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：

Applications of sparse optimization methods to gene regulation studies integrating multiple OMICs

邀请人： 刘歆 副研究员

报告时间：2016 年 5 月 23 日（周一）

上午 **10:00-11:00**

报告地点： 科技综合楼三层

311 报告厅

Abstract：

Recent advancement of high-throughput biological technologies facilitates the generation of various large-scale biological/clinical data, called OMICs (genomics, transcriptomics, epigenomics, etc) data. Inferring transcriptional regulatory networks from these OMICs data is an important step to understand transcriptional regulatory mechanisms in biological processes or diseases, but it is still facing arduous challenges due to the complexity of transcription apparatus. Sparse optimization methods that are very popular in various application areas provide an opportunity to solve this problem. Sparse optimization methods can deal with large-scale data and efficiently infer gene regulation networks from multiple OMICs data. Taking the special structures of gene regulatory networks into consideration, their advantages are shown in improving the accuracy of gene regulatory network inference.

欢迎大家参加！