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# DYNAMIC ANALYSIS OF NEURAL NETWORKS

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In recent years, computational and quantitative studies of modeled neural networks are gaining momentum. Researchers are putting to use powerful mathematical tools such as analysis of non-linear dynamics, network theory and information theory. Neuroscientists have started to make the crucial step of moving from the analysis of single cell dynamics to network dynamics, realizing that only studies of macroscopic systems can help in revealing the mechanisms responsible for the functions of the brain. Although some progress has been made, in most cases networks were studied using simplistic models that cannot give rise to the complex biological reality. Experiments and theoretical work done by our collaborators and us suggest that current models for neural networks are not detailed enough to produce an accurate fit with biology.

Current research into modeling of neural networks focuses mainly on trying to understand what role do the underlying biological properties of the single neuron and synapse in the dynamics of the single cell or of the network. An example of such dynamics can be the natural oscillation generated in cortical neuron, which in many cases is gamma oscillation *(Add references here)* or the firing pattern observed in complex networks consisting of clusters of neurons. Since a biological system is very complex, the idea is to try and understand which biological properties are most important for the biological system to operate correctly. In addition, since many biological processes are unknown, by simulating models based on the observed dynamics we can extrapolate potentially new processes and elements which form an integral part of the system. One of the most and important observed behaviors of networks is synchronization. Figure 1 depicts a raster plot of a recorded neural network from rats. The X axis represents the time on a scale of 1/12 msec (the sampling frequency of the recording is 12 KHz). The figure represents 1 recorded minute of activity. The Y axis represents the number of the recorded electrode. Each line on the figure represents one recorded electrode. We can clearly see from the figure that the neurons of the network fire in a synchronized manner. This may be an important property of network since it is considered that synchronized networks perform a certain task or a computation rather than just fire sporadically.

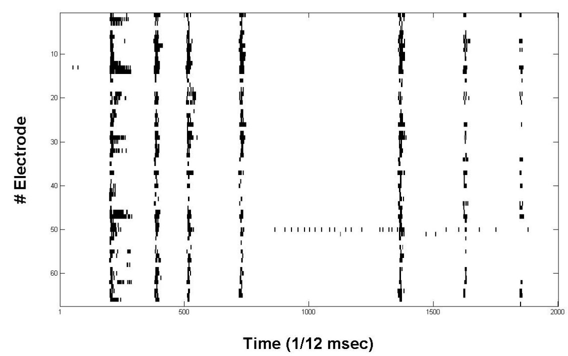


**Figure 1 – Rat Neurons Raster Plot**

In order to study the behavior of a network or a single cell we require a dynamical model which will simulate its behavior. In addition, we require the models to be *biological*, which means that must resemble the recorded biological data both qualitatively and quantitatively. One of the most widely used models is the reduced Morris-Lecar model[1]:

$$C\dot{V} = -g_{Ca}M_{ss}(V)(V-V_{Ca})-g_K W(V-V_K)-g_L(V-V_L)+I_{ext} \quad (1)$$

$$\dot{W} = (W_{ss}(V) - W)/(\phi \cosh[(V - V_3)/2V_4]) \quad (2)$$

$$M_{ss}(V) = (1 + \tanh[(V - V_1)/2V_2])/2 \quad (3)$$

$$W_{ss}(V) = (1 + \tanh[(V - V_3)/2V_4])/2 \quad (4)$$

The model depicts the ion current through ion the main channels on the membrane of the neuron. This determines its *membrane potential*, which can be said to be its output signal. In order to analyze the model and adapt its parameters in order to fit the observed biological behavior. Figure 2 depicts a phase plane portrait of the model when applying a constant external current of $I_{ext} = [uA/cm^2]$. We can clearly see the oscillating behavior and the fixed point which is a stable spiral. We can conclude that if such external current is applied the neuron would fire repeatedly with a fixed frequency.

