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A Bivariate Path Analysis of Fear Data on Twins and Their Parents

M.C. Neale, D.W. Fulker

Institute of Psychiatry, London University

Abstract. A simple path model applicable to twins and their parents and involving both cultural and genetic transmission in the presence of phenotypic assortative mating was extended to cover the bivariate case. The model allows for cross assortative mating as well as cross cultural transmission. It was applied to two correlated measures derived from a fear survey questionnaire given to 1000 subjects. In allowing for the impact of more than one variable, the model allows for a much more realistic picture of cultural transmission than provided by the univariate model. The logic of the model and an application are outlined. (The authors are indebted to Professor R.J. Rose for providing the illustrative data.)

Key words: Path analysis, Twin-family study, Behavior genetics, Multivariate analysis, Fears, Phobias

INTRODUCTION

Path analytic models [15] that attempt to explain the causes of familial resemblance in terms of the combined action of genetic and cultural transmission are currently receiving renewed attention in an attempt to move away from the old "either-or" notions of the nature-nurture controversy and towards a more realistic explanation of individual differences [3-6,10,13,14]. One limitation of all these approaches is their reliance on separation or adoption data to resolve the causal factors. Recently however, Fulker [7] outlined a simple approach based on current ones that is able to separate correlated cultural and genetic effects employing only intact nuclear families, and minimally those of pairs of monozygotic (MZ) and dizygotic (DZ) twins and their parents. The model is, of course, also applicable to other data including those from separation studies, should they be available, and its usefulness thus greatly extended. The purpose of the present paper is to further develop this univariate model to consider the effects of more than one variable on familial transmission and so explore the consequences of combined genetic and environmental multivariate transmission.

THE MODEL

The basic univariate model has been discussed in some detail in a previous paper [7]. It accounts for genetic transmission via the additive genotype of two parents under the action of phenotypic assortative mating, cultural transmission via parental phenotypic influence on the child's environment, and residual shared environmental influences. The model is essentially that of Jencks et al [10] modified by Eaves et al [4], and is shown in Fig 1. The multivariate model is a direct extension of this model.

For the sake of simplicity, the bivariate case is described from which the multivariate case may be inferred. There are four separate aspects of the model to be considered: (1) the effects of assortative mating, (2) the effects of cultural or environmental transmission, (3) the constraints implied by equilibrium, and (4) the implications of the conventional multivariate twin model for the present one.

1. The Effect of Assortative Mating

In the univariate model, assortative mating is measured with the marital correlation μ . The value of this parameter is used to estimate the correlations between the latent variables of parent 1 and the latent variables of parent 2. These correlations, shown at the top of Fig. 1, are estimated under the assumption that assortative mating is phenotypic. Reversed path analysis [4,16], is used to derive all four of the possible correlations, but of these only three are unique, the two δ 's being equal.

The assumption of phenotypic assortative mating is carried through to the bivariate case, the full model for which is shown in Fig. 2. In this diagram each individual is measured on two variables X and Y. It is assumed that people are assortatively mating on the basis of their phenotypes not only within the variables to produce μ_x and μ_y , but also across the variables, producing μ_{xy} and μ_{yx} . The two within-variable assortative mating parameters each yield three unique correlations amongst the latent variables of the parents, $\gamma_x, \delta_x, \epsilon_x$ and $\gamma_y, \delta_y, \epsilon_y$, by the method outlined above for the univariate case. This reversed path analysis technique is applied in an identical fashion to derive the expected correlations between the latent variables of the parents when the two parents are measured on different rather than the same variables. One important difference arises in the induction of these across-variable correlations: all four of the correlations are unique, necessitating an extra subscript to the δ parameters. In total, therefore, there are fourteen correlations between the latent variables of parent 1 and those of parent 2. The expectations, derived by reversed path analysis, are shown in Table 1.

The correlations between latent variables within an individual are of three different types. First, there is the genetic correlation among variables within an individual, g_{xy} , which is a measure of the extent to which the additive genetic causes of variation correlate due to pleiotropy and linkage disequilibrium [5]. Second, there is the environmental correlation, e_{xy} , which is the degree to which the variables are affected in the same way by the environmental events. Third, there are four genotype-environment (G-E) correlations which are induced by combined genetic and environmental transmission. Two of these, s_x and s_y , are equivalent to the univariate G-E correlation s , while the remaining two are across variable correlations, s_{xy} (being rG_xE_y) and s_{yx} (being rG_yE_x). The implications of these induced correlations will be discussed further in Section 3.

2. The Effects of Cultural Transmission

Behaviour genetic analyses of twin studies normally partition environmental sources of variance into two components, the common environment, E_2 , and the specific environ-

ment, E_1 . The inclusion of parents in the model permits a further partitioning of the common environment into parental and non-parental sources of variance. The non-parental sources of variance are described in Section 3, and the parental effects are discussed here. The parental environmental influences are causal pathways from the parent's phenotype to the environment of the offspring, and are designated Z_1 and Z_2 in the univariate model. The bivariate model includes these two parameters for both variables X and Y, leading to four within-variable parameters of cultural transmission, Z_{x1} , Z_{x2} , Z_{y1} and Z_{y2} . However, the bivariate model also permits a further partitioning of the parental environmental influence. The effects of the parental phenotype for variable X upon the environment of the child for variable Y may be specified, being designated Z_{xy} , together with the influence of parental phenotype Y on the child's environment for X, designated Z_{yx} . The partitioning of variance between parent 1 and parent 2 found in the within variable effects such as Z_{x1} and Z_{x2} is also possible in the cross-variable parameters, so a total of four of these parameters can now be specified, namely Z_{xy1} , Z_{xy2} , Z_{yx1} , and Z_{yx2} . The estimation of these cross-variable transmission effects is a major advantage of the bivariate model. Obtaining information concerning cultural transmission of this kind in the presence of, and controlling for, additive genetic effects has not previously been possible. The parent-offspring expected correlations may now be specified, and are given in Table 2.

