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Liquid state machine built of Hodgkin-Huxley neurons–pattern recognition and informational entropy

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Abstract

Neural networks built of Hodgkin-Huxley neurons are examined. Such structures behave like Liquid State Machines. They can effectively process geometrical patterns shown to "artificial retina" into precisely defined output. The analysis of output responses is performed in two ways: by means of Artificial Neural Network and by calculating informational entropy.

1. Introduction and problem statement

The idea of simulating the behaviour of whole brain was suggested by Maass and since then it has been called Liquid State Machine (LSM) [1,2]. In general, the brain (or a fragment of it) is treated as a liquid. Neural microcircuits turn out to be very good "liquids" for computing on perturbations because of the large diversity of their elements, neurons and synapses [3], and the large variety of mechanisms and time constants characterising their interactions, involving recurrent connections on multiple spatial scales [1]. Like Turing machine, the model of LSM is based on strict mathematical framework that guarantees, under ideal conditions, universal computational power as proved in [1]. Idea of the Maass' LSM is shown in Fig. 1. The "liquid" is represented by the column consisting of some integrate and fire neurons. Randomly chosen neurons of the liquid are stimulated by input signals u'*s*. From a formal point of view one can talk about some mapping function realised in the liquid. This function transforms the input into the "readout" layer which gives output signals y'*s*.

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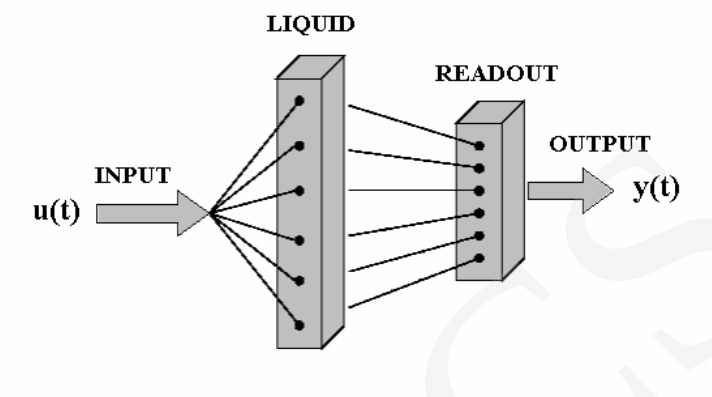

Fig. 1. Scheme of the Maass' LSM

Using the LSM model we simulate some biological visual system. In this paper we will prove that fundamental microcircuits built of Hodgkin-Huxley neurons transform some input signals into output activities in a precisely defined way. This output activities can be effectively analysed by Artificial Neural Network (ANN). ANN conducts reversible operations to the biological system and it will be shown that such a structure can generalise "biological responses" correctly. In order to check generalisation abilities of the visual system we will also discuss the problem in terms of informational entropy, e.g. changes of the entropy for different "patterns" will be analysed in some detail.

2. Concept of neural computations and results

Mammalian brains are built of microcircuits. Microcircuits are organized in columns, and the function of particular microcircuit may be different depending on the part of brain in which it is situated. We want to model the simple biologically based visual system. To be biologically correct we use 4-neuron microcircuits in our structure. An input device (ID) similar to the retina is built of 25 microcircuits. As a part of primary visual cortex we build a set of 25 Hodgkin- Huxley Liquid State Machines (HHLSMs). There are 24 neurons in each HHLSM. Randomly chosen microcircuits of ID are connected with randomly chosen HHLSMs. The same architecture of connections is arranged between the cortex and the "readout" device (see Fig. 2). The readout consists of 100 neurons and its architecture is the same as ID.

All of the structures described above are simulated in GEneral NEural SImulation System (GENESIS) [4]. This simulator lets the user build many different classes of neural circuits and networks. Thanks to the object oriented programming one can implement to each neuron different kinds of modules and connect them using his own rules. The simulator includes two parts: Script

Language Interpreter (SLI) and the X-Windows Display and Output Utility for Simulations (XODUS). The syntax of SLI is close to the syntax of C++ and UNIX shell. XODUS contains a set of objects useful for graphical presentations of results. GENESIS can be run on almost all UNIX systems, including Linux.

The neurons of ID are stimulated by series of 9 different spike patterns (see Fig. 3). The amplitude of spikes is set to be A=0.2 mV. Spike patterns are transformed by the cortex. As a result, some activity responses of the readout are collected.

