



THE UNIVERSITY OF AUCKLAND
NEW ZEALAND


Visualisation of CellML Models

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Objectives

- Research and implement a visual language that can be used to represent all biological processes and state information gathered from a simulation.
 - Develop a specification for building visual templates that support this language and the rules for binding them to biological concepts within the biological ontologies.
 - Develop a visual editing tool, that combines the visual language and biological ontologies, to edit and visualize CellML models.
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Current Status of the Project

- Existing visual languages and tools are being evaluated
 - Kitano's notations and CellDesigner
 - Kohn's notations
 - PATIKA and their ontology
 - Edinburgh pathway notations
 - A basic visual model editor is being developed supporting basic functionality.
 - Developing visual templates to represent CellML ontologies
 - Generating simple visual representation of a CellML model using templates
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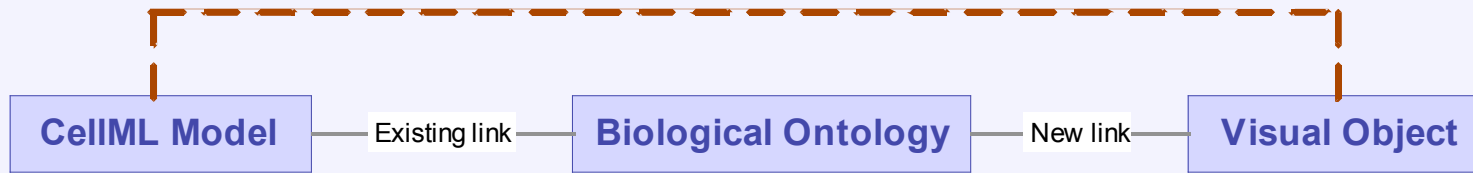


Evaluation of Visual Languages

- Several factors that are being evaluated in a visual language.
 - ☐ The scope of biological concepts it can represent
 - ☐ Extensibility of the visual language
 - ☐ Does the language address scale
 - ☐ Usability of the language
 - ☐ Layout design support
 - ☐ Community support
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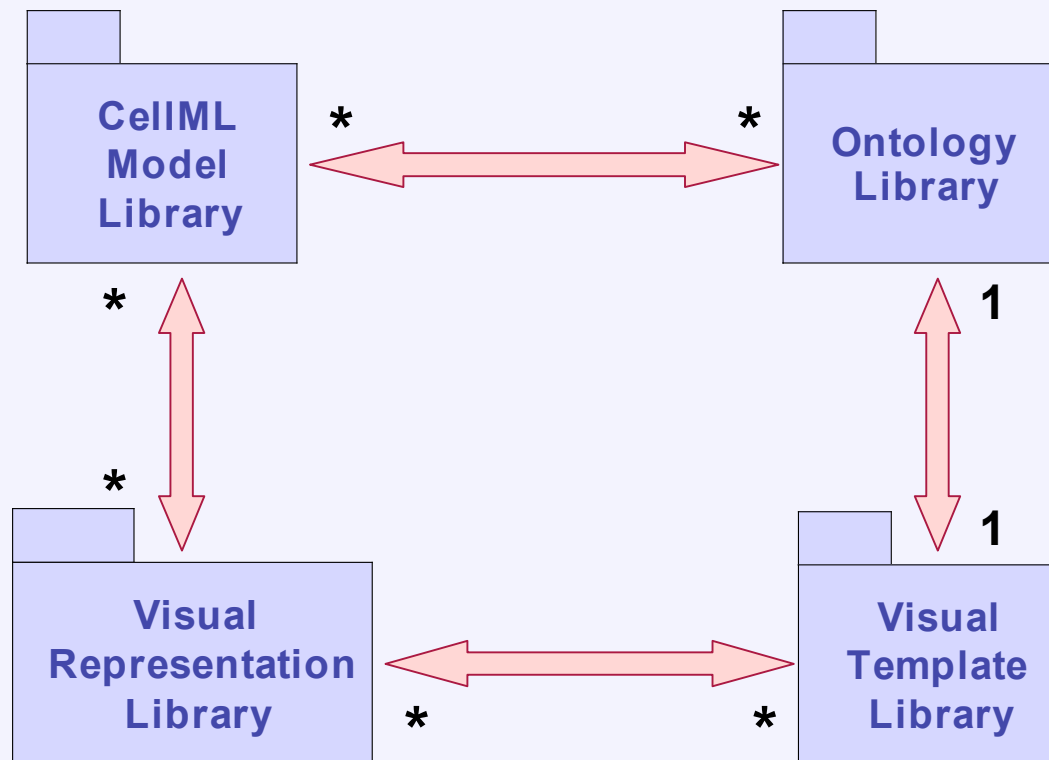
Visual Representation

- The goal is to associate visual elements with CellML models.

