Automating Development of Biophysical Single Cell and Network Models

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Introduction

- Software packages (e.g., NEURON [1]) facilitate the development of simplified and detailed biophysical single cell and network models
- We report on-going work in the development of interfaces to use such software for research, training and outreach purposes

Single Cell Models

- Different single neuron model options have been developed for teaching and self-learning, using NEURON [1], Jupyter Notebook, and brain machine tool kit (BMTK; [2]: (i) using NEURON and GUI; (ii) using Jupyter notebooks with NEURON, BMTK; (iii) with BMTK directly
- We have also developed Jupyter notebook modules for cellular neuroscience topics such as Nernst and rest potential, spike generation, bursting, synaptic transmission, and the development of small networks.
- A JupyterHub server was established on the JetStream cloud computing platform to host several of the notebooks for teaching purposes, an example of which is also provided.

Multi-compartment Jupyter Notebook with segregation

- The user enters passive properties (Tau, Vrest, Rin), FIR curve, morphology information, stimulation input (injected Current or Synaptic Input) and Channels (segregated).
- The software assembles the cell with default conductance values. User can tune the maximal conductances value, Vhalf and slope to tune user input characteristics. An example is shown below.

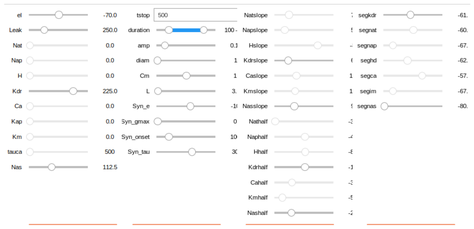


Figure1：One compartment example of the interneuron in Golomb et al. (2007)

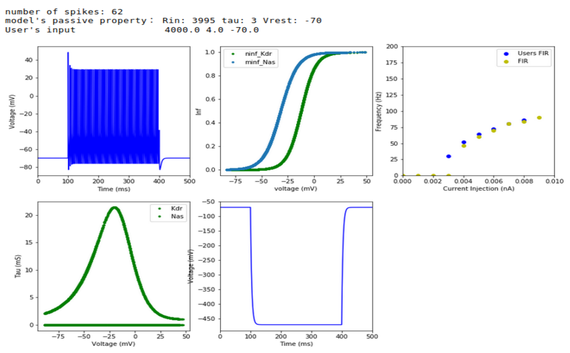
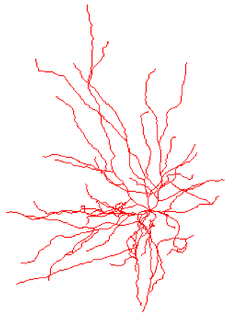


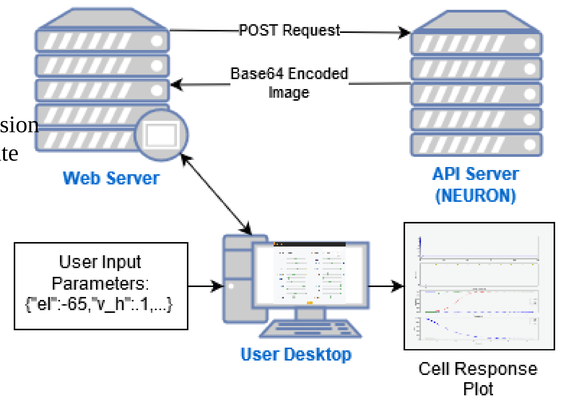
Figure2：BMTK Notebook version of detailed single cell model with segregation of channels in the soma



ON-GOING WORK

- The tonic spiking model shown in the left panel is being expanded to include bursting, low threshold oscillation, high-threshold oscillation
- We will also automate the generation of some of the models, given the user input

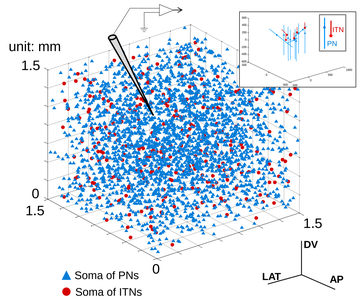
Figure3：Web-based version for training - undergraduate and graduate level



- The user enters their desired cell specifications into the webpage
- The parameters are passed from the simple web server to an API server running NEURON
- The API server runs the specified simulation and a returns base64 encoded text containing an image of relevant plots
- The plots are displayed to the user, and the user is given the option to tune the cell further

Network model Automation

- We are developing an interface where users provide single cell models from the Allen database or their own .hoc files. Then they provide all the network properties such as cell types, proportions, synapse types, and connectivity. The network will then be assembled by BMTK.
- Users can run the network on their local machine. For large networks, They can use SimAgent to interface with HPC resources. The results are automatically downloaded for viewing by the user.
- Software interface will permit tuning of the network parameters and design iteration via the same approach. An example network with 1000 cells is shown in the figure in the next panale.



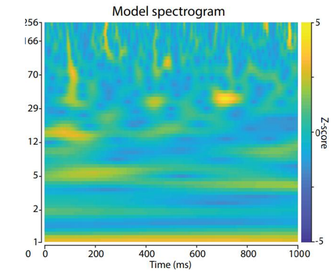


Figure4：A large-scale network model of the rodent amygdala with the spectrogram output (Feng et al. 2019)

CyNeuro Portal

Figure5：Public portal to host research and teaching tools above. Also serves as gateway to HPC resources (e.g., XSEDE), and to coordinate summer programs for training and for outreach to K-12

Outreach - Summer Courses and K-12

We are developing training materials as well as lesson units that include some of the software automation modules, e.g., Jupyter Notebook implementation of basics related to brain waves.

References

1. Carnevale and Hines (2006) The NEURON Book;
2. Gartiy et al. (2018) PLOS ONE
3. Golomb et al. (2007) PLoS Computational Biology
4. Alturki et al. (2016) eNeuro
5. Feng et al. (2019) eNeuro

This project was supported in part by grants NSF OAC-1730655 and NIH MH122023.