3. Constraints Assuming Equilibrium

In the univariate model, the induction of the correlation s between the genotype and environment of an individual is assumed to be entirely attributed to the genetic and cultural influences of the parents, in whom the same degree of G-E correlation is observed. The bivariate model, of course, requires the same assumption of equilibrium over generations to be made with respect to s_x and to s_y , while, in addition, the correlations s_{xy} and s_{yx} must also be assumed to be at equilibrium. The constraints involving all four of these G-E correlations are given in Table 3.

These four equations may be rearranged to give two pairs of simultaneous equations such that those for s_x and s_{yx} will solve for Z_{x1} and Z_{yx1} and those for s_y and s_{xy} will solve for Z_{y1} and Z_{xy1} .

The phenotypic variances of the two variables X and Y are, of course, unaffected by the multivariate extension, so that the constraint on the parameter e [7] in the univariate model is applied to e_x and e_y in an analogous fashion:

$$h_x^2 + 2h_x s_x e_x + e_x^2 = 1.0$$

so

$$e_x = -s_x h_x + (s_x^2 h_x^2 - h_x^2 + 1)^{1/2}$$

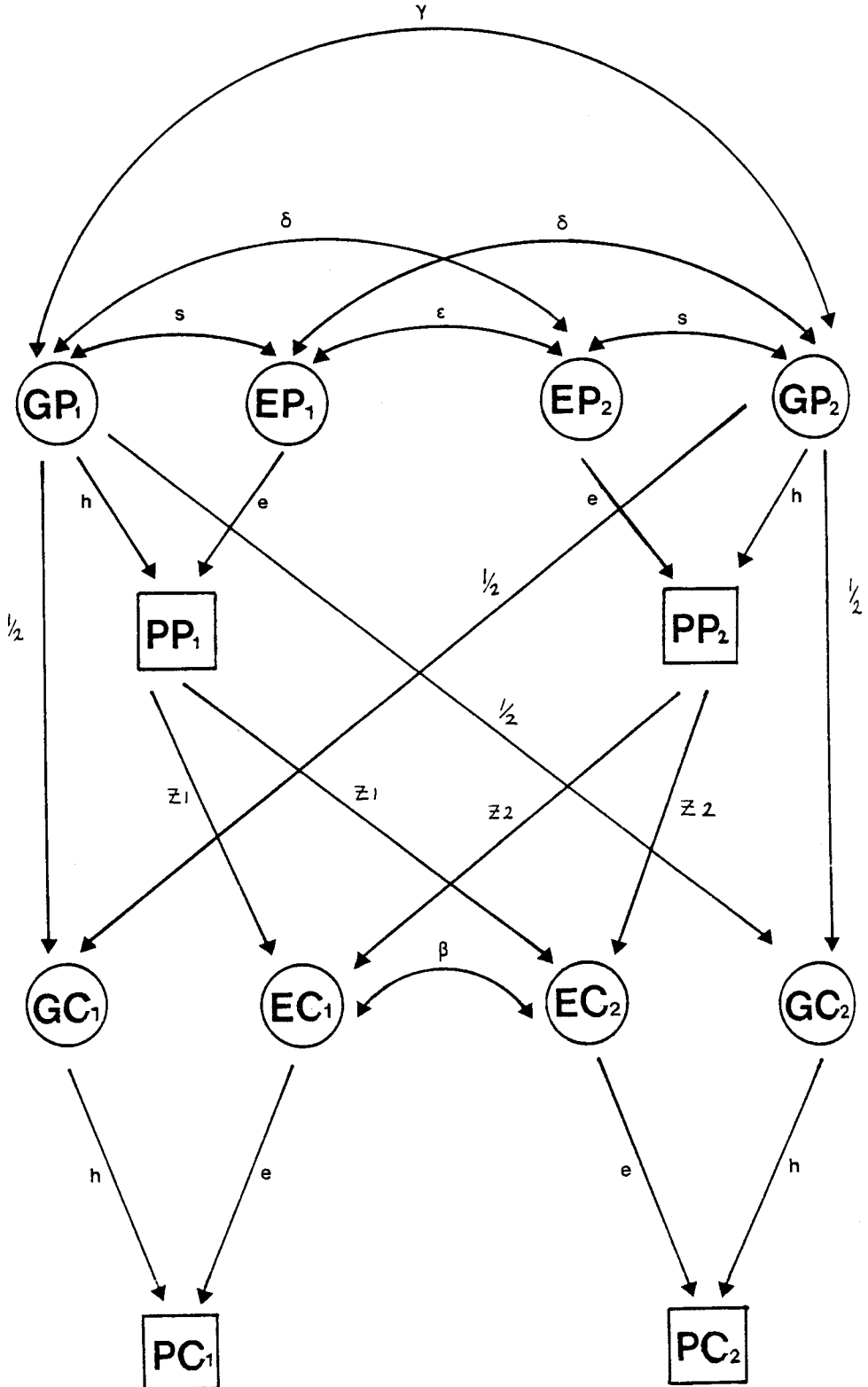
and

$$h_y^2 + 2h_y s_y e_y + e_y^2 = 1.0$$

so

$$e_y = -s_y h_y + (s_y^2 h_y^2 - h_y^2 + 1)^{1/2}$$

assuming both X and Y are standardised variables.



