Nonlinear Behaviour in the MPI-Parallelised Model of the Rat Somatosensory Cortex

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Abstract. Mammalian brains consisting of up to 10^{11} neurons belong to group of the most complex systems in the Universe. For years they have been one of the hardest objects of simulation. There are many different approaches to modelling of neurons, but one of the most biologically correct is Hodgkin-Huxley (HH) model. Simulations that require solving a large number of nonlinear differential equations (fundamental in HH model) are always time and power consuming. The structures discussed in this article simulate a part of the rat somatosensory cortex. We use a modular architecture of the network divided into layers and sub-regions. Because of a high degree of complexity effective parallelisation of algorithms is required. We propose method of parallelisation for the network and the results of simulations using GENESIS parallelised for MPI environment are presented. An occurrence of nonlinear behaviour is demonstrated. Most notably, in large biological neural networks consisting of the HH neurons, nonlinearity is shown to manifest itself in the Poincaré sections generated for the varying value of neural membrane's potential.

Keywords: Hodgkin–Huxley neurons, Poincare sections, nonlinear behaviour.

1. Introduction

The somatosensory pathway in mammalian nervous system brings sensory information from the outside into the brain, in particular from the rat's whisker to the somatosensory cortex. Information from the snout passes along the trigeminal nerve which is responsible for its projection to the trigeminal complex in the brainstem. The brainstem sends projections to the medial ventral posterior nucleus of the thalamus (VPm). Whiskers have representative physical structure in the brain, creating 2-D maps of each whisker pad throughout the pathway. In the cortex, these "maps" are known as barrels. They consist of clusters of stellate cortical neurons, with the cell bodies arranged in a ring and dendrites filling the "hole" in the middle. The dendrites form synapses with multiple axons rising from the VPm (Rat Somatosensory Pathway, 2006).

In physics, the dynamical system is recognised as a part of the world which can be seen as a self-contained entity with some temporal behaviour. In nonlinear dynamics, it usually corresponds to an abstract mathematical system which is a model for such an entity. Generally, dynamical system is defined by its state and by its dynamics (Rasband,

1989). The so-called membrane potential is typical physical variable describing the state of the neuron. Its evolution is ruled by fundamental laws of physics. Large biological neural networks are good examples of dynamical systems.

Our previous experiments showed that HH neurons tend to synchronise very quickly (Wojcik and Kaminski, 2004) during the simulation (which suggests typically periodical behaviour). On the other hand Self-Organised Criticality (SOC) phenomena were found in such systems (Wojcik *et al.*, 2007) and some frequency tuning properties of neurons have been also confirmed experimentally (Garcia-Lazaro *et al.*, 2006). The main objective of the research presented in this article was to check whether nonlinear behaviour occurs in the model of the rat somatosensory cortex? To investigate this we used the method of analysis in Poincaré sections.

Computer-based models of cortical tissues consisting of numerically complicated HH neurons (Hodgkin and Huxley, 1952) are power consuming. However, the simulation time can be shortened using cluster-based parallelised computing. Simulations presented in this contribution were conducted in a parallel version of GENESIS compiled for the MPI environment (Bower and Beeman, 1995; Genesis, 2006). The choice of GENESIS simulator was conscious as it has one of the best implementations of HH equations and allowed us use many processors. It will be shown that good parallelisation of the model can effectively shorten the time of simulation even in the case of a large number of connections requiring the intensive MPI message passing. Remarkably, in this article we will demonstrate that in large HH neural networks nonlinear phenomena do occur and we will show that the membrane's potential trajectory in Poincaré section is diffused. Consequently, the rat somatosensory cortex can be recognised as good example of nonlinear dynamical system, however, the role of such nonlinearity (although commonly known in artificial neural networks (Garliauskas, 2005; Garliauskas, 2007)) in real brains is still unknown.

2. Model and Parallelisation

In the simulations we used slightly modified version of the HH model (Hodgkin and Huxley, 1952). Neurons were relatively simple and consisted of 4 compartments (see Appendix A). The modification was arranged mainly to avoid a rapid synchronisation of the whole simulated system. We added one extra parameter to each synaptic connection and it was responsible for probability of exocitosis. The probability was set for the post-synaptic neuron. One may consider this randomness as a mean effect of the influence of outside. Such a change required a simple modification of original GENESIS code. Pre-compiled version of GENESIS for Linux and the MPI can be downloaded from (Genesis, 2006).

