

数学与系统科学研究院

计算数学所学术报告

报告人: **Dr. Xiangtao Liu**

(*Department of Psychiatry, University of Iowa*)

报告题目:

**A flexible and adaptive association
test for gene sets using summary
statistics**

邀请人: 唐贻发 研究员

报告时间: 2016年2月20日(周六)

下午 15:30~17:00

报告地点: 数学院南楼七层

702 会议室

Abstract:

Genome-wide association studies (GWAS) have been widely used for identifying common variants associated with complex diseases. Despite remarkable success in uncovering many risk variants and providing novel insights into disease biology, genetic variants identified to date fail to explain the vast majority of the heritability for most complex diseases. One explanation is that there are still a large number of common variants that remain to be discovered, but their effect sizes are generally too small to be detected individually. Accordingly, gene set analysis of GWAS, which examines a group of functionally related genes, has been proposed as a complementary approach to single marker analysis. Here, we propose a flexible and adaptive test for gene sets (FLAGS) using summary statistics. Extensive simulations showed that this method has an appropriate type I error rate and outperforms existing methods with increased power. As a proof of principle, through real data analyses of Crohn's disease GWAS data and bipolar disorder GWAS meta-analysis results, we demonstrated the superior performance of FLAGS over several state-of-the-art association tests for gene sets. Our method allows for the more powerful application of gene set analysis to complex diseases, which will have broad use given that GWAS summary results are increasingly publicly available.

Keywords: Complex disease; gene set; association; GWAS; summary statistics

欢迎大家参加！