

CellML

In the Computational Bioengineering Laboratory we are interested in using CellML for the description of mathematical models — primarily models of cellular physiology. We are also actively involved in the development of the base CellML XML language specification and related metadata.

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1. CellML tools

Having strong links to the [Auckland Bioengineering Institute](#), we make use of [CMISS](#) for numerical simulations of tissue and organ models. In particular, we take advantage of the ability of CMISS to easily incorporate cellular electrophysiology models defined in CellML into large scale electrical activation models.

For the development of new models and the modification of existing cellular electrophysiology models we make use of [CellML Simulator](#). CellML Simulator is also being used to develop and test ideas on the exploration of the full potential of annotated CellML 1.1, including support for [graphing metadata](#).

2. Graphing metadata

The lab is researching the development of technology and methods for completely specifying a reference description of cellular electrophysiology models in a machine interpretable and software independent manner. [CellML graphing metadata](#) plays an important role in this work providing the link between CellML model instantiation, numerical simulation result sets, and experimental data.

We have now published some initial work illustrating the potential of this approach to mathematical model description. See the following article for more information:

David P. Nickerson, Alberto Corrias & Martin L. Buist. [Reference descriptions of cellular electrophysiology models](#). *Bioinformatics*, 24(8):1112–1114, Apr 2008.

As part of this work we are currently investigating traditional desktop application-based software development and web-based technology taking advantage of Web 2.0 advances in order to further develop the concepts presented in the above article.