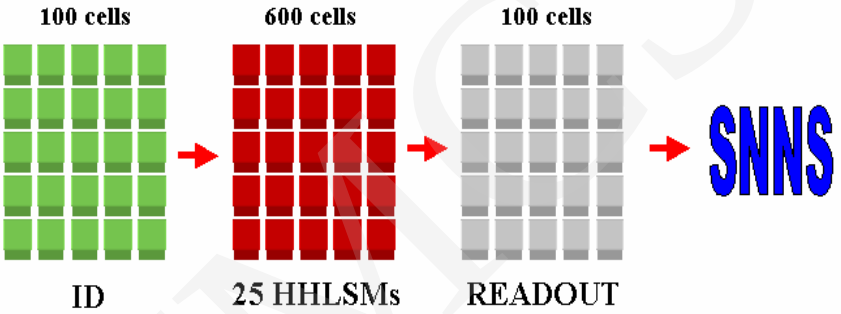

Fig. 2. Scheme of simulated biological-like visual system

Analysis of readout responses is performed using ANN simulated within Stuttgart Neural Network Simulator (SNNS) [7]. The network has 100 inputs, 2 hidden layers and 100 outputs[1] (see Fig. 4). In each hidden layer there are 12 units. The idea of using ANN in order to analyse biological responses comes from Maass works and in our simulations SNNS plays a role of "visual consciousness".

Our aim is to create an artificial structure able to conduct reversible operations of the above mentioned biological system. We train ANN with "biological responses" of the readout. These responses are treated as ANN's inputs. After learning process we stimulate the biological neurons of ID by some patterns slightly different from those presented in the training process. The difference in this case means that i.e. the position of the "diagonal" shown to retina is moved a bit, or the shape of the "square" is "not ideal" (compare with original patterns in Fig. 3). New readout activity patterns are collected on the biological system and given as inputs to trained ANN. In all cases we obtain correct responses (see Fig. 5) thus the ANN can generalize and classify noisy patterns correctly. It turns out that ANN is able to classify effectively given patterns even though it did not see them before. In other words the biological

[1] Full connections are arranged in the system. As a training function we choose RPROP (Resilient Backpropagation) algorithm with learning parameters: 0.1, 30, 40 and 400 training cycles [8].

system maps the diffused inputs in such a way that the responses of its readout are good enough for ANN inputs.

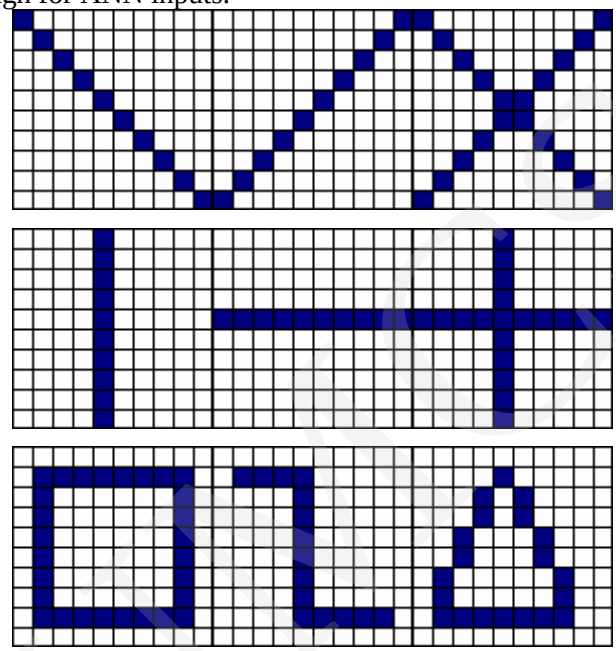

Fig. 3. Set of 9 different patterns shown to the ID

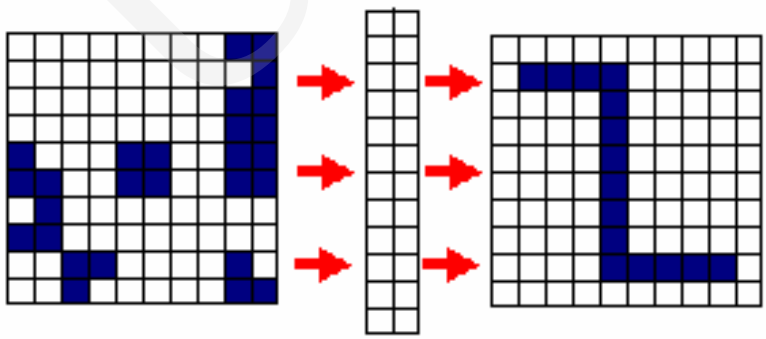

Fig. 4. Structure of ANN. Readout responses from the "visual system" are inputs of ANN (on the left). ANN is trained to show information (on the right) about patterns stimulating the biological ID

Note that the simple ANN, in fact similar to the single biological column (HHLSM) has much better qualification skills. Its work is equal to the work of 25 HHLSMs. Similar observations one can find in De Schutter's and Steuber's work [6] in which the authors compare computational skills of Purkinje cells to such abilities of corresponding ANNs. There is no answer nowadays why such effective structures like ANNs were not created in an evolutional way. Possibly

there are so many neurons in mammalian brains that such extravagance of the nature is quite understandable.

