



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.



Current Status of the Project

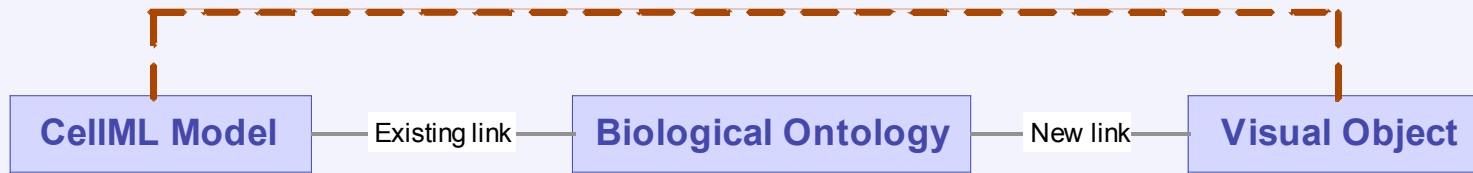
- Existing visual languages and tools are being evaluated
 - Kitano's notations and CellDesigner
 - Kohn's notations
 - PATIKA and their ontology
 - Edinburgh pathway notations
- A basic visual model editor is being developed supporting basic functionality.
 - Developing visual templates to represent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

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

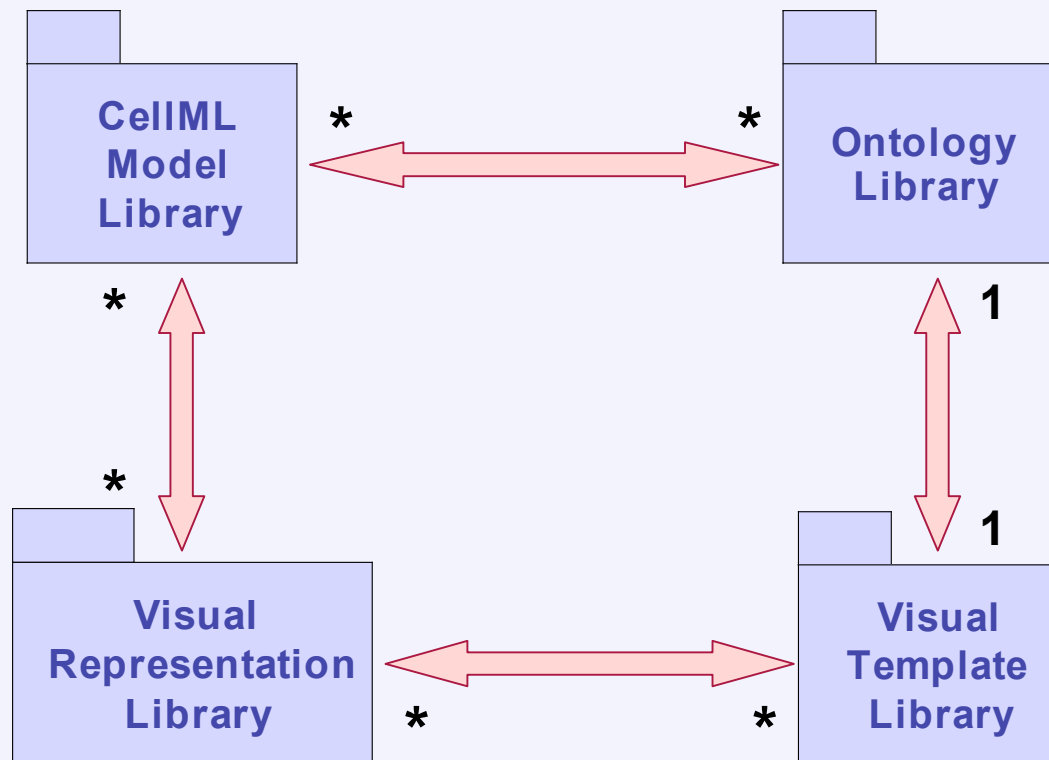
Visual Representation

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

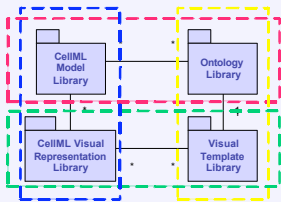


- Currently CellML models are being directly bound to biological ontology.
- Biological ontology refers to physiological and external ontologies such as BioPAX.
- The idea is to integrate visual languages with biological ontology instances that are bound to CellML models.

