数学与系统科学研究院

计算数学所学术报告

报告人： **Prof. Zhaohui Qin**

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报告题目：

Towards the understanding of the three-dimensional genome organization Statistical challenges and opportunities for analyzing Hi-C data

邀请人： 洪佳林 研究员

报告时间：**2013 年 7 月 24 日（周三）**

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：

Understanding how chromosomes fold provides insights into transcription regulation hence functional state of the cell. Recently, chromosomal conformation capture (3C)-related technologies have been developed to provide a genome-wide view of chromatin organization. Despite great technologies, multiple layers of noise and uncertainties stem from the sophisticated experiments, coupled with various sequencing-related artifacts, making the analysis of such data extremely challenging. Here using Hi-C as an example, we review the critical issues of analyzing this latest type of genomics data, including normalization, modeling and inference. We describe a novel Bayesian probabilistic approach, denoted "Bayesian 3D constructor for Hi-C data" (BACH), to infer chromosome three-dimensional (3D) structures from Hi-C data. We also discuss the observations we made when applying BACH to real Hi-C datasets. This is a collaboration with Ming Hu, Ke Deng, Jesse Dixon, Siddarth Selvaraj, Jennifer Fang, Bing Ren and Jun Liu.

欢迎大家参加！