数学与系统科学研究院

计算数学所学术报告

报告人： **Prof. Steve Qin**

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报告题目：

Applying Model-based methods to analyze genomics data

邀请人： 洪佳林研究员

报告时间：**2011 年 8 月 2 日（周二）**

上午 9：30-10：30

报告地点： 科技综合楼三层 **311**

计算数学所报告厅

Abstract：

Designing powerful tools to extract scientific insights from massive and noisy high-throughput data is a key challenge in the post-genomic era. Effective clustering and screening algorithms facilitate the identification of subtle patterns of interest, allowing scientists to quickly pinpoint the target of interest for further validation. Model-based approaches offer numerous advantages over traditional distance-based approaches such as allowing explicit incorporation of biological knowledge and offering reliable statistical inference. In this presentation, we will integrate techniques such as divide-conquer-combine, weighting and feature selection into model-based approaches to analyze DNA sequences and microarray gene expression data. The strengthened model-based approaches will allow us to address some of the pressing biological problems including inference of co-regulated genes in eukaryote species and integrated analysis of multiple microarray gene expression datasets collected under a variety of conditions.

欢迎大家参加！