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Extracting the dynamics of the Hodgkin-Huxley model using recurrent neural networks

Sari Andoni[1], Manish Saggar*[2], Tekin Meriçli[2] and Risto Miikkulainen[2]

Address: [1]Institute for Neuroscience, University of Texas at Austin, Austin TX 78712, USA and [2]Department of Computer Sciences, University of Texas at Austin, Austin TX 78712, USA

Email: Manish Saggar* - mishu@cs.utexas.edu

* Corresponding author

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Overview

A single biological neuron is able to perform complex computations that are highly nonlinear in nature, adaptive, and superior to the perceptron model. A neuron is essentially a nonlinear dynamical system. Its state depends on the interactions among its previous states, its intrinsic properties, and the synaptic input it receives. Some of these factors are included in Hodgkin-Huxley (HH) model, which describes the ionic mechanisms involved in the generation of an action potential. This paper proposes training of an artificial neural network to identify and model the physiological properties of a biological neuron, and mimic its input-output mapping. An HH simulator was implemented to generate the training data. The proposed model was able to mimic and predict the dynamic behavior of the HH simulator under novel stimulation conditions; hence, it can be used to extract the dynamics (*in vivo* or *in vitro*) of a neuron without any prior

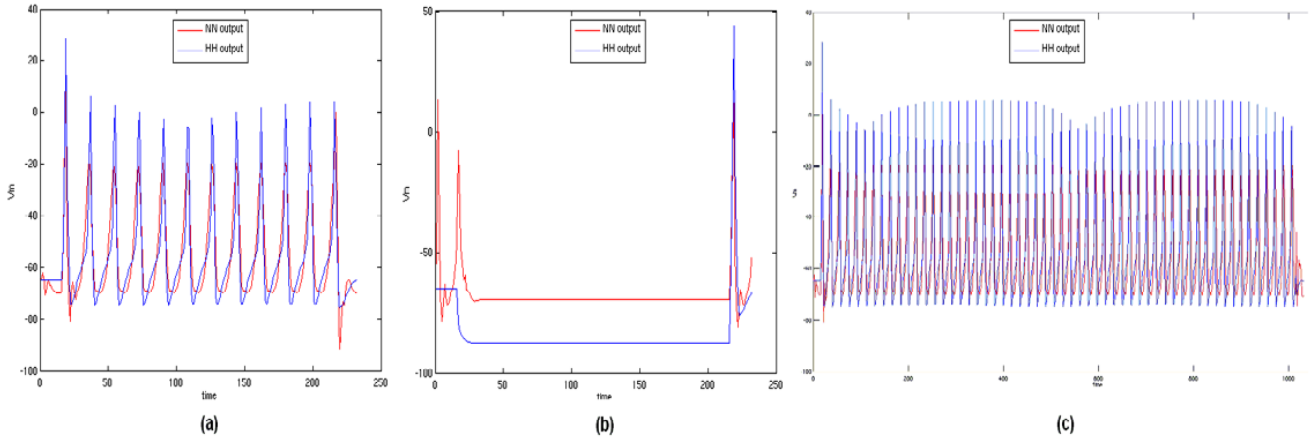

Figure 1
Output of the LRN trained with 232 ms of data on a positive step current, tested on (a) the training data, (b) novel test data that consists of a negative step current, (c) 800 ms of previously unseen data that follow the 232 ms of training data.

knowledge of its physiology. Such a model can in turn be used as a tool for controlling a neuron in order to study its dynamics for further analysis.

Methods and results

To test whether artificial neural networks were able to learn the dynamic behavior of the HH model, four properties of the model were used as testing criteria: thresholding, periodic firing, refractory period, and anode break action potential. Three different neural network architectures were explored: parallel and series-parallel nonlinear autoregressive models with exogenous inputs (NARX [1,2]) and layer-recurrent networks (LRN [3]). All three architectures were able to mimic the behavior of the HH model, provided that they had been trained previously on a similar input. However, among them LRN was the only one that was able to generalize to novel stimuli (Figure 1b). Furthermore, when tested for long-term prediction, LRN outperformed other network architectures by predicting the output for an extra 800 time steps for a positive step signal, although it was trained only once for duration of 232 ms (Figure 1c).

Conclusion

This paper shows that ANNs can learn to behave like the Hodgkin-Huxley model of a biological membrane. In the future it should be possible to apply this approach to modeling biological neurons in vitro. The main advantage of this approach is that it does not require any prior knowledge of the physiological properties of the neuron. After training is completed, the neural process is encoded within the weights of the ANN used to model the neuron. Several ANN architectures were tested in this task, with the recurrency in the LRN architecture proving to be the best. Online modeling using ANNs can provide the necessary tools for capturing the dynamical state of a biological neuron, simulate its output for further analysis, and may provide a more powerful dynamic clamp and online control. Such mechanisms should prove valuable in understanding the behavior of biological neurons in the future.

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