

Applied and Computational Mathematics and Statistics Colloquium

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will give a lecture entitled:

*Preconditioned Bayesian Lasso and Bayesian
Group Lasso for Genome-Wide Association Studies*

Friday, February 18th, 2011
4:00 PM

Location: 129 Hayes-Healy Center

Abstract:

Despite their success in identifying genes that affect complex diseases or traits, current genome-wide association studies (GWAS) are challenged by the high dimensionality of data, the involvement of complex environmental factors, and longitudinal or functional natures of many complex diseases or traits. Motivated by these challenges, we first propose a two-stage procedure for multi-SNP modeling and analysis in GWAS when the response variable is univariate. When response is observed repeatedly over time at individual-specific time points, we develop a nonparametric varying-coefficient model for incorporating functional aspects of phenotypic traits into GWAS and estimate the model parameters through group-lasso penalized linear regression in a Bayesian framework. Our method provides not only point estimates, but also interval estimates of all parameters and automatically constructs the confidence bands of significant time-varying effects. We use the new method to analyze a real GWAS data set from the Framingham Heart Study where the number of observations is less than the number of predictors. Eleven SNPs that are associated with body mass index (BMI) are detected, and their time-varying genetic effects are estimated.