*Behavior Genetics, Vol. 20, No. 5, 1990*

# Alternative Common Factor Models for Multivariate Biometric Analyses

**J. J. McArdle[1] and H. H. Goldsmith [2]**

*Received 4 Apr. 1988—Final 15 May 1990*

*In prior research we have shown how linear structural equation models and computer programs (e.g., LISREL) may be simply and directly used to provide alternatives for the traditional biometric twin design. We use structural equations and path models to define biometric group differences, we write traditional common-factor models in the same way, and then we take a detailed look at some alternative multivariate and biometric models. We contrast the biometric-factors covariance structure approach used by Loehlin and Vandenberg (1968), Martin and Eaves (1977), and others with the psychometric-factors approach used by McArdle et al. (1980) and others. We use the multivariate primary mental abilities data on monozygotic (MZ) and dizygotic (DZ) twins from Loehlin and Vandenberg (1968) to detail fundamental differences in model specification and results. We extend both multivariate biometric approaches using exploratory and confirmatory multiple-factor models. These comparisons show that each alternative multivariate methodology has useful features for empirical applications.*

**KEY WORDS:** twins; multivariate; factor analysis; structural equation models; LISREL; RAM; intelligence; primary mental abilities.

## INTRODUCTION

One of the key insights of evolutionary genetics is that diversity plays an important role in the adaptation of species. This may be true of model building in behavioral genetics as well. For example, Martin and Eaves (1977) begin their

This research has been supported by grants from the National Institute on Aging (AG02695, AG04704, and AG07137) to McArdle, and a Research Career Development Award (HD00694) to Goldsmith.

[1] Department of Psychology, University of Virginia, Charlottesville, Virginia 22903.
[2] Department of Psychology, University of Oregon, Eugene, Oregon 97403.



0001–8244/90/0900–0569$06.00/0 

treatment of multivariate biometric analysis by noting, "The techniques of factor analysis have been used extensively in the behavioral sciences to simplify the representation of relationships among multiple variables. Geneticists, rightly, are sceptical about the use of such methods in genetical research. . . ." This treatment introduced a confirmatory factor analysis with maximum-likelihood estimation for a multivariate form of the covariance among measures of various genetic and environmental factors. Technically, Martin and Eaves (1977) showed how the concepts of Jöreskog's (1970) ACOVS model could be extended to a multiple group case to estimate multivariate biometric models. This presentation formalized the earlier multivariate ideas of many others (e.g., Loehlin and Vandenberg, 1968) and partially allayed behavioral geneticists' skepticism about contemporary issues in factor analysis.

There have been numerous developments in structural equation modeling outside of behavioral genetics (e.g., Jöreskog and Sörbom, 1979; McDonald, 1985). In a 1980 conference paper, we showed how the widely available LISREL computer programs could be used to estimate multivariate biometric models (McArdle *et al.*, 1980). Our LISREL-based calculations directly followed Martin and Eaves (1977) ACOVS analyses but required less novel programming, and this proved to be practically useful. We extended this biometric methodology to other problems and issues in later conference papers and published reports (McArdle *et al.*, 1981; McArdle and Goldsmith, 1984; Goldsmith, 1983; McArdle, 1986; Horn, 1986).

Our work in this area has been recognized by several biometric researchers (e.g., Henderson, 1982; Boomsma and Gabrielli, 1985); independently developed and refined by several behavioral geneticists (e.g., Fulker *et al.*, 1983; Cantor *et al.*, 1983) and the LISREL programming techniques are now widely used (e.g., Martin *et al.*, 1984; Tambs *et al.*, 1984; Boomsma and Molenaar, 1986). In fact, this approach has become so popular that a whole issue of *Behavior Genetics* has been devoted to a conference on "Twin Methodology Using LISREL" (Martin *et al.*, 1989).

Our approach to these problems 10 years ago differed in at least two ways from these subsequent presentations. First, we employed a matrix specification that has little overt resemblence to standard LISREL notation. Our matrix notation is based on general path analysis graphics, and we have used it to demonstrate the convergence of available computer programs such as ACOVSM, COFAMM, LISREL, and COSAN (McArdle, 1980, 1986; McArdle and McDonald, 1984; McArdle and Horn, 1990). Second, and more relevant now, is the fact that we used structural modeling techniques to estimate some novel integrations of biometric and psychometric models. The factor loadings derived from the Martin and Eaves (1977) analyses yield genetic and environmental loadings on each of the observed measures. We termed this the *biometric-factors model* and we recognized it as the standard model in the field. As an alternative,

McArdle *et al.* (1980) and subsequent treatments (Goldsmith, 1984; McArdle, 1986) estimated a different model where the factor loadings represent a psychometric common factor and the genetic and environmental effects relate to this measurement factor. We termed this the *psychometric-factors model* and we treated it as a viable modeling alternative. We continue this comparison of multivariate models here.

In this paper, we elaborate the novel aspects of our previous structural modeling approach. The Methods section provides some elementary structural equation notation for univariate and multivariate biometric models and programming. We also present a few details on the alternative biometric and psychometric common-factor models for multivariate observations. In the Results section we fit and compare these multivariate models using the familiar data from Loehlin and Vandenberg (1968) on *primary mental abilities* (PMA). We extend these comparisons to additional multivariate models, including models without unique factor restrictions, multiple-factor identification problems, and the differences between orthogonal and oblique rotations. The Discussion summarizes these issues and the Appendix provides computer program listings.

This paper bridges a gap between biometrical genetics and psychometric measurement theory. In this sense we try to examine ideas about "the Genetics of IQ," by applying the same modeling standards to the "IQ" as are usually applied only to the "Genetics." We try to demonstrate the utility of alternative models for genetic and environmental influences on common factors derived from the observed measures. To achieve this goal, we bypass several interesting but highly technical controversies of biometric structural modeling. Instead, we are interested mainly in using multivariate biometric structural equation models as one aspect of the validation of psychological constructs.

## METHODS: LINEAR STRUCTURAL EQUATION MODELING

In this section we present some details on the basic models we use. This is not intended to be entirely technical, but we do outline our notation to give the formal basis of our multivariate concepts. Readers more interested in empirical results may skip to the next section.

### Univariate Biometric Models

In Table [1] we present some mathematical notation for a univariate biometric model. We assume that a single behavioral variable $P$ (phenotype) has been measured on a sample of $n = 1$ to $N$ individuals. A linear model for these $P_n$ scores is written in a scalar form as Eq. [1.1]. In this simple model, we assume that $P_n$ can be represented as a weighted linear combination of three unobserved scores: an additive genetic score (genotype) $Ga_n$, a common or

**Table [1].** Mathematical Notation for Biometric Structural Equations

[1.1] Traditional Biometric Linear Model

$$P_n = h\,Ga_n + c\,Ec_n + e\,Ei_n,$$

where, for the n-th individual,
$P_n$ = the observed phenotype or behavioral mean deviate score,
$Ga_n$ = the unobserved additive genetic score (genotype),
$Ec_n$ = the "shared" environment score,
$Ei_n$ = the unobserved independent or error score,
h = the coefficient for genotype upon phenotype,
c = the coefficient for common environments on the phenotype.
and e = the coefficient for independent effects upon the phenotype.

[1.2] Additional Biometric Assumptions

$$E\{Ga\ Ga'\} = E\{Ec\ Ec'\} = E\{Ei\ Ei'\} = 1, \text{ and}$$

$$E\{Ga\ Ec'\} = E\{Ga\ Ei'\} = E\{Ec\ Ei'\} = 0,$$

where scores Ga, Ec, Ei and P are vectors of order (1 × N), and
$E\{*\}$ = the expected value over n = 1 to N individuals.

[1.3] Resulting Phenotype Expectations

$$E\{P\ P'\} = E\{(h\ Ga + c\ Ec + e\ Ei)\ (h\ Ga + c\ Ec + e\ Ei)'\}$$

$$h\,E\{Ga\ Ga'\}\,h' + c\,E\{Ec\ Ec'\}\,c' + e\,E\{Ei\ Ei'\}\,e'$$

$$hh' + cc' + ee'$$

[1.4] A General RAM Matrix Notation (after McArdle & McDonald, 1984)

$\mathbf{v} = \mathbf{vA} + \mathbf{u}$, where

$$\mathbf{v} = [P : Ga : Ec : Ei], \text{ and } \mathbf{A} = \begin{bmatrix} 0 & h & c & e \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$\mathbf{S} = E\{\mathbf{uu}'\}$, where

$$\mathbf{u} = [Z : Ga : Ec : Ei], \text{ and } \mathbf{S} = \begin{bmatrix} 0 & & & \text{sym} \\ 0 & 1 & & \\ 0 & 0 & 1 & \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

$\mathbf{m} = \mathbf{vF} = P$, and $\mathbf{F} = [1\ 0\ 0\ 0]$,

Table [1]. (Continued)

where matrices
**A** = asymmetric coefficients (e.g., regressions, intercepts, arrows),
**S** = symmetric coefficients (e.g., variances, correlations, slings),
**F** = filter elements (e.g., fixed unit values),

and where vectors
**v** = all model variables,
**u** = all endogeneous model variables.
**m** = all manifest model variables,
z = all undefined placeholder nodes.

