NetworkML: Level 3 of the NeuroML Standards for Multiscale Model Specification and Exchange

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NeuroML: THE NEURAL OPEN MARKUP LANGUAGE

Computational models based on detailed neuroanatomical and electrophysiological data have been used for many years to help our understanding of the function of the nervous system. NeuroML is an international, collaborative initiative to develop standards for the exchange of models of neuronal systems and to allow for greater transparency and accessibility of these complex models [1,2]. The standards currently are specified in XML (eXtensible Markup Language) [3]. Exchange of network models will aid the investigation of structure-function relationships in neuroscience including theoretical studies relating connectivity patterns to normal and neurodegenerative network states.

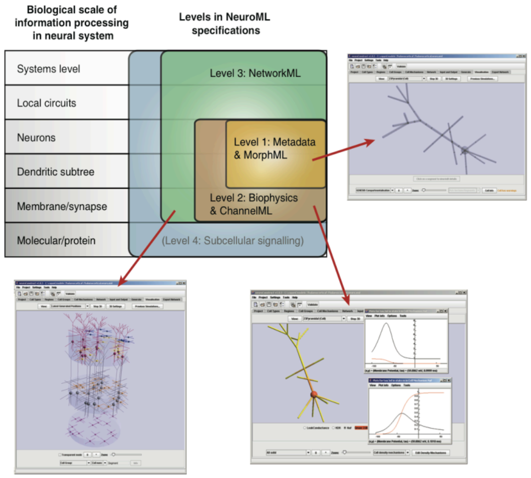
LEVELS IN NeuroML

The standards are arranged into levels, with higher levels adding extra concepts.

Level 1: Includes metadata and neuroanatomical information such as the branching structure of a neuron (MorphML).

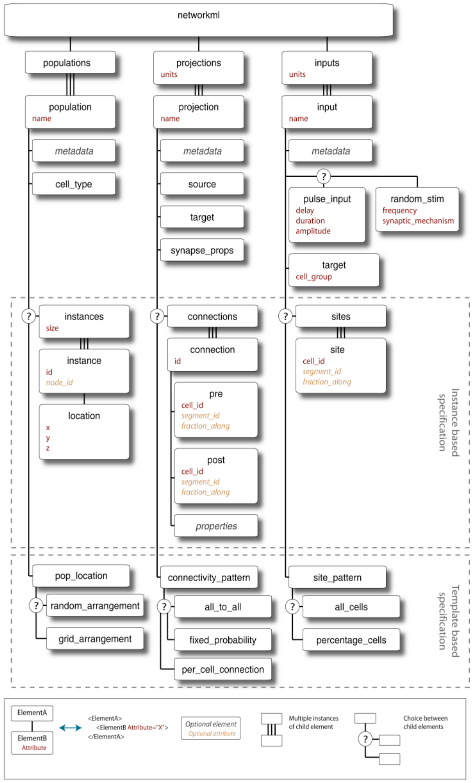
Level 2: Describes the kinetics of models of voltage and ligand gated ion channels, synaptic mechanisms, and the dynamics of intracellular ion concentrations (ChannelML).

Level 3: Describes networks of cells in 3D space including interconnectivity and electrical inputs (NetworkML).


Biological scale of information processing in neural system
Levels in NeuroML specifications
Systems level
Local circuits
Neurons
Dendritic subtree
Membrane/synapse
Molecular/protein
Level 3: NetworkML
Level 1: Metadata & MorphML
Level 2: Biophysics & ChannelML
(Level 4: Subcellular signalling)

Levels in NeuroML and screenshots of corresponding cell, channel mechanisms and network representations in neuroConstruct [4]. neuroConstruct can export generated network structures in NetworkML, and it can import any NetworkML file, regardless of the generating software.

ORGANIZATION OF NetworkML



NetworkML allows for the specification of populations of neurons by:

- providing an explicit list of all neurons and their parameters (instance based specification)
- providing an implicit enumeration (template based specification)

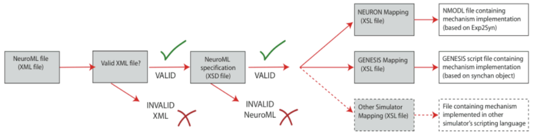
Similarly, connectivity can be specified:

- explicitly using a list of connections
- implicitly by giving an algorithm for defining connectivity such as all-to-all, one-to-one, or fixed probability or by using a fixed number of connections for each presynaptic or postsynaptic cell

Specifications for the properties of synaptic models now also include attributes for the synaptic location on a postsynaptic cell and for delays due to synaptic mechanisms or propagation of action potentials.

CURRENT WORK AND FUTURE PLANS

The latest NeuroML specifications can be found at the NeuroML website at **http://www.neuroml.org**. Samples of valid files are available and users can submit their own NeuroML document files for automatic validation and conversion to a number of different formats including those used by GENESIS [5] and NEURON [6].


NeuroML file (XML file)
Valid XML file?
VALID
INVALID XML
NeuroML specification (XSD file)
VALID
INVALID NeuroML
NEURON Mapping (XSL file)
NMODL file containing mechanism implementation (based on Exp2Syn)
GENESIS Mapping (XSL file)
GENESIS script file containing mechanism implementation (based on synchan object)
Other Simulator Mapping (XSL file)
File containing mechanism implemented in other simulator's scripting language

Process of validation and transformation of NeuroML files

NeuroML schema files define a structure that is used for the specification of models in XML; however, other file formats could take advantage of the same structure. For example, HDF5 files could use the same structure but would provide a more compact method of storing network information.

The node_id attribute in the instance element is useful for specifying how a neuronal network is distributed in a parallel processing environment. For more details see Poster 409.18 titled *Parallel simulations of a 3D cerebellar network created with neuroConstruct*.

The NeuroML standards for networks are compatible with the PyNN initiative to create a Python API for setting up neuronal network models on multiple simulators. Two potential courses for interactions are:

- Given a PyNN script that defines a network template, an instance of the network created by a PyNN compliant simulator could be saved in NetworkML for use in other applications.
- A NetworkML document could be read in by a parser which then calls the appropriate methods in the PyNN API.

More information on PyNN can be found at **http://www.neuralensemble.org/trac/PyNN**.

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MRC Medical Research Council

wellcome trust

NeuroML

XML for Computational Neuroscience

http://www.neuroml.org