数学与系统科学研究院学术报告

报告题目：Control Theoretic Description of Gene Regulatory Network --- A Probabilistic Approach

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摘要：

　　Cell is the universal building block of all living organisms from bacteria to human being. Even in bacteria, the most primitive cell, several thousands of materials are produced, transformed, degradated through a huge material network of chemical reactions in response to environmental changes. The complexity of control network is far beyond that of the largest chemical plants. In this talk, we propose a framework for coping with this complexity of material links of intracellular control from the viewpoint of control theory by identifying the so-called operon, a collection of genes that express simultaneously, as a plant. Inside a cell, all chemical reactions involve only handful molecules due to the smallness of size. The fluctuations thus becomes dominant in every intracellular biochemical process. Probabilistic approach must be taken in quantitative analysis of intracellular regulatory dynamics. In the latter part of this talk, a probabilistic framework of describing biochemical processes including gene regulatory network and metabolic process is given based on master equation. Graph theoretic approach is used tocompute the stationary configuration of protein/protein interactions which plays a key role in quantitatively describing regulatory dynamics. Several specific networks are analyzed in detail based on our approach.

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