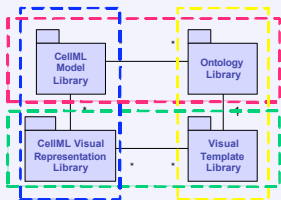


- Currently CellML models are being directly bound to biological ontology.
- Biological ontology refers to physiological and external ontologies such as BioPAX.
- The idea is to integrate visual languages with biological ontology instances that are bound to CellML models.

Library Associations



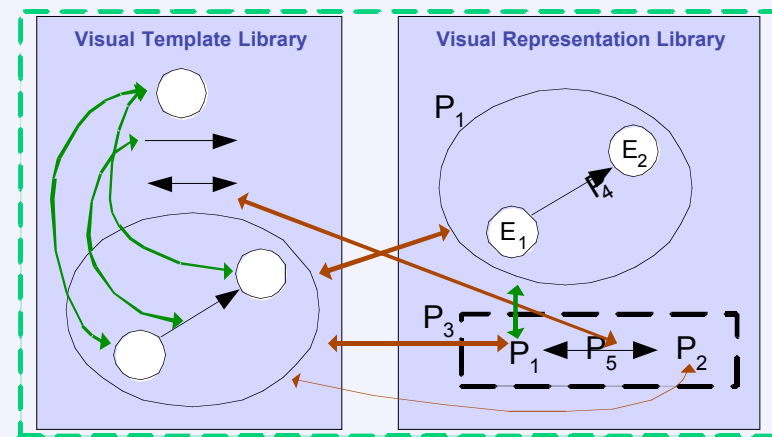
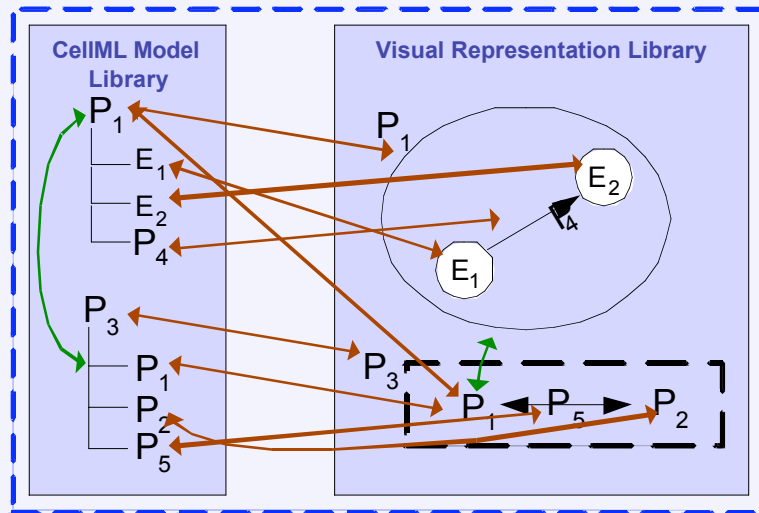
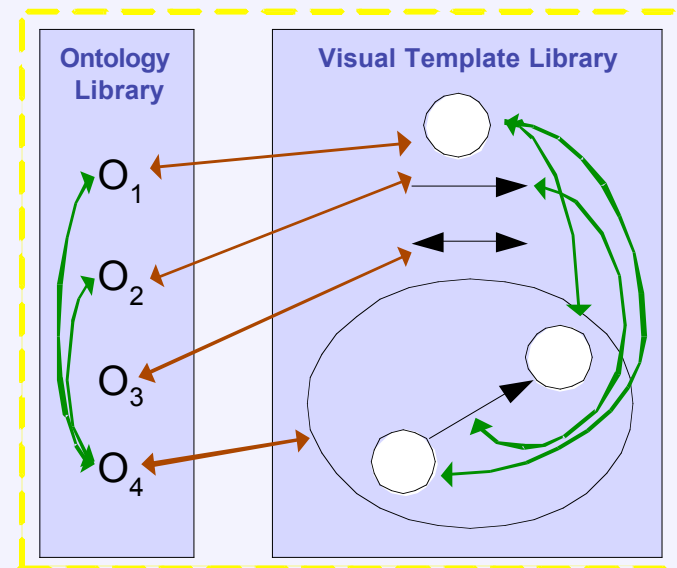
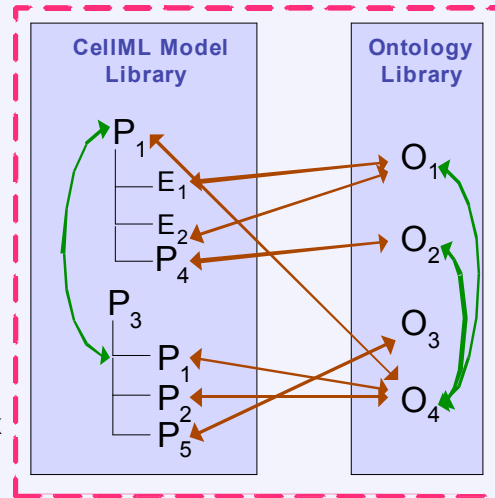
Library Associations