[1.5] The General Matrix Expectations (after McArdle & McDonald, 1984)

$$\mathbf{C} = E\{\mathbf{vv}'\} = E\{(\mathbf{vA} + \mathbf{u})(\mathbf{vA} + \mathbf{u})'\} = E\{[(\mathbf{I}-\mathbf{A})^{-1}\,\mathbf{u}]\,[(\mathbf{I}-\mathbf{A})^{-1}\,\mathbf{u}]'\}$$

$$\mathbf{C} = (\mathbf{I}-\mathbf{A})^{-1}\,E\{\mathbf{uu}'\}\,(\mathbf{I}-\mathbf{A})^{-1'} = (\mathbf{I}-\mathbf{A})^{-1}\,\mathbf{S}\,(\mathbf{I}-\mathbf{A})^{-1'},$$

$$\mathbf{C} = \begin{bmatrix} 1 & h & s & e \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} 1 & 0 & 0 & 0 \\ h' & 1 & 0 & 0 \\ c' & 0 & 1 & 0 \\ e' & 0 & 0 & 1 \end{bmatrix}$$

$$\mathbf{C} = \begin{bmatrix} 0 & h & c & e \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} 1 & 0 & 0 & 0 \\ h' & 1 & 0 & 0 \\ c' & 0 & 1 & 0 \\ e' & 0 & 0 & 1 \end{bmatrix} = \begin{bmatrix} (hh'+cc'+ee') & h & c & e \\ h' & 1 & 0 & 0 \\ c' & 0 & 1 & 0 \\ e' & 0 & 0 & 1 \end{bmatrix}$$

$$\mathbf{X} = \mathbf{F}\,\mathbf{C}\,\mathbf{F}',$$

$$\mathbf{X} = [1\ 0\ 0\ 0] \begin{bmatrix} (hh'+cc'+ee') & h & c & e \\ h' & 1 & 0 & 0 \\ c' & 0 & 1 & 0 \\ e' & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} = (hh'+cc'ee')$$

[1.6] Proportional Expectations from Biometric Theory (after Martin & Eaves, 1977)

$$\mathbf{S}(mzb) = E\{\mathbf{u}(mzb)\,\mathbf{u}(mzb)'\} = \text{diag}\,[.0, 1.0, 2.0, 1.0],$$
$$\mathbf{S}(dzb) = E\{\mathbf{u}(dzb)\,\mathbf{u}(dzb)'\} = \text{diag}\,[.0, .75, 2.0, 1.0],$$
$$\mathbf{S}(mzw) = E\{\mathbf{u}(mzw)\,\mathbf{u}(mzw)'\} = \text{diag}\,[.0, .0, .0, 1.0],$$
$$\mathbf{S}(dzw) = E\{\mathbf{u}(dzw)\,\mathbf{u}(dzw)'\} = \text{diag}\,[.0, .25, .0, 1.0],$$

where the labels mz = monozygotic, dz = dizygotic, b = between, and w = within.

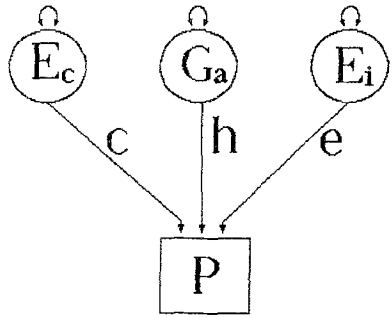
shared environment score $Ec_n$, and an independent environment or random error score $Ei_n$. The structural coefficients for all individuals are given as $h$ for genotype upon phenotype, $c$ for common environments upon the phenotype, and $e$ for the combined effects of independent error and nonshared environments upon the phenotype.

In Eq. [1.2] we define additional assumptions of standardized scaling and orthogonality among the unobserved components. We use these assumptions to obtain a simplified expectation for the variance of the phenotype written as Eq. [1.3]. In this classical variance components (covariance structure) model the term $hh'$ reflects the variance of $P$ due to heredity, the term $cc'$ reflects the variance which is nonheritable and due to shared environments, and the term $ee'$ reflects the residual variance which is nonheritable. When the phenotype $P$ is also standardized (i.e., $E\{PP'\}=1$), these model components of variance in [1.3] are directly interpretable as proportions of variance.

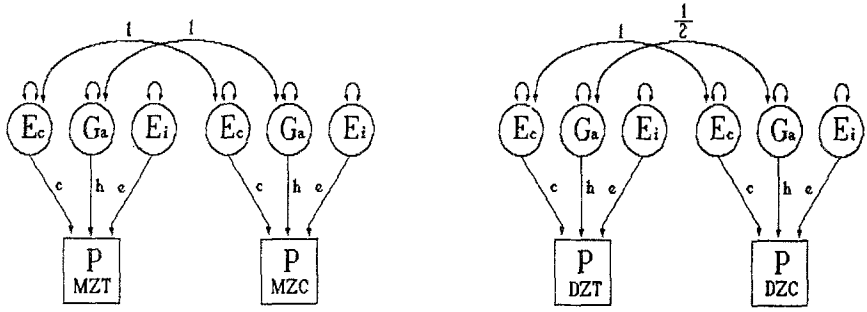
Researchers can translate model [1.1] into other biometric notation, e.g., the scores $Ga = 1/2\ D_r$, $Ei = E_1$, and $Ei = E_2$. These additional model assumptions [1.2] are not generally testable features of the biometric models using the twin data that we discuss here. More complete models that include nonadditive sources of variance, gene–environment correlation, and gene–environment interaction are obviously important and can be incorporated easily into the model framework we use. We use this notation as a simple starting point for our psychometric model development, and we do not now consider more complex biometric issues (but see Eaves *et al.*, 1978).

A graphic display of this biometric model is presented as a structural path diagram in Fig. [1.1]. In our notation, the elements of the algebraic model in Table [1] and the graphic model in Fig. [1.1] are identical. In these pictures (1) the vector **v** lists all variables that are drawn; (2) the matrix **A** contains all one-headed arrows, from column to row variable; (3) the matrix **S** contains all two-headed arrows; and (4) the matrix **F** filters the squares from all variables. This diagram is similar to the typical path analysis diagram except (1) all model variables are considered either observed or unobserved, (2) all model parameters are displayed and labeled in the graphic, and (3) we use a two-headed arrow (termed a "sling") to connect a variable with itself. In most cases here, these two-headed parameters represent a variance or residual variance term, but in all cases they are needed for consistency between the algebra and the graphics.

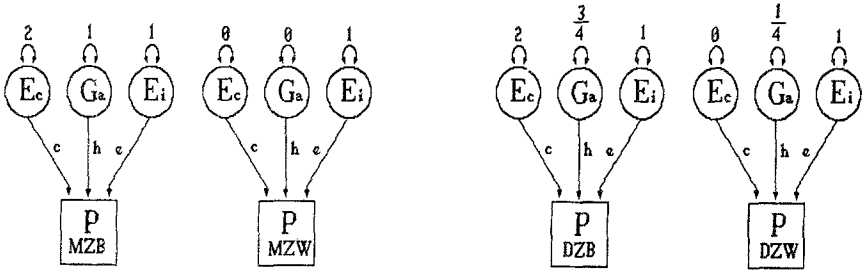
In Eqs. [1.4] and [1.5] in Table [1] we define a matrix notation for this model. In [1.4] we define score vectors **v**, for all variables, **u**, for all unobserved residuals, and **p**, for all observed variables. We also define linear coefficient matrices, **A**, for asymmetric parameters, and **S**, for symmetric parameters, as well as the permutation matrix **F**, to filter observed from unobserved variables In [1.5] we calculate all model covariance expectations **C** by taking the inverse $\mathbf{E} = (\mathbf{I}-\mathbf{A})^{-1}$, specifying **S**, and pre and post multiply to obtain $\mathbf{C} = \mathbf{E}\,\mathbf{S}\,\mathbf{E}'$.




[1.1]: A Theoretical Summary Diagram using RAM notation (McArdle & Horn, 1990)




[1.2]: An Intraclass Covariance Estimation Diagram (after Jaspers & Deleeuw, 1980)




[1.3]: A Mean-Square Covariance Estimation Diagram (McArdle & Goldsmith, 1984)

**Fig. 1.** Univariate structural diagrams of biometric twin models.

The algebraic expectations (of [1.5]) follow a simple and consistent set of path tracing rules (for more details, see McArdle, 1980, 1986; Horn and McArdle, 1980, 1990). Perhaps the most notable feature is that these matrices are largely empty (sparse). Indeed, this algebraic form is overly complex for the simple model considered. On the other hand, this basic matrix representation can be used for *any* structural equation model and forms the *necessary and sufficient* computer programming for any model (see the Appendix). Algebraic features of this model are described in further detail in other presentations (McArdle, 1980, 1986; McArdle and McDonald, 1984; McDonald, 1985; Loehlin, 1987).

## Alternative Data Structures

One clear feature of Eq. [1.3] is that there are three unknown model parameters $h$, $c$, and $e$, and only one observed variance term based on $P$. Thus, the three unknowns cannot all be independently and uniquely estimated from the single variance term. The standard biometric approach to this problem capitalizes on the availability of variance terms from different experimental groups. In the general case, we assume the same measurements made on $g = 1$ to $G$ predefined and measured groups, and we partition the available data. Two alternative data structures are used for twin data: (1) cross-covariances and (2) mean squares. These biometric approaches are described in detail by Jinks and Fulker (1970), Eaves *et al.* (1978), and Cattell (1960, 1982), and Loehlin (1978) demonstrates equivalences between the mean squares and cross-covariance approaches. A few structural modeling aspects of these data are presented in Fig. [1.2] and [1.3].

First, we consider the traditional two-group twin design where twins and cotwins are measured and zygosity is known as either monozygous (MZ) or dizygous (DZ). Given this special group structure, we can estimate $h$, $c$, and $e$ using a "cross-covariance" approach (after Karl Pearson). Here we assume that one member of each twin pair is randomly labeled as a "twin" and the other is labeled as a "cotwin." Figure [1.2] is a structural graphic for a single observed variable. We draw observed variables on a twin and a cotwin for the MZ and DZ pairs. The unobserved model components are assumed

(1) to be standardized (i.e., the two-headed arrows labeled 1);
(2) the $Ga_n$ are correlated at $r = 1.0$ for MZ pairs and at $r = .5$ for DZ pairs;
(3) the $Ec_n$ are correlated at $r = 1.0$ for each pair;
(4) the $Ei_n$ are correlated at $r = 0$ for each pair; and
(5) the $h$, $c$, and $e$ coefficients are repeated (forced to be equal) for all individuals across all effects (one-headed arrows).

This diagram can now be easily translated to matrices **A**, **S**, and **F**, for the generation of expectations required for further computer estimation (Behrman

*et al.*, 1977; Jaspers and DeLeeuw, 1980; McArdle, 1986; Neale and McArdle, 1990).

Another popular data structure for model estimation recasts these same basic expectations into "analysis of variance components" or "expected mean squares" (after R. A. Fisher). These scores are usually calculated in matrix terms by defining a total score cross-products matrix **T**, a between-pair sum score cross-products matrix **B**, and a within-pair cross-products matrix **W** = **T-B.** We can also write and interpret these as score vectors where the between-group scores ($B_n$) are pair sums, and the within-group scores ($W_n$) are pair differences that are further partialed from the pair sums. Using this technique, the obtained $B_n$ and the $W_n$ scores are orthogonal. This mean-square data structure is useful because the cross-sib covariance terms (i.e., $E\{P_{zb}\ P_{zw}'\}$ are redundant or zero and can be dropped from further estimation. The mean square structure yields expectations $E\{\ P_{ij}P_{ik}\ \}$ that differ proportionally over different groups, as defined in [1.6]. That is, the $h$, $c$, and $e$ coefficients are repeated for all individuals across all effects (one-headed arrows) in all groups but the proportions of variance (two-headed slings) change according to biometric theory. Figure [1.3] presents a structural path model based on this mean square data structure.

