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Synchronization of Hindmarsh Rose Neurons by Temporal Evolution of Coupling Strengths

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Abstract

In this study, we observe synchronization on Hindmarsh Rose model which produce spiking-bursting behavior like real biological neurons. We set the same coupling strength parameters. Provided that neurons are synchronized, the coupling strength between the neurons is weakened. Thus, the coupling topology is changed little by little. We observe the synchronization of network.

1. Introduction

We have a lot of neurons in our brain. Neurons have many inputs and one output. Neural network (NN) is formed by connecting neurons. NN is mathematical model represented simulations on the computers that some characteristic features in our brain. We can see spiking-bursting activity which has high-dimensional dynamics for generation. The research about NN was studied by [1–4]. This network is so complex network. The connection between neurons is called coupling strength. Coupling strengths are enhanced by the electrical signals and strengthened the part of more communications. The neurons have output part called axon. Some axons are covered with oligodendrocyte on the Myelin sheaths. Oligodendrocyte is white material which is rich in lipid. Covered axons can communicate quicker than non-covered ones. This phenomenon is called Myelination. For example, we practice to achievement something when we usually try to do it. This action from challenge to achievement is myelination. Therefore, there is a big relation between learning and myelination. The study about myelination has possibility to make more performance for learning by adapting application. In this study, we use Hindmarsh Rose model which produce spiking-bursting behavior like real biological neurons. In this study, we observe the synchronization by changing the temporal evolution of coupling strengths.

2. Hindmarsh Rose Model

Hindmarsh Rose (HR) model is a mathematic model which chaotic behavior molluskan neurons cause reproduces. It can cause chaotic behaviors autonomously without periodic stimulations from external input. We can indicate various oscillations by setting parameters.

2.1. Individual Neuron

This model has three variables. These are the membrane potential $x(t)$, auxiliary variable $y(t)$ representing a set of fast ion channels connected with aspects of potassium and sodium transport, and a slow variable $z(t)$ which captures the slower dynamics of other ion channels. The HR model is described by the following equations.

$$\begin{cases} \dot{x}(t) = y(t) - ax^3(t) + bx^2(t) - z(t) + I \\ \dot{y}(t) = c - dx^2(t) - y(t) \\ \dot{z}(t) = -rz(t) + rS(x(t) - c_x) \end{cases} \quad (1)$$

The parameters are given as $a = 1$, $b = 3$, $c = 1$ and $d = 5$. We use the injected current $I = 3.281$, the voltage $c_x = -1.6$, the scale of the influence of the membrane voltage on the slow dynamics $S = 4.0$ and the time scale for the slow adaptation current $r = 0.0021$. The differential equations are solved by the Runge-Kutta method.

2.2. Electrical Coupling

In this study, we use fully coupled five neurons model shown in Fig. 1. The equations with electrical coupling are given as follows.

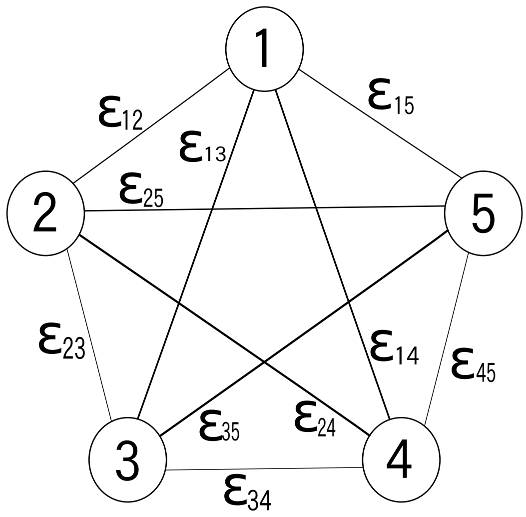

Figure 1: Fully coupled five neurons.

$$\begin{cases} \dot{x}_i(t) = y_i(t) - ax_i^3(t) + bx_i^2(t) - z_i(t) + I - K_i \\ \dot{y}_i(t) = c - dx_i^2(t) - y_i(t) \\ \dot{z}_i(t) = -rz_i(t) + rS(x_i(t) - c_x) \end{cases} \quad (2)$$

where i indicates the neuron number (from 1 to 5). The function K_i is given as:

$$\begin{cases} K_1 = \varepsilon_{12}(x_1 - x_2) + \varepsilon_{13}(x_1 - x_3) \\ \qquad + \varepsilon_{14}(x_1 - x_4) + \varepsilon_{15}(x_1 - x_5) \\ K_2 = \varepsilon_{12}(x_2 - x_1) + \varepsilon_{23}(x_2 - x_3) \\ \qquad + \varepsilon_{24}(x_2 - x_4) + \varepsilon_{25}(x_2 - x_5) \\ K_3 = \varepsilon_{13}(x_3 - x_1) + \varepsilon_{23}(x_3 - x_2) \\ \qquad + \varepsilon_{34}(x_3 - x_4) + \varepsilon_{35}(x_3 - x_5) \\ K_4 = \varepsilon_{14}(x_4 - x_1) + \varepsilon_{24}(x_4 - x_2) \\ \qquad + \varepsilon_{34}(x_4 - x_3) + \varepsilon_{45}(x_4 - x_5) \\ K_5 = \varepsilon_{15}(x_5 - x_1) + \varepsilon_{25}(x_5 - x_2) \\ \qquad + \varepsilon_{35}(x_5 - x_3) + \varepsilon_{45}(x_5 - x_4) \end{cases} \quad (3)$$

where the parameter ε is coupling strength.