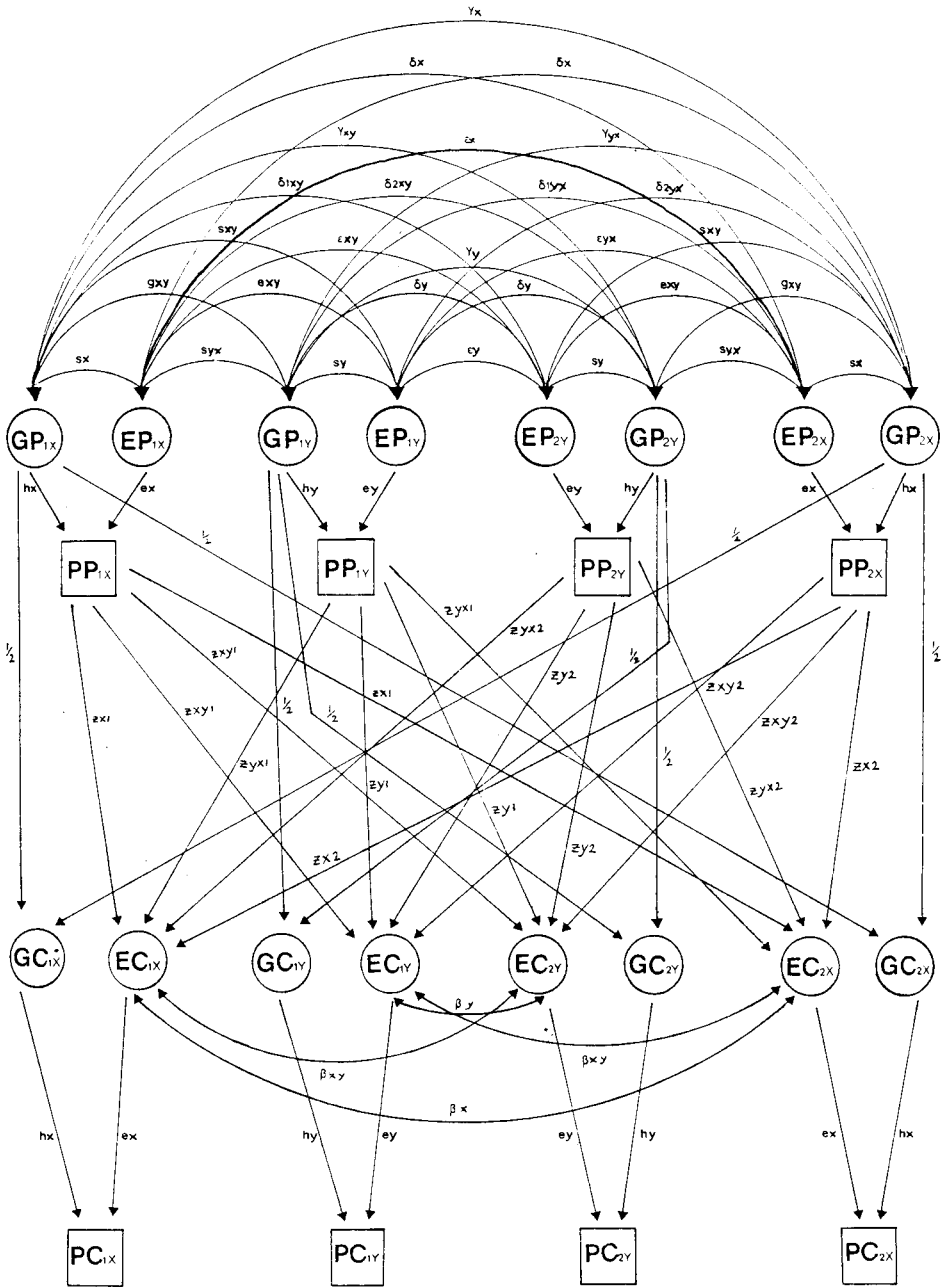


TABLE 1

Symbol	Correlation	Induced expectation
γ_x	$r_{GP_{1x}^{GP_{2x}}}$	$\mu_x (h_x + e_x s_x)^2$
δ_x	$r_{GP_{1x}^{EP_{2x}}, r_{EP_{1x}^{GP_{2x}}}$	$\mu_x (h_x + e_x s_x) (h_x s_x + e_x)$
ϵ_x	$r_{EP_{1x}^{EP_{2x}}}$	$\mu_x (h_x s_x + e_x)^2$
γ_y	$r_{GP_{1y}^{GP_{2y}}}$	$\mu_y (h_y + e_y s_y)^2$
δ_y	$r_{GP_{1y}^{EP_{2y}}, r_{EP_{1y}^{GP_{2y}}}$	$\mu_y (h_y s_y + e_y) (h_y + e_y s_y)$
ϵ_y	$r_{EP_{1y}^{EP_{2y}}}$	$\mu_y (h_y s_y + e_y)^2$
γ_{xy}	$r_{GP_{1x}^{GP_{2x}}}$	$\mu_{xy} (h_x + e_x s_x) (h_y + e_x s_x)$
δ_{1xy}	$r_{GP_{1x}^{EP_{2y}}}$	$\mu_{xy} (h_x + e_x s_x) (h_y s_y + e_y)$
δ_{2xy}	$r_{EP_{1x}^{GP_{2y}}}$	$\mu_{xy} (h_x s_x + e_x) (h_y + e_y s_y)$
ϵ_{xy}	$r_{EP_{1x}^{EP_{2y}}}$	$\mu_{xy} (h_x s_x + e_x) (h_y s_y + e_y)$
γ_{yx}	$r_{GP_{1y}^{GP_{2x}}}$	$\mu_{yx} (h_x + e_x s_x) (h_y + e_y s_y)$
δ_{1yx}	$r_{GP_{1y}^{EP_{2x}}}$	$\mu_{yx} (h_x s_x + e_x) (h_y + e_y s_y)$
δ_{2yx}	$r_{EP_{1y}^{GP_{2x}}}$	$\mu_{yx} (h_x + s_x e_x) (h_y s_y + e_y)$
ϵ_{yx}	$r_{EP_{1y}^{EP_{2x}}}$	$\mu_{yx} (h_x s_x + e_x) (h_y s_y + e_y)$

TABLE 2

Phenotypic correlation	Expectation
$r_{PP_{1x}^{PP_{2x}}}$	μ_x
$r_{PP_{1y}^{PP_{2y}}}$	μ_y
$r_{PP_{1x}^{PP_{2y}}}$	μ_{xy}
$r_{PP_{1y}^{PP_{2x}}}$	μ_{yx}
$r_{PP_{1x}^{PC_{1x}}, r_{PP_{1x}^{PC_{2x}}}$	$\frac{1}{2} h_x (h_x + e_x s_x + (1 + e_x z_{x2}) (h_x \gamma_x + e_x \delta_x)) +$ $e_x^2 z_{x2}^2 (h_x \delta_x + e_x \epsilon_x) + h_x e_x (z_{yx1} (h_x g_{xy} + e_x s_{yx})$ $+ z_{yx2} (h_x \gamma_{xy} + e_x \delta_{2xy})) + e_x e_y (z_{yx1} (h_x s_{xy} +$ $e_x e_{xy}) + z_{yx2} (h_x \delta_{1xy} + e_x \epsilon_{xy})) + z_{x1} e_x$

