An Object-Oriented Data Model for Signal Transduction

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Introduction

- Metabolic, regulatory and signal transduction pathways refer to cellular processes, in which the interactions between the different components form intricate networks, often referred to as biochemical networks. The size of available data on such networks is growing rapidly. Information on such networks and their components is usually stored in various generic and more specialised databases. When available, existing information in a database is limited to one type of biochemical network, and is usually poorly structured. It is therefore difficult to perform elaborated analysis on relationships between different types of biochemical networks.

- We propose an object-oriented data model for signal transduction. This model is an extension of the aMAZE data representation which already deals with metabolic and regulatory pathways [1,2]. Integrated with the latter, it is capable of handling metabolic pathways as well as regulatory and signal transduction pathways, thus covering different types of biochemical networks in a single data representation. The signal transduction data model has been designed to fit a set of about 500 interactions on signal transduction, curated in the aMAZE project. It also integrates protein-protein interactions into their cellular context

A Generic Model of Interactions

- Generic model of interactions : basis of our data representation.
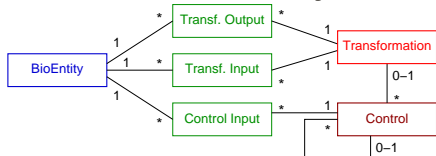
- All the considered interactions are instances of this schema.

- The Transf_Output and Transf_Input objects store information on the particular role of the BioEntities in this reaction (e.g. stochiometry), as well as the cellular location of the different substrates and products.

- Transformation can be controlled by other BioEntity (e.g.catalytic reaction).

- BioEntities can control another control. For instance, Proline can inhibit the ReactionCatalysis (a Control) of a reaction.

Example : Circadian cycle [3]
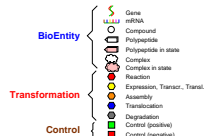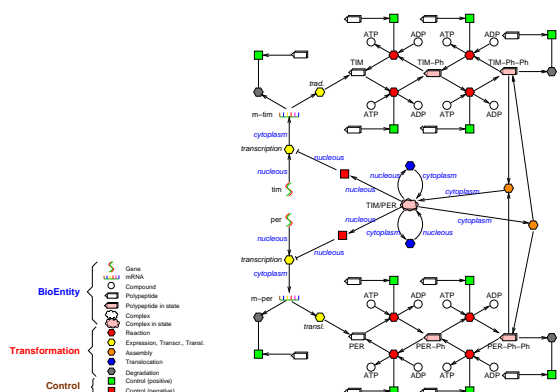
References

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Data Model for Signal Transduction

- By a signal transduction pathway, we mean a biochemical pathway that carries signals from one cellular location (e.g. receptors on the cell-surface) to another (e.g. nucleus).

- In signal transduction, the following elements are particularly important : the cellular location of the BioEntities, the formation and dissociation of complexes and the molecular states of the proteins (e.g. phosphorylation, acetylation, ubiquitylation.).

- Translocation is modeled as a subclass of Transformation. The input and output BioEntities are the same; but the initial location is a property of Transf_Input, and the final location a property of Transf_Output. A translocation can also be controlled by some TransportFacilitator (permeases).

- The Assembly and Dissasembly of complexes is a subclass of Transformation, with its associated AssemblyCatalysis control. Complex is a subclass of BioEntity, but there is an aggregation relation between the complex and all its components. This allows an easy access from a complex to its components.

- Some reactions are very common in signal transduction (phosphorylation, ubiquitylation). No subclass has been defined, but a classification is provided for reactions. This allows a more flexible and extendable structure for existing reactions.

- Polypeptides in a state are modeled as the Polypeptide subclass of BioEntity. A Polypeptide object only contains the information on its states; it is related to its polypeptide reference. P

- Pathways are represented as a directed graph of transformations; arcs relating different pathways are useful to model interactions between pathways as well as subpathways.
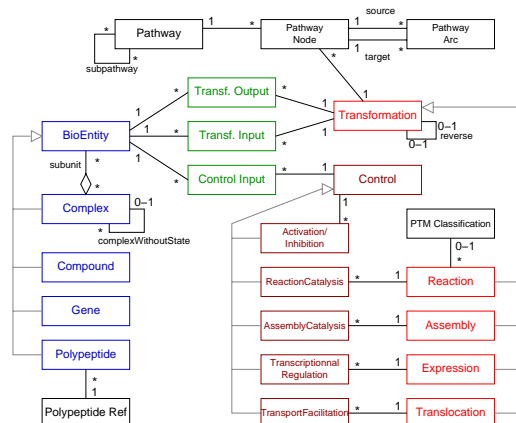
Prototype

- A signal transduction prototype has been integrated into the aMAZE workbench. It contains around 700 BioEntity and about 500 Transfomation and Control.

www.amaze.ulb.ac.be/sigtrans_bench/