

Achievement & Acription in Educational Attainment: Genetic & Environmental Influences on Adolescent Schooling

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Derivation of Model

For each sibling $j = 1, 2$ in a pair one can define 3×1 column vectors

$$\begin{aligned} \mathbf{p}_j &= [p_{1j} \ p_{2j} \ p_{3j}]' = [\text{VIQ}_j \ \text{GPA}_j \ \text{CPL}_j]' \text{ of observed phenotypes,} \\ \mathbf{a}_j &= [a_{1j} \ a_{2j} \ a_{3j}]' \text{ of latent genotypic factors,} \\ \mathbf{c}_j &= [c_{1j} \ c_{2j} \ c_{3j}]' \text{ of latent shared environment factors, and} \\ \mathbf{e}_j &= [e_{1j} \ e_{2j} \ e_{3j}]' \text{ of latent unshared environment factors.} \end{aligned}$$

\mathbf{X} , \mathbf{Y} , and \mathbf{Z} are 3×3 lower triangular matrices representing Cholesky factorizations of the genetic, shared environmental, and unshared environmental structure, respectively, so that

$$\mathbf{X} = \begin{bmatrix} x_{11} & 0 & 0 \\ x_{21} & x_{22} & 0 \\ x_{31} & x_{32} & x_{33} \end{bmatrix} \quad \mathbf{Y} = \begin{bmatrix} y_{11} & 0 & 0 \\ y_{21} & y_{22} & 0 \\ y_{31} & y_{32} & y_{33} \end{bmatrix} \quad \mathbf{Z} = \begin{bmatrix} z_{11} & 0 & 0 \\ z_{21} & z_{22} & 0 \\ z_{31} & z_{32} & z_{33} \end{bmatrix}$$

\mathbf{B} is a 3×3 sub-diagonal matrix representing the direct paths relating the observed variables, so that

$$\mathbf{B} = \begin{bmatrix} 0 & 0 & 0 \\ b_{21} & 0 & 0 \\ b_{31} & b_{32} & 0 \end{bmatrix}$$

The model of Figure 2 can then be represented by the equation

$$\mathbf{p} = \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{B} & 0 \\ 0 & \mathbf{B} \end{bmatrix} \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{X} & 0 \\ 0 & \mathbf{X} \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Y} & 0 \\ 0 & \mathbf{Y} \end{bmatrix} \begin{bmatrix} \mathbf{c}_1 \\ \mathbf{c}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z} & 0 \\ 0 & \mathbf{Z} \end{bmatrix} \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} \quad (1)$$

where \mathbf{p} is the 6×1 vector of observations on the siblings. Carrying out the multiplications yields, for each sibling

$$\mathbf{p}_1 = \mathbf{B}\mathbf{p}_1 + \mathbf{X}\mathbf{a}_1 + \mathbf{Y}\mathbf{Z}\mathbf{c}_1 + \mathbf{Z}\mathbf{e}_1 \quad (2)$$

$$\mathbf{p}_2 = \mathbf{B}\mathbf{p}_2 + \mathbf{X}\mathbf{a}_2 + \mathbf{Y}\mathbf{c}_2 + \mathbf{Z}\mathbf{e}_2 \quad (3)$$

Equations (2) for the first sibling yield

$$\begin{aligned} \mathbf{p}_1 - \mathbf{B}\mathbf{p}_1 &= \mathbf{X}\mathbf{a}_1 + \mathbf{Y}\mathbf{c}_1 + \mathbf{Z}\mathbf{e}_1 \\ (\mathbf{I} - \mathbf{B})\mathbf{p}_1 &= \mathbf{X}\mathbf{a}_1 + \mathbf{Y}\mathbf{c}_1 + \mathbf{Z}\mathbf{e}_1 \\ \mathbf{p}_1 &= (\mathbf{I} - \mathbf{B})^{-1}(\mathbf{X}\mathbf{a}_1 + \mathbf{Y}\mathbf{c}_1 + \mathbf{Z}\mathbf{e}_1) \end{aligned}$$

A similar derivation for the second sibling produces

$$\mathbf{p}_2 = (\mathbf{I} - \mathbf{B})^{-1}(\mathbf{X}\mathbf{a}_2 + \mathbf{Y}\mathbf{c}_2 + \mathbf{Z}\mathbf{e}_2)$$

The expected covariance matrix of the 6 observed variables is

$$\Sigma = E\{\mathbf{p}\mathbf{p}'\} = E\left\{ \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \end{bmatrix} \begin{bmatrix} \mathbf{p}'_1 & \mathbf{p}'_2 \end{bmatrix} \right\} = \begin{bmatrix} E\{\mathbf{p}_1\mathbf{p}'_1\} & E\{\mathbf{p}_1\mathbf{p}'_2\} \\ E\{\mathbf{p}_2\mathbf{p}'_1\} & E\{\mathbf{p}_2\mathbf{p}'_2\} \end{bmatrix} \quad (4)$$

which contains within-sibling covariances on the diagonal and between-siblings covariances off the diagonal. The within-sibling covariance matrix for sibling 1 is derived as

