STANFORD UNIVERSITY

DEPARTMENT OF STATISTICS

DEPARTMENTAL SEMINAR

4:15 p.m., Tuesday, October 19, 2004
Sequoia Hall Room 200
(Cookies at 3:45 in 1st Floor Lounge)

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Genome Scans With Gene-Covariate Interaction

Abstract: Genetic models for gene-covariate interaction are described. Methods of linkage analysis are developed that utilize special features of these models and the corresponding score statistics are derived. Their power is compared with the score statistics of simple genome scans that ignore these special features (naive statistics). Substantial gains in power are observed when the gene-covariate interaction is strong. Both QTL mapping and affected sibpair mapping are discussed. For the latter case, a simpler statistic is proposed which has similar performance to the score statistic, but does not require the estimation of nuisance parameters. Since the nuisance parameters are not estimable solely by affected sibpair data, this statistic is much easier to apply in practice. Similarities with linkage analysis of models for multivariate phenotypes and for longitudinal data are also briefly discussed. Approximations for the genome wide p-value and power are derived under the framework of local alternatives.

This is joint research with Jie Peng and Hsiu-Khuern Tang.