These alternative model organizations do not alter our interpretation of the model parameters $h$, $c$, and $e$. The cross-covariance approach [1.2] and the mean square approach [1.3] are simply two ways to organize the parameters of the fundamental biometric model [1.1]. Many researchers prefer one approach over the other, but the reasons for these preferences typically involve technical issues of estimation. We now use the summary diagram in Fig. [1.1] as a convenient way to draw a complete model of the biometric decomposition and to represent *any biometric group*. This graphic simplification will prove useful in the presentation of models with more variables and extended kinships.

## Alternative Estimation and Comparison

There are several simple ways to estimate the parameters $h$, $c$, and $e$. Many researchers have used the familiar "double entry" formula to obtain the intraclass data for MZ and DZ groups. These intraclass statistics are used to obtain information about the parameters. Such simple correlational estimations are still popular, but they are subject to some difficult statistical and mathematical problems (Jinks and Fulker, 1970; Goldsmith, 1983). For example, it is often unclear how to constrain the parameter estimates, how to obtain adequate statistical tests, or how to use information from samples of different sizes effectively.

These problems with the simple correlational approach led researchers to examine a simultaneous equations model-fitting approach (described in

detail by Cattell, 1960; Eaves *et al.*, 1978; Fulker, 1978). First, we rewrite the model observations $O_g$ and expectations $X_g$ for $g = 1$ to $G$ groups to define model misfits or residuals $R_g = (O_g - X_g)$ (McDonald, 1985). Second, we can calculate a discrepancy function based on weighted least squares or as a *likelihood-ratio criterion* (LRC). Finally, we obtain parameter values and produce expectations $X_g$ that minimize the residuals $R_g$. The computation of these "best" estimates requires the a priori definition of a multiple group LRC($g$). Since we assume that the groups are independent, the LRC for the entire model is calculated as a simple sum of the $g$ independent LRC($g$) for the $G$ separate groups. The numerical minimization of this function produces a *minimum chi-square* for the assessment of goodness of fit, as well as approximate *maximum-likelihood estimates*(MLE) and standard errors (SE) for all free parameters. More complex estimation techniques are well developed (Lange and Boehnke, 1983; also see Bock, 1989), but these are required only for more complex kinship designs.

Most problems inherent in the assessment of goodness of fit in analysis of variance, multiple regression, and factor analysis also pertain to biometric structural modeling. Given certain regularity conditions on the function, the LRC($G$) for the entire model can be considered a chi-square variate with degrees of freedom (df) equal to the numerically independent information (McDonald and Krane, 1979). A test of the null hypothesis can be translated in $Z$ score units (Horn and McArdle, 1980; McArdle, 1986). Relatively large chi-square (and $Z$) values reflect nonrandom residuals, but the size of the nonrandom effects is often indexed in other ways. For example, we could define a specific test size (i.e., $p < .01$) for model fit and use this as a rigorous standard of statistical inference. Alternatively, we could guide our modeling decisions by the search for a minimal number of parameters, each of which has a clear substantive interpretation. These are important modeling issues, and we present further details later.

There are many alternative ways to calculate biometric parameters for these univariate model estimates (for general proof, see McArdle and McDonald, 1984). A listing of one LISREL program for this kind of univariate analysis is presented in the Appendix. This approach is identical to our earlier work (e.g., McArdle *et al.*, 1980) but differs in several ways from more recent work in this area (e.g., Boomsma and Molenaar, 1986). The programming of only three matrices has a direct resemblance to the diagrams in Fig. 1: the "arrows" are placed in one matrix and the "slings" are placed in another. We think this programming approach is effective because it includes all necessary and sufficient features, it allows path analysis to be carried out in any metric, and it allows flexibility in multivariate extensions (McArdle, 1986; McArdle and McDonald, 1984; McArdle and Horn, 1990; McArdle and Boker, 1990).

## Common-Factor Models

The extension of the previous univariate biometric model to a multivariate form is compelling but not obvious. In this section we examine models where the observed phenotype **P** is defined as a $(M \times N)$ matrix for $m = 1$ to $M$ different measures. There are many sensible multivariate approaches to this problem, but we focus on the common factor model defined in Table [2]. The scalar model of Eq. [2.1] and matrix form of [2.2] follow the classic structural model of Spearman (1904); it includes one factor, $F$, common to all variables, and one factor, $U[m]$, unique to each phenotype $P[m]$.

This single-factor model can be examined in exactly the same way as the previous biometric models, but we require multiple measures rather than multiple groups. As in all previous latent variable models, unique estimates require at least one scaling constraint on each independent latent variable, so we use the typical standardization and model constraints of Eq. [2.3]. These additional assumptions lead to the simplified set of variance expectations of [2.4] and the covariance expectations of [2.5]. These expectations are restrictive because they require proportionality constraints among all covariances, and these restrictions permit a test of the suitability of the single common-factor model (McDonald, 1985).

The single-factor model is drawn as a structural graphic in Fig. [2.1]. The associated structural model matrices, **A**, **S**, and **F**, are defined in Table [2.6]. Because the algebra can be obtained directly from this graphic, there is usually no need to present both algebra and graphics.

## The Biometric-Factors Model

Fulker (1978, 1979) provides an informative historical perspective on multivariate biometric analyses. He reports that Tukey (1951; as reported by Fulker, 1978) originally suggested the calculation of between- and within-pair cross-product matrices for a variety of measures followed by separate principal-components analysis of these matrices. Additional statistical contributions to this approach were made by Kempthorne and Osborne (1961), Bock and Vandenberg (1968), Meredith (1968), Loehlin and Vandenberg (1968), and Crawford and DeFries (1976). Contemporary advances in this methodology were offered by Martin and Eaves (1977), Behrman *et al.* (1977), Chamberlain and Grilliches (1977), and Fulker (1978, 1979). These later developments used the same basic mean square approach but added several features, including (1) the estimation of a single common factor model including unique factors, (2) numerical approximations to obtain maximum likelihood estimates and standard errors for all model parameters, and (3) multivariate hypothesis testing based on likelihood-ratio tests.

**Table [2]:** Traditional Multivariate Factor Equations (e.g., Spearman, 1904)

[2.1] A Single Common Factor Model

$$P[m]_n = L[m]\, F_n + u[m]\, U[m]_n$$

where, for the ith individual,

$P[m]_n$ = the observed score on the m-th measure,
$F_n$ = the common factor score,
$U[m]_n$ = the unique factor score,
$L[m]$ = the factor loading of P on F, and
$u[m]$ = the unique loading of P on U[m].

[2.2] Matrix Form of [4.1]

$$\begin{bmatrix} P[1] \\ P[2] \\ P[3] \\ \cdots \\ P[M] \end{bmatrix} = \begin{bmatrix} L[1] \\ L[2] \\ L[3] \\ \cdots \\ L[M] \end{bmatrix} F +$$

$$\begin{bmatrix} u[1] & & & & \\ & u[2] & & & \\ & & u[3] & & \\ & & & \cdots & \\ & & & & u[M] \end{bmatrix} \begin{bmatrix} U[1] \\ U[2] \\ U[3] \\ \cdots \\ U[M] \end{bmatrix}$$

[2.3] Additional Scale Constraints

$E\{F\, F'\} = 1$, and $E\{U[m]\, U[m]'\} = 1$.

[2.4] Diagonal Variance Expectations

$$\begin{aligned} E\{P[m]\, P[m]'\} &= E\{(L[m]\, F_n + u[m]\, U[m]_n)\, (L[m]\, F_n + u[m]\, U[m]_n)'\} \\ &= L[m]\, E\{F\, F'\}\, L[m]' + u[m]' + u[m]\, E\{U[m]\, U[m]'\}\, u[m]', \\ &= L[m]\, L[m]' + u[m]\, u[m]', \end{aligned}$$

[2.5] Off-Diagonal Covariance Expectations

$$\begin{aligned} E\{P[i]\, P[j]'\} &= E\{(L[i]\, F_n + u[i]\, U[i]_n)\, (L[j]\, F_n + u[j]\, U[j]_n)'\} \\ &= L[i]\, E\{F\, F'\}\, L[j]' = L[i]\, L[j]. \end{aligned}$$

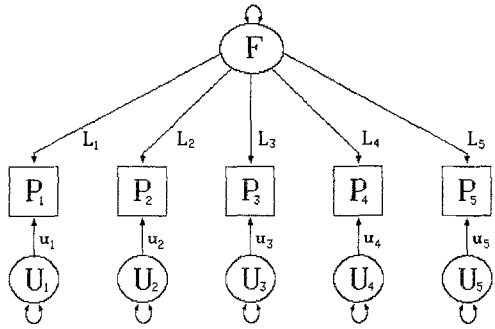
[2.6] A General Matrix Model (after McArdle & McDonald, 1984)

$$\mathbf{v} = [P[M] : F : U[M]], \text{ and } \mathbf{A} = \begin{bmatrix} 0 & L[M] & u[M] \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$\mathbf{u} = [Z[M] : F : U[M]], \text{ and } \mathbf{S} = \begin{bmatrix} 0 & & \text{sym} \\ 0 & Q & \\ 0 & 0 & I \end{bmatrix}$$

$$\text{and } \mathbf{F} = [I[m]\ 0\ 0[m]],$$

where, in general, X[M] are matrices with m = 1 to M rows or columns.



