

# NeuroML : A lingua franca for computational modeling in Neuroscience

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## ABSTRACT

NeuroML [2, 4] is an XML based declarative language for specifying simulation models of neural structures from sub-cellular to network levels, intended as a common exchange format. It is a collaborative effort involving authors of modeling packages such as NEURON [6], GENESIS [7], CATABOMB [5], BLISS [3] and NEOSIM [1].

Existing neuronal modeling packages tend to perform well for the level of models for which they were designed - and less well at higher or lower levels of scale and abstraction. For example Catacomb includes a good user interface for describing and simulating kinetic scheme models of ion channels, and BLISS includes powerful high level constructs for building structured networks of neurons. Each simulation package also uses its own peculiar format for saving models (often as a script program). This makes it hard for people to run and test other people's models unless they happen to use the same simulator, and even harder to link simulators to build multi-scale models. But these are precisely the things which are required to further our understanding of neuronal systems.

The NeuroML approach is to define a simulator-independent declarative format for describing models, where the vocabulary of NeuroML matches the conceptual structures used by modelers. For example membrane channel conductances are defined in terms of well-known equations, neurons can be described in terms of membrane sections having a certain distribution of channels, and structured networks of neurons are defined in terms of populations and projections. An individual simulator can convert this description into an executable simulation model optimised for efficiency. NeuroML also includes code interfaces to let different simulation modules work together to run multi-scale models.

We have developed a NeuroML software development kit which includes libraries for reading and writing models, GUI tools for building models and visualisation plug-ins for viewing the running state of a simulation.

One of the benefits of standardising model description formats and interfaces is that it becomes possible to link NeuroML-enabled simulation tools to similar efforts for intracellular modeling (such as SBML/SBW), and also to extend up-

wards to support more abstract neural-network style models. It also meshes well with attempts by Gardner and others (BrainML) to establish a common data model for neuroscience.

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