数学与系统科学研究院

计算数学所学术报告

报告人： **Prof. Kevin Burrage**

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报告题目： **Multi–scale stochastic modelling of biochemical systems**

邀请人: **洪佳林研究员**

报告时间： **2007年5月22日(周二)**
下午1:30—2:30

报告地点： **科技综合楼三层311**
计算数学所报告厅

Abstract： **Understanding the roles of noise in cellular dynamics is a crucial driver of Cell Biology. The Stochastic Simulation Algorithm (SSA) is an important technique for**

simulating the interactions of small numbers of molecules in cellular environments and in particular genetic regulation. In this talk we focus on two issues. Firstly we will discuss modifications to the SSA that allows us to model delays in transcription and translation and we will illustrate these ideas via the Hes 1 gene regulatory clock in mouse. In the second part of the talk we will address multiscale issues associated with the solution of the chemical master equation (CME), that describes the evolution of the probability density function (pdf) associated with modelling intrinsic noise. The CME is typically difficult to solve, since the state-space involved can be very large. Recently a finite state projection method (FSP) that truncates the state-space has been suggested by Munsky and Khammash and shown to be effective on small scale problems. We present a Krylov FSP algorithm based on a combination of state-space truncation, inexact matrix-vector product routines and aggregation ideas. These techniques allow significantly larger-scale cellular models to be studied than was previously the case using CME approaches.

欢迎大家参加！