Liquid Computations and Large Simulations of the Mammalian Visual Cortex

Grzegorz M. Wojcik and Wieslaw A. Kaminski

Institute of Computer Science
Department of Complex Systems and Neurodynamics
Maria Curie-Sklodowska University
Plac Marii Curie-Sklodowskiej 5, 20-031 Lublin, Poland
gmwojcik@gmail.com

Abstract. Large artificial Hodgkin-Huxley neural networks are examined. The structures discussed in this article simulate the cortex of the mammalian visual system. We use a modular architecture of the cortex divided into sub-regions. Results of parallel simulations based on the liquid computing theory are presented in some detail. Separation ability of groups of neural microcircuits is observed. We show that such property may be useful for explaining some edge or contrast detection phenomena.

1 Introduction

The human brain and its cortex are probably the most complex systems known. A structure built of about 10^{11} interacting neural cells is always a hard object for simulation, even for the fastest super-computers. A new idea of brain modelling was suggested by Maass [1] and since then it has been called Liquid State Machine (LSM) [2]. In general, the brain (or its fragment) is treated as a liquid. The cortex is built of neurons organised in microcircuits [3] which form columns and the function of each column depends on its location in the brain. Cortical microcircuits turn out to be very good "liquids" for computing on perturbations. They are characterised by the large diversity of their elements, neurons, synapses, the large variety of mechanisms and time constants characterising their interactions, involving recurrent connections on multiple spatial scales. Like the Turing machine, the model of LSM is based on a strict mathematical framework that guarantees, under ideal conditions, universal computational power [1]. Applying ideas of liquid computing [1] allows to decrease the number of neurons in the constructed model. In addition, the simulation time can be dramatically shortened using cluster-based parallelised simulations of groups of microcircuits.

It has been discovered that simple cells in cat's primary visual cortex (V1) are specialised for the orientation of light and dark borders [4]. The orientation selectivity of simple cells in V1 comes from an oriented arrangement of the input from the Lateral Geniculate Nuclei (LGN). Namely, ON-centre LGN inputs have receptive fields centres aligned over simple cell's ON sub-regions, and similarly for OFF-centre inputs [5]. Some observations of monkey cortex suggest that the microstructure of V1 is spatially periodic [6]. Thanks such architecture many

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phenomena of signal processing occurring in visual systems can be explained. Visual pathway and detailed description of ON-OFF centres can be found elsewhere [7].

In this paper we present some results of mammalian visual cortex simulations. We prove that our model can help to understand some edge or contrast detection phenomena.

2 The Model of Mammalian Visual System

Discussed model of mammalian visual system consists of two main modules (Fig. 1). Because the idea of LSM calls for such an architecture, our model includes "Input" (Retina) and "Liquid" (Cortex) [1]. All simulations discussed in this paper are conducted in parallel version of GENESIS for MPI environment (for parallelisation effectiveness, time of typical runs and other detail see Appendix A). Neurons used in the simulations are built according to the Hodgkin-Huxley model [8] and are relatively simple (for detail see Appendix B).

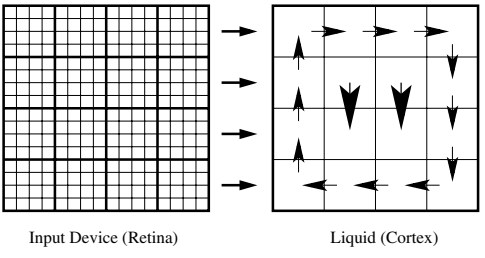

Fig. 1. The model of simulated visual system. The arrows represent connections of HHLSM columns (for detail see text).

The Retina is built on 16×16 square-shaped grid and divided into 16 patches (4×4). Each patch is connected with one of 16 HHLSM (Hodgkin- Huxley Liquid State Machine) columns which simulate LGN and the ensemble of cortical microcircuits (retinal cells are connected only with LGN). HHLSM consists of 1024 cells put on a $8 \times 8 \times 16$ grid. There are layers arranged in each column (Fig. 2) and the set of columns simulates the Liquid. There are 80% of excitatory connections established among layers and neurons of each layer and 20% of inhibitory connections. In addition, layers L6 of some columns are connected with LGNs of other HHLSMs in the same way, simulating the corticothalamic feedback. Intercolumn connections are presented in Fig. 1. Each connection in the model is characterised with some "delay" parameter and random weight. The thick arrows in Fig. 1 represent connections with short delays ($d_1 = 10^{-4}$ s) and the thin arrows correspond to connections with long delays ($d_2 = 10^{-3}$ s). We choose such topology to model ON and OFF-centre subregions of V1. We can treat the "Liquid" as a hypercolumn in some part of periodic structure of the cortex.

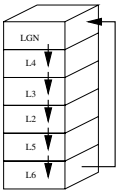

Fig. 2. Structure of HHLSM column as the fundamental microcircuit

Such a model can be easily scaled into multiprocessor simulation. In discussed research each column and its corresponding retinal patches should be simulated on one node. It should be noted that 16 processors were required for the best realisation of the model and additional one for the simulation control. However, the Retina may be easily divided into 4 (2×2), 64 (8×8) or 256 (16×16) patches, depending on the number of processors available. Thus, if each patch is connected with corresponding HHLSM column - it should be possible to conduct a simulation of about 256 thousands Hodgkin-Huxley neural cells.