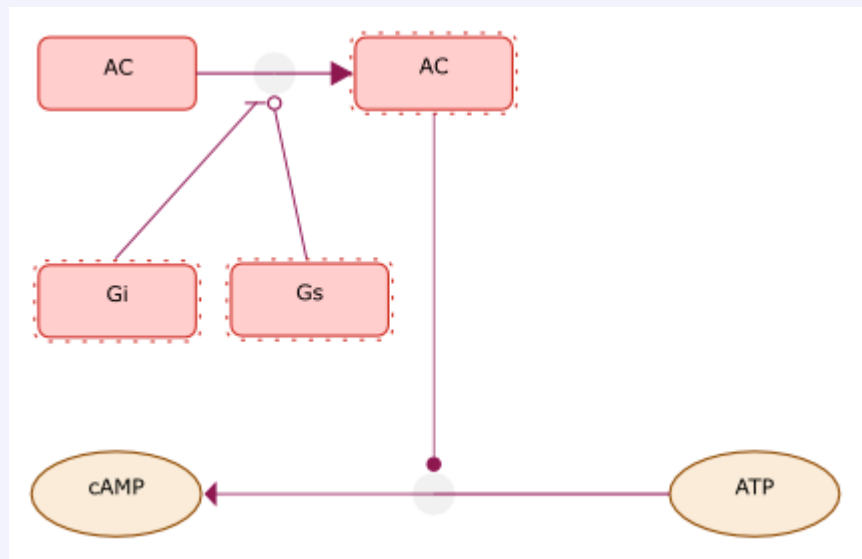
Ex = Element x

Px = Process x

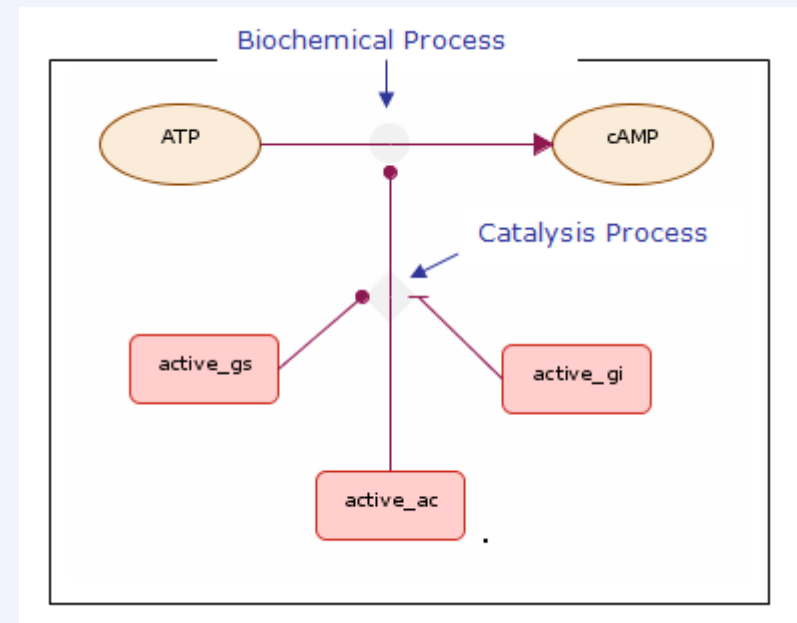
Ox = Ontology concept x



Visualising Interactions



- A diagram created using existing notations



- A diagram created using new notations – supports BioPAX representation



Current Problems with Using BioPAX

- There is no notion of active and inactive states
- There is no differentiation between various types of proteins.
 - Receptors
 - kinases ect.
- There is no API support



CellML Model Editor in Action

- CellML model editor used to draw cAMP/PKA Signalling Cascade Regulation of Cardiac L-type Calcium Channel Activity model
- Technologies used
 - Java
 - SVG
 - Batik
- Main features supported
 - Visualisation of basic entities and transitions
 - Manual Layout
 - Loading files with ontology information
 - Saving and reloading generated SVG files