The constructed network consisted of 2025 neurons placed on a square-shaped grid with 45 rows and 45 columns. The pair of integer numbers from 0 to 44 identified each neuron. All the cells were divided into 22 groups, so called layers, numbered from 1 to 22 (from inner to outer). Communication (actually the MPI message passing) between

neurons was established based on the following principles – the output signal from each neuron from the layer m was transported in one direction to all the cells from layers: $m + 1, m + 2, m + 3, \ldots, m + N_s$, where N_s (called the number of neighbourhoods) was the natural number, not greater than the number of layers (see Fig. 1). Such a structure (2-D with dense "neural rings") imitated the structure of rat cortical barrels (Rat Somatosensory Pathway, 2006).

This structure can be effectively parallelised, so the problem was split into 15 processors.

The idea of parallel version of GENESIS is to simulate a given number of cells on a single node. When there are to many neurons or connections simulated on a single machine some of the lack of memory problems may appear and the simulation crashes. In the parallel version, each node is waiting for the end of computations on the nodes that is is exchanging messages with, the special mechanism of so-called barriers provides us with the proper and synchronous work of the whole system.

That is why the network was divided into 15 zones. The same number of neurons was simulated in each zone. Zones were numbered from 1 to 15. Zones arranged thereby are presented in Fig. 1. Such a choice allowed us run simulations in optimal way, without the barriers being timed out. The complexity of the system increases rapidly with N_s, so
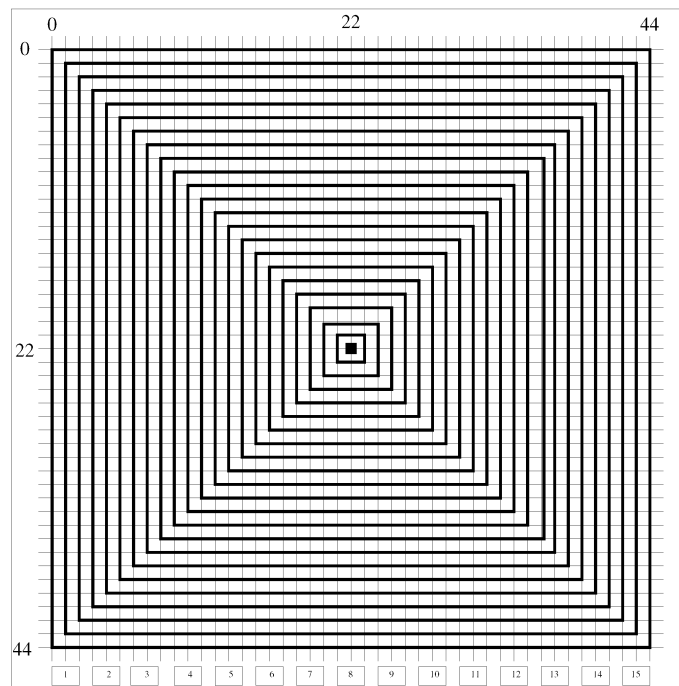

Fig. 1. Scheme of the simulated network. Layers are highlighted by thick lines. Stimulating neuron is marked with the black square and all other neurons are put on the intersections of grid lines. Neurons coordinates are marked on the top and the left side of the scheme. In each zone there are 3 columns of neurons as marked at the bottom. The choice of columns belonging to particular zones is arbitrary.

does the time of simulation. In this case parallelisation not only shortens the simulation time, but most often makes the model executable at all. This is main reason justifying the use of parallelisation techniques. Such a way of problem's solving is priceless especially when the biological correctness and all properties of HH are required, especially when the built system includes a large number of synapses.

