The Fourteenth International Symposium on Artificial Life and Robotics 2009 (AROB 14th '09),
B-Con Plaza, Beppu, Oita, Japan, February 5 - 7, 2009

Possible roles of pre-synaptic connections in neural circuits

H. Watanabe
Graduate School of
Information Science and Technology,
The University of Tokyo

K. Aihara
Graduate School of
Information Science and Technology,
The University of Tokyo,

ERATO Aihara Complexity
Modelling Project, JST
Institute of Industrial Science,
University of Tokyo
Tokyo, Komaba 4-6-1. 153-8505

Institute of Industrial Science,
University of Tokyo
Tokyo, Komaba 4-6-1. 153-8505

Abstract

A recent study suggests a new form of inhibitory circuits, in the cortex, in which a pyramidal cell directly excites pre-synaptic terminal of an inhibitory interneuron [1]. This circuit allows action potentials generated in a single pyramidal (excitatory) neuron to evoke reliable constant-latency inhibition in other nearby pyramidal neurons. However, tangible effects of this direct inter-pyramidal inhibition in neural circuits are still unclear. In the present paper, we examine effects of the direct inter-pyramidal inhibition by numerical simulations.

1 Introduction

Inhibitory circuits in the neocortex were thought to be so simple. Excitatory synapses from pyramidal neurons excite the dendrites or soma of interneurons, and generate action potentials that propagates the axons to trigger the release of inhibitory neuronal transmitters onto postsynaptic cells. The neocortex has been thought to have only this classical inhibitory circuit. Recently, however, Ren et al proposed an extraordinary form of synaptic circuitry that allows one pyramidal cell to rapidly inhibit other pyramidal neurons [1]. They suggests a new form of inhibitory circuit, in which the excitatory synaptic terminal from one pyramidal cell directly connects to the presynaptic terminal of an inhibitory interneuron. In the classical inhibitory pathway, considerable integration of synaptic inputs onto interneurons is needed for triggering spikes in the interneurons, one spike in one pyramidal cell is not enough. In contrast, the new circuits suggested by Ren et al allows action potentials generated in a single pyramidal neuron to evoke reliable, constant-latency inhibition in other nearby pyramidal neurons. Instead of weakly exciting one another, pyramidal cells arranged in this way can strongly inhibit one another.

The work of Ren et al suggests both a new inhibitory function and its surprising cellular mechanism that allows one neuron to violate Dale's principle. But there are many problems to be solved. However, one of the most important problems is what the functional differences is between classical inhibitory pathways and this new inhibitory mechanisms. To verify this problem, we simulated the effects of direct inter-pyramidal inhibition on dynamics of neural ensembles using the spiking neuron model. The results shows that there are large differences of network dynamics between classical and new type inhibition, even when all parameters and setting are identical except the type of inhibitory mechanism.

2 Model

2.1 Neural model

In simulations of dynamics of neural ensembles we can use physiologically realistic models like the Hodgkin-Huxley one. However, we have to find a compromise between computational e ciency and physiological plausibility. In this work we use spiking neuron model proposed by Izhikevich [3].

$$\frac{dv}{dt} = 0.04v^2 + 5v + 140 - u + I \qquad (1)$$

$$\frac{du}{dt} = a(bv - u) \tag{2}$$

with the auxiliary after-spike resetting

$$if \quad v \geq 30mV \quad then \quad v \leftarrow c, \quad u \leftarrow u + d \tag{3}$$

Here, the variable v represents the membrane potential of the neuron and u represents a membrane recovery variable, which accounts for the activation of K^+ ionic currents and inactivation of Na^+ ionic currents, and it provides negative feedback to v. The variables a, b, c, and d are dimensionless parameters, and t is the time. After the spike reaches its apex (+30 mV), the membrane voltage and the recovery variable are reset according to the (3). Synaptic currents or injected dc-currents are delivered via the variable I.

The reasons for using this model are that it is as biologically plausible as the Hodgkin-Huxley model, yet as computationally e cient as the integrate-and-fire model, and depending on four parameters, the model reproduces spiking and bursting behavior of known types of cortical neurons (pyramidal neuron, fast spiking neuron and so on).

