

Overview

The CellML language is an open standard based on the XML markup language. CellML is being developed by the Auckland Bioengineering Institute at the University of Auckland and affiliated research groups.

The purpose of CellML is to store and exchange computer-based mathematical models. CellML allows scientists to share models even if they are using different model-building software. It also enables them to reuse components from one model in another, thus accelerating model building.

Although CellML was originally intended for the description of biological models, it has a broader application (for an example, see the classical Mooney-Rivlin Constitutive Material Law). CellML includes information about model structure (how the parts of a model are organizationally related to one another), mathematics (equations describing the underlying processes) and metadata (additional information about the model that allows scientists to search for specific models or model components in a database or other repository).

CellML includes mathematics and metadata by leveraging existing languages, including MathML and RDF. In the future, CellML may also use other existing languages to specify data and define simulation and rendering information.

The CellML project is closely affiliated with another XML-based language project currently underway at the University of Auckland, FieldML. Combined, these languages will provide a complete vocabulary for describing biological information at a range of resolutions from the subcellular to organism level.

FieldML can be used to describe spatially and temporally varying field information. It is appropriate for storing geometry information and spatial distribution of parameters inside compartments in CellML, or the spatial distribution of cellular model parameters across an entire organ.