

**University of California, Irvine
Statistics Seminar**

***Variance Component Testing and Selection
for a Longitudinal Microbiome Study***

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(Bldg. #314 on campus map)**

High-throughput sequencing technology has enabled population-based studies of the role of the human microbiome in disease etiology and exposure response. Due to the high cost of sequencing technology such studies usually have limited sample sizes. We study the association of microbiome composition and clinical phenotypes by testing the nullity of variance components. When the null model has more than one variance parameters and sample sizes are limited, such as in longitudinal metagenomics studies, testing zero variance components remains an open challenge. In this talk, I first introduce a series of efficient exact tests (score test, likelihood ratio test, and restricted likelihood ratio test) of testing zero variance components in presence of multiple variance components. Our approach does not rely on the asymptotic theory thus significantly boosts the power in small samples. Furthermore, to further conquer limited sample size and high dimensional features of metagenomics data, we introduce a variance component selection scheme with lasso penalization. We propose a minorization-maximization (MM) algorithm for the difficult optimization problem. Extensive simulations demonstrate the superiority of our methods vs existing methods. Finally, we apply our method to a longitudinal microbiome study of HIV infected patients.