2.2 Short term synaptic plasticity and Synaptic activity

In the real brain, the synaptic strength of each synapse can be depressed or facilitated on a short time scale of hundreds of milliseconds by a scalar factor (Short term synaptic plasticity). To reconstruct short term synaptic plasticity, this scalar factor, different for each synapse, is modeled by the following one-dimensional equation [4].

$$\frac{dr_{ij}}{dt} = \frac{1 - r_{ij}}{\tau_r} \tag{4}$$

$$if \ presynaptic \ spike \ arrive \ then \ r_{ij} \leftarrow p_r r_{ij} \tag{5}$$

r_{ij} is scalar factor of synapse from neuron j to neuron i. r_{ij} tends to recover to the equilibrium value $r_{ij} = 1$ with the time constant τ_r, and it is reset by each spike of the presynaptic cell to the new value p_r. The parameter $p_r > 1$ decreases r_{ij} and results in short-term synaptic depression, whereas $p_r < 1$ results in short-term synaptic facilitation. (In the present simulation, we use only short-term synaptic depression.)

In addition, synaptic activity is modeled by following one-dimensional equation [4].

$$\frac{dg_{ij}}{dt} = -\frac{g_{ij}}{\tau_g} \tag{6}$$

$$if \ presynaptic \ spike \ arrive \ then \ g_{ij} \leftarrow g_{ij} + w_{ij} r_{ij} \tag{7}$$

Here g_{ij} is the activity of synaptic terminal from neuron j to neuron i, w_{ij} is strength of synaptic connection, and r_{ij} is short term plasticity factor mentioned above. When spike from neuron j reach neuron i with synaptic delay t_{dij}, g_{ij} is increased by $w_{ij} r_{ij}$, and then g_{ij} tends to decrease to the equilibrium value $g_{ij} = 0$ with the time constant τ_g.

After all, total input to neuron i is described by following equation.

$$I_i = (V_E - v_i) \sum g_{ij} + (V_I - v_i) \sum g_{ij} + I_0 \tag{8}$$

Here, v_i is the membrane potential of the neuron i, V_E and V_i represent reversal potentials of excitatory and inhibitory synaptic input, respectively. I_0 is external input.

2.3 Network structure

The network consists of N neurons. The network topology is random, and all neurons are connected with equal probability $\epsilon \in [0, 1]$, regardless of their identity. The only constraint is that all neurons receive same number of excitatory and inhibitory synapses. Figure 1 shows the schematic structure of network we use.

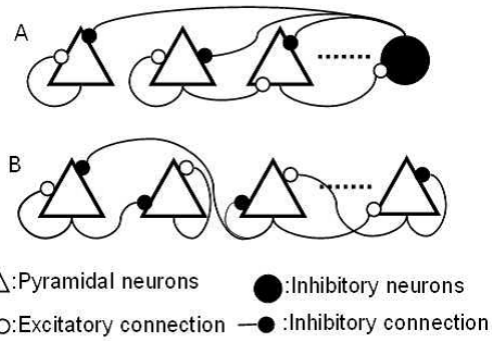

Figure 1: Schematic structure of network. In classical type inhibition system (Figure 1-A), one neuron either excites all postsynaptic neruons or inhibit them. On the other hand, in new type inhibition system (Figure 1-B), one neuron can make both type of synaptic connections for each postsynaptic target.

Small open circle indicate excitatory connections, whereas small filled circle indicate inhibitory connections. Large open triangle indicate a pyramidal neuron, and large filled circle means an inhibitory neuron, respectively.

In figure 1-A, traditional type of inhibition, there are βN excitatory neurons and $(1 - \beta)N$ inhibitory

neurons in the network ($\beta \in [0, 1]$). On the other hand, in figure 1-B, there are no discrimination between excitatory and inhibitory neuron. Instead, $100\times\beta$ percent of all connections are excitatory, and the others are inhibitory (violation of Dale's principle). In both cases, one neuron receives $\epsilon\beta N$ excitatory synapses and $\epsilon(1-\beta)N$ inhibitory synapses.

