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：

Bayesian model-based methods for analyzing ChIP sequencing data

邀请人：　　唐贻发研究员

报告时间：**2010** 年 **7** 月 **26** 日（周一）

上午 **10：00**

报告地点：　　科技综合楼三层 **311**

计算数学所报告厅

Abstract：

Protein-DNA interaction constitutes a basic mechanism for genetic regulation of target gene expression. Deciphering this mechanism is challenging due to the difficulty in characterizing protein-bound DNA on a genomic scale. The recent arrival of ultra-high throughput sequencing technologies has revolutionized this field by allowing quantitative sequencing analysis of target DNAs in a rapid and cost-effective way. ChIP-Seq, which couples chromatin immunoprecipitation (ChIP) with next-generation sequencing, provides millions of short-read sequences, representing tags of DNAs bound by specific transcription factors and other chromatin-associated proteins. The rapid accumulation of ChIP-Seq data has created a daunting analysis challenge. Here we propose a hidden Markov model (HMM)-based algorithms to detect genomic regions that are significantly enriched by ChIP-Seq. We also propose a multi-level hierarchical HMM that will allow integration of data from both ChIP-Seq and ChIP-chip experiments. Finally, we will discuss some issues related to post-processing ChIP-Seq data to obtain new biological insights.

欢迎大家参加！