Contd

$rPP_{2x}^{PC} r_{1x}, rPP_{2x}^{PC} r_{2x}$	$\frac{1}{2}h_x(h_x + e_{xx} s_x + (1 + 2e_{xx} Z_{x1}) (h_{xy} + e_{xx} \delta_x)) +$ $e_x^2 Z_{x1} (h_x \delta_x + e_{xx} \epsilon_x) + h_x e_x (Z_{yx2} (h_x g_{xy} + e_{xx} s_{yx}))$ $+ Z_{yx1} (h_x \gamma_{yx} + e_{xx} \delta_{1yx}) + e_x e_x (Z_{yx2} (h_x s_{xy} +$ $e_x e_x) + Z_{yx1} (h_x \delta_{2yx} + e_{xx} \epsilon_{yx})) + Z_{x2} e_x$
$rPP_{1y}^{PC} r_{1y}, rPP_{1y}^{PC} r_{2y}$	$\frac{1}{2}h_y(h_y + e_{yy} s_y + (1 + 2e_{yy} Z_{y1}) (h_{xy} + e_{yy} \delta_y)) +$ $e_y^2 Z_{y1} (h_y \delta_y + e_{yy} \epsilon_y) + h_y e_y (Z_{xy1} (h_y g_{xy} + e_{yy} s_{xy}))$ $+ Z_{xy2} (h_y \gamma_{yx} + e_{yy} \delta_{2yx}) + e_y e_y (Z_{xy1} (h_y s_{yx} +$ $e_y e_y) + Z_{xy2} (h_y \delta_{1yx} + e_{yy} \epsilon_{yx})) + Z_{y1} e_y$
$rPP_{2y}^{PC} r_{1y}, rPP_{2y}^{PC} r_{2y}$	$\frac{1}{2}h_y(h_y + e_{yy} s_y + (1 + 2e_{yy} Z_{y1}) (h_{xy} + e_{yy} \delta_y)) +$ $e_y^2 Z_{y1} (h_y \delta_y + e_{yy} \epsilon_y) + h_x e_y (Z_{xy2} (h_y g_{xy} + e_{yy} s_{xy}))$ $+ Z_{xy1} (h_y \gamma_{xy} + e_{yy} \delta_{1xy}) + e_x e_y (Z_{xy2} (h_y s_{yx} +$ $e_y e_y) + Z_{xy1} (h_y \delta_{2xy} + e_{yy} \epsilon_{yx})) + Z_{y2} e_y$
$rPP_{1x}^{PC} r_{1y}, rPP_{1x}^{PC} r_{2y}$	$Z_{xy1} e_y + (\frac{1}{2}h_y + Z_{y1} e_y h_y) (h_x g_{xy} + e_{xx} s_{yx}) + e_y^2 Z_{y1}$ $(h_x s_{xy} + e_x e_x) + h_x e_x Z_{xy2} (h_x \gamma_x + e_{xx} \delta_x) +$ $e_x e_x Z_{xy2} (h_x \delta_{xx} + e_{xx} \epsilon_x) + (\frac{1}{2}h_y + Z_{y2} h_y e_y) (h_x \gamma_{xy}$ $+ e_x \delta_{2xy}) + e_y^2 Z_{y2} (h_x \delta_{1xy} + e_{xx} \epsilon_{xy})$
$rPP_{2x}^{PC} r_{1y}, rPP_{2x}^{PC} r_{2y}$	$Z_{xy2} e_y + (\frac{1}{2}h_y + Z_{y2} e_y h_y) (h_x g_{xy} + e_{xx} s_{yx}) +$ $e_y^2 Z_{y2} (h_x s_{xy} + e_x e_x) + h_x e_x Z_{xy1} (h_x \gamma_x + e_{xx} \delta_x)$ $+ e_x e_x Z_{xy1} (h_x \delta_{xx} + e_{xx} \epsilon_x) + (\frac{1}{2}h_y + Z_{y1} h_y e_y)$ $(h_x \gamma_{yx} + e_x \delta_{1yx}) + e_y^2 Z_{y1} (h_x \delta_{2yx} + e_{xx} \epsilon_{yx})$