3. Proposed Method

First, we define the synchronization condition by the following equation:

$$|x_a - x_b| < 0.01 \quad (4)$$

Figure 2 shows definition of the synchronization. We determine the synchronization only when the case synchronization continues for 130000 iterations with the step size $h = 0.05$.

We explain the way to change the coupling strengths. The coupling strength is weakened 0.001 in the case of synchronization between neurons. At that moment, other coupling strengths are enhanced 0.001/9. Those actions are done in the case of synchronization every 130000 iterations consecutively.

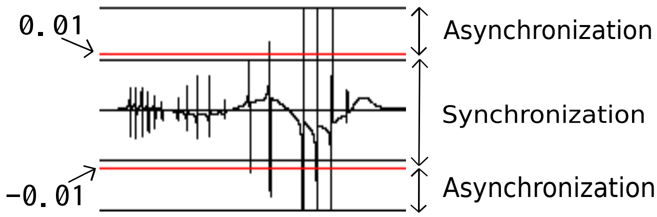

Figure 2: Definition of the synchronization. Lines show synchronization between neurons.

4. Simulation Results

In this paper, we use initial condition for which the steady states become a decoupled synchronization in Fig. 3. This decoupled synchronization appears for $t \geq 9608.5$ when all coupling strengths are fixed as $\varepsilon_{ij} = 0.2$. Neurons 1, 2 and 4 are synchronized. Neurons 3 and 5 also are synchronized. However, the neurons 1, 2 and 4, and the neurons 3 and 5 are not synchronized.

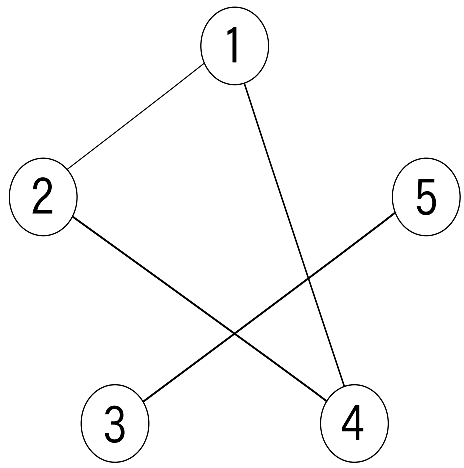

Figure 3: Decoupled synchronization. Lines show synchronization between neurons.

All coupling strengths are fixed 0.2 at the start. We observe the synchronization with all neurons on the network. Figure 4 illustrates the temporal evolution of the membrane potential around $t \simeq 7500$. Figure 5 shows difference waveforms between each neurons around $t \simeq 7500$. We can confirm the synchronization in Fig. 5 (a), (c), (f) and (i). Thus, the network exhibits the same decoupled synchronization as Fig. 3. This synchronization is completed in $t = 7001.05$. Namely, this synchronization is achieved earlier than unchanging coupling strengths simulation.

We obtain results Fig. 6 and 7 after a period of time. Figure 6 illustrates the temporal evolution of the membrane potential. Figure 7 shows difference waveforms between each neurons. As Fig. 7 shows, all neurons are synchronized. This full synchronization for all neurons is completed in $t = 15541.25$.

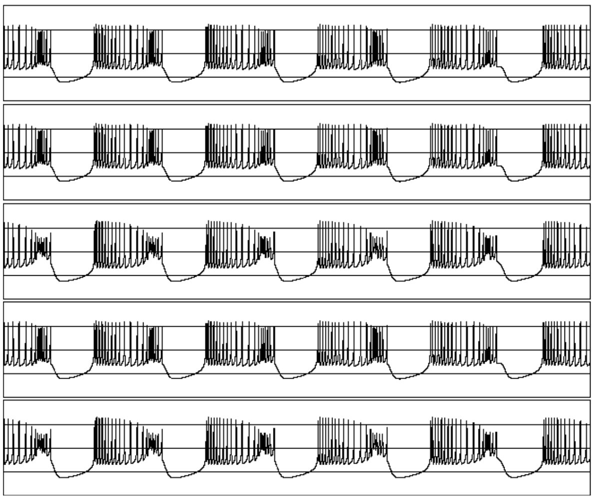

Figure 4: The temporal evolution of the membrane potential in the beginning. (a) The membrane of neuron 1. (b) The membrane of neuron 2. (c) The membrane of neuron 3. (d) The membrane of neuron 4. (e) The membrane of neuron 5.

