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TITLE: Nature of Nurture Analysis via Structural Equation Modeling

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ABSTRACT:

While behavioral genetics is often viewed as being concerned with cataloging genetic variation and its determinants across traits, there has traditionally been great interest in understanding how family members directly impact each other in non-genetic ways. However, because family members share both genetic and environment factors, it is hard to disentangle variation due to genetic factors from variation due to familial shared environment factors by modeling only covariances between relatives.

Recently, Kong *et al.* developed a method to understand whether parental phenotypes directly influence their offspring phenotypes (“vertical transmission”) using the covariance between a polygenic risk score from non-transmitted parental genotypes (which imperfectly reflects parental phenotype) and offspring phenotype. Here, we show how structural equation models (SEM) can both simplify and improve upon the method introduced by Kong *et al.* To estimate parameters of SEM model, we performed maximum likelihood (ML) estimation via openMX package in R.

To verify our SEM model works similar to Kong *et al.*, we used GeneEvolve to simulate several scenarios, including parent-to-offspring vertical transmission, assortative mating, and additive genetic effects. We show that our proposed method provides unbiased estimates of the full variance due to vertical transmission as well as estimates of genetic

variation and (passive) gene-environment covariance. Path analysis provides an intuitive approach to modeling genetic nurture and allows the method to be expanded in a systematic and rigorous manner.

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