$$\begin{aligned} \Sigma_W &= E\{(\mathbf{p}_1\mathbf{p}'_1)\} \\ &= E\{(\mathbf{I} - \mathbf{B})^{-1}(\mathbf{X}\mathbf{a}_1 + \mathbf{Y}\mathbf{c}_1 + \mathbf{Z}\mathbf{e}_1) \\ &\quad \cdot ((\mathbf{I} - \mathbf{B})^{-1}(\mathbf{X}\mathbf{a}_1 + \mathbf{Y}\mathbf{c}_1 + \mathbf{Z}\mathbf{e}_1))'\} \\ &= E\{(\mathbf{I} - \mathbf{B})^{-1}(\mathbf{X}\mathbf{a}_1 + \mathbf{Y}\mathbf{c}_1 + \mathbf{Z}\mathbf{e}_1)(\mathbf{a}'_1\mathbf{X}' + \mathbf{c}'_1\mathbf{Y}' + \mathbf{e}'_1\mathbf{Z}')((\mathbf{I} - \mathbf{B})^{-1})'\} \\ &= (\mathbf{I} - \mathbf{B})^{-1}(E\{\mathbf{X}\mathbf{a}_1\mathbf{a}'_1\mathbf{X}'\} + E\{\mathbf{Y}\mathbf{c}_1\mathbf{c}'_1\mathbf{Y}'\} + E\{\mathbf{Z}\mathbf{e}_1\mathbf{e}'_1\mathbf{Z}'\})((\mathbf{I} - \mathbf{B})^{-1})' \\ &= (\mathbf{I} - \mathbf{B})^{-1}(\mathbf{X}\mathbf{X}' + \mathbf{Y}\mathbf{Y}' + \mathbf{Z}\mathbf{Z}')((\mathbf{I} - \mathbf{B})^{-1})' \end{aligned}$$

Simplifications of the vector cross products in the derivation above can be made because the vectors \mathbf{a} , \mathbf{c} , and \mathbf{e} are assumed uncorrelated within siblings, so that for sibling 1

$$E\{\mathbf{a}_1\mathbf{c}'_1\} = E\{\mathbf{a}_1\mathbf{e}'_1\} = E\{\mathbf{c}_1\mathbf{e}'_1\} = \mathbf{0}$$

and the components of each vector are orthogonal with unit variance so that

$$E\{\mathbf{a}_1\mathbf{a}'_1\} = E\{\mathbf{c}_1\mathbf{c}'_1\} = E\{\mathbf{e}_1\mathbf{e}'_1\} = \mathbf{I}$$

Defining matrices $\mathbf{A} = \mathbf{X}\mathbf{X}'$, $\mathbf{C} = \mathbf{Y}\mathbf{Y}'$, $\mathbf{E} = \mathbf{Z}\mathbf{Z}'$, and $\mathbf{W} = (\mathbf{I} - \mathbf{B})^{-1}$, the covariance matrix for sibling 1 becomes

$$\Sigma_W = \mathbf{W}(\mathbf{A} + \mathbf{C} + \mathbf{E})\mathbf{W}' \quad (5)$$

The same result holds for sibling 2.

Because of the names of the matrices involved, the classic behavior genetic decomposition of the phenotypic covariances embedded within Equation (5) – with genetic component \mathbf{A} , shared environment \mathbf{C} , and unshared environment \mathbf{E} – is traditionally called the **ACE** model.

A similar derivation can be carried out for each off-diagonal block of Σ containing the between-siblings covariances, for example $E\{\mathbf{p}_2\mathbf{p}'_1\}$. Simplifications of the vector cross-products in the derivation can be made because by assumption the pattern of covariances of the vectors \mathbf{a} , \mathbf{c} , and \mathbf{e} across siblings is such that

$$E\{\mathbf{a}_2\mathbf{c}'_1\} = E\{\mathbf{a}_2\mathbf{e}'_1\} = E\{\mathbf{c}_2\mathbf{e}'_1\} = \mathbf{0}$$

and

$$E\{\mathbf{a}_2\mathbf{a}'_1\} = k \otimes \mathbf{I} \quad E\{\mathbf{c}_2\mathbf{c}'_1\} = \mathbf{I} \quad E\{\mathbf{e}_2\mathbf{e}'_1\} = \mathbf{0}$$

The between-siblings covariance can thus be represented by the 3×3 matrix

$$\Sigma_B = \mathbf{W}(k \otimes \mathbf{A} + \mathbf{C})\mathbf{W}' \quad (6)$$

which contains the covariances of the observed values for sibling 1 (in the columns) and sibling 2 (in the rows). The expression $k \otimes \mathbf{A}$ is the Kronecker product of k by \mathbf{A} ; since k is a scalar the expression is equivalent to the ordinary multiplication of matrix \mathbf{A} by k . (Scalar multiplication is implemented as a Kronecker product in the program Mx.) k represents the degree of genetic relatedness of siblings. It is set $k = 1$ for MZ twins; assuming random mating $k = .5$ for DZ twins and full siblings, $k = .25$ for half siblings, $k = .125$ for cousins, and $k = 0$ for non related siblings. The unshared environmental factors associated with the matrix \mathbf{E} are assumed uncorrelated across siblings and thus do not contribute to the between-siblings covariances in Equation (6).

The complete 6×6 matrix Σ of expected covariances among all observed variables, with rows and columns corresponding to the three observations for sibling 1 followed by the three observations for sibling 2 (in the order VIQ₁, GPA₁, CPL₁, VIQ₂, GPA₂, CPL₂) can be written as the partitioned matrix

$$\Sigma = \begin{bmatrix} \mathbf{W}(\mathbf{A} + \mathbf{C} + \mathbf{E})\mathbf{W}' & \mathbf{W}'(k \otimes \mathbf{A} + \mathbf{C})\mathbf{W}' \\ \mathbf{W}(k \otimes \mathbf{A} + \mathbf{C})\mathbf{W}' & \mathbf{W}(\mathbf{A} + \mathbf{C} + \mathbf{E})\mathbf{W}' \end{bmatrix} \quad (7)$$

With only small notational changes, this is the way the expected covariance matrices that are fitted to observed covariances \mathbf{S} are represented in the Mx script. The parameters implicit in (7) are estimated by maximum likelihood to simultaneously fit the observed covariance matrices for the six groups of siblings. The Mx script used to estimate the parameters of the model and the output are shown in separate documents.