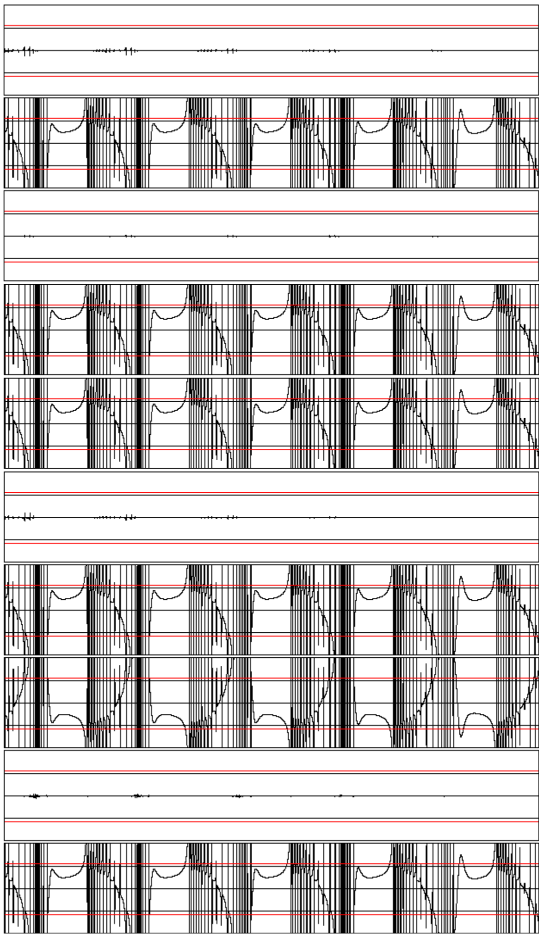

Figure 5: Waveforms show difference between two neurons in the beginning. Threshold illustrates red line.

5. Conclusions

In this study, we use the synchronization with the fully coupled five neurons on Hindmarsh Rose model. The synchronization with all neurons is not completed in the case of unchanging coupling strengths. Moreover, the result also indicates that all neurons is the synchronization by changing the temporal evolution of coupling strengths. In our future works, we would like to do the simulation with large scale model.

References

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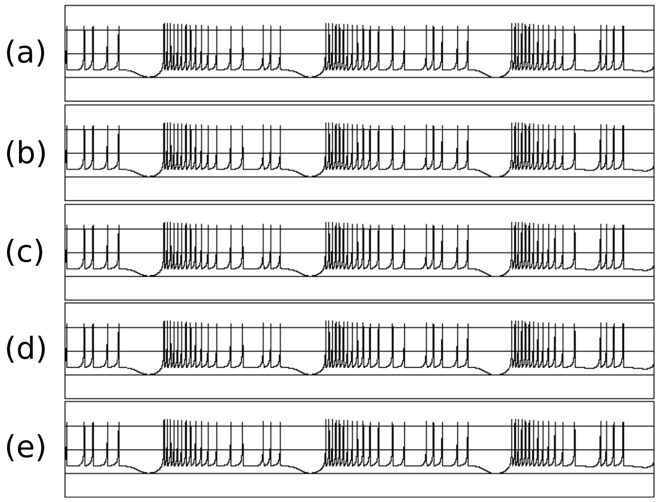

Figure 6: The temporal evolution of the membrane potential in each neuron. (a) The membrane of neuron 1. (b) The membrane of neuron 2. (c) The membrane of neuron 3. (d) The membrane of neuron 4. (e) The membrane of neuron 5.

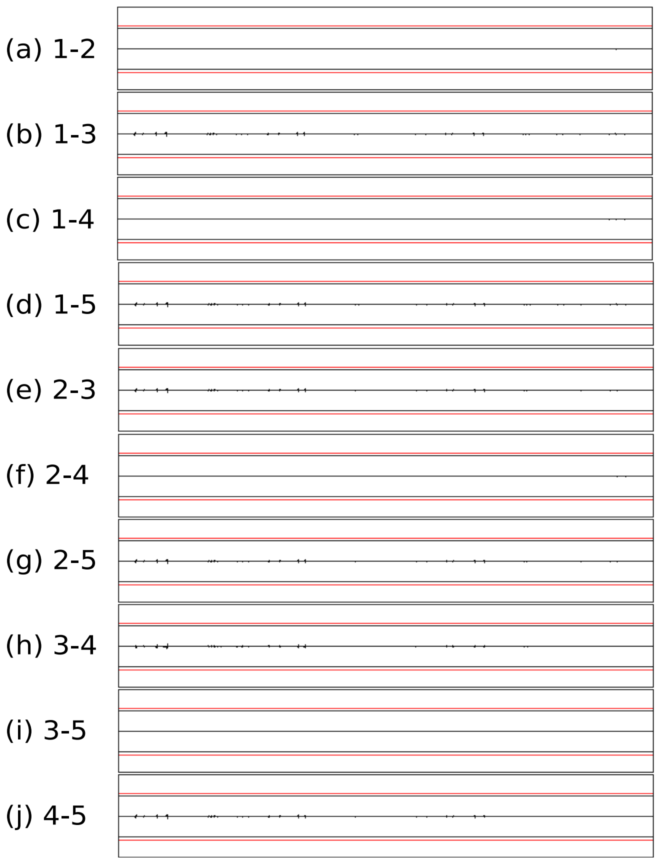

Figure 7: Waveforms show difference between two neurons. Threshold illustrates red line.