数学与系统科学研究院

计算数学所学术报告

报告人：**Asso. Prof. Steve Qin**

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报告题目：

Model-based methods for analyzing NGS data

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报告时间：**2011 年 12 月 30 日（周五）**

下午 16：00-17：00

报告地点：　科技综合楼三层 **311**

计算数学所报告厅

Abstract：

The next generation sequencing (NGS) technologies have been rapidly adopted in an array of diverse applications. Although extremely promising, the massive amount of data generated from NGS, substantial biases and correlation pose daunting challenges for data analysis. By treating observed data as random samples from probability distributions, model-based methods can accommodate uncertainties explicitly and also automatically leads to rigorous statistical inference. Inspired by the success of model-based methods in the analysis of other high throughput genomics data such as microarray, we attempted to develop novel model-based methods to analyze data generated from the new NGS-based experiments. RNA sequencing (RNA-seq) is a powerful new technology for mapping and quantifying transcriptome. We propose a spatial model-based method named POME to characterize base-level read coverage within each exon. The underlying expression level is included as a key parameter in this model and large base-specific variations and between-base correlations are also taken into account. Simulated and real data analysis demonstrated significant improvement when comparing POME to existing approaches. I will also discuss how model-based methods can help other applications of NGS. This is a joint work with Ming Hu, Michael Zhu and Jun Liu.

欢迎大家参加！