Three parameters characterised each synaptic connection: weight w, time delay τ and the already mentioned probability of exocitosis p. The p was set to be a constant and was the same for all the synapses ($p = 0.5$).Values of two other parameters depended on the coordinates of both the pre-synaptic and post-synaptic neurons. For each pair of neurons (from the m-th and the n-th layer) the parameters w and τ were calculated according to following rules:

$$w = \frac{w_0}{|m - n|}, \tag{1}$$

$$\tau = 10^{-4}|m - n|\,[s], \tag{2}$$

where w_0 was a positive constant (in our simulations $w_0 = 2$). The network was stimulated by the neuron $N[22, 22]$ that corresponded to the main receptor of activities from outside of the net (i.e., glass capillary stimulating the rat's whisker (Garcia-Lazaro *et al.*, 2006) or an electrode transmitting some random stimulus directly into the cortex). As a result, the receptor was producing a periodic spike potential with a frequency of about 80 Hz. In addition, the simulation was characterised by the parameter T that corresponded to the system's working time usually, in our simulations, $T = 15$ s.

3. Simulations and Results

For some chosen neurons the time of spike potential occurrence was collected. The central neuron was transmitting the stimulation to all other cells in agreement with network's architecture. The activity of the whole system was examined, however, because of high degree of symmetry in the network we generated Poincaré sections only for the neurons with the first coordinate equal 25 (as a kind of cross section that does not go through the centre).

Generally, in the theory of nonlinear systems, when the trajectory drawn in Poincaré section is diffused, we can talk about the nonlinear behaviour. That means that it is impossible to predict some next positions of for example the pendulum basing on its previous states (Rasband, 1989).

Figs. 2–5 prove that neurons in simulated part of the rat somatosensory cortex behave in nonlinear way. What's more, the degree of curve diffusion depends both on the distance of particular neurons from the central neuron and on network's complexity. In Fig. 2 the $N_s = 1$, the number of connections in the network is relatively small and neuron $[25, 22]$ shows small evidence of nonlinearity. Presumably, small nonlinear behaviour results of the correlation of spike potentials occurring on neurons that are situated near the centre of the net. Their work is both highly regular and synchronised with the central neuron
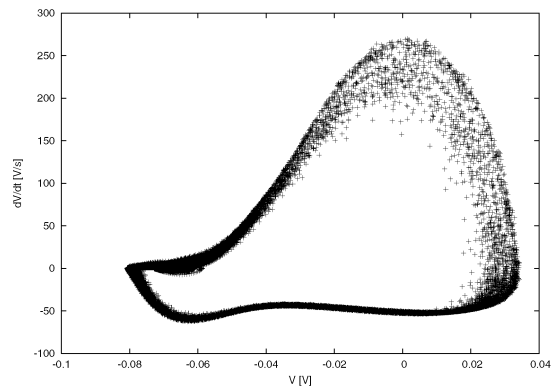
Fig. 2. Poincaré section for membrane potential generated for neuron [25,22] ($N_s = 1$ and $T = 15$ s).
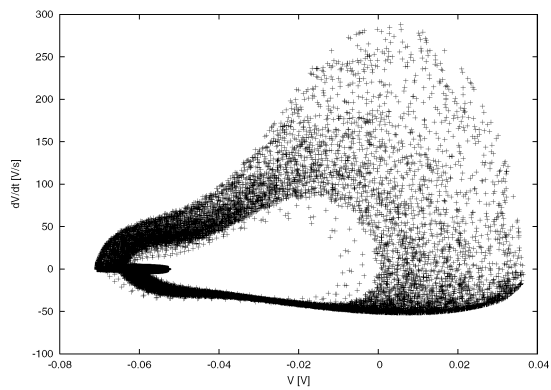

Fig. 3. Poincaré section for membrane potential generated for neuron [25,0] ($N_s = 1$ and $T = 15$ s).

receiving impulses from the outside. Nevertheless, Fig. 3 presents the Poincaré section for the network with the same number of neighbourhoods ($N_s = 1$) but generated for neuron $[25, 0]$ which is far from the central stimulating unit. The nonlinear behaviour can be clearly observed there. The degree of nonlinearity also increases together with the number of connections (actually N_s) present in the system. Figs. 4–5 show Poincaré sections obtained for $N_s = 6$ and $N_s = 13$.

