

Neurospaces Parameter Handling

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In neuro-biological modeling, no good software technologies currently exist that are memory efficient and give access to all the mathematical details of a model. Mainly two categories of data models are being used to store a model in the main memory of a computer. On the one hand, the full model can be stored in a hierarchical way. This is used by simulators like Genesis and has advantage that all the details of the model are accessible, something that is crucial to validate complicated models[1, 2]. Nevertheless this is very memory expensive. Since complicated models tend to be large, this data model impedes the simulation of these complicated models. As a result, in PGenesis, the parallel version of Genesis intended for the simulation of very large and complicated models, the model is distributed over a parallel computer, which hampers again model validation, since not all the details of the model are accessible from one node of the parallel computer[5].

On the other hand, to solve the above mentioned problems, a number of modeling packages currently use a reference based data model to store neuro-biological components in the main memory of a computer[3, 4]. The references allow to store repetitive components in a memory inexpensive manner, so the advantage of this data model is memory efficiency. The drawbacks are twofold : first, the repetitive components are shared by the references and thus always exactly the same, which, in the context of biological relevance, is not always desirable. Second and more importantly, it becomes impossible to distinguish between two axonal connections going to or coming from a shared subcomponent of two different references.

One of the main goals of our research when implementing the modeling package Neurospaces, has been to allow memory efficient storage of neuro-biological models, while keeping the validation requirement. In practice this means that we want to give the modeler access to the hierarchical data model as used by Genesis, but implement it behind the scene using references.

Model validation and inspection, is always done by accessing individual parameters. By creating distinct categories for the different parameter types present in a neuronal model, it becomes possible to handle them in an appropriate way. Furthermore we distinguish between symbolic values for parameters, direct numeric values and transformed numerical values. We discuss here two categories of parameters in a neuro-biological model :

1. Coordinates : The coordinate of a biological component always gets a direct default value of zero. The transformed coordinate is defined to be the direct coordinate of the component plus the transformed coordinate of the parent of the component.

The advantage of this technique is that it allows not to specify coordinates for components that are at the same location as the parent component, e.g. a channel in a segment inherits the location of the segment. Furthermore when coordinates are attributed to references in a referenced based data model, the coordinates of different references will propagate to the shared components, such that the shared components have different locations depending on the way you access them. Nevertheless the shared components occur in memory only once.

2. Conductances : It is a well known fact that maximal channel conductances in neuroscience papers are often given as conductance densities, expressed in conductance per unit area. Neurospaces knows about the difference between conductance density and maximal conductance. The conductance density is a direct attribute to the channel, while the transformed value of the conductance density is the absolute maximal conductance of the channel. The transformed value is obtained by retrieving the surface of the parent biological component of the channel and multiplying the surface with the conductance density.

Neurospaces knows many more categories of parameters : segment capacitance, segment axial resistance, concentration time constant etc... A function that implements the parameter transformation is

called a parameter handler. The parameter handlers are implemented at the level of the types of the biological components, e.g. the channel type uses a parameter handler that is responsible for scaling of conductance density to an absolute maximal conductance. Also the default values are taken care of by the parameter handlers. Parameter handlers can be shared by a many biological types e.g. the coordinate handler is shared by all the types.

The advantage of the above summarized techniques is that it allows user extensions to be written in a modular way, and it keeps the reference based data model invisible to a modeler. One of the main results is the memory efficiency of Neurospaces.

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