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***Statistical Methods for the Design and
Analysis of Microarray Experiments***

Abstract:

My talk will focus on three projects. The first addresses the experimental design question of whether or not pooling mRNAs prior to hybridization is useful. The second concerns microarray time course experiments, where it is of interest to identify genes differentially regulated across multiple conditions over time. The last considers expression trait loci (ETL) mapping studies, where each mRNA abundance measurement is considered as a phenotype for quantitative trait loci (QTL) mapping. I will review our approaches to each of these problems and illustrate their performance using data from simulations and case studies.

**Tuesday, February 15th, 2005
4:00 p.m.**

Genetics/Biotechnology Center Auditorium
425 Henry Mall