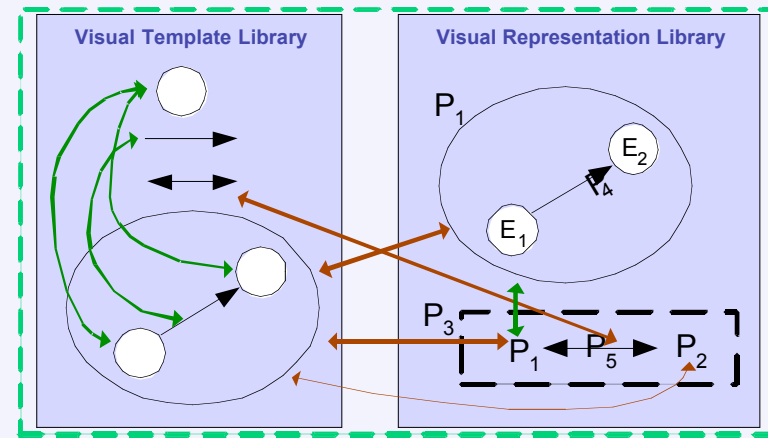
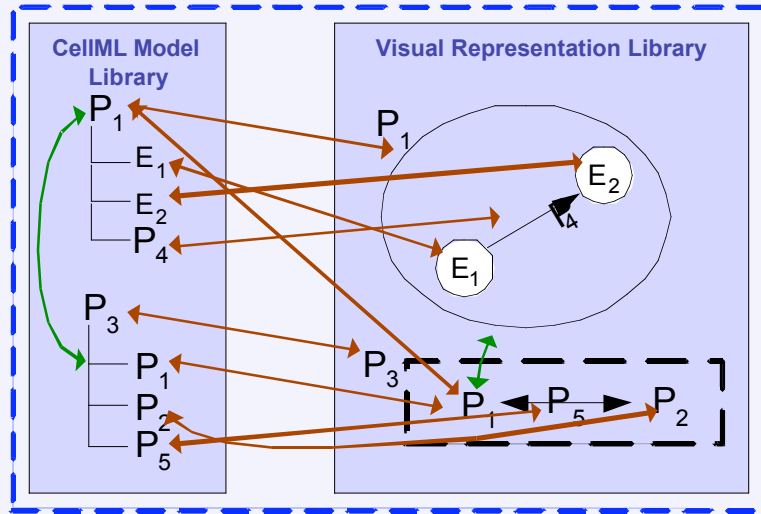
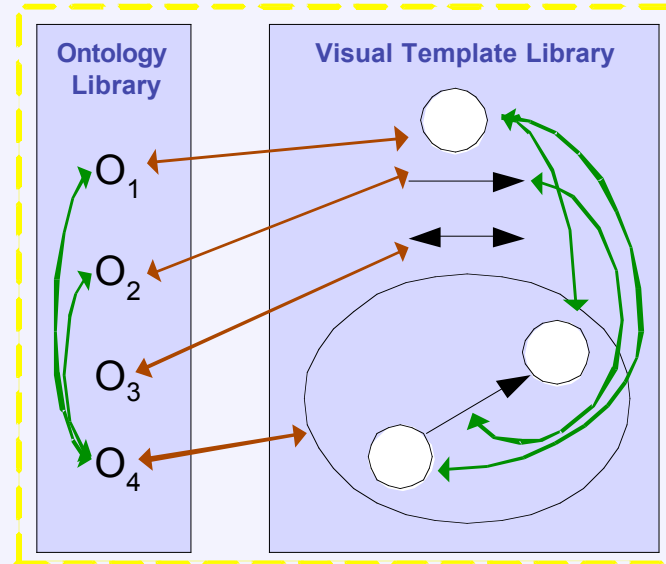
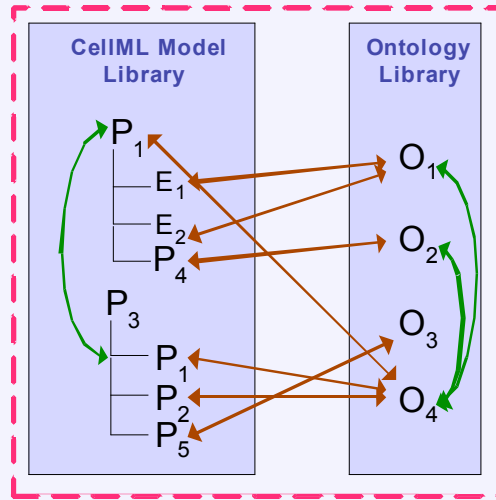
Library Associations