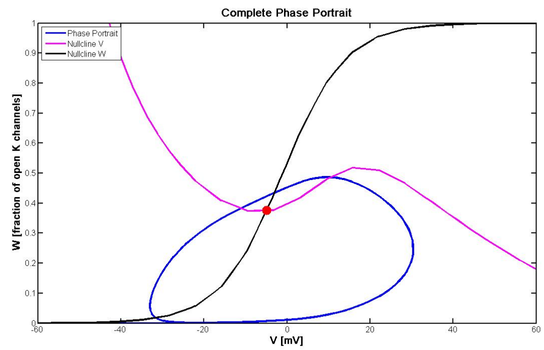


**Figure 2 – Rat Neurons Raster Plot**

However, in order to transmit this signal to other neurons it must transmit it through it axons. In most studies of networks, due to computational complexity the axons are considered to be perfect conductors. At the end of the axons, where it connects to other neurons it forms synapses. As it is for the neurons, there are many dynamical models for synapses. One of the most prevalent ones is the Tsodyks-Uziel-Markram (TUM) synapse model[2]:

$$\dot{x} = z/\tau_{rec} - ux\delta(t - t_{AP}) \tag{5}$$

$$\dot{y} = -y/\tau_I + ux\delta(t - t_{AP}) \tag{6}$$

$$\dot{z} = y/\tau_I - z/\tau_{rec} \tag{7}$$

$$\dot{u} = -u/\tau_{facil} - U(1-u)\delta(t - t_{AP}) \tag{8}$$

The *x,y,z* variables depict the amount of synaptic resources which are recovered, active and inactive respectively. Thus, it must hold that $z = x + y$. $u$ denotes the amount of resources which are released when an incoming AP reaches the synapse. When we model networks, a neuron can have multiple inputs which it must integrate and which define its underlying behavior.

As we have seen previously, one of the key features in a neural networks is its ability to synchronize. Thus, we need a quantitative measure of synchronization which can be calculated from the raster plot. Such a model has been developed in our group[3]. The synchronization between a pair of neurons is defined to be the phase synchronization, or the difference in phase, between the firing events of the two neurons. The instantaneous phase of neuron *j* is denoted by $\theta_j(t, n)$. The instantaneous difference in phase between two neurons *j,k* is denoted by $\delta\theta(j, k)$. The total phase synchronization between the two neurons throughout the simulation is denoted by $S(j, k)$.

$$\theta_j(t, n) = 2\pi n + 2\pi(t - t_j(n))/(t_j(n+1) - t_j(n)) \tag{9}$$

$$\Delta\theta(j, k) = \theta_j(t, n) - \theta_k(t, m) - 2\pi(n - m) \tag{10}$$

$$S(j, k) = \left| \left\langle e^{i\Delta\theta(j,k)} \right\rangle_t \right| \tag{11}$$

We can see that this measure detects both the differences in the phase between two firing events with the same index and between events of different indices. In order to produce a single value for the entire simulation, the phase difference is averaged over he time span of the simulation. After calculating the phase differences between all neuron pairs, a phase synchronization map is produced. It graphically depicts the differences throughout the network. In order to correctly arrange the neurons in the map, a dendrogram clustering algorithm is used. In order to test the applicability of our models, we need our network of simulated neurons to reproduce this ability. Figure 3 depicts a phase synchronization map of a simulated neural network with two clusters. A warmer color signifies higher synchronization.

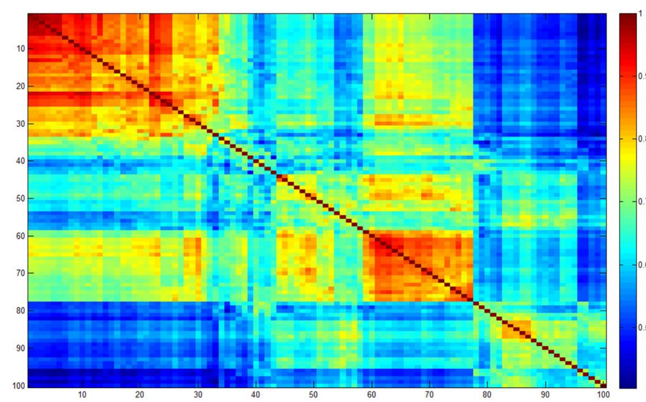

**Figure 3 – Phase Synchronization Map**

We can clearly see the formation of the clusters in the network. The clusters are highly synchronized inside themselves, when in between the synchronization is much weaker.

Our current work consists of developing more accurate model parameters, adding more biological elements to the network (such as electrical synapses) and developing models for network evolution as they do in the brain. The network evolution properties are speculated to be the biological basis for learning and memory.

## References

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