Applied and Computational Mathematics and Statistics Colloquium

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will give a lecture entitled:

A Semiparametric Bayesian Model for Genetic Mapping with Bivariate Sparse Longitudinal Data

> Monday, January 24th, 2011 4:00 PM Location: 129 Hayes-Healy Center

Abstract:

Most of the biological, agricultural and medical studies result in longitudinal data measured at subject specific time points. Despite difficulty, such data can be analyzed efficiently with some advanced methods developed in longitudinal or functional data analysis literature. However, when the studies result in bivariate response measured longitudinally, traditional method of using two separate models for two responses might not be quite effective simply because two responses might be highly correlated. The challenge in such situations is to model the mean response and the covariance matrix which is non-negative definite. In this talk, I propose a semiparametric approach for joint modeling of the mean and covariance for such data. Penalized spline is used to model the mean curve and an extended generalized linear model is used to estimate the covariance structure. Model parameters are estimated by MCMC, using Gibbs sampler and Metropolis Hastings algorithm. We applied our method on blood-pressure data from Framingham Heart Study (FHS) to locate the quantitative trait loci (QTLs) controlling human blood pressure. Extensive simulations studies are performed to check the validity and utility of the proposed model. The current approach will be a powerful tool to reveal the genetic control of the dynamic traits which are bivariate in nature.