



Neural activity and new methods of computational analysis in the model of mammalian brain cortex

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Abstract

Analysis of the real brain's neural activity can be performed in many different ways like for example electroencephalography. Sometimes the value of neural membrane potential is collected even from particular cells, using electrodes in neurophysiological experiments. However, this invasive method can be performed only on animals and in most cases leads to death of the experiment's subject. Computer modelling and simulation are often very important for the design of real experiments and in this paper we present the set of three new methods of neurodynamical analysis, two of them analogical to the probing used in neurophysiology and electroencephalography. We show that in some cases our approach can be even more effective than the techniques used in bio-medical laboratories.

1. Introduction

First attempts of the brain bioelectrical activity analysis are dated to the end of 19th century [1]. Caton investigated the correlation of the simple behaviour with the brain cortex electrical activity using specially constructed electrodes attached to the rabbit's skull. Later works of Berger [2] and Cybulski [3] began the rapid development of electroencephalographic techniques.

The main idea of electroencephalography (EEG) is to collect the potential changes generated by synchronic activity of neurons in some chosen part of the brain. Nowadays, more and more sensitive electrodes put on the head's skin are used to register potential changes and then the signal is transformed by special filters and amplifiers finally reaching the PC with appropriate software.

However, there are still many disadvantages of EEG: the data can be collected only from the cortex (where the neural activity is on the highest level), mainly from pyramidal neurons (which are most active), and the final results

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come from thousands of synchronically working neural cells. What's more, it is very hard to cut out all the electric noise coming not only from the outside (the PC, some other electrical devices necessary for conducting the experiment), but also from heart beating and electrical activity of the subject's body and muscles.

Nevertheless, using EEG methods can still be helpful in estimating regions of the cortex responsible for wide range of behavioural functions.

In 1952 Hodgkin and Huxley [4] ran experiments on the axon of the *Giant Squid* and in empirical way they formulated sets of equations describing the behaviour of biological neurons. In their model each neural cell can be treated as the ensemble of several (sometimes several thousands) equivalent electrical circuits, each described by the precisely defined set of nonlinear differential equations. Such equations can be integrated only numerically and after a few decades we have computers able to solve a problem consisting of hundreds of thousands of neurons modelled in such a way. Thanks that we construct models with relatively high degree of complexity and during the simulation the data resembling precisely the real dynamics of particular cells is collected.

In this paper we present three methods of data acquisition from the simulated biological neural networks. Our approach allows us to have the insight view into the dynamics both of the single neurons and the large parts of neural tissues using techniques similar to that known from medicine. Analysis resembling EEG can be performed with omitting the noise and what's more – the software approach makes possible the investigation of deeper than the top-cortex structures in the modelled brain. The methods described in this article are intended to be applied to the results obtained from completely new language and simulation system developed by our group. In future it will be also possible to analyse results obtained from commonly known neural simulators i.e., GENESIS [5], NEURON [6].

Single Neural Network Modelling Language (SNNML) is used to implement all of the three abovementioned tools. The new language is created in order to make simulations faster with the possibility of effective model construction by many independent neuroscientific groups and keeping the script as clear as possible.

2. Recording potential changes in single cells

The first device is called the Probe and it is responsible for collecting data from single cells. Its construction allows for the observation of potential changes on the membrane of the simulated neuron. Thanks to the Probe it is possible to create plots of spiking activity. Each Probe can be associated with given cell. There may be many Probes defined in the model, each of them is represented by the set of parameters:

$$P \equiv \{id_p, id_c, x, y, z, G, T\}, \tag{1}$$

where id_p and id_c are the unique Probe's and cell's identifiers, $[x,y,z]$ are its coordinates, G stands for the amplifier (multiplier of data collected) and T is its working time given in seconds or simulation steps in the model.

The output of the Probe is characterised as the function of membrane potential multiplied by G :

$$P(t) = G \cdot V(t). \tag{2}$$

Associating of the Probe with particular cell can be arranged in two ways: by putting the Probe in space and then it is connected to the closest neuron (Fig. 1A) or by giving the unique cell identifier (Fig. 1B) to which the Probe is to be attached.

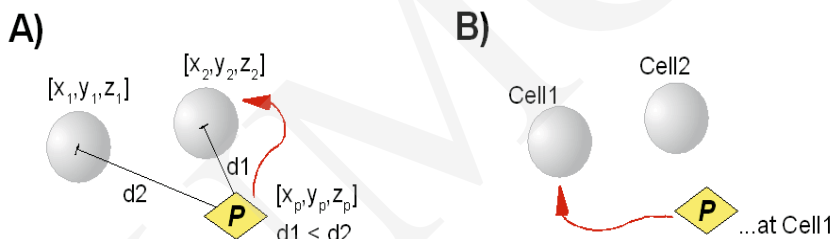


Fig. 1. The two ways of connecting the Probe to the cell (for detail see text)

The Probe and its potential analysis allows us to compare the bioelectric activity of simulated cells with neurophysiological data collected in *in vitro* or *in vivo* experiments. An example of two plots generated thanks to the application of the Probe are presented in Fig. 2.

