

Reply to Abdellaoui et al.: Interpreting GAM

Abdellaoui et al. (1) question our (2) finding that spouses are more genetically similar than nonspouses because they believe that we are only measuring ethnically based social sorting indexed by population stratification and not genetic assortative mating (GAM). To address this possibility, we evaluated GAM among a racially homogeneous group, we adjusted for genetic variation with principal components (PCs), and we adjusted for geographic region. One of these results, based on direct controls for PCs, where the residualized GAM was not significantly different from zero, is the primary focus of their critique. The main thrust of their note challenges our interpretation rather than our methods.

We believe that PC-based controls are heavy handed because the calculation of PCs and GAM both rely on genome-wide similarity. If individuals are mating with others who are more genetically similar to them compared with random mating, correlations in PCs will not be zero. The critique of our analysis is that we are overinterpreting social segregation by ethnicity as a deeper evolutionary process. Indeed, it may be the case that ethnicity is one of the primary phenotypes through which nonrandom mating is guided. This does not, however, change the importance of quantifying this process.

Moreover, the confounding role of ethnicity is speculation because neither we nor

Abdellaoui et al. (1) have detailed measures of self-reported ethnicity. Only future researchers with spousal genetic data and detailed ethnicity measures will be able to extend our study and determine whether our attempt to proxy ethnic background through geography was successful and/or the degree to which GAM works through ethnic sorting (and vice versa). Researchers may also wish to study unique populations such as island isolates or global cities to determine how GAM depends on the local distribution of genetic and ethnic variation.

In sum, we believe that this is an important area of research and we welcome discussion of these issues. We also believe that the logic and conventions of genome-wide association study (GWAS) analysis are the wrong framework from which to interpret our results. Unlike typical GWAS analysis, where the goal is to hold constant ancestral differences when examining genetic associations at the SNP level, our goal was to document genetic similarity between spouses—presuming that potential spouses are actually sorting on observable phenotypes (not on unobservable SNPs). Indeed, many traits (e.g., height, education, appearance, and even political views) on which spouses are known to sort have a genetic basis. As such, in a highly admixed population such as that of the United States, we believe it implausible that GAM is merely

due to sorting on ancestry. We view our paper as a descriptive exercise that lays the foundation for future work in this area—i.e., specific SNP, gene, and pathway level sorting within the marriage market.

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1 Abdellaoui A, Verweij KJH, Zietsch BP (2014) No evidence for genetic assortative mating beyond that due to population stratification. *Proc Natl Acad Sci USA* 111:E4137.

2 Domingue BW, Fletcher J, Conley D, Boardman JD (2014) Genetic and educational assortative mating among US adults. *Proc Natl Acad Sci USA* 111(22):7996–8000.

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The authors declare no conflict of interest.

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