum_{j=1}^N A_{ij} h(\xi_j), \ i = 1, \dots, N,$$
 (1)

where g_s is the overall coupling strength. We look for conditions on the matrix $g_s A = \{g_s A_{ij}\}$ in order to obtain identical synchronization among the subsystems, *i.e.*, in order to get

$$\xi_1(t) = \xi_2(t) = \ldots = \xi_N(t) = \xi(t).$$
 (2)

For the synchronous manifold described by Eq. (2) to be invariant, we need the row sum of A to be zero, *i.e.*, $\sum_{j} A_{ij} = 0$ [7]. In this paper, the *master stability equation/function* approach [7] is used, because it permits to separate the contribution of the identical isolated cells from that of the topology of the network to infer the synchronization conditions. More precisely [7], a linear transformation is applied to the variational equation of system (1) on the synchronous manifold described by Eq. (2) to decompose it in N uncoupled systems with evolution given by

$$\begin{cases} \dot{\xi} = f(\xi), \\ \dot{\delta}_k = \left(Df(\xi) + (\alpha_k + i\beta_k) Dh(\xi) \right) \delta_k, \ k = 1, \dots, N, \end{cases}$$
(3)

where $Df(\xi)$ and $Dh(\xi)$ are the Jacobian matrices of $f(\xi)$ and $h(\xi)$, respectively, whereas $(\alpha_1 + i\beta_1), \ldots, (\alpha_N + i\beta_N) \in \mathbb{C}$ are the eigenvalues of $g_s A$. We restrict our study to symmetric coupling, then all the eigenvalues of the coupling matrix are real and non positive [8]. Henceforth, we assume the following ordering for the real eigenvalues: $0 = \alpha_1 \ge \alpha_2 \ge \ldots \ge \alpha_N$.

The motion along $\alpha_1 = 0$ is the motion on the synchronous manifold, so in order to study its stability we can focus on the remaining eigenvalues, which take into account the orthogonal modes. Since the N systems of Eq. (3) are uncoupled, we can drop the index k and call $\Lambda(\alpha)$ the maximum Lyapunov exponent of system (3). This is called the Master Stability Function (MSF), and can be numerically evaluated by using, for instance, the algorithm proposed in [9]. A coupling scheme described by a symmetric matrix $g_s A$ such that $\Lambda(\alpha) < 0$ for all $\alpha_2 \dots, \alpha_N$ eigenvalues of $g_s A$ (except $\alpha_1 = 0$) will lead to a stable synchronous manifold, as all the variations perpendicular to the synchronous manifold will fade exponentially.

III. MSF FOR THE HR MODEL

We consider networks of identical Hindmarsh-Rose (HR) neurons [5] symmetrically coupled in a linear way. Being $\xi_i = [x_i(t), y_i(t), z_i(t)]^T$ the state of the *i*-th neuron in the network $(i = 1, ..., N, \xi^T$ denotes transpose of vector ξ), the equations governing the system evolution are

$$\begin{cases} \dot{x}_{i} = y_{i} - z_{i} + I - x_{i}^{3} + bx_{i}^{2} + g_{s} \sum_{j=1}^{N} A_{ij} x_{j}, \\ \dot{y}_{i} = -y_{i} + 1 - 5x_{1}^{2}, \\ \dot{z}_{i} = \mu \left(s(x_{i} - x_{0}) - z_{i} \right), \end{cases}$$

$$\tag{4}$$

with b = 2.96, s = 4, $\mu = 0.01$, $x_0 = -1.6$. The coupling is on variable x, which plays the same role as the membrane potential in a biological neuron. The parameter I plays the same role as the input membrane current in a biological neuron.

Define the Global Quadratic Error (GQE) as

$$e^{2}(t) = \left(\operatorname{std}(x(t))\right)^{2} + \left(\operatorname{std}(y(t))\right)^{2} + \left(\operatorname{std}(z(t))\right)^{2}.$$
 (5)

In Eq. (5) x(t), y(t) and z(t) are defined as $x(t) = [x_1(t), \dots, x_N(t)]^T$, $y(t) = [y_1(t), \dots, y_N(t)]^T$, and

 $z(t) = [z_1(t), \ldots, z_N(t)]^T$ and std denotes the standard deviation. If the network reaches identical synchronization at time t_0 , then $e^2(t) = 0$ for any $t \ge t_0$, as this condition implies that the dispersion is zero in each of the three dimensions. As a figure of merit for this behavior, we use the time average of the GQE $e^2(t)$:

$$\left\langle e^2 \right\rangle = \lim_{T \to \infty} \frac{1}{T} \int_{t_0}^{t_0 + T} e^2(\tau) \,\mathrm{d}\,\tau. \tag{6}$$

We approximate Eq. (6) with a time average over an interval large enough after the initial transient has been discarded. More precisely, we used $t_0 = 10^4$, $T = 2 \cdot 10^3$, and sampling time $\Delta t = 0.1$.