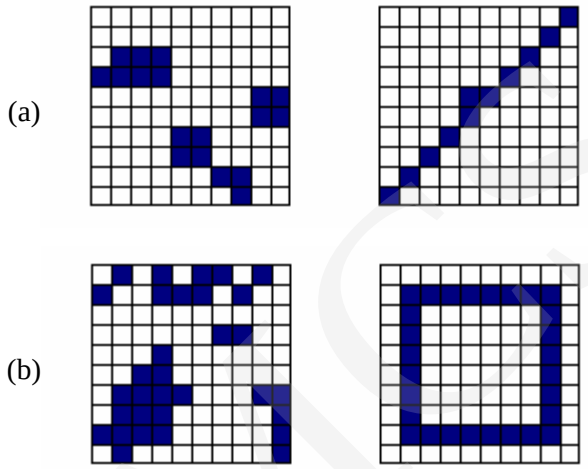

Fig. 5. Input (on the left) to ANN for "diagonal pattern" (a) and "square" pattern (b). On the right ANN's correct classification answers

In order to investigate thermodynamics of the system we apply a version of entropy based on the classical definition of Shannon's informational entropy [9-10]. Simulating the T=50 ms of biological system's work N spike potentials on the readout were obtained for each of 9 patterns shown to ID. Of course, number of spikes is different for each defined pattern shown to ID. Thus one can introduce probability of observation of n_i spikes occurred during a period[2] t_i=0.1 ms:

$$p_i = \frac{n_i}{N}. \tag{1}$$

Such a probability can be interpreted as a chance of giving the whole information in i^{th} part of time T. Of course, all probabilities for time T sum up to 1.

$$\sum_{i=1}^{500} p_i = \frac{n_1 + n_2 + ... + n_{500}}{N} = \frac{N}{N} = 1. \tag{2}$$

Using probability p_i one can introduce individual entropy as follows:

$$S_0^i = -p_i \cdot \ln(p_i). \tag{3}$$

More general global entropy reads:

[2] The entropy does not depend on the time interval of t_i <0.8 ms. For longer t_i the simulation time T ought to be longer.

$$S = \sum_i S_0^i = -\sum p_i \ln(p_i)\,. \tag{4}$$

Fig. 6. shows the changes of the readout entropy for 9 patterns shown to ID. Solid lines represent the entropy S and give the information about the global entropy increase in the first few milliseconds. Dashed lines provide us with information about individual entropy S_0 changes in the t_i intervals of time. For each of 9 patterns, the changes of entropy are slightly different. Basing on such thermodynamical analysis one can, in principle, differentiate with satisfying accuracy pattern shown to the ID. However, in our opinion, there have to be used some more sophisticated statistical methods like i.e. mutual information in order to improve recognition abilities of the system.

