IMPERIAL COLLEGE LONDON

ELECTRICAL AND ELECTRONIC ENGINEERING DEPARTMENT

Interim Report

Project title
STRUCTURE AND DYNAMICS OF LARGE NETWORKS OF INTERACTING NEURONS

Author
ALEJANDRO GILSON CAMPILLO CID: 01112712

Supervisor
PROF. PIER LUIGI DRAGOTTI

Second Marker
DR. WEI DAI

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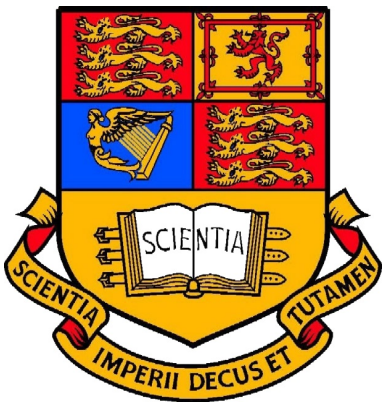

1 Introduction

The brain is a complex machine, it allows the human being to think, communicate and feel. It does so thanks to the billions of neurons that communicate in a dense network through synapses. However, little is known about how it works. By studying how the neurons structure to to store and process information we can understand how the brain as a whole functions. This could have important applications in medicine for curing diseases such as Parkinson [1] and epilepsy [2], and in machine learning for the development of more intelligent neural networks.

In order to infer the network structure of a set of neurons, they are treated as a diffusion network where electrical spikes increase the likelihood of connected neurons to spike and therefore transmit a signal that travels as if it were a disease. By evaluating the time of "infection", the relationship between two neurons can be probabilistically estimated. After computing the relationship between all of the neurons, an estimate of the topology of the network can be obtained.

Previous work on this topic [3, 4] evaluated the feasibility of using a maximum-likelihood estimator algorithm, NetRate [5], for the structure inference of biological neural networks. A network was simulated using the Izhikevic neuron model [6] and the brian simulator [7]. The connections between the neurons were then estimated, compared to the original network and the performance of the algorithm was evaluated.

The aim of this project is to improve on the state of the art research of network inference and the understanding of the underlying structure of the brain. There are many ways in which this can be done such as scalability and the addition of different types of neurons to the model.It would also be useful to test the accuracy of the algorithm on real interacting neurons. Developments in technology allow us to obtain spike data from individual neurons [8, 9, 10].

2 Background

2.1 Definition of connectivity

The definition of connectivity between neurons has a history of lack of consensus among the scientific community [11]. Connectivity studies from different researches may lead to different results depending on how they define it, as they may be looking at different aspects of connectivity. The two main accepted definitions that are used are functional and effective connectivity.

Functional connectivity is the temporal correlation between spatially remote neurophysiological events [12]. Studies on this topic began with electroencephalography (EEG) measurements. Some methods to measure functional connectivity include the evaluation of the correlation in the frequency domain between EEG signals at different scalp locations [13], and the cross-correlation of the time series measurements from a pair of electrodes [14]. However, due to the volume conduction of brain tissue, the electrical activity from the scalp cannot infer the individual neuron behaviour below the electrode [11].

Effective connectivity was defined in [12] as the influence that one neural system exerts on another. Effective connectivity can be measured in terms of efficacy and contribution. At a synaptic level it can be expressed as in eq.1, where x_j is the post-synaptic response to many pre-synaptic inputs x_i and $\mathbf{W}_{ij}$ is the efficacy of the connections between neurons

i and j. Contribution is reflected in eq.2 as the effect of i on j relative to all pre-synaptic inputs. Using this definition, directional effects are taken into account and a richer representation of the network can be attained. Following the approach in [4], this project will focus on the effective connectivity of neurons in a network.

