Computational and Experimental Approaches to the Study of Genetic Networks

By

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Abstract

Mathematical and computational modeling is becoming increasingly important for understanding the complex dynamical interactions in genetic regulatory systems. In light of recent development of high-throughput genomic technologies, modeling efforts have the potential to move from theory into practice. The understanding of the underlying mechanisms employed by genetic networks not only sets the stage for a systematic view of physiology and pathophysiology, but also carries tremendous practical potential in the context of model inference from real measurement data. Because the implications of the logic of genetic networks are difficult to deduce solely by means of experimental techniques, computational and mathematical modeling plays a vital role.

In this talk, the role of probabilistic Boolean networks will be discussed in the elucidation of genetic interactions by means of transcriptional profiling studies. The focus will be on inference, generation of sub-networks, steady-state analysis, and several classes of regulatory rules for constraining the inference. Recent results obtained from human glioma gene expression studies in our laboratory will be presented.

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