

Modeling intracellular systems at multiple levels of abstraction

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Key Word: biochemical and genetic reaction networks, simulation, dynamics, databases

Biological regulatory networks are the circuitry that control cellular function and malfunction. The chemistry underlying the function of these networks is extraordinarily complex and difficult, if not impossible to understand knowing only a list of the parts (genes, proteins, and other chemicals) and a list of which parts react with which other parts. Just as when analyzing and diagnosing complex electronic circuits, mathematical models and computational tools for analysis and simulation are necessary if we are to understand, control and even design our own biological and genetic reaction networks. Mathematical methods for analyzing these multiscale systems with mixed levels of abstraction are just becoming available.

In this talk we will describe our efforts at modeling bacterial genetic systems from the stochastic processes of gene expression to spatial effects in cell-cell adhesion and the mathematical and computational challenges of doing so accurately. We will demonstrate analyses of various microbial systems from phage to *Bacillus subtilis* and the challenges faced in understanding the “engineering principles” of control in these systems. We will also describe our efforts at creating a framework for biological data analysis and simulation to aid in these efforts.