$$x_j = \Sigma \mathbf{W}_{ij} \times x_i \tag{1}$$

$$\frac{\mathbf{W}_{ij}}{\Sigma \mathbf{W}_{ij}} \tag{2}$$

2.2 Izhikevich neuron model

In order to understand how the brain works we must be able to replicate the behaviour of individual neurons applying simple and accurate models. However, meeting both criteria can be challenging. The Hodgkin–Huxley model [15] is very accurate as it can emulate the rich firing patterns of many types of neurons. However, it is very computationally expensive and only a few neurons can be computed in real time. The integrate-and-fire model has the opposite problem: it is computationally simple but it is an unrealistic representation of the neuron since it does not capture the firing patterns with sufficient accuracy [6]. In contrast, the Izhikevich neuron model [6] meets both criteria. Tens of thousands of spiking cortical neurons can be simulated in real time by simplifying the Hodgkin-Huxley model into the two dimensional system of differential equations shown below.

$$v' = 0.04v^2 + 5v + 140 - u + \mathbf{I} \tag{3}$$

$$u' = a(bv - u) \tag{4}$$

with the auxiliary after-spike reseting

$$\text{if } v \geq 30\text{mV, then } \begin{cases} v & \leftarrow c \\ u & \leftarrow u + d \end{cases} \tag{5}$$

Here, the dimensionless variables v and u represent the membrane potential of the neuron and the membrane recovery, respectively. When a spike reaches its apex (30 mV), both these variables are reset according to eq. 5. Synaptic or injected DC currents are represented by the variable $\mathbf{I}$. The threshold is not fixed, just as with real neurons and it's based on previous spikes.

On the other hand, a, b, c and d are dimensionless parameters. a determines the speed of the recovery variable u, b defines the sensitivity of the recovery variable u to sub-threshold fluctuations of the membrane potential v. Finally, c and d determine the after-spike reset value of the recovery variables v and u, respectively.

The relevance of this algorithm stems from the fact that, different combinations of the parameters provide the model with a rich variety of firing patterns. When analysing the neocortical neurons in the mammalian brain, a number of different classes of excitatory neurons can be found [16, 17] such as RS (regular spiking), IB (intrinsically bursting) and CH (chattering). From the inhibitory type of neurons, two classes can be found: FS (fast spiking and LTS (low-threshold spiking). Other interesting classes of neurons are the TC (thalamo-cortical) and the RZ (resonator). It is of great importance to understand what

types of neurons can be found so that a simulated network can become a closer representation of what can be found on a real brain. In order to simplify the network to be inferred, the only type of neurons simulated in the network were the regular spiking neurons. This was achieved by setting the parameters to $a = 0.02$, $b = 0.2$, $c = -65$ and $d = 8$. This type of neuron is the most common type of excitatory neuron in the brain. There is also a ratio of excitatory and inhibitory neurons of 4 to 1 in the mammalian brain, respectively [6].

2.3 Netrate

2.3.1 Diffusion processes

In order to infer the underlying structure of a network, [4] employed NetRate algorithm developed by Rodriguez [5] by treating the network as a diffusion process.

The study of diffusion network is based on the observation of the nodes in a system when they take a certain action: get infected by a virus, share a piece of information, etc. A problem concerning this kind of studies lies on the fact that we can only understand when and where these nodes propagate but not how or why the do so. An example of this is the propagation of a virus in a population. We can tell who and when somebody got infected but not who infected him. For the rest of this section we will refer to the propagation of an infection as the object of study of the network.

To infer the mechanisms behind diffusion processes the time of infection is analysed. A model needs to be created with some assumptions about the structures that generate diffusion processes:

1. The network in a diffusion process is fixed, unknown and directed.
2. Infections are binary, they can only be infected or not infected, no partial infections are considered.
3. Infections across the edges of the network occur independently from one another.
4. The likelihood of a node a infecting node b at time t is modelled by a probability distribution dependent on a, b and t.
5. All infections in a network are observed during a recorded time window.

NetRate aims to describe how infections occur during a period of time in a fixed network. This is achieved by finding the optimal network and transmission rates that maximizes the likelihood of a set of observed cascades to occur. The mathematical definitions that construct this model will be explained in the following section.

2.3.2 Mathematical definitions

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