3 Simulation and Results

We investigated the model consisting of 16640 neurons (as the Liquid is simulated by the ensemble of 16 HHLSM columns). Twelve patterns were arranged on the Input Device (Fig. 3). Retinal cells chosen for each pattern were then stimulated with random spike trains. The input signal was encoded in Liquid's state. We define the state of the Liquid by a multidimensional vector with binary coordinates 0 for a "sleeping neuron" and 1 for an "active" neuron. The "dead-state" corresponds to the Liquid with all neurons "sleeping".

We simulated 500 ms of biological work of our system. The main objective of current research was to check the Euclidean distance of states of the liquid for different couples of input patterns.

The results confirm liquid computing abilities of neural microcircuits. In each case a meaningful difference in states of the liquid was observed for different

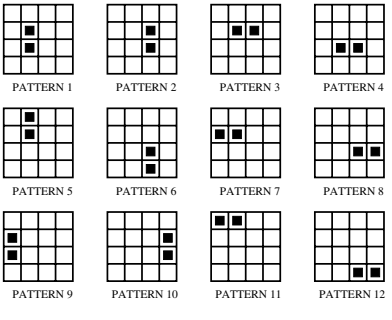

Fig. 3. Set of input patterns stimulating the retina

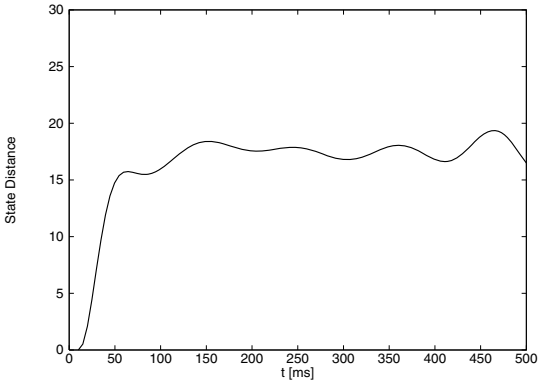

Fig. 4. The liquid state distance for two different spike trains given as an input to retinal pattern 1

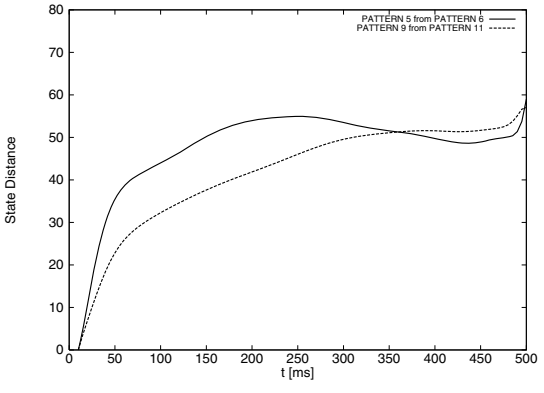

Fig. 5. Liquid state distances for different input spike trains given as input to retinal patterns 5,6 (solid line) and 9,11 (dashed line)

spike trains stimulating even the same retinal pattern (Fig. 4). It is usually a very typical behaviour for LSM. However, Maass' LSM has been built of integrate and fire neurons, while our structure consists of much more biologically realistic Hodgkin- Huxley neural cells. Additionally, for the states of two geometrically different input patterns even larger "distance of liquids" was observed (Fig. 5).

In general, we can divide the set of input patterns into three groups: the Retina for patterns $1-4$ (group 1) has ON-centre receptive fields stimulated, patterns $9-12$ (group 2) stimulate the OFF-centre sub-regions and patterns $5-8$ (group 3) send impulses both to ON and OFF-centre patches of the Input Device. Figs. 6-8 present the state of liquids measured as the distance from the so-called "dead state" (liquid is in the "dead-state" when nothing is stimulating its cells). One can note different tendencies for each of three pattern groups. In Figs. 6-7 we present typical plots from pattern group 1 and 2 respectively. Network's architecture implies such behaviour: large delays in OFF-centre V1 microcircuits