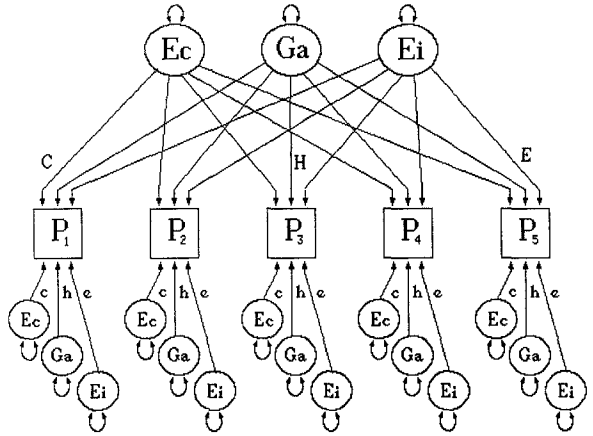

[2.1]: A Single Common Factor Model (after Spearman, 1904)

**Fig. 2.** Multivariate structural diagrams of biometric twin models.

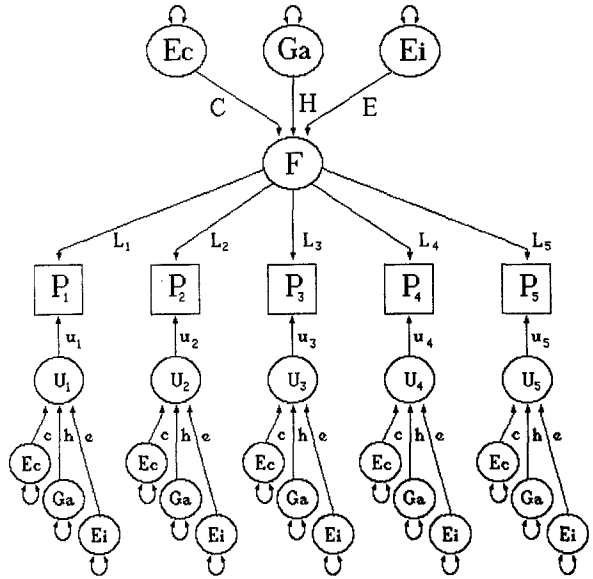
Table [3] is a listing of a multivariate biometric model presented by Martin and Eaves (1977). Equation [3.1] presents a scalar form of the linear model for multiple phenotypes. In this model we allow six sources of variance for each phenotype. The factors *common* to all measures are labeled *Ga*, *Ec*, and *Ei* (without subscripts) with common factor loadings *H*[*m*], *C*[*m*], and *E*[*m*]. The factors *unique* to a specific measure $m=1$ to *M* are labeled *Ga*[*m*], *Ec*[*m*], and *Ei*[*m*] with unique loading coefficients *h*[*m*], *c*[*m*], and *e*[*m*]. These components are all orthogonal in this model, so the coefficients can simply be squared, added, and scaled to obtain variance proportions. In sum, this model assumes that each phenotypic matrix can be formed from common and unigue factors that represent genetic and nongenetic factors.

This structural organization can be clearly seen in the matrix form of Eq. [3.2]. The additional scale constraints and model conditions in [3.3] are required for all latent variables. Given these assumptions, this multivariate model produces expectations for the variances of all *P*[*m*] variables in [3.4] and for the covariances of pairs of *P*[*i*] and *P*[*j*] variables in [3.5]. These expectations are slightly more complex than the proportionality restrictions of the traditional factor model. Unique parameter estimation requires both multiple psychometric measures and multiple biometric groups.

Figure [2.2] displays the basic structure of the multivariate linear model of Table [3] in a summary form. Estimation of these parameters requires the subpartitioning of the matrix data into either cross-covariance or mean square matrices for the four groups described earlier, but this picture is largely redundant and is not presented here [see Fig. [1.3] and McArdle *et al.* (1980)]. On the other hand, the current diagram [2.2] is especially clear about the sources of variance [3.4] and [3.5] for any variable in the model, and this is the key modeling issue.




[2.2]: The Biometric Common Factors Model (after Martin & Eaves, 1977)




[2.3]: The Psychometric Common Factor Model (after McArdle, Connell & Goldsmith, 1980)

**Fig. 2.** Continued.

## A Psychometric-Factor Alternative

The biometric-factors model in Table [3] uses the basic logic of the common factor model in Table [2], and this can be informative. But the model in Table

**Table [3]:** Traditional "Biometric Factors" Model Equations (e.g., Martin & Eaves, 1977)

[3.1] Scalar Representation of Multiple Phenotypes

$$P[m]_n = H[m]\,Ga_n + C[m]\,Ec_n + E[m]\,Ei_n + h[m]\,Ga[m]_n + c[m]_n + c[m]\,Ec[m]_n + e[m]\,Ei[m]_n,$$

where, for each measure m = 1 to M,
Ga, Ec, and Ei (without subscripts) are common to all measures,
Ga[m], Ec[m], and Ei[m] (with M subscripts) are unique to each measure,
coefficients H[m], C[m], and E[m], are common factor loadings, and
h[m], c[m], and e[m] are unique factor loadings.

[3.2] Matrix Expansion of [3.1]

$$\begin{bmatrix} P[1] \\ P[2] \\ P[3] \\ \cdots \\ P[M] \end{bmatrix} = \begin{bmatrix} H[1] \\ H[2] \\ H[3] \\ \cdots \\ H[M] \end{bmatrix} Ga + \begin{bmatrix} C[1] \\ C[2] \\ C[3] \\ \cdots \\ C[M] \end{bmatrix} Ec + \begin{bmatrix} E[1] \\ E[2] \\ E[3] \\ \cdots \\ E[M] \end{bmatrix} Ei +$$

$$\begin{bmatrix} h[1] & & & & \\ & h[2] & & & \\ & & h[3] & & \\ & & & \cdots & \\ & & & & h[M] \end{bmatrix} \begin{bmatrix} Ga[1] \\ Ga[2] \\ Ga[3] \\ \cdots \\ Ga[M] \end{bmatrix} + \begin{bmatrix} c[1] & & & & \\ & c[2] & & & \\ & & c[3] & & \\ & & & \cdots & \\ & & & & c[M] \end{bmatrix}$$

$$\begin{bmatrix} Ec[1] \\ Ec[2] \\ Ec[3] \\ \cdots \\ Ec[M] \end{bmatrix} + \begin{bmatrix} e[1] & & & & \\ & e[2] & & & \\ & & e[3] & & \\ & & & \cdots & \\ & & & & e[M] \end{bmatrix} \begin{bmatrix} Ei[1] \\ Ei[2] \\ Ei[3] \\ \cdots \\ Ei[M] \end{bmatrix}$$

[3.3] Multivariate Model Scale Constraints (with Proportionality [1.6] assumed)

$$E\{Ga\ Ga'\} = E\{Ec\ Ec'\} = E\{Ei\ Ei'\} = 1,$$

$$E\{Ga[m]\ Ga[m]'\} = E\{Ec[m]\ Ec[m]'\} = E\{Ei[m]\ Ei[m]'\} = 1,$$

[3.4] Multivariate Model Variance Expectations

$$E\{P[m]\ P[m]'\} = H[m]\,H[m]' + C[m]\,C[m]' + E[m]\,E[m]' + h[m]\,h[m]' + c[m]\,c[m]' + e[m]\,e[m]'$$

[3.5] Multivariate Model Covariance Expectations

$$E\{P[i]\ P[j]'\} = H[i]\,H[j]' + C[i]\,C[j]' + E[i]\,E[j]'.$$

[3] is not the only way to use the common-factor model in Table [2]. In our earlier reports, we studied a different kind of model based on psychometric considerations (McArdle *et al.*, 1980; Goldsmith, 1983; McArdle, 1986). In Table [4], we present the basic algebra for this psychometric variation.

In [4.1] we assume that each phenotype $P[m]$ can be decomposed into a single common factor $F$ and unique factors $U[m]$. In a second equation we then assume that these common and unique factor scores have biometric sources of influence; i.e., the common factor $F$ comes from common sources $Ga$, $Ec$, and $Ei$, with effects $H$, $C$, and $E$, whereas the unique factor $U[m]$ comes from common sources $Ga[m]$, $Ec[m]$, and $Ei[m]$, with effects $H[m]$, $C[m]$, and $E[m]$. These simultaneous equations are also written in a "reduced form" to show the proportional assumptions of the second-order biometric model directly on the zero-order phenotypes. The basic factor structure of this model is also presented in Fig. [2.3]. The pattern of influences clearly shows that the first-order common psychometric factor $F$ is influenced by second-order biometric sources $Ga$, $Ec$, and $Ei$. The unique factors have a similar higher-order structure. This model has standard psychometric components which themselves have a biometric source.

The independent estimation of parameters for both the common-factor loadings $L[m]$ and $U[m]$ requires the usual restrictions on the model parameters. These scale constraints (in Table [4.3]) lead to variance expectations (in Table [4.4]) and covariance expectations (in Table [4.5]). These expectations represent our alternative psychometric model.

## Alternative Multivariate Model Comparisons

In the psychometric model above we assume (1) a first-order psychometric separation into a common factor $F_n$ and $M$ unique factors $U[m]$ and (2) a second-order separation of the biometric sources $Ga$, $Ec$, and $Ei$ of these common and unique factors. This is different from the more traditional biometric model. The formal difference between the two multivariate models is expressed by three differences in structural expectations in Tables [3] and [4].

*(1) The Psychometric Factors Model Is a Subset of the Biometric Factors Model.* The two models can produce identical expectations under conditions where the loadings of the biometric-factors structure can be written as $H[m] = L[m]\,H$, $C[m] = L[m]\,C$, and $E[m] = L[m]\,E$, where $L[m]$ is a common-factor loading for the $m$th variable. That is, this psychometric model is a biometric model with the additional constraint of proportionality of loadings $H[m]$, $C[m]$, and $E[m]$ across all $m$ manifest variables.

*(2) The Psychometric Factors Model Is Usually More Restrictive.* The psychometric model estimates $M+3$ common-factor parameters $L[m]$, $H$, $C$, and $E$, whereas the biometric model requires $M*3$ common-factor parameters

**Table [4]:** Non-Traditional "Psychometric Factors" Biometric Model Equations (e.g., McArdle, Connell & Goldsmith, 1980)

[4.1] Biometric Additions

$$P[m]_n = L[m]\, F_n + u[m]\, U[m]_n,$$

$$F_n = H\, Ga_n + C\, Ec_n + E\, Ei_n,$$

$$u[m]_n = h[m]\, Ga[m]_n + c[m]\, Ec[m]_n + e[m]\, Ei[m]_n,$$

or, in reduced form,

$$P[m]_n = L[m]\{H\, Ga_n + C\, Ec_n + E\, Ei_n\}$$
$$+ u[m]\{h[m]\, Ga[m]_n + c[m]\, Ec[m]_n + e[m]\, Ei[m]_n\},$$

where H, C, and E are now (1 × 1) scalars representing the second-order impact of the biometric components upon the psychometric factor.

