



## Frequency transitions in synchronized neural networks

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### ABSTRACT

Temporal organization of events can emerge in complex systems, like neural networks. Here, random graph and cellular automaton are used to represent coupled neural structures, in order to investigate the occurrence of synchronization. The connectivity pattern of this toy model of neural system is of Newman–Watts type, formed from a regular lattice with additional random connections. Two networks with this coupling topology are connected by extra random links and an impulse stimulus is either constantly or periodically applied to a unique neuron. Numerical simulations reveal that this model can exhibit a variety of dynamic behaviors. Usually, the whole system achieves synchronization; however, the oscillation frequencies of the stimulus and of each network can be different. The dynamics is evaluated in function of the network size, the amount of the randomly added edges and the number of time steps in which a neuron can remain firing. The biological relevance of these results is discussed.

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### 1. Introduction

Synchronization of neuronal firings has been hypothesized to support sensory and cognitive functions [1,2]. For instance, experimental observations relate image perception to synchronous oscillatory activities in mammalian visual system [3,4]. Abnormal cortical synchronization, however, has been associated to brain disorders, such as autism and epilepsy [5,6]. Therefore, researches on synchrony in neural networks can help to understand the functioning of healthy and pathological nervous systems [7]. Numerical and analytical studies usually take into account a unique network and employ differential or difference equations [8,9] to represent the neuronal activity.

Here, the occurrence of synchronism between two neural networks is investigated via computational simulations. Our intent is to explore how the neuronal connectivity affects the synchronizability of coupled structures, which can achieve synchrony at distinct oscillation frequencies. For instance, in mammals, synchronized oscillatory responses of neurons in retina, lateral geniculate nucleus of the thalamus and cerebral cortex are detected after visual stimulation, in a time scale of the order of 100 ms [3,4,10–12]. The typical range of the synchronization frequency of these three neural structures excited by static visual stimuli is 60–120 Hz. However, for dynamic stimuli, the typical ranges are 30–60 Hz in the visual cortex, and 60–120 Hz in the lateral geniculate nucleus and in the retina [10,14]. Thus, synchronization between retina and thalamus happens in the same frequency band, but between thalamus and cortex can occur in distinct bands [10,13,14]. The goal here is to examine phenomena like this.

This manuscript is organized as follows. In Section 2, our model is described. This model of interconnected neural structures is based on deterministic cellular automaton and complex random graph. In Section 3, the dynamics is evaluated

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by varying topological features of the whole system and the results numerically obtained are presented. In Section 4, the relevance of these results is stressed.

## 2. The model

The brain presents a modular architecture [15]. In this work, the aim is to determine how the topology of synaptic links influences on the emergence of synchronized activity between two interconnected neural structures.

Our complex network is built according to the following procedure. Start from a two-dimensional lattice composed of  $m \times n$  neurons, in which  $n$  is an even number. In this regular graph, the edges are undirected and a cross-like coupling pattern is employed; thus, each neuron is connected to the ones to the left, right, up and down. Therefore, each neuron initially has four regular neighbors (except the nodes placed at the boundaries, which have two or three neighbors). Then, remove the links among the neurons at the columns  $n/2$  and  $(n+2)/2$ ; hence, two regular lattices are created, in which each one contains  $m$  rows,  $n/2$  columns,  $N = mn/2$  neurons and  $M = ((n/2) - 1)m + (m - 1)n/2$  edges. These lattices are called part-1 and part-2. Finally, randomly add  $qM$  links in each part and include this same amount of  $qM$  links for connecting these parts. For instance, for  $m = 10$ ,  $n = 20$  and  $q = 5\%$ , then in each part there are  $N = 100$  neurons connected by  $M = 180$  regular links plus  $qM = 9$  additional random links; also, there are  $qM = 9$  random links joining both parts. In this case, the full network is composed of  $100 + 100 = 200$  nodes and  $180 + 180 + 9 + 9 + 9 = 387$  edges. In this network, the nodes are mainly locally connected [16,17]. This topology has small-world features [18], because the “long-range” random connections make “small” the average shortest path length  $l$  (that is,  $l \sim \ln(N)$  instead of  $l \sim N$  as in regular lattices). Such a coupling pattern is similar to the one proposed by Newman and Watts [19].

