

DEPARTMENT OF MATHEMATICS AND STATISTICS
MISSISSIPPI STATE UNIVERSITY

COLLOQUIUM

Nonparametric Modeling of Large Longitudinal Covariance Structure in Functional Mapping of Quantitative Trait Loci

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Allen 14

Abstract. Estimation of the covariance structure of longitudinal processes is a fundamental prerequisite for the practical deployment of functional mapping designed to study the genetic regulation and network of quantitative variation in dynamic complex traits. We present a nonparametric estimation approach for the covariance structure of a quantitative trait measured repeatedly at a series of times. Specifically, we adopt Huang et al.'s (2006) approach of invoking the modified Cholesky decomposition and converting the problem into modeling a sequence of regressions of responses. A regularized covariance estimator is obtained using a normal penalized likelihood with an L2 penalty. This approach, embedded within the mixture likelihood framework of functional mapping, leads to enhanced power of this dynamic mapping method while preserving its biological relevance. Extensive simulation studies are performed to reveal the statistical properties and advantages of the proposed method. A real example from a mouse genome project is analyzed to illustrate the utilization of the methodology. The new method will provide a useful tool for genome-wide scanning for the existence and distribution of quantitative trait loci underlying a dynamic trait important to agriculture, biology and health sciences.

Mr. Yap is a candidate for a position in our department. There will be a reception for him in Allen 467 at 3:00 pm following his talk.

Contact Michael Neumann, neumann@math.msstate.edu or (662) 325-7159, for additional information.