[4.2] A Matrix Form of [4.1]

$$\begin{bmatrix} P[1] \\ P[2] \\ P[3] \\ \cdots \\ P[M] \end{bmatrix} = \begin{bmatrix} [1] \\ L[2] \\ L[3] \\ \cdots \\ L[M] \end{bmatrix} [H : C : E] \begin{bmatrix} Ga \\ Ec \\ Ei \end{bmatrix} +$$

$$\begin{bmatrix} h[1] & & & \\ & h[2] & & \\ & & h[3] & \\ & & & \cdots \\ & & & h[M] \end{bmatrix} \begin{bmatrix} Ga[1] \\ Ga[2] \\ Ga[3] \\ \cdots \\ Ga[M] \end{bmatrix} + \begin{bmatrix} c[1] & & & \\ & c[2] & & \\ & & c[3] & \\ & & & \cdots \\ & & & c[M] \end{bmatrix}$$

$$\begin{bmatrix} Ec[1] \\ Ec[2] \\ Ec[3] \\ \cdots \\ Ec[M] \end{bmatrix} + \begin{bmatrix} e[1] & & & \\ & e[2] & & \\ & & e[3] & \\ & & & \cdots \\ & & & e[M] \end{bmatrix} \begin{bmatrix} Ei[1] \\ Ei[2] \\ Ei[3] \\ \cdots \\ Ei[M] \end{bmatrix}$$

[4.3] Factor Scale Constraints

$$E\{Ga\ Ga'\} = E\{Ec\ Ec'\} = E\{Ei\ Ei'\} = 1,$$

$$E\{Ga[m]\ Ga[m]'\} = E\{Ec[m]\ Ec[m]'\} = E\{Ei[m]\ Ei[m]'\} = 1,$$

[4.4] Diagonal Variance Expectations

$$E\{P[m]\ P[m]'\} = L[m]\,(H\,H' + C\,C' + E\,E')\,L[m]'$$
$$+ h[m]\, h[m]' + c[m]\, c[m]' + e[m]\, e[m]'$$

[4.5] Off-Diagonal Covariance Expectations

$$E\{P[i]\ P[j]\} = L[i]\,\{H\,H' + C\,C' + EE'\}\,L[j]'.$$

$H[m]$, $C[m]$, and $E[m]$. It follows that, when the number of measures $M \geq 3$, the degrees of freedom for DF{psychometric} > DF{biometric}.

*(3) All Differences Come from the Common Factor Structure.* The unique factor structure is identical in both models, and in later applications we ignore the biometric structuring of the unique factor variances.

The three structural contrasts above imply that these two models are always *testable alternatives* (given $m > 3$). In the next section, we provide a demonstration of these multivariate differences.

## RESULTS: COMMON FACTOR MODELS OF THE PMA

We now present results for the fitting of several multivariate models to the five-variable PMA matrices presented by Loehlin and Vandenberg (1968; see Appendix here). These summary statistics were previously fitted using a biometric-components approach by Loehlin and Vandenberg (1968) and a biometric factors approach by Martin and Eaves (1977) and again by Boomsma and Molenaar (1986). McArdle *et al.* (1981) reported the LISREL estimation of the biometric factors model and compared these with the psychometric factors model applied to these data. Some aspects of this comparison follow.

### Initial Model Comparisons

The second column in Table [5] gives maximum-likelihood estimates for the Martin and Eaves (1977) biometric-factors model [4] fitted to the $M = 5$ measures of the PMA. This listing includes all common factor loadings in standardized form, shows a few loading parameters which are not significant, and yields an LRC = 33 on df = 30. This is obviously an excellent fit, and these results match the earlier report of Martin and Eaves (1977).

The third column in Table [5] gives the standardized results for a slight variation on this model. Martin and Eaves (1977) originally suggested that a proportional patterning of the factor loadings $H[m]$ for common additive genetic $Ga$ and the loadings $C[m]$ for common shared environments $Ec$ could be used to structure an assortative mating coefficient ($Ma$) within the classical twin design. To wit, Martin and Eaves fit a model where $Ga[m] = b * Ec[m]$, and the standardized estimates for this model are reproduced in column 3 in Table [5]. This model yields the MLE($b$) = .704 and an overall LRC = 52 on df = 34, which is also a reasonably good fit.

This second model shows that Martin and Eaves (1977) clearly recognized the possibility of more complex constraints upon their model (also see Fulker, 1978, 1979). However, Martin and Eaves (1977) did not use further proportionality constraints on the factor loading matrices, nor did they allow correlation among the factor scores. The additional constraints [5.4] and [5.5] can be made

**Table [5]:** Alternative Multivariate Models fitted to the Primary Mental Abilities Twin Data.

| | | | Model 1: Genetic Factor | Model 2: Proportional Ec Factor | Model 3: Psychometric Factor | Model 3: Psychometric Expectations |
|---|---|---|---|---|---|---|
| Additive Genetic First-Order Factor Loadings | | | | | | |
| Ga --> | PMA[N] | := H[1] | .758 | .533 | .0** | .429 |
| Ga --> | PMA[V] | := H[2] | .348 | .569 | .0** | .526 |
| Ga --> | PMA[S] | := H[3] | .434 | .335 | .0** | .262 |
| Ga --> | PMA[W] | := H[4] | .382 | .436 | .0** | .403 |
| Ga --> | PMA[R] | := H[5] | .423 | .543 | .0** | .503 |
| Common Environment First-Order Factor Loadings | | | | | | |
| Ec --> | PMA[N] | := C[1] | .410 | .533 | .0** | .517 |
| Ec --> | PMA[V] | := C[2] | .782 | .569 | .0** | .633 |
| Ec --> | PMA[S] | := C[3] | .239 | .335 | .0** | .316 |
| Ec --> | PMA[W] | := C[4] | .463 | .436 | .0** | .485 |
| Ec --> | PMA[R] | := C[5] | .616 | .543 | .0** | .605 |
| Indpendent Environment First-Order Factor Loadings | | | | | | |
| Ei --> | PMA[N] | := E[1] | .024* | .018* | .0** | .193 |
| Ei --> | PMA[V] | := E[2] | .299 | .300 | .0** | .237 |
| Ei --> | PMA[S] | := E[3] | .043* | .025* | .0** | .118 |
| Ei --> | PMA[W] | := E[4] | .244 | .218 | .0** | .181 |
| Ei --> | PMA[R] | := E[5] | .277 | .265 | .0** | .223 |
| Psychometric First-Order Factor Loadings | | | | | | |
| F --> | PMA[N] | := L[1] | .0** | .0** | .699 | |
| F --> | PMA[V] | := L[2] | .0** | .0** | .857 | |
| F --> | PMA[S] | := L[3] | .0** | .0** | .427 | |
| F --> | PMA[W] | := L[4] | .0** | .0** | .656 | |
| F --> | PMA[R] | := L[5] | .0** | .0** | .819 | |
| Psychometric Second-Order Factor Loadings | | | | | | |
| Ga[1] --> | F[1] | := M[1,4] | 1.0** | 1.0** | .614 | |
| Ec[1] --> | F[1] | := M[1,5] | .0** | .0** | .739 | |
| Ei[1] --> | F[1] | := M[1,6] | .0** | .0** | .276** | |
| Ec[2] --> | F[2] | := M[2,8] | 1.0** | .704 | .0** | |
| Ei[3] --> | F[3] | := M[2,12] | 1.0** | 1.0** | .0** | |
| Goodness of Fit Indices | | | | | | |
| Likelihood Ratio [DF] | | | 33 [30] | 52 [34] | 72 [38] | |
| Residual Z Statistic | | | .46 | 1.96 | 3.18 | |

Notes:

(1) Scores on all Primary Mental Abilities obtained from the five PMA covariance matrices listed by Loehlin & Vandenberg (1968), with matrix error corrected;
(2) "MLE" = Maximum Likelihood Estimate and "SE" = Standard Error;
(3) All symmetric coefficients fixed at value determined by biometric model;
(4) Single asterisk denotes a parameter which is not greater than twice its standard error (i.e., P/SE[P] < 2.00);
(5) Double asterisks denotes a parameter which has been "fixed" at a value;
(6) LRC = Likelihood Ratio Test Statistic ["LISREL Chi-Square" Value]; Z = {[LRT/Df]**(1/2) − [1−[2/9]/Df]**(1/3)} = Null Model Normal Z-score (Horn & McArdle, 1980).

from psychometric theory, and the MLE for this restricted model are presented in the fourth column in Table [5].

The usual requirements of latent variable scaling apply to both first- and second-order factors for Model 3, and there are many ways to achieve this result (see [5.3]; Appendix). In standardized form, the MLE loadings $L = \{ .699, .857, .427, .656, .819 \}$ are relatively large, so we interpret $F$ as a common factor of all PMA subtests except spatial (S) ability. Simultaneously, the biometric decomposition of this single-factor score $F$ yields MLE for $B = \{ .614, .739, .276 \}$. The biometric proportion of variance can be calculated as $B^2 = \{.377, .546, .076\}$. These biometric results are common to all five measures and demonstrate a major effect of shared environments *E*c and additive genetic effects *G*a and only a minor effect of independent environments *E*i. In this psychometric factors model, the common factor score $F$ is a perfectly reliable variable; thus, in some contexts, these effects may be called the *reliable biometric effects*.

This analysis leads to a reasonable question: How do the biometric estimates for the latent variable correspond to simpler models, such as an unweighted linear combination of the manifest $Z$ scores or a weighted principal-components score? In these data we have found that the latent variable parameters do not dramatically differ among these models. Nevertheless, the psychometric factors model is consistent with contemporary latent variable path analysis (McDonald, 1985; Loehlin, 1987). We usually assume that variables are measured with error or specificity, so the univariate estimation of $ee'$ is always an overestimate of the variance of independent environments *E*i. Even in the rare case where all loadings $L[j]$ are equal, the ratio of $hh'$ to $cc'$ could be estimated without bias but the $ee'$ would still be overestimated. The prior calculation of sum scores, component scores, or even factor scores can eliminate some unwanted variance due to errors of measurement. These psychometric calculations are not based on any biometric model. In contrast, the latent variable factor loadings $L[j]$ above are the most likely loadings given all other biometric equations, and simultaneously, the biometric effects $b$ are the most likely effects given the psychometric equations. This psychometric approach also leads to several interesting structural hypotheses that cannot be reliably tested with a single univariate score (see the next section).

Multivariate differences between the biometric and the psychometric organizations can be seen in the parameter estimates listed in Tables [5] and [6]. The effect of adding the biometric constraints can be seen by a direct comparison of the second and third columns in Table [5]; the last column lists the psychometric model predictions. Here, for example, the parameter for the common *G*a effect on PMA[$N$] is .429. This comes from $L[i]*B[j] = .614*.699$. This estimate can be compared to the corresponding estimate of .758 from the biometric-factors model (column 2). Note that the largest psychometric factor loading for

Ga is PMA[V] = (.526), but the corresponding loading is relatively small (.348) in the biometric-factor model.