3 Simulation and Results

3.1 Simulation settings

To reproduce the behavior of regular spiking neurons, we set parameter $a = 0.02$, $b = 0.2$, $c = -55$, $d = 6$ in the equation (1), (2) and (3). (In the real brain, spiking characteristics are different between excitatory and inhibitory neurons. However, for purely making a comparison of difference by the type of inhibition, we set same parameter to all neurons in both classical type inhibition and new inhibition mechanism suggested by Ren et al.) Initial values of u and v of each neurons are randomly set. And for other parameters, we use following values; $V_E = 0$ (mV), $V_I = -70$ (mV), $\tau_r = 150$ (ms), $\tau_g = 6.0$ (ms), $p_r = 0.6$,

$$w_{ij} = \begin{cases} 0.02 & \text{if the synapse } j \to i \text{ is excitatory} \\ 0.2 & \text{if the synapse } j \to i \text{ is inhibitory} \\ 0 & \text{if the synapse } j \to i \text{ is not exist} \end{cases}$$

and synaptic transmission delay is fixed to 2 (ms).

And we set the number of neurons $N = 250$, proportion of excitatory neurons (synapses) $\beta = 0.8$, and connection probability $\epsilon = 0.8$ (So in classical inhibitory mechanism simulations, there are 200 excitatory neurons and 50 inhibitory neurons.) In both cases, one neuron receives 160 excitatory synapses and 40 inhibitory synapses.

Changing the type of inhibitory mechanism, we observe the spiking dynamics of the network.

3.2 Results

In each type of inhibition mechanism, we ran simulations by 40 times. Figure 2 shows the one example of raster plot and population histograms when we add the constant input to the network ($I_0 = 10.0$). Figure 2-A is the result of classical inhibitory mechanism simulation, and Figure 2-B is that of new type mechanism simulations.

As shown by numerical simulation of otherwise identical systems, the difference of inhibitory mechanism causes the large difference of network dynamics.

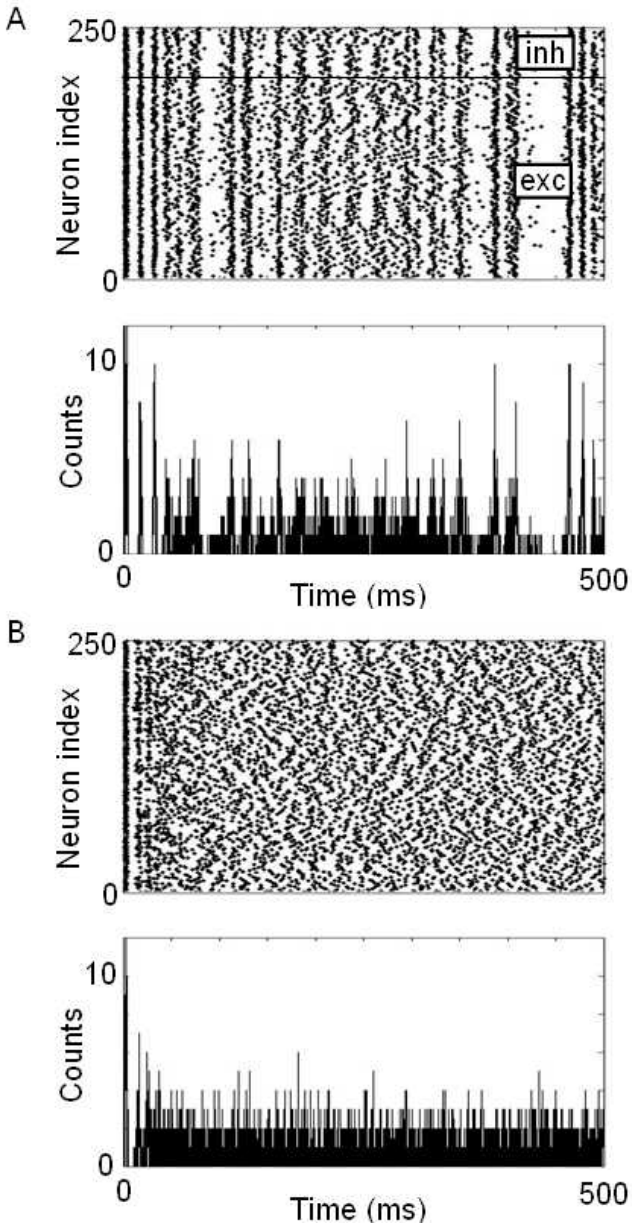

Figure 2: Population spiking activity in classical inhibition mechanisms (Figure 2-A) and new inhibition suggested by Ren et al (Figure 2-B). Spiking activity (dot displays) for networks of size N = 250 neurons (200 excitatory and 50 inhibitory neurons in A) and population histograms (lower panels of each figure; bin size 0.1 ms) in classical inhibition mechanism and new type inhibition (see section 3.1 for network and simulation parameters). Even though all other parameters and the number of synaptic connections are identical, network dynamics are largely different between two type inhibition mechanisms.

