An Object-Oriented Model for the Representation of Biochemical Networks

Renato Mancuso[1], Matthew Eldridge[1], Jacques van Helden[1], and Shoshana J. Wodak [1,2], [1]EMBL Outstation, EBI, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SD, UK; [2]Unite de Conformation de macromolecules Biologiques, CP 160-16, Universite Libre de Bruxelles, Ave. F. Roosevelt, 1050 Brussels Belgium.
E-mails: Mancuso@ebi.ac.uk; Shosh@ebi.ac.uk

In just a few years the complete sequences of more than 100 genomes will be known. This may finally allow us to address fundamental issues of cellular function and dynamics in ways that have not been possible before. For this to become a reality it is essential to establish proper relationships between sequence data and corresponding biological functions. This will require combining a large body of biological, biochemical and structural data coming from very different levels of organisation and detail.

A crucial body of data is represented by the information on biochemical networks present in a given cell or tissue, and constituted by data about metabolic pathways, gene regulation, metabolite transport and signal transduction. The ability to access such information electronically should be a very valuable tool for the assignment and the understanding of gene function, as well as for the interpretation of data collected from high-throughput gene expression experiments.

Here we describe the ongoing development of an object-oriented database covering metabolic pathway data from different organisms and tissues and underpinned by detailed information on enzyme function extracted from the publicly accessible BRENDA database. In particular, we describe aspects of our object model for representing metabolic pathways and its extensions for representing other types of functional networks (regulatory, signal transduction). In addition we present the features of a graphical pathway editor developed in C++.

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