

**University of California, Irvine  
Statistics Seminar**

*Large-scale Covariance Estimation with Applications in Biology*

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**Thursday, May 24, 2018  
4 p.m., 6011 Bren Hall  
(Bldg. #314 on campus map)**

Understanding the function of biological molecules requires statistical methods for assessing covariance across multiple dimensions. To address these issues, I develop a Bayesian model-based method for evaluating heterogeneity among multiple covariance matrices when the number of features,  $p$ , is larger than the sample size,  $n$ . We use an empirical Bayes method to identify a low-dimensional subspace which explains variation across all groups and use an MCMC algorithm to estimate the posterior uncertainty of eigenvectors and eigenvalues on this subspace. I will illustrate the utility of our method for exploratory analyses of high-dimensional multivariate gene expression and metabolomics data.

For directions/parking information, please visit <https://uci.edu/visit/maps.php> and <http://www.ics.uci.edu/about/visit/index.php>