In Table [6] we present a comparative display of the proportions of manifest variable variance attributed to common and unique influences for both models. This standardization of all model components is a by-product of the computer output as long as the three-matrix form is used (see Appendix; McArdle *et al.*, 1980; cf. Boomsma and Molenaar, 1986). In Table [6] we list the common proportions separately, accumulated over the specific effects for the two main models. Some of these differences are also noteworthy, especially the common genetic contribution to PMA number facility and PMA vocabulary and the decreased specific variance in the biometric model.

The validity of the multivariate model interpretation rests on a comparison of goodness of fit. Here the psychometric "one factor" model fits with LRC = 72 on df = 38 (Z = 3.18), and the genetic one-factor model fits with LRC = 33 on df = 30 (Z = .46), so the difference between them is a difference *d*LRC = 39 on *d*df = 8 (Zd = 4.34). The size of this difference illustrates the potential power to distinguish between these two alternatives. This test of the constraints of Eq. [4.5] seems to show that biometric factors model fits better than the psychometric factors model. Before we rest on this initial conclusion, we consider a few more complex alternatives.

## Ignoring Unique Biometric Structure

In most multivariate analyses the common factors are of primary importance and the unique factors are less essential for interpretation. Of course, the estimation of unique factors makes the common factor approach different from, say, the principal components approach. Also, unique parameters can be statistically related to common factor parameters. As discussed earlier, both the biometric and the psychometric models assume exactly the same unique factor decomposition, so these considerations do not differentiate the models.

These theoretical results lead to a practical device for simplifying multivariate modeling problems. We can rewrite the simultaneous equations in Table [3] or [4] to allow the unique variance to take on any MLE (i.e., a separate estimate in all groups). In either factor model this relaxation of the unique variance structure does not alter the covariance expectation [3.5] or [4.5] and these restrictions lead to considerable simplification of the required programming (because the number of total variables within each group is much smaller; see the Appendix).

In the first set of models in Table [7], we examine the necessity for the biometric structuring of unique factors. The initial model in Table [7] (labeled #0) allows all unique variance terms to be estimated in an unstructured way.

**Table [6]:** Decomposition of Manifest Variable Variance for Common and Unique Biometric Influences for Two Alternative Factor Models of PMA

| | Common Ga | Common Ec | Common Ei | Unique |
|---|---|---|---|---|
| PMA Number Facility | | | | |
| Biometric Factors: | .574 | .169 | .001 | .257 |
| Psychometric Factor: | .184 | .267 | .037 | .512 |
| Difference: | .390 | −.098 | −.036 | −.255 |
| PMA Vocabulary | | | | |
| Biometric Factors: | .121 | .612 | .089 | .178 |
| Psychometric Factor: | .277 | .401 | .056 | .266 |
| Difference: | −.156 | .211 | .033 | −.088 |
| PMA Spatial Relations | | | | |
| Biometric Factors: | .189 | .058 | .002 | .757 |
| Psychometric Factor: | .067 | .100 | .014 | .817 |
| Difference: | .122 | −.042 | −.012 | −.060 |
| PMA Word Fluency | | | | |
| Biometric Factors: | .146 | .214 | .060 | .580 |
| Psychometric Factor: | .162 | .235 | .033 | .570 |
| Difference: | −.016 | −.021 | .027 | .010 |
| PMA Reasoning | | | | |
| Biometric Factors: | .179 | .380 | .077 | .365 |
| Psychometric Factor: | .253 | .367 | .051 | .329 |
| Difference: | −.074 | .013 | .026 | .036 |

Notes:
(1) All percentages are MLE from squared parameter estimates of Table [6].
(2) Composite Standard Error and Confidence Boundaries can be obtained from MLE and Information Matrix elements.

This model is typically labeled the "null" or "zero-factors" model because all variances are free but all covariances are restricted to be zero. The fit of this model is indexed by an LRC = 588 on df = 40 ($Z = 19.5$) which is large. Obviously this model does not fit, but it can be used as a baseline for judging the need for more complex structure in the covariances.

The next model, labeled #O + U, adds the three-parameter restrictive biometric structure to each of the unique variances. The absolute fit of this model is indexed in Table [7.1] by a $Z = 19.4$, and the loss due to structuring unique variance is indexed in Table [7.2] by a $Zd = .51$. The same approach is used with models labeled #B1 + U and #P1 + U. The unique components are left unstructured and then structured and the differences in fit examined in Table [7.2]. In general, we conclude that the unique variances can be structured by biometric restrictions without any loss of fit so this substructure is not essential to our further model comparisons.

## Single-Factor Alternatives

The models in Table [7] listed as #B1 and #P1 all represent single-common factor alternatives. The set of models labeled #B1 has a biometric factors interpretation and fits the PMA data exceedingly well. The difference models in Table [7.2] show that the genetical covariance model substantially improves the fit of the model ($Zd = 19.8$), and the addition of the biometric constraints ($Zd = 3.12$) is not as serious a loss of goodness of fit. From a mathematical point of view, this full biometric model #B1 or #B1 + U may be an "over-parameterized" structure and the simpler #B1 + B model (i.e., with $H[m] = b^*S[m]$) fits these data very well. (cf. Martin and Eaves, 1977; and see column 3, Table [5], here).

The models labeled #P are based on the psychometric factors models. The first model, #PO, fits a single-factor model with an invariant factor pattern but no biometric constraints. The goodness-of-fit values detect some departure from fit ($Z = 3.32$), but one common factor is a dramatic improvement over no factors at all (#0, $Zd = 18.3$), and the additional biometric constraints are acceptable (#P1, $Zd = .47$). The difference in fit between biometric model #B1 and psychometric model #P1 is indexed by a $Zd = 4.25$. But once again, the biometric-factor model is a considerably complex set of model parameters, so we continue to ask the question, Are the psychometric constraints acceptable?

The next single-factor models test various hypotheses about the equality of the common biometric effects on the common factor $F$. The direct comparison of model #P1 to model #PE yields a test of "Are the biometric effects on the factor of equal size?" and the results show $Zd = 6.71$. These comparisons illustrate the statistical flexibility of this approach but also point out the complexities

**Table [7]:** Goodness-of-Fit Indices for A Selected Set of Alternative Multivariate Genetic Models to Primary Mental Abilities Twin Data

[7.1]: Absolute Goodness-of-Fit Indices for Alternative Factor Models of the PMA

| Model and Parameter Description | | | | | Goodness-of-Fit Indices | | |
|---|---|---|---|---|---|---|---|
| | Psychometric Factors | Biometric Factors | Common Effects | Unique Effects | Df | LRT | Z |
| #0 | := None | None | None | Free | 40 | 588 | 19.5 |
| #0+U | := None | None | None | h, c, e | 45 | 594 | 19.4 |
| #B1 | := None | One | H, C, E | Free | 25 | 29 | .63 |
| #B1+U | := None | One | H, C, E | h, c, e | 30 | 33 | .46 |
| #B1+B | := None | One | H=bC, E | h, c, e | 34 | 52 | 1.96 |
| #B1−E | := None | One | H, C, E=0 | Free | 30 | 85 | 4.91 |
| #B2 | := None | Two [Ortho] | H, C, E | Free | 13 | 14 | .32 |
| #P0 | := One | None | Free | Free | 32 | 66 | 3.25 |
| #P1 | := One | None | H, C, E | Free | 33 | 67 | 3.33 |
| #P1+U | := One | None | H, C, E | h, c, e | 38 | 72 | 3.18 |
| #P1−E | := One | None | H, C, E=0 | Free | 34 | 96 | 5.19 |
| #PE | := One | None | H=C=E | Free | 35 | 128 | 6.87 |
| #PE+U | := One | None | H=C=E | h, c, e | 40 | 132 | 6.63 |
| #P2+O | := Two [Ortho] | None | H, C, E | Free | 27 | 35 | 1.08 |
| #P2+C | := Two [Oblique] | None | H, C, E | Free | 26 | 31 | .75 |
| #P2+S | := Two [Simple] | None | H, C, E | Free | 28 | 34 | .84 |

[7.2]: Relative Goodness-of-Fit for Difference Comparisons among Alternative Models

| Comparison | | Key Structural Hypothesis | Difference-of-Fit Indices dDf | dLRT | Zd |
|---|---|---|---|---|---|
| #0 | vs #0+U := | Can unique or variances be structured? | 5 | 6 | .51 |
| #B1 | vs #B1+U := | [same] | 5 | 4 | .56 |
| #P1 | vs #P1+U := | [same] | 5 | 5 | .21 |
| #PE | vs #PE+U := | [same] | 5 | 5 | .21 |
| #B1 | vs #0 := | Is biometric factor model unnecessary? | 15 | 588 | 19.8 |
| #B1+U | vs #B1+B := | Are H=bS model constraints acceptable? | 4 | 19 | 3.12 |
| #B1-E | vs #B1 := | Is the independent environment common? | 5 | 56 | 6.08 |
| #PO | vs #0 := | Is psychometric factor unnecessary? | 8 | 522 | 18.3 |
| #P1 | vs #P0 := | Are biometric constraints on factor OK? | 1 | 1 | .47 |
| #P1 | vs #B1 := | Are psychometric constraints acceptable? | 8 | 38 | 4.25 |
| #PE | vs #P1 := | Are biometric effects on factors equal? | 2 | 61 | 6.71 |
| #P1-E | vs #P1 := | Is independent environment effect common? | 1 | 29 | 4.87 |
| #P1 | vs #P2 := | Is second biometric factor unneccessary? | 12 | 15 | .70 |
| #P1 | vs #P2+0 := | Is second orthogonal factor unneccessary? | 6 | 21 | 2.89 |
| #P1 | vs #P2+C := | Is second oblique factor unnecessary? | 7 | 36 | 4.25 |
| #P2+0 | vs #P2+C := | Are the oblique relatinos unnecessary? | 1 | 4 | 1.72 |
| #P2+S | vs #P2+C := | Is the simple factor pattern acceptable? | 2 | 3 | .77 |

of inferential statistical testing in models. In general, these differences are not large and we may need external substantive criteria to make a clear choice.

