A multidisciplinary survey of modeling techniques for biochemical networks

James Decraene[1], Peter Dittrich[2], Thomas Hinze[2], Thorsten Lenser[2], Barry McMullin[1], George Mitchell[1]

1: Dublin City University, Dublin, Ireland
2: Friedrich-Schiller-Universitat Jena, Jena, Germany

james.decraene@eeng.dcu.ie

All processes of life are dominated by networks of interacting biochemical components. The purpose of modeling these networks is manifold. From a theoretical point of view it allows the exploration of network structures and dynamics, to find emergent properties or to explain the organization and evolution of networks. From a practical point of view, in silico experiments can be performed that would be very expensive or impossible to achieve in the laboratory, such as hypothesis-testing with regard to knock-out experiments or overexpression, or checking the validity of a proposed molecular mechanism.

The literature on modeling biochemical networks is growing rapidly and the motivations behind different modeling techniques are sometimes quite distant from each other. To clarify the current context, we present a systematic overview of the different philosophies to model biochemical networks. We put particular emphasis on three main domains which have been playing a major role in the past, namely: mathematics with ordinary and partial differential equations, statistics with stochastic simulation algorithms, Bayesian networks and Markov chains, and the field of computer science with process calculi, term rewriting systems and state based systems.

For each school, we evaluate advantages and disadvantages such as the granularity of representation, scalability, accessibility or availability of analysis tools. Following this, we describe how one can combine some of those techniques and thus take advantages of several techniques through the use of bridging tools. Finally, we propose a next step for modeling biochemical networks by using artificial chemistries and evolutionary computation.

This work was funded by ESIGNET (Evolving Cell Signaling Networks in Silico), an European Integrated Project in the EU FP6 NEST Initiative (contract no. 12789).