$rPP_{1y}^{PC} r_{1x}, rPP_{1y}^{PC} r_{2x}$	$Z_{yx1} e_x + (\frac{1}{2}h_x + e_x Z_{x1} h_x) (h_x g_{xy} + e_{xx} s_{yx}) +$ $e_x^2 Z_{x1} (h_x s_{yx} + e_x e_x) + h_x Z_{yx2} e_x (h_x \gamma_y + e_{yy} \delta_y)$ $+ e_x e_x Z_{yx2} (h_x \delta_{yy} + e_{yy} \epsilon_y) + (\frac{1}{2}h_x + Z_{x2} h_x e_x)$ $(h_x \gamma_{yx} + e_y \delta_{2yx}) + e_x^2 Z_{x2} (h_x \delta_{1yx} + e_{yy} \epsilon_{yx})$
$rPP_{2y}^{PC} r_{1x}, rPP_{2y}^{PC} r_{2x}$	$Z_{yx2} e_x + (\frac{1}{2}h_x + e_x Z_{x2} h_x) (h_x g_{xy} + e_{xx} s_{yx}) +$ $e_x^2 Z_{x2} (h_x s_{yx} + e_x e_x) + h_x Z_{yx1} e_x (h_x \gamma_y + e_{yy} \delta_y)$ $+ e_x e_x Z_{yx1} (h_x \delta_{yy} + e_{yy} \epsilon_y) + (\frac{1}{2}h_x + Z_{x1} h_x e_x)$ $(h_x \gamma_{xy} + e_y \delta_{1xy}) + e_x^2 Z_{x1} (h_x \delta_{2xy} + e_{yy} \epsilon_{xy})$

4. Twins and Genetic Information

The difference between the genetic correlations of MZ twins and of DZ twins is the key

TABLE 3

Correlation	Expectation
$r_{PC_{1x}PC_{2x}}$	$\alpha_x h_x^2 + 2h_x s_x e_x + e_x^2 (z_{x1}^2 + z_{x2}^2 + z_{yx1}^2 + z_{yx2}^2) + 2P_{xy} (z_{x1} z_{yx1} + z_{x2} z_{yx2}) + 2Z_{yx1} z_{yx2} \mu_y + 2Z_{x1} z_{x2} \mu_x + 2Z_{x1} z_{yx2} \mu_{xy} + 2Z_{x2} z_{yx1} \mu_{yx} + \beta_x)$
$r_{PC_{1y}PC_{2y}}$	$\alpha_y h_y^2 + 2h_y s_y e_y + e_y^2 (z_{y1}^2 + z_{y2}^2 + z_{xy1}^2 + z_{xy2}^2) + 2P_{xy} (z_{y1} z_{xy1} + z_{y2} z_{xy2}) + 2Z_{xy1} z_{xy2} \mu_x + 2Z_{y1} z_{y2} \mu_y + 2Z_{y1} z_{xy2} \mu_{yx} + 2Z_{y2} z_{xy1} \mu_{xy} + \beta_y)$
$r_{PC_{1x}PC_{2y}}, r_{PC_{1y}PC_{2x}}$	$\alpha_{xy} h_x h_y + e_x h_y s_{yx} + e_y h_x s_{xy} + e_x e_y (z_{x1} z_{xy1} + z_{x2} z_{xy2} + z_{y1} z_{yx1} + z_{y2} z_{yx2}) + P_{xy} (z_{x1} z_{y1} + z_{x2} z_{y2} + z_{yx1} z_{xy1} + z_{yx2} z_{xy2}) + \mu_x (z_{x1} z_{xy2} + z_{x2} z_{xy1}) + \mu_y (z_{y1} z_{yx2} + z_{y2} z_{yx1}) + \mu_{xy} (z_{x1} z_{y2} + z_{xy1} z_{yx2}) + \mu_{yx} (z_{x2} z_{y1} + z_{xy2} z_{yx1} + 2\beta_{xy})$
α_x, α_y for MZ twins	1.0
$\alpha_x,$ for DZ twins	$\frac{1}{2}(1 + \gamma_x)$
$\alpha_y,$ for DZ twins	$\frac{1}{2}(1 + \gamma_y)$
$\alpha_{xy},$ for MZ twins	g_{xy}
$\alpha_{xy},$ for DZ twins	$\frac{1}{2}g_{xy} + \frac{1}{4}(\gamma_{xy} + \gamma_{yx})$
P_{xy}	$h_x h_y g_{xy} + h_x e_y s_{xy} + h_y e_x s_{yx} + e_x e_y e_{xy}$