In two final single-factor models, #B1-E and #P1-E, we test the hypothesis that no $E$ effect at the factor level is needed. These models offer a direct test of the hypothesis of "Are common independent environmental effects needed?" In both cases the model with $E=0$ fits the data rather poorly ($Z=4.91$ and $Z=5.19$). We conclude that there should be an environmental effect common to the PMA subtests which is not shared by cotwins.

More importantly, the last two models offer a potentially informative way to separate independence from unreliability using multivariate measures. In theory, the unique factor effects $E[m]$ are confounded with both independent environmental effects and random error or unreliability, but, because the common factor $F$ is a purely psychometric construct with only reliable variance, the common factor effect $E$ contains only pure independent environmental effects. Likewise, in the biometric-factors model the $Ei$ factor reflects only the common components so the model does account for unreliable variation. Either multivariate approach allows the hypothesis testing of a concept that is not usually tested at the univariate level and is of substantive interest to behavioral geneticists (Plomin and Daniels, 1987; cf. McArdle and Gottesman, 1987).

## Multiple Factor Model Identification

We have treated the biometric factors model and the psychometric factor model as special kinds of "one factor" models. However, as is obvious from Table [3], the biometric factors model has three orthogonal factors that combine to produce the manifest observations, whereas the psychometric factor model has only one common factor strategically deployed to account for the same manifest observations. Some aspects of these differences can be clarified by further examination of the mathematical properties of multiple factor solutions.

The common factor model [3] is frequently written to include multiple common factors. For example, we may wish to assume two common factors $F[1]$ and $F[2]$. In this two-factor model we usually retain scale constraints and orthogonality between common and unique factors, but we also allow a covariation $Q$ between the two factor scores. The model expectations for the covariances among $m=1$ to $M$ measures again follows directly. The traditional variance and covariance expectations show how the increasing complexity of the model structure reflects an increasing complexity of the sources of variance.

These results also lead to an increasing complexity in the independent estimation of parameters for both the common factor loadings $L[m]$ and the unique loadings $u[m]$. The identification constraints required in the multiple-factor model are complex but the general results on factor identification for the $K$-factor model can be summarized simply: in most cases, $K*K$ fixed parameters

are required to estimate the remaining values in matrices $L$ and $Q$. The scaling restriction of unit variance used above places $K$ constraints on the model so only $K*(K\text{-}1)$ additional restrictions are required.

In the oblique models, a correlation $Q$ among the factors is estimated, and there is one fixed zero loading for each of the two factors scores. These oblique models differ from the orthogonal models only in the location of the required $K*(K\text{-}1)$ constraints. The main problem with any final choice between the orthogonal and the oblique models is that they can produce the same expectations about the covariances. That is, even though the parameters are all uniquely identifiable, the model structure can be rotated without loss of fit.

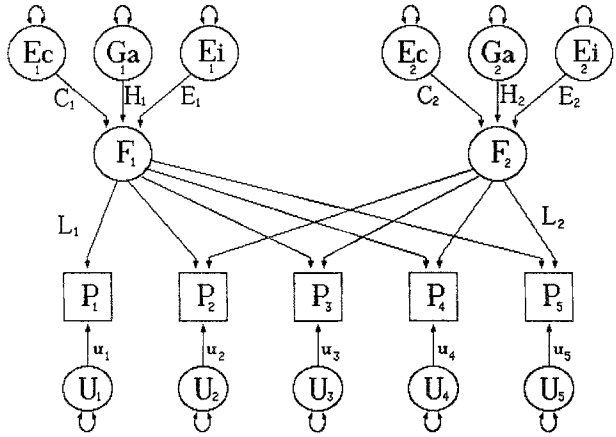
This leaves us with the fundamental question of factor rotation—What is the best way to deploy the remaining $K*(K\text{-}1)$ required restrictions? There is no single mathematical criterion for model simplicity that is uniformly palatable. In the typical application, the final choice between these models rests on substantive and practical considerations. To describe some of these multiple factor alternatives, we use the new path diagrams in Fig. 3 and the new parameter estimates in Table [8]. As we now demonstrate, novel options obtain with some multiple-group structural equation models.

## Exactly Identified (Exploratory) Alternatives

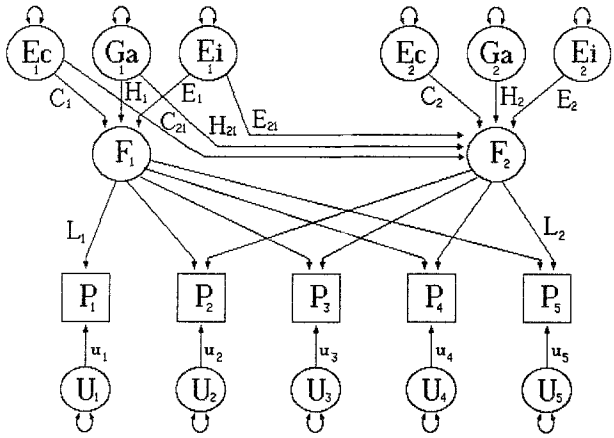
One resolution to the identification problem to use the "orthogonal" factor restrictions. This rotation of the parameter space essentially forces the correlation among the factors to be zero ($Q=0$) and also fixes one of the loadings on the second factor to be zero (i.e., a triangular restriction). In this case, the first orthogonal factor scores are interpretable as a common general to all variables. The second common factor is general to all variables except the variable with the loading forced to be zero.

Referring to Table [7], the model labeled #B2 starts with the biometric-factors model of Martin and Eaves (1977) and adds a second orthogonal factor to each component. The first factors were identified as in #B1, and the second factors were identified by imposing orthogonal restrictions on each factor and forcing one of the loadings in the second factor to be zero. This results in a six common factor orthogonal model. The results yield a $Z=.32$ for the overall fit and a $Zd=.70$ (not shown in Table [7])] for the improvement over the one-factor model. The addition of a second component for each source did not improve the fit of the original three common biometric factors model.

The model labeled #P2+0 in Table [7] adds a second orthogonal factor to the psychometric model. This model has two psychometric factors, which in turn have orthogonal biometric components. This model was identified by forcing one zero loading for the spatial PMA[*s*] subtest (in the second column of the factor pattern) and by having each factor identified by the fixed loading in




[3.1]: An Orthogonal Factors Influence Model

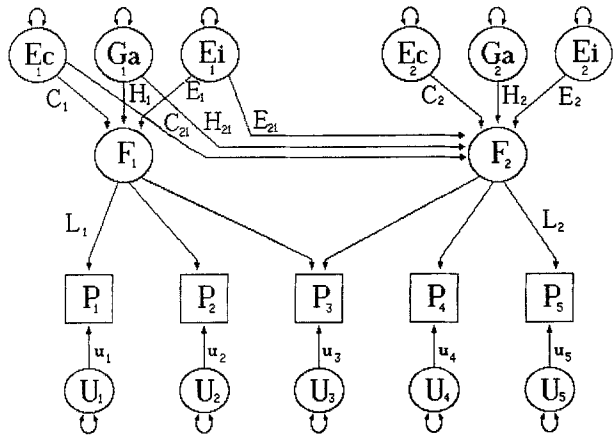



[3.2]: An Oblique Factors with Common Influence Model

**Fig. 3.** Multiple-factor psychometric and biometric alternatives.

the respective *Ei*[1] and *Ei*[2] loadings *E*[1] and *E*[2]. The results of this model show a good overall fit $Z = 1.08$ and a potential improvement over the one-factor model with $Zd = 2.89$.

The MLE for this psychometric model #P2+O are listed in the second column in Table [8]. These results show the same general factor plus a second factor which is neither Spatial (which was fixed at zero) or Number (which was




[3.3]: A Restrictetd Oblique Factors Model

**Fig. 3.** Continued.

estimated at approximately zero). The biometric components of these factors seem to have different patterns: the source of the first factor is now largely *Ga*, whereas the second factor has no *Ga* effects. This psychometric model, although restricted by the position of the zero loading, allowed the emergence of a simple patterning of the biometric components.

Next in Tables [7] and [8] are the familiar oblique psychometric factor models. Although there are many ways to allow factor correlations in these models, we assume a structure that allows separate biometric components for each of two factors, and where the biometric components of the first factor, *Ga*[1], *Ec*[1], and *Ei*[1] are used as a source of both psychometric factors *F*[1] and *F*[2]. A path diagram of this model is provided in Fig. [3.2]. This oblique and invariant model: (1) allows correlations among *F*[1] and *F*[2], (2) provides a test of the utility of the previous orthogonal restrictions, (3) restricts the correlations in a mathematically useful way (i.e., to positive semidefinite form), and (4) restricts the covariance structure in a biometrically informative way.

The practical implication of this last-mentioned property (4) is that we can depict two factor models wherein the genetic and environmental sources of variation on one factor exert an influence on the other factor. These effects contrast with a model where latent variables of one factor merely correlate with latent variables of the other factor. Such directed influences are implied in most longitudinal biometric designs (Loehlin, 1979; McArdle, *et al.*, 1980; Goldsmith, 1984) and in theoretical relationships [such as that between fluid and crystallized intelligence (McArdle *et al.*, 1981)].