Benchmark tests of the local cluster (see Appendix B) and GENESIS for the MPI were also performed. The length of a typical run for $T = 15$ s was about 12000 s (3.5 hours) when the problem was parallelised for 15 nodes. For discussed simulations the speedup of about 2.78 was obtained if compared to 3-processor run. Of course the time of simulation depends on the number of connections established in the system. Fig. 6 presents the simulation's time as function of N_s. The jump in simulation time for $N_s > 12$ originates from the high increase of the connections number in the system. After reaching some critical number of synapses on a single node the simulation rapidly slows down and the communication among particular machines becomes more intensive. For example on a
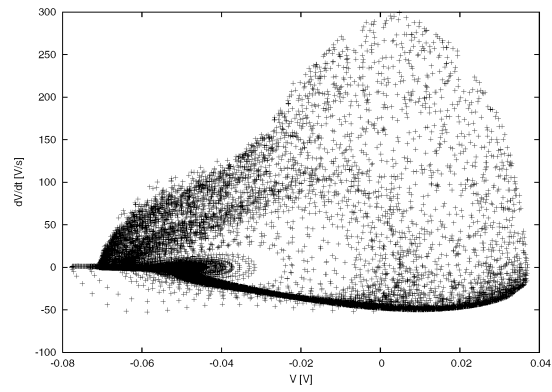
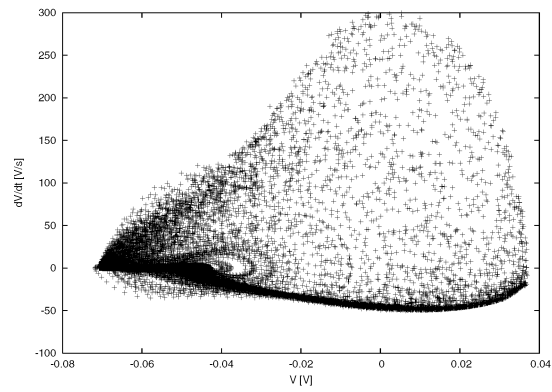Fig. 4. Poincaré section for membrane potential generated for neuron [25,5] ($N_s = 6$ and $T = 15$ s).

Fig. 5. Poincaré section for membrane potential generated for neuron [25,44] ($N_s = 13$ and $T = 15$ s).
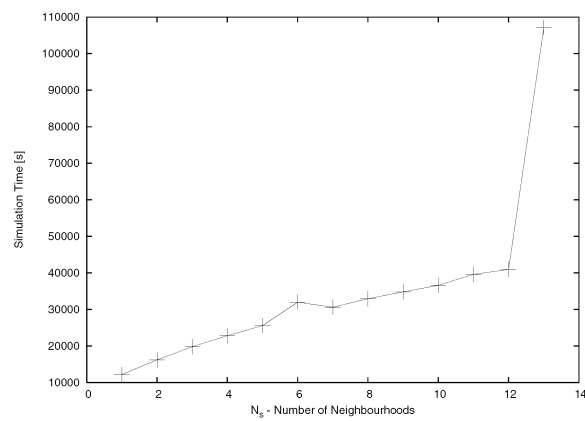

Fig. 6. Time of simulation as a function of N_s ($T = 15$ s).

single machine it is not possible to run a simulation for $N_s > 10$ in a reasonable time. In the first view the speedup of 2.78 is not very optimistic, however, for networks with $N_s > 6$ simulation on one SPARC 400 MHz node takes longer than three weeks.

Our cluster is only a part of the large CLUSTERIX grid project. With an access to 800 processors we will be able to run simulations of millions of neural cells, covering in the constructed model, the whole tissues of mammalian brain. However, initial results of investigating nonlinearity, chaos and self-organisation seem to be very promising.

4. Conclusions

Results of the rat somatosensory cortex simulations were presented. The system's modular structure makes possible a good parallelisation as the particular zones can be simulated on separate nodes. Presented model is scalable and the number of neurons in each zone can be easily increased. Initially we simulated about 2000 of HH neurons. Some biologically-inspired topology was arranged and results proved that processes pertinent to other complex systems take place. In particular, neurons in such systems tend to behave in nonlinear way. In planned experiments we are going to investigate in theoretical way the biological reasons for such a behaviour. Good theoretical and experimental understanding of nonlinearity in brain microcircuits may result in new field of computational neuroscience research.

