

MorphML: Extending NeuroML to facilitate collaborative representations of neuronal morphology

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Abstract

We describe the XML application MorphML which was developed as a common data format for neuronal morphology data. MorphML is distributed as part of NeuroML but can be used as a stand-alone application. We have developed a Java Application Program Interface for MorphML including routines to parse and generate documents to and from an instantiated Java object tree and have also created tools for generating MorphML documents corresponding to digitized morphology files for several data formats. We also describe collaborative efforts to provide interactions between MorphML and existing simulation environments and tools for viewing and manipulating three-dimensional structures in MorphML documents.

Introduction

Existing neuronal morphology data have been obtained using many different neuron tracing systems such as Eutectic's Neuron Tracing System, Microbrightfield's Neurolucida, the Nevin binary branch tree (BBT) syntax, and the Douglas syntax (e.g. [2]). Generally, these systems represent neuronal structure using a collection of points and connections in three dimensions. The different tracing systems use a variety of representations and vocabularies to describe the connectivity between points based on different conceptual models for the morphology data. In each case, the generated files

are flat text files so that cell structure is not available explicitly without reconstructing the cell. Consequently, each system requires a different reconstruction tool for use in spatial analysis or for creating compartmental models for simulation studies.

Due to growing interest in defining a common data format for describing and exchanging neuronal cell and model information using Extensible Markup Language (XML) technology, the XML application NeuroML was developed to support discussion, development, and exchange of neuronal models [3]. In this work we describe the XML application MorphML which was developed as a common data format for neuronal morphology data, and we also describe associated tools. MorphML can be used separately from NeuroML as a stand-alone XML application for representing morphological data (Qi and Crook, submitted); however, it was developed to replace the original cell morphology representation in NeuroML and is included in the current release of NeuroML.

MorphML: An XML Application for Neuronal Morphology Data

XML provides a portable format for computer documents where data are surrounded by text that describes the structure and semantics of the data; that is, the important details about the content of the document are explicitly described by a set of tags known as a markup [4,6]. MorphML provides a markup for representing digitized neuronal morphology files. Our chosen vocabulary is an abstract representation language that is independent of any particular digitization. MorphML documents can then have the same format regardless of the syntax of the original digitized morphology files. The MorphML schema was designed so that morphology data converted to (or from) MorphML will be equivalent to the original digitization in anatomical structure, membrane surface area, and volume.

Because MorphML documents are designed to be stored in databases, viewed by visualization tools, and passed to a variety of analysis and simulation software, the data format has not been modeled on the internal structure of any particular software application. MorphML simply provides reusable information about cell structure essential for all of these downstream applications.

By including cell structure explicitly, relevant data representing cell membrane properties can be linked to the morphology data representing a particular structure. For example, values for membrane resistance and capacitance as well as information about ion channels can be associated with a portion of the dendrite of a neuron. In this way MorphML can easily represent or provide connections to all of the information that is needed for creating models for simulating cell behavior (e.g. [1,5]). The Hines group at Yale University is currently developing software to provide interactions between MorphML and the NEURON simulation environment [5].

Software Tools

We have developed a Java Application Program Interface (API) for MorphML including routines to parse and generate MorphML documents to and from an instantiated Java object tree. We have also developed tools for generating MorphML documents corresponding to digitized neuronal morphology files for several data formats including NeuroLucida and the Nevin BBT syntax. In each case, a neuron is first reconstructed in memory from the input data file. Then these tools use functions provided in the NeuroML API to generate the correct tags for encoding in MorphML based on the dynamic tree structure. We are currently adapting an existing C++ tool for viewing and manipulating three-dimensional cell structure to read and write

MorphML documents. This tool will likely be converted to Java to use the MorphML API directly.

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