We now fix I = 2.5, a value which leads to a bursting behavior in both the HR and PWL models [6]. In Fig. 1 we plotted the MSF $\Lambda(\alpha)$ (solid line) with $\alpha \in [-10,0]$. To achieve identical synchronization, we must have $\alpha < -0.5$ approximately. To validate this result, let us consider a network



Figure 1. MSF for the real HR neuron (Eq. (4), solid line) and PWL approximation (Eq. (10), dashed line). The dashed grey lines highlight the abscissa of the intersection between $\Lambda = 0$ and the two MSFs.

of 100 neurons coupled in a diffusive way as a ring, so that the coupling matrix is

$$g_{s}A = g_{s} \cdot \begin{bmatrix} -2 & 1 & 0 & \cdots & 0 & 1 \\ 1 & -2 & 1 & 0 & \ddots & 0 \\ 0 & 1 & -2 & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & \ddots & 0 \\ 0 & \cdots & 0 & \ddots & -2 & 1 \\ 1 & 0 & \cdots & 0 & 1 & -2 \end{bmatrix}.$$
 (7)

The spectrum of matrix A is given by $\gamma_1 = 0$, $\gamma_{2,3} = -3.9510^{-3}$, ..., $\gamma_{100} = -4$. As $\alpha = g_s \gamma$, in order to obtain identical synchronization we should have $g_s > 500/3.95 \approx 126$. A time domain analysis confirms the result. In fact, in

the plot of the time average of the GQE for different values of g_s reported in Fig. 2 (upper panel, solid line) for $g_s > 126$ (see the vertical dashed grey line) approximately, we have an extremely low mean value.

If we consider an all-to-all coupling, so that matrix A is described by

$$\begin{cases} A_{ii} = -99, \\ A_{ij} = 1, \quad i \neq j, \end{cases}$$

$$\tag{8}$$

for i, j = 1, ..., N, then the spectrum of A is $\gamma_1 = 0$, $\gamma_{2,...,100} = -100$. The condition to obtain identical synchronization is now $g_s > 0.5/100 = 0.005$. Again, the plot of the time average of the GQE for different values of g_s reported in Fig. 2 (lower panel, solid line) confirms the result, as for $g_s > 0.005$ (see the vertical dashed grey line) approximately, we have an abrupt decrease of the mean value.



Figure 2. Time average of GQE for networks of 100 HR (solid line) or PWL (dashed line) neurons with two-nearest-neighbors ring coupling (upper panel) and all-to-all coupling (lower panel). The dashed grey lines highlight the value of g_s where the transition from the asynchronous state to the synchronous one occurs.

IV. MSF FOR THE PWL MODEL

We now consider a model of bursting neurons derived from Eq. (4) by approximating the nonlinear part of the vector field on the righthand side with a PWL function [6]. More precisely, if $\{\varphi_1(x), \ldots, \varphi(x)_L\}$ is the chosen base of PWL functions, we have that

$$\begin{cases} x^{3} - bx^{2} = \sum_{\ell=1}^{L} w_{\ell}^{1} \varphi_{\ell}(x), \\ 5x^{2} = \sum_{\ell=1}^{L} w_{\ell}^{2} \varphi_{\ell}(x), \end{cases}$$
(9)

so the model for the *i*-the neuron is now

$$\dot{x}_{i} = y_{i} - z_{i} + I - \sum_{\ell=1}^{L} w_{\ell}^{1} \varphi_{\ell}(x_{i}) + g_{s} \sum_{j=1}^{N} A_{ij} x_{j},$$

$$\dot{y}_{i} = -y_{i} + 1 - \sum_{\ell=1}^{L} w_{\ell}^{2} \varphi_{\ell}(x_{i}),$$

$$\dot{z}_{i} = \mu \left(s(x_{i} - x_{0}) - z_{i} \right).$$
(10)

The chosen approximation is the simplest one presented in [6], which is suitable for analog implementation and where L = 16.

We recomputed the MSF for this model, with I = 2.5 as in the previous case, and obtained the plot shown with a dashed line in Fig. 1. It is evident that the limit to achieve synchronization is again -0.5, approximately.

To validate this statement, we considered two networks of 100 neurons, with the same coupling matrices as in the HR case. The plots of the time average of the GQE for different values of g_s shown in Fig. 2 (upper and lower panel, dashed lines) confirm the result. Even if in this case the decrement of GQE time average is not as evident as in the case of HR model, its order of magnitude (10^{-10}) is still low enough to assure complete synchronization.

Figures 3 (two-nearest-neighbors ring coupling) and 4 (allto-all coupling) provide further qualitative comparisons between the HR network (left column) and the PWL network (right column) with 100 neurons in the two considered topologies. The raster plots show the variable x(t) (coded by a grey level) for the 100 neurons (with random initial conditions) in each network: Lighter grey levels correspond to the presence of spikes. The three rows correspond to three different coupling strengths: $g_s = 0$ (upper row), $g_s = 50.67$ (middle row), $g_s = 506.77$ (lower row) for the ring coupling and $g_s = 0$ (upper row), $g_s = 0.002$ (middle row), $g_s = 0.02$ (lower row) for the all-to-all coupling. The vertical patterns in the third row evidence that, after a transient, both networks synchronize on a similar state.

V. CONCLUDING REMARKS

We conducted some numerical experiments to validate the PWL approximation of the HR neuron with respect to the synchronization properties in some simple networks, focusing on regular symmetric diffusive couplings. The preliminary results show that the PWL networks exhibit the same collective properties as the original HR ones, giving credit to this kind of approximation in order to simulate large networks. We are currently working on testing less regular structures of larger size, different values of the b and I parameters and on weakening the assumption of having identical systems.



Figure 3. Raster plots for the 100-neurons two-nearest-neighbors ring coupling HR (left column) and PWL (right column) networks (see text).

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Figure 4. Raster plots for the 100-neurons all-to-all coupling HR (left column) and PWL (right column) networks (see text).

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