TABLE 4

$$\begin{aligned}
 rGC_{XEC_X} = s_X &= \frac{1}{2} [(Z_{x1} + Z_{x2}) (s_X e_X + (1 + \gamma_X) h_X + \delta_X e_X) + Z_{yx1} ((g_{xy} + \gamma_{yx}) h_Y + (s_{xy} + \delta_{2yx}) e_Y) + Z_{yx2} ((g_{xy} + \gamma_{yx}) h_Y + (s_{xy} + \delta_{1xy}) e_Y)] \\
 rGC_{YEC_X} = s_{YX} &= \frac{1}{2} [(Z_{yx1} + Z_{yx2}) (s_Y e_Y + (1 + \gamma_Y) h_Y + \delta_Y e_Y) + Z_{x1} ((g_{xy} + \gamma_{xy}) h_X + (s_{yx} + \delta_{2xy}) e_X) + Z_{x2} ((g_{xy} + \gamma_{yx}) h_X + (s_{yx} + \delta_{1yx}) e_X)] \\
 rGC_{YEC_Y} = s_Y &= \frac{1}{2} [(Z_{y1} + Z_{y2}) (s_Y e_Y + (1 + \gamma_Y) h_Y + \delta_Y e_Y) + Z_{xy1} ((g_{xy} + \gamma_{xy}) h_X + (s_{yx} + \delta_{2xy}) e_X) + Z_{xy2} ((g_{xy} + \gamma_{yx}) h_X + (s_{yx} + \delta_{1xy}) e_X)] \\
 rGC_{XEC_Y} = s_{XY} &= \frac{1}{2} [(Z_{xy1} + Z_{xy2}) (s_X e_X + (1 + \gamma_X) h_X + \delta_X e_X) + Z_{y1} ((g_{xy} + \gamma_{yx}) h_Y + (s_{xy} + \delta_{2yx}) e_Y) + Z_{y2} ((g_{xy} + \gamma_{xy}) h_Y + (s_{xy} + \delta_{1xy}) e_Y)]
 \end{aligned}$$

to all twin designs. The presence of assortative mating increases the DZ genetic correlation α to $\frac{1}{2}(1 + \gamma)$ where γ is the genetic correlation between the parents. The bivariate model expresses α_x and α_y as $\frac{1}{2}(1 + \gamma_x)$ and $\frac{1}{2}(1 + \gamma_y)$. The genetic correlation between the variables X and Y is similarly estimated from the twins' genetic similarity. The MZ twins have a genetic correlation between variables equal to that for individuals, namely g_{xy} , while the DZ twins have half of this correlation plus the appropriate adjustment for assortative mating, giving

$$\frac{1}{2} (g_{xy} + \frac{1}{2} (\gamma_{xy} + \gamma_{yx}))$$

The twin data also provide the necessary information for the estimates of the common environment parameters. These parameters are assumed to be equal for the two types of twins, in common with almost all twin models. The univariate model contains the parameter β , which is seen in the bivariate models as β_x and β_y . The bivariate model requires the specification of a further parameter β_{xy} , which represents the effects of environmental events that are shared by a pair of twins that also affect both the variables X and Y. Since the environmental correlations $rEC_{1X}EC_{2Y}$ and $rEC_{1Y}EC_{2X}$ are expected to be the same, there is no parameter β_{yx} .

The full twin-cotwin expectations are given in Table 4.

It is interesting to note that β_{xy} is a part of the total environmental correlation of an individual across variables, e_{xy} , and may therefore be subtracted from this correlation, along with the parental effects through the various z pathways, to provide an estimate of residual environmental association across variables, namely, the specific environmental correlation of an individual.

We propose to illustrate the full model with data on common fears and phobias.

METHOD

The "Fear Survey Schedule II" (or FSS-II) [8,9], was administered to 144 pairs of MZ twins, 106 pairs of DZ twins, and to all the parents of the twins, totalling 1000 subjects in all. The twins were volunteer members of a register maintained by R.J. Rose at Indiana University, Bloomington. A factor analysis of FSS-II revealed the presence of seven factors, of which two are analysed with the bivariate model: factor 1, labelled fear of social criticism; and factor 5, labelled fear of meeting people and of leadership. These two factors were chosen because of their broad similarity in phenotypic structure. The score of an individual was computed by reducing the matrix of factors loadings to one including only 1's for strong loadings, and 0's for weak loadings. The data on the family pedigrees were age corrected and standardised, and two 8×8 covariance matrices were computed, corresponding to the MZ and DZ families. These covariance matrices are assumed to approximate to a Wishart distribution. The model was therefore fitted with a maximum likelihood function [12], which is asymptotic to χ^2 for large samples, and is given by