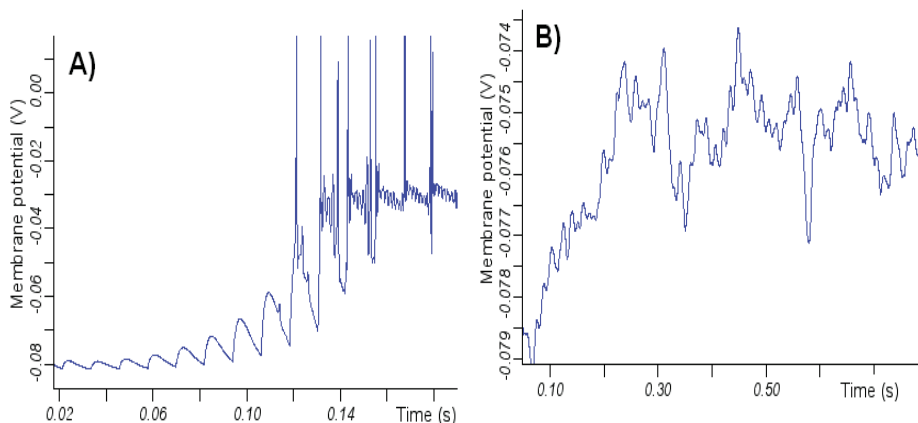


Fig. 2. Changes of single cells potential registered by the Probe. (A) Synaptic excitation leading to a series of spike potentials. (B) Balancing potential in a basket cell

3. Investigating activity of the region

Good observation of the activity in large group of neurons in chosen cortical area would make us implement a large number of Probes in the model and such an operation would dramatically complicate and elongate the simulation. It is also difficult to construct an algorithm responsible for the summation of many single cells activities.

That is why we present a special instrument collecting the neural activity from the selected area. So-called Probe Array has the formal definition:

$$M \equiv \left\{ \begin{array}{l} id_m, x_A, y_A, z_A, x_B, y_B, z_B, x_n, y_n, z_n, \\ \varepsilon, I(d), G, T, R_x, R_y \end{array} \right\}, \quad (3)$$

where the id_m parameter is the unique Probe Array identifier, $[x_A, y_A, z_A]$, $[x_B, y_B, z_B]$, $[x_n, y_n, z_n]$ are the coordinates of two points identifying the plane in space and its normal vector, ε stands for the maximum distance under which the element is regarded as a member of the plane, $I(d)$ – the function mapping the membrane potential value on the array, G – the multiplier, T – the working time and R_x, R_y set the two-dimensional probing resolution.

The Probe Array can be represented as the matrix $M = [M_{ij}]$ where $i = 0 \dots x$, $j = 0 \dots y$ and x and y are derived from the plane dimension, R_x and R_y . Elements of the matrix are calculated on the basis of membrane potential value collected from the neurons belonging to the defined part of the plane in five steps:

1. In the first step the plane of the Probe Array is situated in the space. This step is made before the simulation, during the compilation of the model.
2. The neurons that belong to the surface are localised with the precision of ε parameter. This step is made before the simulation as well.
3. Estimating so-called points of data acquisition P_{ij} for which the potential is calculated using R_x and R_y .
4. Calculating the Euclidean distance of considered neurons from each point of the surface P_{ij} .
5. Finally, elements M_{ij} are calculated for each point P_{ij} according to the rule:

$$M_{ij} \equiv V_{P_{ij}} = G \cdot \sum_{k=0}^n I(d(P_{ij}, C_k)) \cdot V_{C_k}, \quad (4)$$

where n is the number of neurons localised on the considered surface, $I(d)$ maps the membrane potential and is the function of $d(P, C)$ (the distance of k -th cell from the point P_{ij}), G – the multiplier and V_{C_k} is the value of the membrane potential collected from the cell C_k .

Probe Array does not have its equivalent in medical methods of brain analysis. However, it was designed in order to generate the detailed maps of network activity in precisely defined regions of investigated models. It is still

hard or impossible to achieve this using the EEG or even the tomography. Example of such maps is presented in Fig. 3.