At each time step  $t$ , assume that each neuron can be in one of three states: susceptible ( $S$ ), active ( $A$ ) or refractory ( $R$ ). The input of  $i$ -th neuron at  $t$  is calculated from  $\sum_j w_{ij} y_j(t) + I_i(t)$ , in which the index  $j$  labels the neurons connected to the  $i$ -th neuron,  $w_{ij}$  is the synaptic weight linking the  $j$ -th to the  $i$ -th neuron,  $y_j(t)$  is the output of the  $j$ -th neuron and  $I_i(t)$  represents an external stimulus applied at  $t$ . If the  $j$ -th neuron is active at  $t$ , then its output is  $y_j(t) = 1$ ; if it is susceptible or refractory, then  $y_j(t) = 0$ . As in neural discrete-time models based on cellular automaton [16,20], consider that the time evolution of this system is governed by a set of rules of state transitions. In this model, a  $S$ -neuron at the time step  $t$  becomes an  $A$ -neuron at the time step  $t + 1$  if its input at  $t$  is equal to or greater than the threshold  $T$ . An neuron that was activated at the instant  $t$  remains in the state  $A$  up to the instant  $t + d$  while its received input is equal to or greater than  $T$ . An  $A$ -neuron firing at  $t, t + 1, t + 2, \dots, t + d$  becomes a  $R$ -neuron at  $t + d + 1$  independently of its input. A  $R$ -neuron at  $t$  becomes a  $S$ -neuron at  $t + 1$ . Notice that these rules concerning the transitions  $S \rightarrow A$ ,  $A \rightarrow R$  and  $R \rightarrow S$  are deterministic. The states of all neurons are simultaneously updated throughout a simulation.

The threshold  $T$  and weights  $w_{ij}$  are assumed to be equal to 1; therefore, it seems that this model takes into account only excitatory effects. However, this is not the actual picture. Inhibition, a crucial feature for synchronizing biological neural systems [21,22], is considered in this model by choosing a finite value for  $d$ . This parameter represents the presence of hidden inhibitory synapses which would force a neuron to inactivity after firing during  $d$  consecutive time steps (even if it remains stimulated enough to fire). The lower the value of  $d$ , the stronger the inhibitory effects.

Let  $x_1(t)$  and  $x_2(t)$  be the numbers of active neurons in the part-1 and in the part-2 at the time step  $t$ , respectively. Let  $p_1$  and  $p_2$  be the oscillation periods of  $x_1(t)$  and  $x_2(t)$ , respectively. Both parts are said to be  $r_1 : r_2$  synchronized if, after a transient,  $x_1(t)$  and  $x_2(t)$  periodically oscillate such that  $p_1/r_1 = p_2/r_2$ ;  $r_1$  and  $r_2$  being integer numbers [23,24].

Let an impulse stimulus of magnitude  $I$  and period  $P$  be applied to a unique neuron at the first column at the part-1. Here, we numerically investigate how the dynamic behavior is affected by the values of  $n$ ,  $q$  and  $d$ . Notice that  $n$  and  $q$  are explicitly topological parameters and  $d$ , a parameter related to the transition rule  $A \rightarrow R$ , can also be associated to the connectivity pattern of the network; that is, to the synaptic excitation-inhibition balance.

Assume that one time step corresponds to one millisecond of real time, because this is the characteristic time interval of the state transitions  $S \rightarrow A$  and  $R \rightarrow S$  in actual neurons [15]. Therefore, in order to simulate biological phenomena like the one described in Section 1, synchronization in our model should be observed within a time window of 100 time steps [3,4,10–14].

## 3. Numerical results

In spite of the random graph being unweighted and the threshold being the same for all neurons, we found a richness of dynamic behaviors. For instance, simulations showed that both parts can be synchronized with either  $p_1 = p_2$  or  $p_1 \neq p_2$ . They also showed that either  $p_1 = P$  or  $p_1 \neq P$ .

At first, consider a random graph created in accordance with the procedure described in the last section with  $m = 10$ ,  $n = 20$  and  $q = 5\%$ . Take  $d = 1$ . At  $t = 0$ , assume that all neurons are susceptible. A simulation comprises 100 time steps. During this time interval, an impulse stimulus of magnitude  $I$  and period  $P$  is applied to a unique neuron at the first column of the part-1 and the states of all neurons are updated at each instant  $t$ . The stimulus has magnitude  $I = 1$  and period  $P \in \{1, 2, 3, \dots, 20\}$ . For instance,  $P = 3$  means that, at each three time steps, a stimulus with  $I = 1$  is applied to that selected neuron. Notice that  $P = 1$  corresponds to a static forcing and  $P > 1$  to a periodic forcing. If the forcing is removed, the network activity eventually vanishes.

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