$$\chi^2 = \sum_{i=1}^2 N_i (\ln (|\Sigma_i| / |S_i|) + \text{tr } S_i \Sigma_i^{-1} - c)$$

where $|S_i|$ denotes the determinant of the matrix S_i , tr denotes the trace of a matrix, and $c = 8$, being the order of the covariance matrices. The expected correlations generated by the application of path analysis to the diagram in Fig. 2 were multiplied by a scale variance parameter, either V_x^2 , or V_y^2 , or $(V_x V_y)$, according to whether the element involved was in the 4×4 block diagonal for x or for y , or in the off-diagonal 4×4 block (correlations between the variables), respectively. The function was minimised with a FORTRAN program MINUIT [2].

RESULTS AND DISCUSSION

The results of fitting the full model involving 21 free parameters are given in Table 5 together with their associated standard errors (as computed by the MINUIT routine HESSE). The two data matrices (shown in the Appendix) involve 72 statistics giving 51 df for the goodness of fit $\chi_{51}^2 = 49.2$ ($P = 0.55$).

Assortative mating is present to a significant extent both within and between variables; as demonstrated by the 4 values of μ_x , μ_y , μ_{xy} , and μ_{yx} , which vary from 0.16 to 0.21, all more than twice their standard errors. It is interesting to note that μ_{yx} is lower than μ_{xy} , and that, while the difference between these parameters is not large enough to be statistically significant, the implication is that there may be slightly more assortative mating for female fear of leadership and male fear of social criticism than vice versa.

TABLE 5

Parameter	Free parameters		Constrained parameters	
	Value	SE	Parameter	Value
h_x	0.77	.13	e_x	.74
h_y	0.82	.13	e_y	.76
s_{xy}	0.82	.11	Z_{xl}	-.10
s_x	-.12	.09	Z_{yl}	-.21
s_y	-.20	.11	Z_{xy1}	-.08
s_{xy}	-.19	.10	Z_{yx1}	-.07
s_{yx}	-.12	.08	γ_x	.08
e_{xy}	0.56	.08	γ_y	.09
μ_x	0.17	.06	γ_{xy}	.09
μ_y	0.21	.06	γ_{yx}	.07
μ_{xy}	0.20	.06	δ_x	.07
μ_{yx}	0.16	.06	δ_y	.08
Z_{x2}	-.12	.16	δ_{1xy}	.08
Z_{y2}	-.09	.15	δ_{2xy}	.09
Z_{xy2}	-.15	.13	δ_{1yx}	.07
Z_{yx2}	-.04	.13	δ_{2yx}	.06
β_x	0.15	.15	ϵ_x	.07
β_y	0.05	.18	ϵ_y	.09
β_{xy}	-.05	.14	ϵ_{xy}	.08
V_x	1.01	.05	ϵ_{yx}	.06
V_y	0.99	.05	P_{xy}	.65

Appendix - Variance-Covariance Matrices (Diagonal and Above) and Correlation Matrices (lower triangle) for MZ and DZ Families on 2 Factors, Fear of Social Criticism and Fear of Leadership, labelled x and y respectively.

	x				y				
	F	M	T1	T2	F	M	T1	T2	
MZ families									
x	F	.90	.11	.25	.16	.58	.15	.14	.14
	M	.11	1.11	.09	.21	.09	.61	-.01	.10
	T1	.28	.08	.95	.49	.16	.06	.67	.29
	T2	.18	.21	.54	.89	.11	.13	.34	.52
y	F	.61	.09	.16	.11	.98	.18	.15	.16
	M	.16	.57	.06	.13	.18	1.02	.06	.14
	T1	.14	-.01	.69	.37	.15	.06	.99	.49
	T2	.16	.10	.31	.59	.18	.15	.53	.88
DZ Families									
x	F	1.08	.21	.14	.10	.54	.24	.05	.01
	M	.21	.91	.24	.16	.21	.64	.21	.03
	T1	.13	.23	1.21	.32	.09	.24	.94	.19
	T2	.09	.16	.29	1.03	.09	.16	.25	.74
y	F	.54	.23	.09	.09	.90	.04	.04	.03
	M	.23	.68	.23	.16	.23	.96	.29	.17
	T1	.04	.20	.79	.22	.04	.26	1.19	.26
	T2	.01	.04	.18	.74	.03	.18	.25	.96

The correlations between the latent variables of the parents, which are induced by the assortative mating, vary between 0.06 and 0.09, the largest being the genetic correlation between spouses for variable Y (fear of leadership), and the smallest that between the environment of the father for variable X and the environment of the mother for variable Y.

The parameters which relate to the phenotypic variances and covariance of an individual are of three main types: the genetic, environmental, and G-E covariance parameters, and are examined in that order. Since negative values of s would lead to negative percentages of variance, percentage figures given here refer to the proportion of a component relative to the sum of the absolute values of the components. First, the genetic parameters: $h_x = 0.77$ which represents 46% of the phenotypic variance of fear of social criticism. Similarly, $h_y = 0.823$, and is associated with 45% of the phenotypic variance of the fear of leadership. The genetic correlation of 0.82 between these two variables is high and this represents 51% of the phenotypic covariance between the variables for an individual.

