Computational ability of LSM ensemble in the model of mammalian visual system

Grzegorz M. Wójcik[*], Wiesław A. Kamiński

Department of Complex Systems and Neurodynamics, Institute of Computer Science, Maria Curie-Skłodowska University, Pl. Marii Curie-Skłodowskiej 5, 20-031 Lublin, Poland

Abstract

Ensembles of artificial Hodgkin-Huxley neural microcircuits are examined. The networks discussed in this article simulate the cortex of the primate visual system. We use a modular architecture of the cortex divided into columns. The 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 pattern recognition phenomena.

1. Introduction

The primate brains and their cortex are said to be 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 seem 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]. Application of liquid computing ideas [1] allows to decrease the number of neurons in the constructed model. In addition, the simulation time can be significantly shortened using cluster-based parallelised simulations of groups of microcircuits.

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[*]Corresponding author: *e-mail address*: gmwojcik@gmail.com

In this paper we present some results of mammalian visual cortex simulations. We prove that our model can help to understand some pattern recognition phenomena thanks to the separation abilities of cortical microcircuits ensembles.

2. The model of mammalian visual system

The discussed model of the 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].
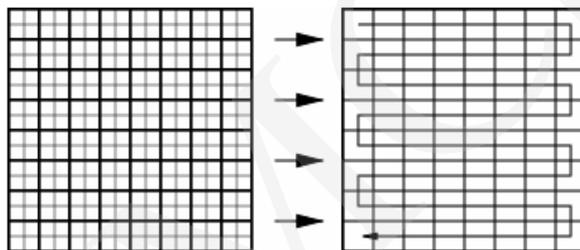

Fig. 1. The model of simulated visual system. The arrow represents possible connections of HHLSM columns (for detail see text)

All simulations discussed in this paper were 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 [5] and are relatively simple (for detail see Appendix B).

The Retina is built on 16×16 square-shaped grid and divided into 64 patches (2×2). Each patch is connected with one of 64 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 8×8×16 grid. There are layers arranged in each column (Fig. 2) and the set of columns simulates the Liquid.
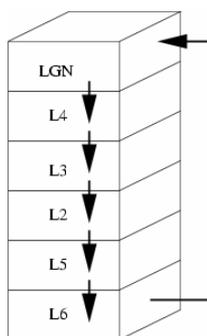

Fig. 2. Structure of HHLSM column as the fundamental microcircuit

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 (i.e. with the probability of 30%), simulating the corticothalamic feedback. The pathway of the possible intercolumn connections is presented in Fig. 1. Each connection in the model is characterised with some "delay" parameter and random weight. We can treat the "Liquid" as a hypercolumn in some part of periodic structure of the cortex.

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

3. Simulation and results

The model consisting of 65792 neurons (as the Liquid is simulated by the ensemble of 64 HHLSM columns) was investigated.

In the first series of simulations we stimulated all the Retinal cells with random spike trains. The input signal was encoded in the Liquid 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. We simulated 500 ms of biological work of our system. The main objective of this research was to check the Euclidean distance of states of the liquid for different couples of changing in time or geometrically different 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 spike trains stimulating the "whole retinal" pattern (Fig. 3). In Fig. 3 the distance of the Retina state was marked with solid line. It is clearly notable that the distance of the liquid is much larger. Such separation ability is usually a very typical behaviour of 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 the separation ability was also observed. Fig. 4 presents the state distance of both the Retina and the Liquid for the case when only 30% of the Retinal cells were stimulated.
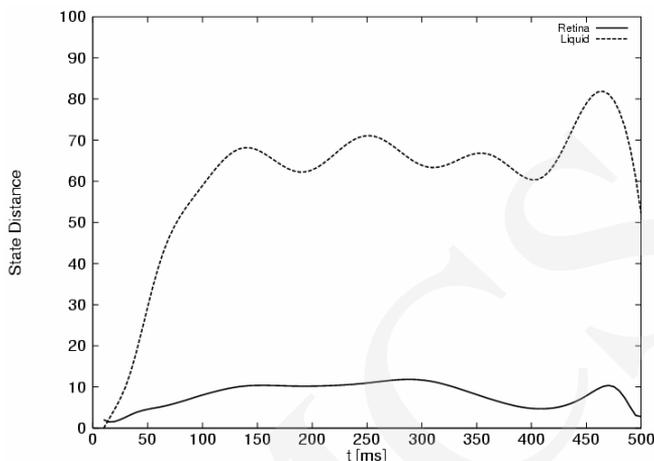
Fig. 3. State difference of the Liquid (dashed line) and the Retina (solid line) states
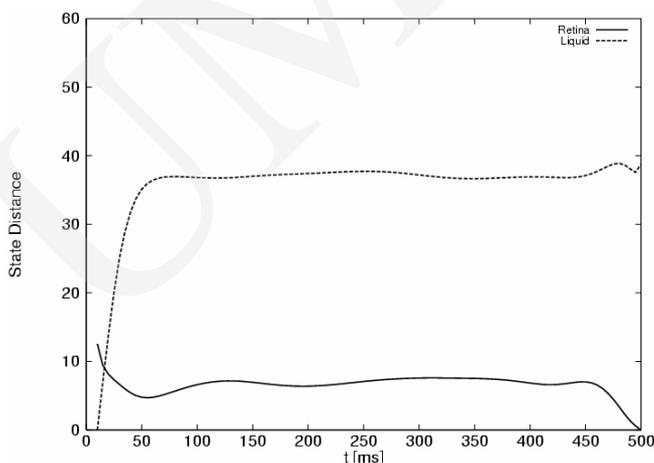for two changing in time spike trains stimulating all cells of the Retina

Fig. 4. State difference of the Liquid (dashed line) and the Retina (solid line) states for two
changing in time spike trains stimulating 30% cells of the Retina

Following Maass' [1] ideas and applying a readout for liquid state analysis
we can imagine some expert-devices able to classify geometrically different and
changing in time patterns. Implementing neural models and arranging a proper
architecture of the simulated cortex can then lead to a better understanding of,
for example, pattern recognition phenomena taking place in the real brains.

Conclusions

In this paper we report the results of the mammalian visual cortex'
simulations. We simulated about 65 thousands Hodgkin-Huxley neurons
organised in layers and cortical microcircuits. The results prove that such

organisation of the cortex has good separation ability characteristic of LSM and model used for this article can explain some natural pattern recognition phenomena.

The modular structure of visual cortex makes application of good parallelisation possible 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 models of visual cortex. Most of the discussed simulations were conducted on the local cluster. Our machine is part of the CLUSTERIX grid project [6]. 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 a new field of computational complex systems research.

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 12000 s. The problem was parallelised for 64 nodes.

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 that of some electrical circuit [6]. Thus, each circuit is characterised by a typical for the 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 $G_{Na} = 1200 \; \Omega^{-1}$. Most of these parameters originate from neurophysiological experiments [6] and were 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
[6]. More details concerning the Hodgkin-Huxley model can be found elsewhere
[4].

References

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