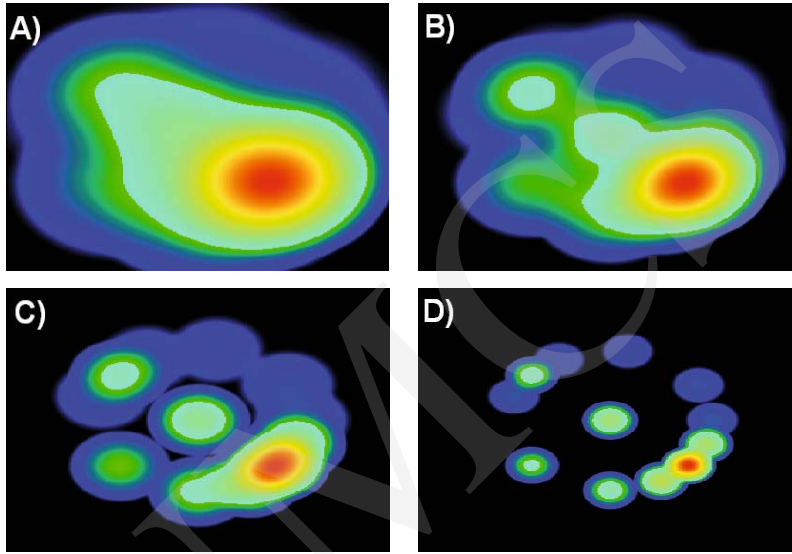


Fig. 3. Activity of a single hypercolumn registered by the Probe Array with different values of ε ($\varepsilon_A < \varepsilon_B < \varepsilon_C < \varepsilon_D$)

4. The Electrode

The Electrode is designed to get the results similar to these collected in EEG, however, we do not simulate exactly the physical behaviour of the real electrode. Instead of doing this we define the function:

$$E \equiv \{id_e, x, y, z, r, G, T, \rho(d)\}, \quad (5)$$

where id_e is the unique electrode's identifier, $[x, y, z]$ are its coordinates, r is the range of the sphere which the electrode "covers", G – the multiplier, T – working time and $\rho(d)$ is the sensitivity function calculating the value of activity depending from the distance from the electrode.

After calculating the distance and having estimated the neurons located in the Electrode's range, the summary current registered by the instrument is calculated according to the rule:

$$I_e = \sum_k \rho(d_k) \cdot I_k, \quad (6)$$

where $k = 0 \dots n$ stands for indexes of all neurons included in the r -ranged sphere, $\rho(d_k)$ is the function of the Electrode sensitivity and I_k is the value of the current flowing through k -th cell. The key-aspect of electrode modelling is the choice of its sensitivity function. In our simulator it can be constant, linear, Gaussian or

depending on the square of the distance, nevertheless, it is possible to define many other.

In Fig. 4 we present typical plots generated using the Electrode method of analysis.

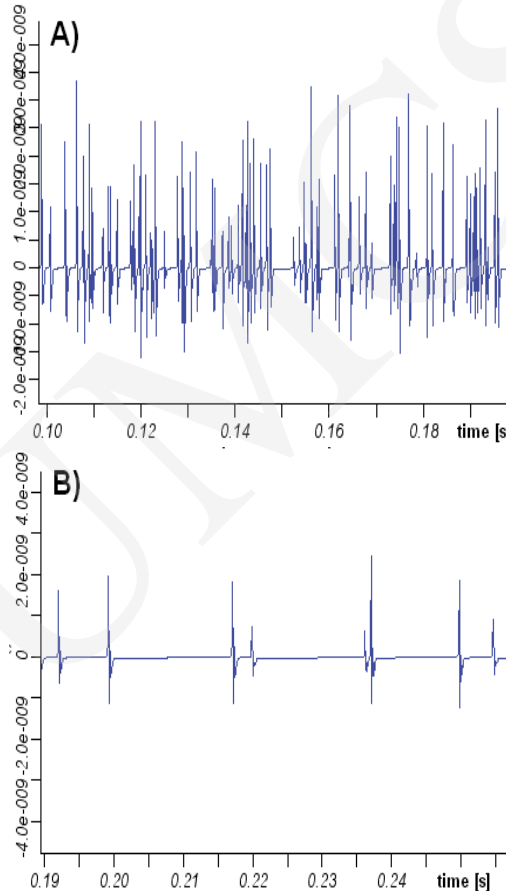


Fig. 4. The activity registered by the Electrode in (A) active and (B) inactive hypercolumn

5. Summary

We propose three instruments useful in the electrical analysis of activity in simulated biological neural networks. Two of them (the Probe and the Electrode) are inspired by neurophysiology and electroencephalography, the Probe Array has not its equivalent in medicine, however it gives us data still impossible to collect in experimental way. Results presented in this contribution are part of the large project realised in our labs. Together with newly constructed neural

simulation language, abovementioned methods can start a new chapter in computational neuroscience research.

Acknowledgements

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