

# Department of Applied and Computational Mathematics and Statistics Colloquium

**Hal Stern**

Department of Statistics  
University of California, Irvine

will give a lecture entitled:

## *Spatial Statistical Models for Genome-wide Association Studies*

### Abstract

Genome-wide analyses are now commonplace approaches to identifying genetic risk factors for disease. The standard analysis is based on a series of tests for association between individual genetic markers (known as SNPs) and disease status. This approach ignores known relationships among the markers. This motivates our work on methods that incorporate dependence among markers. In this study, we develop Bayesian hierarchical models to analyze multiple markers simultaneously. Our basic approach begins with the traditional single-marker test statistic, which is presumed to be a noisy version of the underlying effect of that location on the genome. Two types of prior probability models are introduced to capture dependence among SNPs: a model allowing for dependence as a function of distance between SNPs and a model integrating dependence among multiple markers within a gene. We illustrate the models on simulated data and on a real Alzheimer's disease dataset.



**Friday, December 9<sup>th</sup>, 2011  
10:00 a.m. to 11:00 a.m.  
127 Hayes-Healy Center**