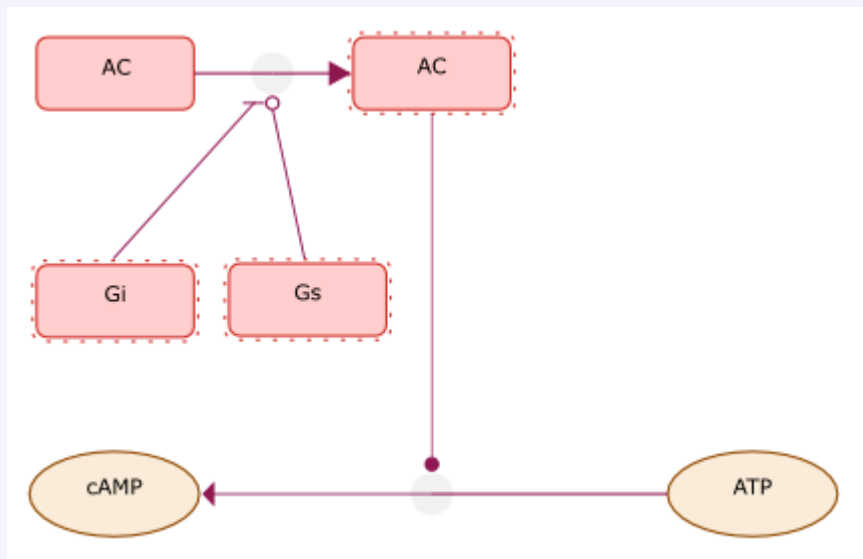
Library Associations



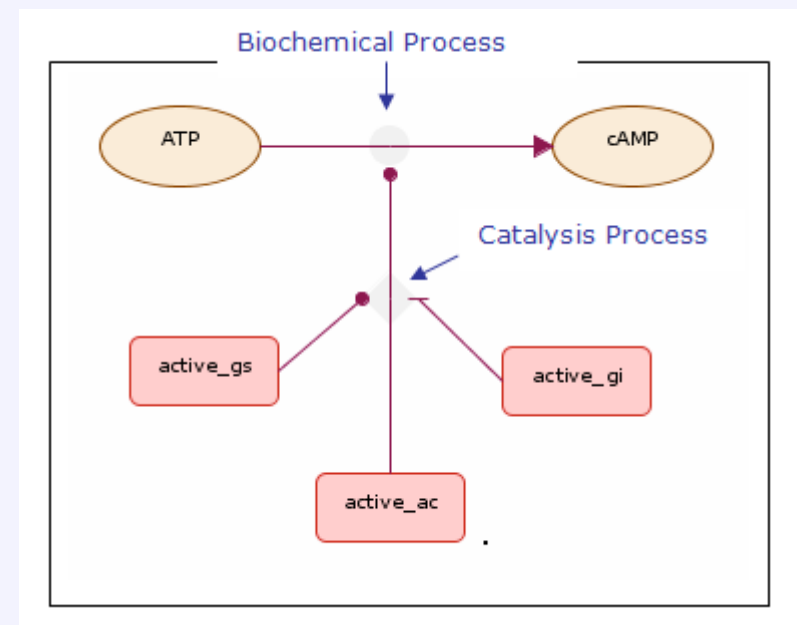
Ex = Element x
 Px = Process x
 Ox = Ontology concept x



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

