



THE UNIVERSITY OF  
**CHICAGO**

Department of Statistics

STATISTICS COLLOQUIUM

JOINT SEMINAR WITH THE DEPARTMENT OF HUMAN GENETICS

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Disentangling Nature and Nurture  
Using Genomic Family Data

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#### ABSTRACT

Heritability measures the relative contribution of genetic inheritance (nature) and environment (nurture) to trait variation. Estimation of heritability is especially challenging when genetic and environmental effects are correlated, such as when indirect genetic effects from relatives are present. An indirect genetic effect on a proband (phenotyped individual) is the effect of a genetic variant on the proband through the proband's environment. Examples of indirect genetic effects include effects from parents to offspring, which occur when parental nurturing behaviours are influenced by parents' genes. I show that indirect genetic effects from parents to offspring and between siblings are substantial for educational attainment. I show that, when indirect genetic effects from relatives are substantial, existing methods for estimating heritability can be severely biased. To remedy this and other problems in heritability estimation, such as population stratification, I introduce a novel method for estimating heritability: relatedness disequilibrium regression (RDR). RDR removes environmental bias by exploiting variation in relatedness due to random Mendelian segregations in the probands' parents. We show mathematically and in simulations that RDR estimates heritability with negligible bias due to environment in almost all scenarios. I report results from applying RDR to a sample of 54,888 Icelanders with both parents genotyped to estimate the heritability of 14 traits, including height (55.4%, S.E. 4.4%), body mass index (BMI) (28.9%, S.E. 6.3%), and educational attainment (17.0%, S.E. 9.4%), finding evidence for substantial overestimation from other methods. Furthermore, without genotype data on close relatives of the proband - such as used by RDR - the results show that it is impossible to remove the bias due to indirect genetic effects and to completely remove confounding due to population stratification.

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