The distribution of population spike counts is comparably broad and skewed in classical type inhibition networks, whereas it is narrow and uniform for the new type inhibition network.

The average spike count per one neuron is not so different between two inhibition type (classical type; 19.1866, new type; 20.6374, slightly larger in new type inhibition). However, variance of spike count among neurons in one simulation running is somewhat different. Simulation results show that in new type inhibition, spike count variance is about 5 times larger than in classical type inhibition (classical type; 2.1306, new type; 10.4955). These result suggest that new type inhibition mechanism has stronger desynchronizing effect on network dynamics than classical inhibition.

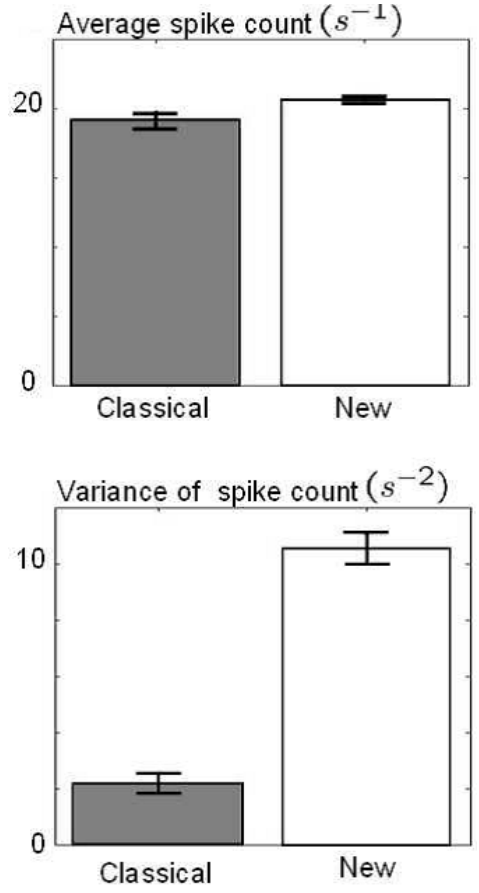

Figure 3: Average spike count (upper panel) and variance of spike count among neurons in one simulation (lower panel). These figure shows the differences of each value averaged over 40 simulations. Error bars mean standard deviation. Spike count variance in new type inhibition is about 5 times larger than that in classical type inhibition, while average spike count per one neuron is not so different.

4 Summary

We have simulated the dynamics of spiking neural networks, and compared the difference of effects on network dynamics between traditional initiatory circuits and new inhibitory circuits suggested by Ren et al. Even though all other parameters and the number of synaptic connections are identical, network dynamics are largely different between two type inhibition mechanisms. Our result has indicated that the new type inhibition mechanism has stronger desynchronizing effects on network dynamics than classical inhibition.

To investigate whether these characteristic features are useful for information processing in the brain cortex is one of our future problems.

Acknowledgements

This work was supported by a *kakenhi* Grant-in-Aid for Scientific Research (A).

References

[1] Ren, M., Yoshimura, Y., Takada, N., Horibe, S., Komatsu, Y. "Specialized inhibitory synaptic actions between nearby neocortical pyramidal neurons" *Science*, Vol. 316, pp. 758-761, 2007.

[2] Connors, B. W., Cruikshank, S. J. "Bypassing interneurons: Inhibition in neocortex," *Nat.Neurosci*, Vol. 10, pp. 808-810, 2007.

[3] Izhikevich, E. M. "Simple model of spiking neurons" *IEEE Transactions on Neural Networks*, Vol. 14, No. 6, pp. 1569-1572, 2003.

[4] Izhikevich, E. M., Edelman G. M. "Large-scale model of mammalian thalamocortical systems" *PNAS*, Vol. 105 No. 9, pp. 3593-3598, 2008.

[5] Dyan, P., Abbot, L. F. *Theoretical Neuroscience*, The MIT Press, 2001.

[6] Shepherd, G. M., *THe Synaptic Organization of the Brain*, The OXFORD University Press, 2004.

[7] Izhikevich, E. M. *Dynamical Systems in Neuroscience*, The MIT Press, 2001.