A Petri Net Framework for the Representation of Biological Knowledge
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It is often acknowledged that the application of bioinformatics to biological networks (e.g. metabolism, gene regulation or signal transduction) will result in the discovery of processes and pathways which are too complex to be elucidated by human scientists. However, there remains a general problem of organising biological knowledge into a form which is readily manipulated by a computer. For example, although several databases exist for information on enzymes and metabolic pathways, it still requires a great deal of effort to extract a metabolic subnetwork and convert it into a computer model. Recently, various types of Petri Net have been successfully used in the qualitative and quantitative modelling of biological processes. We propose a modelling language built on Petri Net concepts which is conceptually very simple, yet flexible and powerful enough to represent any kind of biological network within a single unified database. Subnetworks from such a database could easily be exported for any kind of analysis. We are working on the development of a metabolic reconstruction system which will identify potential pathways within a generic metabolic network and compare these against genomic information from particular organisms. This should help scientists to clarify which pathways are functioning in that organism, and to highlight enzymes which should be present in the genome but have not yet been characterised.