



HPC Newsletter

Speaker Series Edition

Issue No. 6

Dr. Guang Guo, *University of North Carolina at Chapel Hill*

This HPC Seminar was enhanced by the participation of Prof. James Taylor, a biological scientist who studies the upstream science of genetics within the Department of Biology, JHU, and Prof. Xiaobin Wang, a Pediatrician who studies epigenetics based on a large birth cohort's data within the School of Public School, JHU. These two scholars provided informal comments during the seminar. Alongside these commentators, Dr. Guo led an informal post-seminar workshop of 1.5 hours, spurring exciting discussions and potential research ideas.

Dr. Guang Guo

Dr. George and Alice Wells Distinguished Professor of Sociology at University of North Carolina, Chapel Hill

Seminar title: **Genomics and Population Studies**

What does genomic information add to social science research?

Conventional social science research assumes that individuals are more or less identical at birth. Differences among individuals can be attributed to nurture rather than nature. In recent years, social scientists have started to explore the impact of genes, and such efforts have recently started to cultivate fruit. 10 to 15 years ago, the addition of genetic information at the individual level was unthinkable, but now it has become a regular component of many studies.

Rapid advances in genomics alongside increased interdisciplinary collaborations among researchers have created strong challenges to the age-old assumption of the absence of heritability. Specifically, inheritance likely impacts socioeconomic status (SES) outcomes, health, and other type of behaviors, such as smoking and drinking. The incorporation of genomic information in social science studies will allow us to better address sociological questions about inequality.

How did social scientists assess genetic influence prior to molecular data?

Twin and sibling studies have been around for 20-30 years, preceding the advent of individual DNA data. In his 2005 article "The social influences on the Realization of Genetic Potential for Intellectual Development," Dr. Guo applies a sibling approach to assessing the importance of ascribed and achieved characteristics for social mobility. Using a large sibling sample from Add Health, the study finds that when individuals are subject to similar social environmental impact, parental unemployment and ethnicity have a significant effect on the extent to which genetic potential for intellectual development is realized. Specifically, in using random-effects models to calculate the heritability of SES sub groups, this study showed that SES disadvantaged groups tend to have lower heritability for cognitive scores.

Where do social scientists apply individual genetic information?

Since 2000, many researchers have employed the candidate gene approach which examines associations between certain genes and diseases or other phenotypic expressions. This approach is also often used in animal studies. Dr. Guo and his colleagues (2008) use the candidate gene approach in the article, "The Integration of Genetic Propensities into Social-Control Models of Delinquency and Violence among Male Youths," and they implement regression to estimate genotype effects on delinquency. Specifically, using the third wave of Add Health where the saliva DNA of more than 2000 siblings and twins was collected, a small number of candidate genes were coded as variables and included in the models as covariates. They found that three particular genetic polymorphisms were highly significant predictors of delinquency, and most importantly, that the genetic effects of these genes are conditional on and interact with social processes.

Finally, starting in the late 2000s, genome-wide association studies (GWAS) have been available for researchers. These studies look for genetic variants within particular phenotypical manifestations of traits or diseases. In a GWAS on factors that influence binge drinking among college students, Dr. Guo and colleagues (2015) found that while randomly assigned roommates do influence binge drinking behavior, and peer influence showed a medium level of genetic propensity for alcohol use among youths. Those with a low or high genetic propensity for alcohol use were not influenced by peer drinking behaviors. The genetic data collected for this study was procured from 2000 randomized roommates at a large public university in the South and came from saliva DNA, enabling researchers to test several hundreds of genetic variants.

What are the recent advancements that GWAS has contributed to existing debates and findings?

Currently, genomic findings tend to be used primarily in health outcomes. In the 2010 GWAS consortium, an analysis of 249,796 individuals, revealed that 18 new loci associated with body mass index (BMI) in addition to the existing 14 known genes. In 2016, GWAS further discovered 65

additional BMI genes based on data from up to 339,224 individuals. With these large samples, the extent to which the impact of each gene becomes increasingly reliable.

Regarding a common sociological concern, a 2016 GWAS identified 74 loci associated with years of schooling, and the number of originally known genes increased... While these findings and modern methods contribute valuable new information to a well-established question, it is necessary to keep in mind that educational attainment is measured very crudely, and environmental processes modify and reshape genetic processes. Nevertheless, with R^2 values that reach between 11-13% for educational attainment, the use of GWAS identified genes in social science research will continue.

How have scholars taken gene-environment interaction into account?

Gene-environment interaction, or "G by E" studies, help us explain social outcomes. In a 2015 article, Dr. Guo and his colleague used GWAS results to study how lifetime socioeconomic status, historical context, and genetic inheritance shape BMI in middle and late adulthood. Using the Health and Retirement Survey (HRS) with a sample of more than 9,000 individuals with GWAS data (upwards of 2 million genetic variables), they model the interactive effect between genotype and SES. They found that genetic obesity raised the mortality rate among black females by more than 100%; the "G by E" interaction analysis indicates that a higher level of educational attainment attenuates negative effects of genetic obesity.