

数学与系统科学研究院

计算数学所学术报告

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报告题目:

**On the Mathematical Modeling and
Analysis of Gene Network Inference
and Cell Polarization**

邀请人: 袁亚湘 院士

报告时间: **2012 年 10 月 16 日 (周二)**

下午 15:30~16:30

报告地点: 科技综合楼三层 311

计算数学所报告厅

Abstract:

Spatial organization of the embryo plays a role in determining how different cells are to develop. An early event in the development of the embryo is the differentiation of the mesoderm and endoderm germ layers, and defining the regulatory circuit that controls this differentiation is one of the main goals of modern developmental biology. In this talk, we use two inference models with different underlying assumptions, a linear ODE model for steady-state data and a linear Markov model for time series data, to elucidate regulatory circuits from the heterogeneous biological samples and then test the ability of the inferred networks to predict spatial gene expression for *Xenopus Tropicalis*.

Cell polarization, in which substances previously uniformly distributed become asymmetric due to external or/and internal stimulation, is a fundamental process underlying cell mobility and cell division. For example, during mating, the yeast cells *S. cerevisiae* sense shallow external spatial gradients and respond by creating steeper internal gradients of protein aligned with the external cue. Understanding the complex regulations during yeast mating polarization is critical to studying many important characteristics in cell polarization including signal amplification, tracking dynamic signals, and potential trade-off between achieving both objectives in a robust fashion. In this talk, we study some of these questions by analyzing several models with different spatial complexity: two compartments, three compartments, and continuum in space. The step-wise approach allows detailed characterization of properties of the steady state of the system, providing more insights for biological regulations during cell polarization.

欢迎大家参加!