The genetic architecture of economic and political preferences

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Relevance for Social Science

- The extent to which these promises of molecular genetic data will be fulfilled hinges crucially on the molecular genetic architecture of the traits in question.
- Molecular genetic architecture: joint distribution of effect sizes and allele frequencies in a population.

Prerequisites for Applications

1. Biological mechanisms typically requires an ability to identify individual variants or genes.

2. For prediction, interventions and OVB, may be enough that the genetic variants jointly have predictive power.

3. Genes as instrumental variables (Davey-Smith, 2002; Ding et al., 2007) requires detailed knowledge of the pathways through which the genetic variants affect the outcome of interest.

- Use the method of Yang et al. (2001) - GREML - for estimating the proportion of variance explained jointly by all the SNPs measured in a GWAS.
- Carry out prediction analyses in the spirit of Purcell (2009).
- Conduct GWAS analysis.

GREML: Key Identifying Assumption

- Idea is to see how the correlation in phenotype between pairs of individuals relates to the genetic distance, estimated from SNP data, between those individuals.
- Among individuals who are unrelated—i.e., distantly related, since all humans are related to some extent—environmental factors are uncorrelated with differences in the degree of genetic relatedness.
- More random variation in the realized degree of genome sharing relative to the expected degree as the expected relatedness declines.
- Realized relatedness should be independent across chromosomes.

GREML: Interpretation

- We should expect the estimated relationship between phenotype and genetic relatedness to be attenuated because relatedness is measured imperfectly; the common SNPs typed may not be perfectly representative of the causal variants (Yang et al., 2010; Visscher, Yang and Goodard, 2010).
- GREML estimates are a lower bound of narrow heritability.
- Output can be interpreted as the ultimate predictive value that can be obtained from dense SNP data.
- Can test for diffuse effects by checking whether longer chromosomes explain more variation.

Economic Preferences

- Risk - Questions from Barsky et al. (1997) and Dohmen et al. (2006).
- Trust - Questions from World Value Survey.
- Fairness - Questions from World Kahneman Knatsch and Thaler (1986)
- Discounting - Three Questions Comparing Immediate to Delayed Payoffs.

Political Attitudes

- Derived from a factor analysis of a 34 item battery of policy proposals.
- Results suggest five distinct factors: attitudes toward immigration, economic policy, environmentalism, feminism and international affair.

- Years of educational attainment from SALT survey.

GREML Analyses

	Economics					Political				
	Edu	Risk	Patient	Fair	Trust	Crime	Econ Pol	Environ	Femin	Foreign
v(g)	0.158	0.137	0.085	0.000	0.242	0.203	0.344	0.000	0.000	0.354
p	0.004	0.186	0.285	0.150	0.046	0.079	0.012	0.500	0.500	0.009
N	5,727	2,327	2,399	2,376	2,410	2,368	2,368	2,368	2,368	2,368
Chrom	0.442	0.118	-0.195	-0.111	0.460	0.118	0.496	-0.311	0.247	0.462
p	0.039	0.601	0.623	0.031	0.031	0.601	0.019	0.159	0.268	0.030

- Virtually no predictive power for any of the traits studied.
- No genome-wide hits for any of the preference variables.

- These results consistent with these traits having a complex architecture, with highly diffuse and small genetic effects scattered across the genome.
- Implies that in the field of genetics and social science, as it is presently being pursued, we should expect a high false discovery rate.
- Three constructive responses.
  - Use other statistical approaches that make efficient use of the information contained in the entire genome.
  - Gather large samples.
  - Study relatively large and replicated associations.