Environmental influences which are represented by the parameters e_x and e_y have the values 0.74 and 0.76 respectively. Environmental variation makes up 43% of the total variance of the social criticism factor, and 38% of the variance of fear of leadership. The correlation between the environments of these two variables is 0.56, and is associated with approximately 31% of the phenotypic covariation between the two measures for an individual.

G-E covariance for an individual is measured by the parameters s_x , s_y , s_{xy} , and s_{yx} . For the fear of social criticism, s_x constitutes about 11% of the total phenotypic variance, and is not significant with respect to its standard error (see Table 5). The parameter value is negative, suggesting that a small amount of disassociation exists between additive genetic and environmental sources of variation for this phenotype. A similar but larger effect is observed for the second variable, fear of leadership, which is reflected by s_y at -0.20. This parameter value is significantly different from zero, as measured by its standard error, and it is associated with some 17% of the phenotypic variance for this character. The G-E covariance between the variables of an individual is reflected in the size of the correlations s_{xy} and s_{yx} , which are -0.19, and -0.12 respectively. The former can be regarded as significantly different from zero, while the latter cannot. Together, they are associated with about 18% of the covariance between the two variables.

The presence of negative G-E covariance parameters implies the presence of some negative pathways from the parental phenotype to the environment of the child, since these paths are the sole cause of this covariation. In fact, all 8 of the Z parameters are negative in value, ranging from -0.04 to -0.21. Z_{xy2} is the only across variable Z parameter which is larger than its standard error, and while it is not significant for this sample, if it represents a consistent effect it implies that the mother's fear of social criticism has an opposite effect via her influence on the fear of leadership in the offspring. It seems plausible that the mother's fear of criticism may provide an increased opportunity for leadership in the child. The only significant Z parameter is that of Z_{y1} , which suggests that paternal fear of leadership has a similar effect on the offspring fear for the same factor as the mother's fear of social criticism (Z_{xy2}). Such effects are reminiscent of Cattell's theory of coercion to the bio-social mean [1] where extreme offspring tendencies are moderated by the parents. In the present case, the coercion is in the opposite direction to the genotypic influences of the parents. These negative paths reflect the fact

that the parent-offspring resemblance is slightly lower than expected from the heritability estimated from the twins. Some caution is in order with the possibility that the estimates of heritability derived from the twins may be higher than those from the parent-offspring resemblance, perhaps due to genotype × age interaction, possible dominance or epistasis, or a failure of the equal environments assumption for MZ and DZ twins. More extensive designs such as adoption studies are required to substantiate the model. None the less, the present readily accessible design does provide an economical source of potentially fruitful hypotheses.

The partitioning of the twin environments in the bivariate parents of twins model can be considered in three main parts: the environment for fear of social criticism, the environment for fear of leadership, and the covariation between the two factors. The variance of E for twin 1 on variable X, EC_{1x} , which is accounted for or explained by the model, is given by

$$\begin{aligned} VEC_{1x} = & Z_{x1}^2 + Z_{x2}^2 + Z_{yx1}^2 + Z_{yx2}^2 + \\ & 2P_{xy}(Z_{x2}Z_{xy2}) + 2Z_{yx1}Z_{yx2}\mu_y + 2Z_{x1}Z_{x2}\mu_x + \\ & 2Z_{x1}Z_{yx2}\mu_{xy} + 2Z_{x2}Z_{yx1}\mu_x + \beta_x + \beta_{xy} \end{aligned}$$

(assuming residual common environments to be causal paths). Since the variances of latent variables in standardised path analysis are unity, there exists a specific environment residual which influences EC_{1x} to the extent $1 - VEC_{1x}$. This is equivalent to the specific environment of the typical twin study [11]. This residual variance is 79% for fear of social criticism, and makes up the majority of the environmental variance. Of the remaining variance which is associated with sources that twins share, about a quarter or 6% of total variance has parental origins, and three-quarters or 15% of total comes from non-parental sources. If we break down the environmental variance for fear of leadership, we find that 80% of the variance lies with the residual ‘specific environment’ term, while three-quarters or 15% of total is parental in origin, and one quarter or 5% of total is non-parental. The covariance between the environments of the two factors can be partitioned in an analogous fashion, although no residual parameter is present. Approximately 58% of the covariance between the environments of the twins across variables is associated with non-parental sources of covariation, while the remaining 42% is parental in origin. However, the total covariation is very small ($c_{xy} = 0.032$), even though this includes a small negative non-parental component ($\beta_{xy} = -0.023$).

To conclude, the analysis of the two fear factors concerning social criticism and leadership implies that both factors have approximately equal environmental and additive genetic components, with a small amount of negative G-E covariance induced by parental phenotypic influences on their offspring. Assortative mating is present to a mean level of 0.189 both between and within factors. The fit of the model is sufficient to conclude that the data do not depart from the expected covariances to a significant degree. The data demonstrate that the bivariate parents of twins model can estimate parental environmental influences on their offspring both between and within variables in the presence of G-E covariance and phenotypic assortative mating, although such influences are mild for the two fear factors analysed.

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Correspondence: M.C. Neale, Animal Psychology Laboratory, Institute of Psychiatry, Bethlem Royal Hospital, Monks Orchard Road, Beckenham BR3 3BX, England.