

University of Houston, Department of Mathematics

Statistics Seminar

Daniel Schaid, PhD

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**Multivariate Analysis in Genetic Studies: Pleiotropy and
Disentangling Statistical Confusion**

Friday September 18, 2015, 11:00 am – 12:00 pm

Conference Room 646A, PG Hoffman Hall

Abstract

The statistical association of a single trait with genetic data has revolutionized human genetic medicine, with many genome-wide association studies completed and providing guidance on genetic factors influencing human health. Although human diseases are often characterized by multiple measured traits, it is common to evaluate the association of a gene with each trait separately. For a long time, animal breeders have known what the human genetics community is beginning to discover: analyzing multiple correlated traits simultaneously can give greater power to detect underlying causal genes. Yet, the statistical methods are somewhat disorganized, with “newly invented methods” unknowingly reinventions from existing methods. This talk will focus on recent developments of statistical models that are intended to simultaneously analyze how multiple traits are associated with a measured gene. Some methods will be familiar to biostatisticians, based on multivariate regression and canonical correlation, while other methods based on mixed models — the tools of animal breeders — will offer alternative insights of pleiotropy: multiple traits caused by a single gene. Furthermore, I will present a novel statistical method to test the existence of pleiotropy. By illustration of the some of the methods on existing data, strengths and limitations of the methods will be emphasized.

Please contact Dr. Wenjiang Fu (fuw@math.uh.edu) for meetings with the speaker.