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Parallel simulations of a 3D cerebellar network created with neuroConstruct

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Abstract:

The properties of ion channels and synapses can have a profound effect on higher level behaviour of neural systems. Linking these low level mechanisms to high level neural network behaviour can be aided by the development of biophysically realistic computational models. However, such models are very complex and can require large computational resources. We have recently developed a software application, neuroConstruct, which facilitates the construction of such network models. Models of cells with detailed morphologies and voltage and concentration-dependent membrane conductances can be created through a graphical user interface, and are based on open standards (NeuroML) ensuring transparency of the underlying physiological parameters and portability of the models to multiple simulation platforms. Complex connectivity patterns between groups of cells placed in 3D space can also be generated. neuroConstruct automatically generates code for running NEURON and GENESIS, which carry out the numerical simulation. The initial version of neuroConstruct generated code for a single processor, limiting the size of networks that could be simulated.

Here we present recent developments towards the next generation of neuroConstruct. This includes adding support for the generation of scripts for the parallel version of NEURON allowing execution in a distributed computational environment. This parallelization will permit much larger simulations to be run on clusters allowing simulations on a scale (numbers of neurons and synapses) much close to biologically realistic levels found in specific brain regions. Network models of a number of brain areas have been tested, but the main focus of our research, the granule cell layer of the cerebellum, will be discussed in detail. This model has been used to investigate how signals are processed in the granule cell layer. We have generated networks with 50,000 cells distributed over multiple processors. We have also developed an alpha version of a Python-based scripting interface to neuroConstruct, which allows greater flexibility in network creation beyond the functionality available through the interface. It also facilitates the creation and management of multiple simulations and optimization procedures used for parameter searching.

These new features, which will be included in the next release of neuroConstruct, will increase the biological realism of the network models that can be simulated and extend its functionality for neural network research.

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