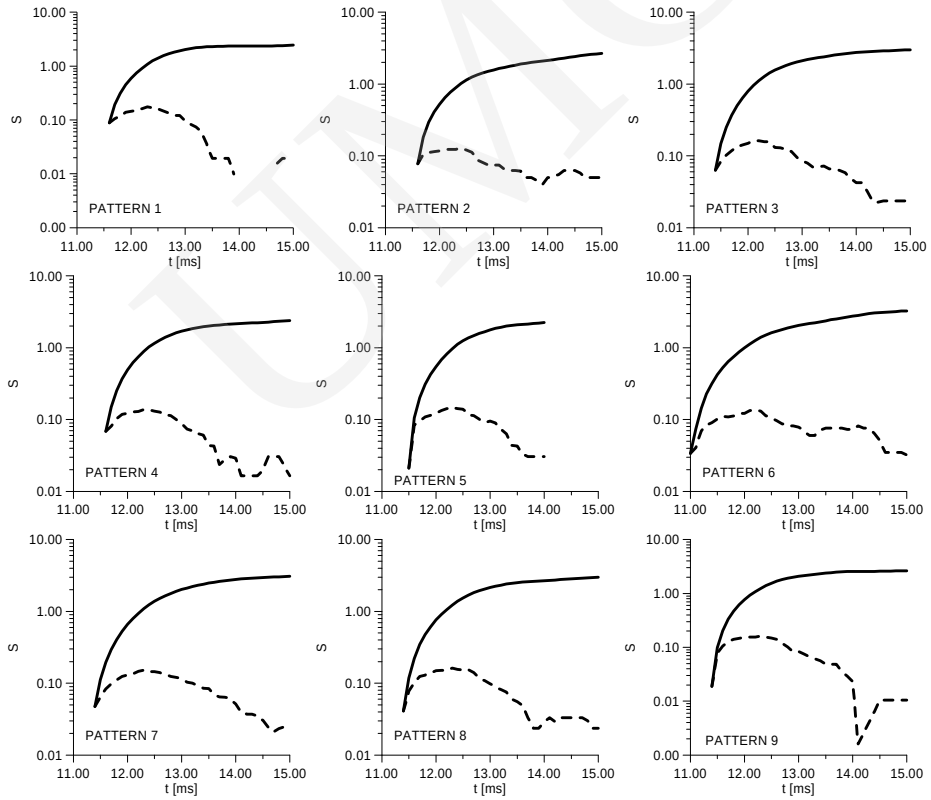

Fig. 6. Individual entropy S_0 (dashed line) and global entropy S (solid line) for 9 different patterns (as in Fig. 3) shown to ID

3. Summary

In conclusion, we simulated biological visual system using the LSM model. We showed that networks of Hodgkin-Huxley neurons are effective in

realisation of some computational functions like pattern recognition. Analysis of system's thermodynamics shed some light on the recognition process in the visual system. However, understanding this process in detail requires further and more precise research.

Appendix A – Details of Hodgkin-Huxley Neurons

Our HHLSMs consist of multicompartmental neurons with two dendrites compartments, a soma, and an axon. The dendrites contained a synaptically activated channel and the soma had voltage activated Hodgkin-Huxley sodium and potassium channels. The behaviour of each compartment is described by the differential equation:

$$C_m \frac{dV_m}{dt} = \frac{(E_m - V_m)}{R_m} + \sum_k [(E_k - V_m)G_k] + \frac{(V_m^{'} - V_m)}{R_a^{'}} + \frac{(V_m^{''} - V_m)}{R_a} + I_{inject} . \qquad (5)$$

Each sub-circuit was characterised by a group of parameter set as follows: resistances R_a=0.3 Ω, R_m=0.333333 Ω, 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 was chosen to be: G_K=360Ω^{-1} and G_{Na}=1200 Ω^{-1}. The soma had a circular shape with the diameter of 30μm, while the dendrite and axon were cable like with the length of 100 μm. All other parameters were chosen as suggested by GENESIS authors to simulate behaviour of the biological-like neurons [4]. More details concerning the Hodgkin-Huxley model one can find in [5].

References

[1] Maass W, Natschlaeger T, Markram H, *Real-time Computing Without Stable States: A New Framework for Neural Computation Based on perturbation*, Neural Computations, 14 (2002) 2531.

[2] Holden AV, Tucker JV, Thompson BC, *Can excitable media be considered as computational systems?*, Physica D, 49 (1991) 240.

[3] Gupta A, Wang Y, Markram H, *Organizing principles for a diversity of GABAergic interneurons and synapses in the neocortex*, Science, 287 (2000) 273.

[4] Bower JM, Beeman D, *The Book of GENESIS – Exploring Realistic Neural Models with the GEneral NEural SImulation System*, Telos, New York, (1995).

[5] Hodgkin A, Huxley A, *Currents carried by sodium and potassium ions through the membrane of the giant axon of Loligio*, Phyiol., London, (1952).

[6] Steuber V, De De Schutter E, *Long-term depression and recognition of parallel fibre patterns in a multi-compartmental model of Purkinje cell*, Neurocomputing, 38-40 (2001) 383.[7] Stuttagrt Neural Network Simulator (SNNS); website: http://www-ra.informatik.uni-tuebingen.de/SNNS.

[8] SNNS – Stuttgart Neural Network Simulator, User Manual, Version 4.2. http://www-ra.informatik.uni-tuebingen.de/SNNS.

[9] Shannon C. E., *A mathematical theory of communication.* Bell Systems Technical Journal, 27 (1948) 623.

[10] Cover T. and Thomas J., *Elements of Information Theory*. Wiley, New York.