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Modeling a single dendritic compartment using Neurospaces and GENESIS-3

Hugo Cornelis*, Huo Lu, Angelica Esquivel and James M Bower

Address: Research Imaging Center, University of Texas Health Science Center at San Antonio, TX, USA

Email: Hugo Cornelis* - hugo.cornelis@gmail.com

* Corresponding author

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Modeling a single dendritic compartment

The standard technical approach to realistic modeling of single neurons involves dividing the cell and especially its dendrites into a series of compartments assumed to be effectively isopotential. During simulation a single membrane voltage is calculated for each of these compartments. Recent cerebellar network and Purkinje cell single cell modeling efforts in our laboratory have suggested, however, that membrane dynamics may depend on a finer level of control of membrane voltage within the dendrite [1]. Accordingly, we have now identified the precise dendritic geometries and positions of excitatory and inhibitory synapses using serial electron microscopy. This paper describes our efforts to construct an electrical/chemical model of the resulting fully reconstructed segments ranging from 5 to 10 microns in length.

Technical challenges

Modeling these small dendritic segments realistically poses several technical challenges. Beyond issues of how to represent space, the project is also inherently multiscale, as the behavior of segments must be interpreted in the context of the larger compartmental simulation of the dendrite, and second, at a finer scale, molecular and cellular processes (Ca diffusion for example), also come into play.

Completing the software tool chain

This project is being undertaken in the context of two ongoing computational software development projects, the GENESIS 3.0 project and Neurospaces. GENESIS 3.0 is a major redevelopment effort focused on the development of a state of the art Graphical User Interface and Database structure for the GENESIS project. The Neurospaces project http://www.neurospaces.org involves the development and elaboration of a new open, modular framework for essential tools used in computational simulations in biology, and defines the hooks required for collaborative software components, that work on the same modeling project. This poster will describe the latest tools of the Neurospaces project in the context of our efforts to simulate small segments of the Purkinje cell dendrite. As an example, we have developed algorithms to slice the volume obtained from serial EM into small cylinders intended for simulation. The cylinders can be visualized, validated and compared with the original volume. The compartmental solver Heccer, also part of the Neurospaces project, simulates the model, using the spatial and temporal precision appropriate for these fine scale models.

Conclusion

The tools developed in the context of this project, give a detailed insight in the level of control of inhibition and excitation on membrane dynamics in a small dendritic segment of a Purkinje cell. Additionally, in the context of larger compartmental simulations of the entire dendritic tree, the interpretation of the effect of these dynamics on dendritic signal processing is likely to have important

functional consequences for the regulation of dendritic dynamics in the Purkinje cell.

References

1. Santamaria F, Bower JM: **Background synaptic activity modulates the response of a modeled Purkinje cell to paired afferent input.** *J Neurophysiol* 2005, **93:**237-250.