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Determine the assortative mating pattern of the phenotypes by using covariance structures of the haplotypic polygenic scores.

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ABSTRACT:

Assortative mating (AM) can bias estimates of genetic effects from family/twin-based and genomics-based approaches. Properly adjusting estimates requires knowing whether the AM is at equilibrium or not. Here, we show how different types of AM (at equilibrium vs. AM for one or two previous generations) lead to different patterns of 6 unique covariances between the haplotypic polygenic scores (hPGS's) of spouses. For example, all covariances are expected to be zero between hPGSs of spouses when there is no AM, all 6 are expected to be positive and equal under equilibrium AM, and 4 of the 6 are expected to be positive under a single generation of AM. In addition, the 4 variances of the hPGS are similarly informative. We show how a goodness of fit test on these hPGS variance/covariances matrices (e.g., using openMx) can be used to test whether the data best fits a single generation of AM model vs. an equilibrium AM model. We show further that spousal data that is "gametically phased" (such that the chromosomes inherited from different parents are differentiated) can be used to test for AM that has occurred for one generation vs. two generations vs. many generations.

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