Appendix A: Properties of HH Neurons

Our model consists of multicompartmental neurons with two dendrite compartments, a soma, and an axon. The dendrites contain synaptically activated channel and the soma has voltage activated HH sodium and potassium channels. The behaviour of each compartment is equivalent to the behaviour of some electrical circuit (Bower and Beeman, 1995). Thus, each circuit is characterised by a group of parameters (these parameters are typical for GENESIS) set as follows: resistances $R_a = 0.3\,\Omega$, $R_m = 0.33\,\Omega$, capacity $C_m = 0.01$ F, and potential $E_m = 0.07$ V. For the soma compartment $E_k = 0.0594$ V and for the dendrite $E_k = 0.07$ V. Conductance for each type of ionic channels is chosen to be: $G_K = 360\,\Omega^{-1}$ and $G_{Na} = 1200\,\Omega^{-1}$. These parameters originate from neurophysiological experiments (Bower and Beeman, 1995) and are chosen to make the model biologically more realistic. The soma has a circular shape with the diameter of 30 μm, dendrites and axon are cable-like with the length of 100 μm. All the other parameters are chosen as suggested by GENESIS authors to simulate the behaviour of the biological-like neurons (Bower and Beeman, 1995). More details concerning the HH model can be found elsewhere (Bower and Beeman, 1995; Hodgkin and Huxley, 1952).

Appendix B: Details of Simulations' Hardware and Software Environment

The local cluster used for all simulations and discussed in this contribution was built of 12 machines and 1 additional machine – the so-called "access node". Each SMP machine had two 64-bit 1.4 GHz Itanium2 IA64 processors with 4 GB of RAM memory. The cluster works under control of Debian Linux Sarge (v. 3.1) and 2.6.8-1 kernel version. The model is simulated in GEneral NEural SImulation System GENESIS v.2.2.1 with its MPI extension. A gcc was used for the system compilation. The compilation of GENESIS for LINUX and MPI required some tuning of its code and can be found in (Genesis, 2006). The 2.2 version of GENESIS was originaly predicted to be run on PVM machines. Ours changes made it compilable for LINUX MPI. The newest versions of GENESIS (2.3 and higher) have the support for MPI environment.

Acknowledgements

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G.M. Wojcik was born in 1976 at Nisko in Poland and is working and living in Lublin. In the year of 2000 he was awarded the master of science degree at the Faculty of Mathematics, Physics and Informatics of Maria Curie Sklodowska University (Lublin) and in 2004 gained the PhD in computational physics. His scientific interests cover computational artificial intelligence, modelling of biological systems, thermodynamical and informational analysis of large biological neural networks, since 2004 high performance computing.

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Netiesiškumas žiurkės somatosensorinės žievės MPI-išlygiagretintame modelyje

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Žinduolių smegenys priklauso pačių sudėtingiausių sistemų visatoje grupei. Atitinkamai, tai yra vieni iš sudėtingiausių modeliavimo objektų. Straipsnyje neurono modeliavimui buvo pasirinktas vienas iš biologiškai korektiškiausių – Hogkin–Huxley modelis. Šį modelį sudaro netiesinių paprastųjų diferencialinių lygčių sistema, kurios skaitinis sprendimas yra gana brangus, todėl neuroninių tinklų modeliavimas jo pagalba reikalauja didelių skaičiavimų resursų. Lygiagrečiųjų technologijų panaudojimas šioje srityje leidžia ne tik ženkliai sumažinti modeliavimo laiką, bet ir iš esmės išplėsti išsprendžiamų uždavinių klasę. Straipsnyje skaitinis modeliavimas atliekamas paketo GENESIS (GEneral NEural SImulation System) lygiagrečiosios versijos pagalba. Darbe buvo sudarytas tinklas iš 2025 neuronų, aprašantis žiurkės somatosensorinės žievės dalį. Skaičiavimuose tinklas buvo paskirstytas tarp 15 procesorių. Gauti rezultatai rodomi atskirų neuronų membranos potencialo Puankare pjūviuose. Potencialų trajektorijų difuzija parodo sistemos netiesiškumą. Biologinės šio netiesinio elgesio priežastys yra nežinomos. Jas planuojama tirti tolimesniuose darbuose.