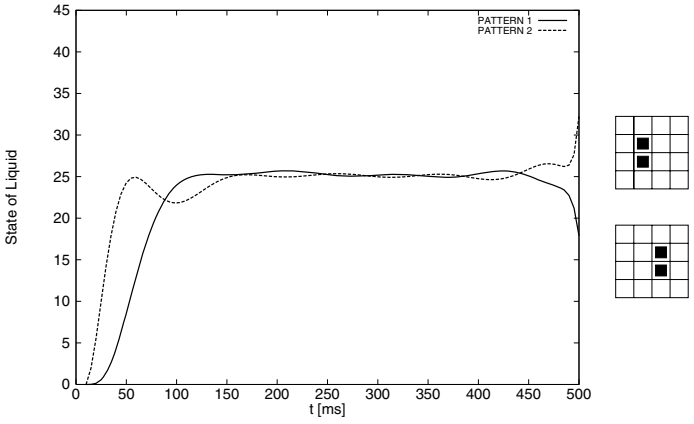

Fig. 6. Liquid distance from the dead-state for two patterns from group 1

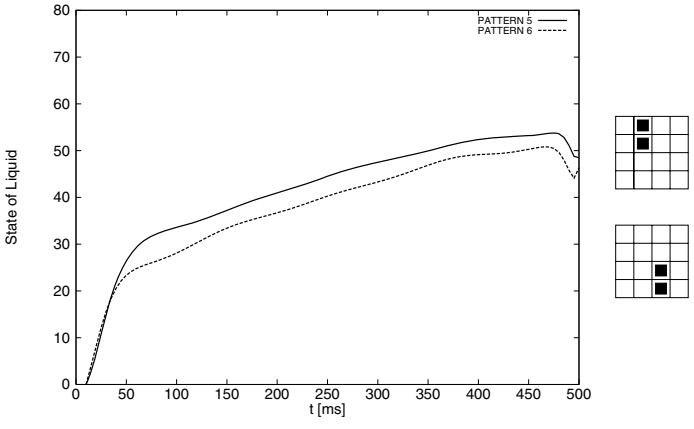

Fig. 7. Liquid distance from the dead-state for two patterns from group 2

cause more action spike potentials in the late phases of simulations. In addition, for patterns from the 2nd group we obtain activity of both ON and OFF-central HHLSMs. Fig. 8 shows characteristics for patterns 7 and 12. It should be noted that 12th pattern belongs to the 3rd group. In this case only the OFF-centre area of the cortex is stimulated and whole liquid activity is relatively smaller.

The distance curve in Figs. 6-8 goes down after 475 ms as result of intended and decreased retinal activity in the end of simulation. In the case of simulations longer than 500 ms the typical behaviour (like from 100 ms - 400 ms parts of the plots) was observed.

Following Maass' [1] ideas and applying a readout for liquid state analysis we can imagine some expert-devices able to classify ON and OFF-central patterns. Implementing different delays for connections and arranging a proper architecture of the simulated cortex can then lead to a better understanding of, for example, contrast or edge detection phenomena.

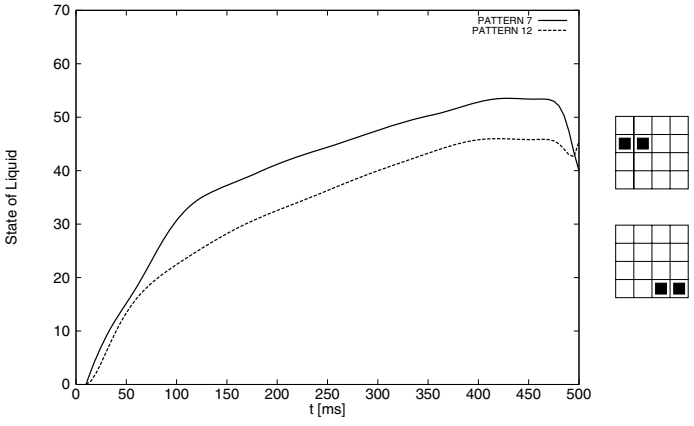

Fig. 8. Liquid distance from the dead-state for two patterns from group 2 and 3

4 Conclusions

In this paper we report results of the mammalian visual cortex' simulations. We simulated about 16 thousands Hodgkin-Huxley neurons organised in layers and cortical microcircuits. Some biologically-inspired topology was arranged. The results prove that such organisation of the cortex has good separation ability characteristic for LSM and model used for this article can explain some natural pattern recognition phenomena.

The modular structure of visual cortex makes possible the application of good parallelisation as particular microcircuits can be simulated on separate nodes. Our model is scalable and we can easily increase the number of neurons in each cortical column which will let us run simulations consisting of more than 256 thousands Hodgkin-Huxley neurons. This will help us build more realistic model of visual cortex. Most of the discussed simulations were conducted on the local cluster. Our machine is part of the CLUSTERIX grid project [10]. With access to 800 processors and by increasing the number of simulated microcircuits a structure consisting of several millions of neural cells simulated in a similar way can be imagined. This could lead to the creation of very sophisticated models and such possibility can open for us quite new field of computational complex systems' research.

Acknowledgements

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Appendix A: 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 compiler was used for the general system configuration.

The length of a typical run was about 3000 s. The problem was parallelised for 17 nodes. Some benchmarking was done for the parallelisation. The speedup of $11 - 12$ if compared to $1 - 2$ processor runs was obtained.

Appendix B: Properties of Hodgkin-Huxley Neurons

Our HHLSMs consist of multicompartmental neurons with two dendrite compartments, a soma, and an axon. The dendrites contain synaptically activated

channel and the soma has voltage activated Hodgkin-Huxley sodium and potassium channels. The behaviour of each compartment is equivalent to the behaviour of some electrical circuit [9]. Thus, each circuit is characterised by a typical for GENESIS group of parameters 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 whilst 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 [9] and are chosen to make the model biologically more realistic. The soma has a circular shape with the diameter of 30 μm, while 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 [9]. More details concerning Hodgkin-Huxley model can be found elsewhere [8].