Automatic estimation of neural properties for Hodgkin-Huxley type models

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Abstract: Detailed neuron models based on measured ionic currents are still exceptional when considering the bewildering variety of cell types investigated because determining ionic currents requires very favorable experimental conditions. The situation is still worse for multi-compartment models, but such models are required for detailed simulations of complex neural networks. To alleviate these difficulties, we propose a method that allows estimating ionic currents and passive properties based on simple electrophysiological responses and assumptions concerning the types of currents involved.

Keywords: Genetic algorithm, Parallel computing, NEURON, Compartmental modeling, Electrophysiology simulation

1. INTRODUCTION

Nervous systems are capable of solving problems that pose considerable difficulties to conventional computing methods. An example of such a problem is the chemical plume tracking problem, solved by male silkmoths (*Bombyx mori*) displaying odor-source orientation behaviour[1]. We use various approaches to elucidate the solution of this problem are followed using a combination of robotics, models, silkmoths, and their brains[2, 3].

In particular, the use of neural network models as robot controllers is promising as behavior at different levels can be directly compared to the biological system. However, a suitable level of detail is required for the implementation of such neural network models because much of the properties of the neurons reside in their complex morphological and electrical properties. Generally, it is not feasible to obtain complete biophysical characterisations of all the neurons of interest. Therefore, it is highly desirable to obtain at reasonable estimates of the actual biophysical properties from more restricted experimental data. The number of parameters to be estimated is a drawback in this strategy: an automated fitting scheme is required, notably when expanding estimations to allow for multi-compartment models including neural morphology.

To address this problem, we have developed a system in which parameter estimates can be carried out automatically by including the simulation of the neurons in the fitting process. Due to the computational demands, we implemented our system on the RIKEN integrated Cluster of Clusters (RICC) and KEI facilities.

2. MATERIALS AND METHODS

2.1 Neuron Model Construction

We adopted silkmoths antennal lobe (AL) projection neuron model as example (Fig. 1). This model is composed of four parts: dendrite, soma, spike generator and axon. Dendrite and soma compartments have passive membrane potentials. Spike generator and axon compartments have Hodgkin-Huxley (HH) type membrane potentials[4] with three types of channels: Na^+, K^+ and Ca^{2+}

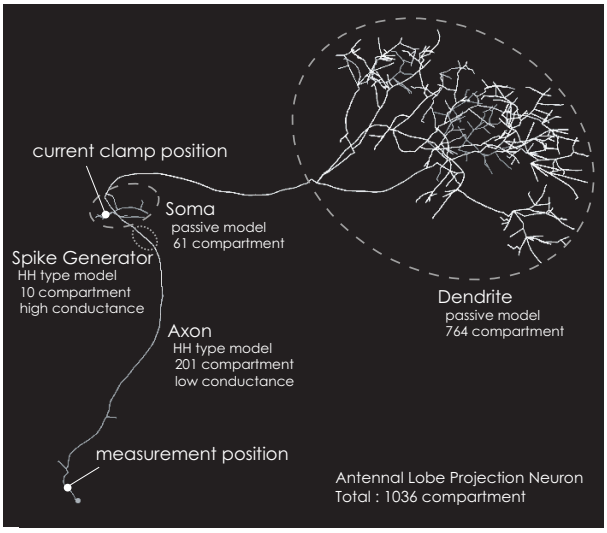

Fig. 1 The model of antennal lobe projection neuron of the silkmoth, using in the simulation.

transit. Spike generator compartments have higher ionic conductance than axon compartments.

This model neuron was simulated by "NEURON"[6], an empirically-based neuron simulator. At the simulation, neuron was subjected to a simulated experimental current clamp, injecting a depolarizing ramp or ramp + sin wave current. The voltage responses of the model neurons to this stimulus were used as target data for re-estimating the parameters used to construct the model neurons.

2.2 Parameter Estimation

We adopted the real-coded genetic algorithm (RCGA)[5] for parameter estimation because of its good parallel efficiency. Parameters to estimate were property of spike generator: position on axon, number of compartments, a K^+ conductance (G_K), a Na^+ conductance (G_{Na}), and a Ca^{2+} conductance (G_{Ca}).

During parameter estimation, we simulated the model neuron with the parameters of each gene, determining voltage responses to the current injections.Based on

these potential changes $P(t)$ and the target data potential changes $T(t)$, we defined fitness (F) as:

$$F = \frac{1}{\int_0^{t_{\max}} [\int_0^a (P(t) - T(t))dt]^2 da}$$

Reproduction on the GA, we apply uniform mutation as mutation algorithm and BLX-α as crossover algorithm. Additionally, some genes were mutated normal random value for local searching.

Parameter estimates were done under the following conditions:

- **Processor:** 256 cores
- **Number of genes:** 2048
- **Number of generations:** 200
- **Simulation time step:** 0.025 msec
- **Simulation time range:** 0 - 400 msec
- **Estimation range:**
  - position of spike generator on axon: 0 - 200
  - compartment number of spike generator: 1 - 50
  - $\overline{G_K}$ of spike generator: 0.0001 - 1.0000 S/cm^2
  - $\overline{G_{Na}}$ of spike generator: 0.0001 - 10.000 S/cm^2
  - $\overline{G_{Ca}}$ of spike generator: 0.00001 - 0.10000 S/cm^2

3. RESULT

We estimated parameters by using three types of current clamp. Results of the estimations are shown in Fig.2.

