SEMINAR

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10:30 - 13:00

Greetings and Introduction
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Exploring the role of genetics data in a model of life-cycle health behavior

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Exploring the role of genetics data in a model of life-cycle health behavior

Titus Galama, Dean R. Lillard, Kevin Thom,

Recent developments in genetics have dramatically lowered the time and expense of sequencing individual human genomes. As a result, the number of people who contribute genomic data for research purposes is growing. As this sample grows, researchers are also collecting for those same people information on social and economic behaviors. Consequently, the data needed to run genome-wide association studies (GWAS) is expanding in both sample size and the scope of available phenotypes. Further, the single nucleotide polymorphism (SNP) variants are being associated with social and economic outcomes at a pace that far outstrips the development of knowledge about the underlying mechanisms and possible biological pathways. Second, physicians and patients face increasing pressure to decide whether or not to learn one's genetic profile (polygenic scores or PGS).
The latter, more practical and immediate need motivates our project. Primary care physicians need evidence that will inform whether and when they counsel patients to learn about their genetic profiles. As importantly, physicians need to advise patients now. Because of the growing pressure about PGS, physicians and patients cannot wait for the scientific community to delve deeply to understand whether and what biological mechanisms link SNP variants to observed phenotypic variation.

This presentation introduces the outline of a model of dynamic health decisions that aims to incorporate genetics and yield testable predictions. We are extending Galama & van Kippersluis' (2018) theory of health by adding genetic heterogeneity and the potential for misinformation or uncertainty about the effects of unhealthy behaviors and one's own genotype. We are building the model with two primary goals. First, we want to generate predictions about how genotypes influence health behavior over the life-cycle when individuals are forward-looking. Second, we want predict how behavior and health will change when people get information about either their genetic make-up or the consequences of health behaviors. We focus on two relevant dimensions of genetic heterogeneity: a genotype related to unhealthy behaviors (e.g. smoking and drinking), and a genotype related to the propensity for cognitive decline.

The model suggests three ways that genes might impact the life-cycle path of behavior and health outcomes: (1) shifting preferences for unhealthy goods through a genetic "taste" parameter; (2) altering the relationship between consumption, investment, and depreciation in health, (3) changing the rate of cognitive decline, which in turn affects the marginal productivity of health investments.

The model we have developed so far assumes that individuals are perfectly informed about their genotype and how health inputs and unhealthy behaviors affect health. Our primary motivation in building this model is to investigate the consequences of mistaken or uncertain beliefs related to these parameters.

Although still not complete, we present preliminary empirical evidence related to the model predictions.

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