

DEPARTMENT OF STATISTICS COLLOQUIUM SERIES  
Texas A&M University

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**HYPOTHESIS TESTING FOR HIGH DIMENSIONAL DATA:  
STUDYING RARE VARIANT EFFECTS IN SEQUENCING  
ASSOCIATION STUDIES**

**ABSTRACT:**

Whole exome and whole genome sequencing studies are increasingly being conducted to identify rare variants associated with complex traits. The classical single marker test, which is popular for studying common variant effects in genome-wide association studies, has little power for testing rare variant effects. Multi-marker analysis is hence needed. We will discuss challenges in such testing problems, and discuss several methods for testing for composite null hypotheses in high-dimensional data especially when the design matrix is sparse and signals are sparse. We will discuss difficulties using the oracle estimators developed for variable selection for testing, and strategies of improving testing power by incorporating biological knowledge in analysis.

**DATE:** Thursday, February 16, 2012  
**TIME:** 3: 45 p.m. – 4:45 p.m.  
**PLACE:** Room 113, Blocker