4. DISCUSSION

Genetic algorithm in conjunction with the simulation of neuron models allows parameter estimates for model neurons. However, comparing each results of estimation, case of ramp stimulation was not accurate as others (Fig.2). It probably suggests that stimulation optimizing is very important for estimation.

In the present study, we used model neurons and simulations both for target data and for determining the fitness. In the next step, we will employ complete electrophysiological data from real neurons. To avoid overfitting due to errors (and noise) in the experimental data, an error evaluation function may be implemented or the fitness function may have to be modified, for example by using spike timing and number.

Our approach can easily be extended for application to more detailed multi-compartment models. However, such systems need very large computational resource. To tackle this problem, we will use more CPUs (ex. 8192 cores on RICC or >10000 cores on KEI) and extend GA like the island model GA.

REFERENCES

[1] R. Kanzaki, N. Sugiand and Shibuya T, "Self-generated zigzag turning of Bombyx mori males during pheromone-mediated upwind walking", *Zoological Science* Vol. 9, pp. 515–527, 1992.

[2] S. Emoto, N. Ando, H. Takahashi and R. Kanzaki, "Insect-controlled robot - evaluation of adaptation ability -", *The Journal of Robotics and Mechatronics* Vol. 19, pp. 436–443, 2007.

[3] A. Takashima, R. Minegishi, D. Kurabayashi and R. Kanzaki, "Estimation of Feedback System during Programmed Behavior Exhibited by Silkworm Moth", 2010 Second World Congress on Nature and Biologically Inspired Computing (Fukuoka), pp. 92–97, 2010.

[4] AL. Hodgkin and AF. Huxley, "A quantitative description of membrane current and its application to conduction and excitation in nerve", *The Journal of Physiology*, Vol. 117, No. 4, pp. 500–544, 1952.

[5] AH. Wright, "Genetic algorithms for real parameter optimization", *Foundations of Genetic Algorithms*, pp. 205–218, 1991.

[6] NEURON web, "http://www.neuron.yale.edu/neuron/".

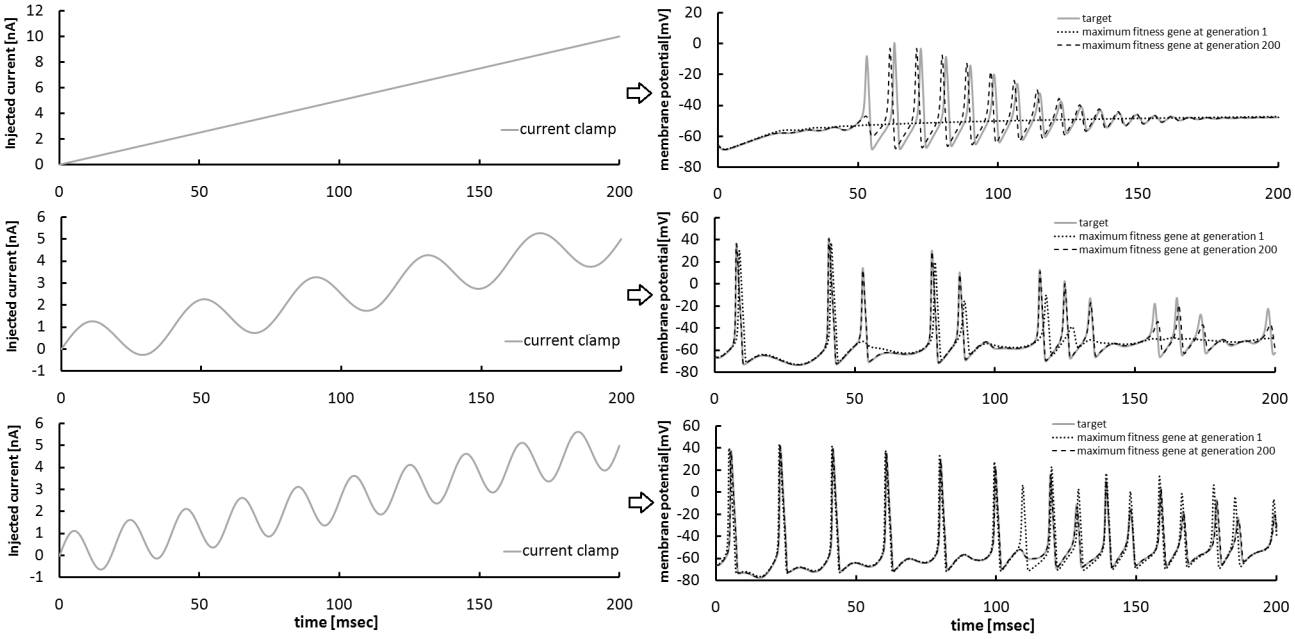

Fig. 2 **Result of estimation** Top: ramp stimulus current, Middle: ramp + sin wave (low frequency) stimulus current, Bottom: ramp + sin wave (high freqency) stimulus current.