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Modeling assortative mating and other selection with OpenMx

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ABSTRACT:

Resemblance between spouses has numerous potential sources, including: direct phenotypic homogamy, population stratification and marital interaction. Even within phenotypic assortment, spouse resemblance for one trait may be due to mate selection on a correlated trait. Multivariate modeling of spousal resemblance can help to distinguish between such primary and secondary mechanisms. To date, modeling these alternative mechanisms has proved challenging, especially when they are considered jointly. Recent developments to OpenMx software have facilitated the specification of such models in two ways. First, Pearson-Aitken selection matrix functions that calculate the covariances of all measured variables following selection on a subset of them are useful for matrix-based analyses. Second, and apparently a first for structural equation modeling software, it is possible to use co-paths, represented by lines with no arrowheads, to represent direct phenotypic homogamy. In the multivariate context, homogamy for some variables may precede that for others. Accordingly, it is possible to specify the order in which the assortment for different variables occurs. For substance use, marital resemblance is substantial.

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