**Table [8]:** Multivariate Estimates for "Two Factor" Psychometric PMA Alternatives

| | | | Alternative Factor Models | | | |
|---|---|---|---|---|---|---|
| | | | Orthogonal | Oblique | Simple-I | Simple-II |
| First-Order Factor 1 Loadings | | | | | | |
| F[1] | -->PMA[N] | := L[1,1] | .901 | 1.100* | 1.470 | .858* |
| F[1] | -->PMA[V] | := L[2,1] | .698 | .0 ** | .0 ** | .0 ** |
| F[1] | -->PMA[S] | := L[3,1] | .480 | .479* | .437 | .500* |
| F[1] | -->PMA[W] | := L[4,1] | .551 | .189* | .0 ** | .0 ** |
| F[1] | -->PMA[R] | := L[5,1] | .680 | .209* | .807 | .101* |
| First-Order Factor 2 Loadings | | | | | | |
| F[2] | -->PMA[N] | := L[1,2] | −.083* | −.251* | −.744 | .0** |
| F[2] | -->PMA[V] | := L[2,2] | .556 | .901 | .891 | .875 |
| F[2] | -->PMA[S] | := L[3,2] | .0** | .0** | .0** | .0** |
| F[2] | -->PMA[W] | := L[4,2] | .333 | .479 | .646 | .653 |
| F[2] | -->PMA[R] | := L[5,2] | .680 | .612 | .0** | .726 |
| Second-Order Factor 1 Loadings | | | | | | |
| Ga[1] | -->F[1] | := M[1,4] | .738 | .409 | .533 | .461 |
| Ec[1] | -->F[1] | := M[1,5] | .652 | .816 | .769 | .803 |
| Ei[1] | -->F[1] | := M[1,6] | .171** | .258** | .249** | .248** |
| Second-Order Factor 2 Specific Loadings | | | | | | |
| Ga[2] | -->F[2] | := M[2,7] | .002 | .181* | .0* | .140* |
| Ec[2] | -->F[2] | := M[2,8] | .848 | .002* | .0* | .004* |
| Ei[2] | -->F[2] | := M[2,9] | .530** | .258** | .249** | .248** |
| Second-Order Factor 2 Common Loadings | | | | | | |
| Ga[1] | -->F[2] | := M[2,4] | .0** | .828* | .662 | .881* |
| Ec[1] | -->F[2] | := M[2,5] | .0** | .544* | .701* | .469* |
| Ei[1] | -->F[2] | := M[2,6] | .0** | .137 | .249 | .059 |
| Goodness of Fit Indices | | | | | | |
| Likelihood Ratio [DF] | | | 35 [27] | 31 [26] | 34 [28] | 34 [28] |
| Residual Z Statistic | | | 1.08 | .75 | .84 | .84 |

Notes:

(1) Scores on all Primary Mental Abilities obtained from the five PMA covariance matrices listed by Loehlin & Vandenberg (1968), with matrix errors corrected;
(2) "MLE" = Maximum Likelihood Estimate and "SE" = Standard Error;
(3) All symmetric coefficients fixed at value determined by biometric model;
(4) Single asterisk denotes a parameter that is not greater than twice its standard error (i.e., P/SE[P] < 2.00);
(5) Double asterisks denote a parameter that has been "fixed" at a value;
(6) LRC = Likelihood Ratio Test Statistic ["LISREL Chi-Square" Value]; Z = {[LRT/Df]**(1/2) − {1 − [2/9]/Df]} / {[[2/9]/Df]**(1/3)} = Null Model Normal Z-score (Horn & McArdle, 1980).

The empirical results for this oblique model are presented as model #P2 + C in Table [7] and in the third column in Table [8]. The model is identified by forcing one zero loading in each column of the factor pattern matrix. In this example the factor $F[1]$ was identified as "Not Vocabulary" and the factor $F[2]$ was identified as "Not Spatial." The MLE show poor overall behavior, as seen in the mixed loadings on Number.

We think it is useful to examine model features at the level of the latent biometric factors. For example, the common environmental effect *E*s is the strongest input to the first Not Vocabulary factor ($E[1,1] = .816$), with the additive genetic (*G*a) input being moderate. On the other hand, the *G*a effect common to the first and second psychometric factors contributes strongly to variation in the second Not Spatial factor ($H[2,1] = .828$). Of the three modestly sized biometric inputs to residual variation in the second factor, the effect of the specific environmental factor *E*i is greatest ($E[2,2] = .258$). If we overlook the instability of these factor loadings, the model yields a very differentiated mapping of genetic and environmental influences on latent psychometric factors. Also, this oblique model fits very well ($Z = .75$) and represents a clear improvement over the orthogonal case ($Zd = 4.25$).

## Overidentified (Confirmatory) Alternatives

We do not pursue the exactly identified models in further detail because these rotation problems lead us to the use of the third and final model in Fig. [3.3]—the "confirmatory" or "restricted" factor model. Here the oblique model is used as a starting point and many additional factor loadings are set equal to zero. This model offers the most power when these strong restrictions are made by an *a priori* hypothesis. This confirmatory approach leads to "overidentified" parameter estimates, less rotational indeterminacy, and numerous degrees of freedom to test the basic model hypothesis. More complex cases have been dealt with in the literature (Jöreskog and Sörbom, 1979; McDonald, 1985).

The last model, #P2-S, in Table [7] gives the fits obtained when a Thurstone (1947) "simple structure"-based approach is required of the psychometric factors. In this example we have forced two more loadings to be zero by psychometric hypothesis. The fourth column in Table [8] shows that this model is restricted so the factor $F[1]$ has zero loadings on Vocabulary and Word Fluency, while the second factor $F[2]$ has zero loadings on both Spatial and Reasoning. The model fit is certainly acceptable ($Z = .84$), and the loss due to the added zero restriction is trivial ($Zd = .77$).

This pattern is an elementary way to represent a biometric basis for the theory of "fluid and crystallized intelligence" (Cattell, 1982; Horn, 1986; Loehlin and Vandenberg, 1968; McArdle *et al.*, 1981). The interpretation of the MLE factor loadings would lead us to define factor $F[1] = Gf$ (fluid) and factor

$F[2] = Gc$ (crystallized), except for the odd behavior of the PMA Number measure. The biometric component estimates suggest that the small independent environment $Ei$ component is the only specific component of the $Gc$ factor not already accounted for by $Gf$.

The last model, labeled "Simple-II," uses the same basic model but forces the Number variable to be aligned with one factor $F[1]$. The fit of this model is necessarily the same and the behavior of the MLE improves, but large standard errors suggest this alternative rotation is actually much worse. For these reasons, we think the model labeled "Simple-I" is the best restricted psychometric model for these data.

## Statistical Model Comparisons

In any structural modeling experiment we need to address the question of goodness of fit of alternative models. In a mathematical sense our two main models are nested, so we can prescribe statistical rules to describe the degree to which the two models fit the same manifest covariances. If we proceed to define *a priori* significance levels, we can rigorously test the null hypothesis (*Ho*) of the adequacy of any model subset against the alternative (*Ha*) of any model superset. Unfortunately, the traditional LRC model comparison logic is limited in many ways, and we typically use other less formal devices to judge the key differences between alternatives (Jöreskog, 1969, p. 201; McDonald, 1985, p. 55; Loehlin, 1987, pp. 215–216).

In Fig. 4 we have plotted the LRC as a function of the DF for most of the models presented earlier. To distinguish the two approaches, biometric model fits are listed with an x, whereas psychometric model fits are listed with an ○. We have also fitted a regression line to these indices where $LRC[\#] = B * DF[\#]$ for all models (except the null models) so the resulting $B = 2.08$ reflects the empirical LRC penalty for each DF (McArdle, 1988). Models below the line are good in the sense of giving a good fit for each DF, whereas models above the line give a bad fit. The model labeled #B1 + U is farthest below this line, so this is the best-fitting model. This model was also chosen by Martin and Eaves (1977) using rigid statistical criteria.

But Fig. 4 also shows that the model #B1 + U is not much better than several others. For example, the psychometric model #P2 + S has a similar benefit in LRC given its DF, so it may be a reasonable choice as well. The overview in Fig 4 is important because the psychometric model #P2 + S has two common factors, all biometric influences, and no uniqueness structure. This means that psychometric factor model #P2 + S *is not nested* within biometric-factor model #B1 + U. These results are limited to the narrow subspace defined by models fitted, but other models and indices demonstrate similar comparisons.

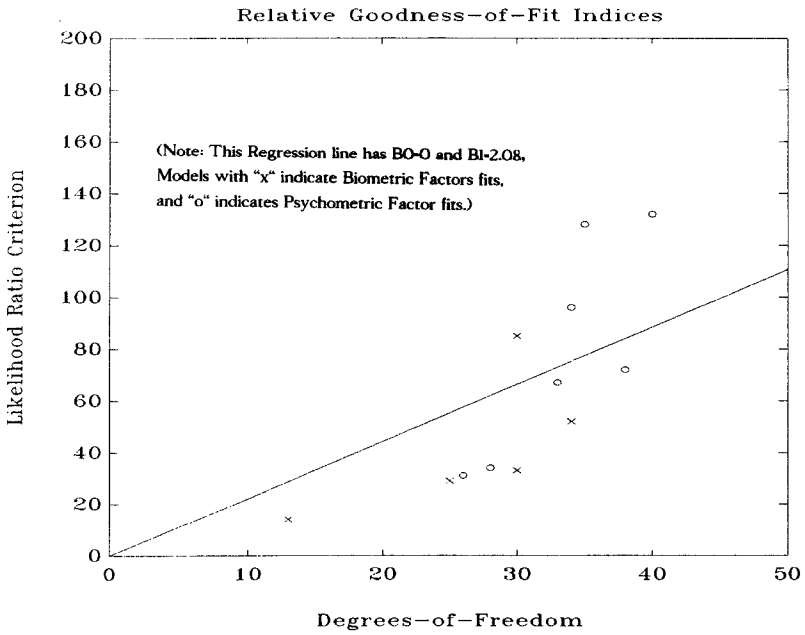



**Fig. 4.** The relative goodness of fit of various multivariate PMA models.

From these results we conclude that the fit of the one factor biometric and the two factor psychometric models are indistinguishable.

## DISCUSSION: MERGING PSYCHOMETRIC AND BIOMETRICS

In this paper we compared some structural models for multivariate twin data. In doing so we reexamined aspects of a traditional biometric factors model (e.g., Martin and Eaves, 1977) and elaborated a different psychometric factors model (e.g., McArdle *et al.*, 1980). In our alternative model we directed the investigator's attention to genetic and environmental influences on a common factor derived from the observed measures. We also extended this model to include multiple factors.

### Methodological Issues

The consumer of these models may wish for a nontechnical, even somewhat intuitive, treatment of the relative virtues of each model alternative. Figure 2 is probably the most direct or clearest comparison we can make. The first differ-

ence that strikes the eye is that the psychometric factors model contains a latent factor, $F$, that is assumed to produce the phenotypic manifestations. Multiple latent variables, $F[1]$ and $F[2]$, represent realistic organizational principles that are common and useful. If one is interesting in drawing inferences about such latent factors per se, our psychometric approach seems preferable. This may not always be the case.

Our figures also readily show benefits of the biometric factors model. This model allows a more differentiated view of genetic covariation. A pattern of loadings of each manifest variable on the genetic factor is obtained, in comparison to the one genetic loading in our one factor model. Thus, the degree of attractiveness of the notion of a "genetic" factor might influence choice of models. The notion of a psychometric factor, as in our model, needs little discussion.

A second difference between these models comes because the psychometric factors model specifies fewer parameters for comparable models (e.g., #B1 vs. #P1, #B2 vs. #P2 + 0). In this sense, the psychometric factors model is more parsimonious. Parsimony is a traditional philosophical criterion for evaluating models, and it has often been relied upon in biometrics, so it is relevant here. The main differences arise because the biometric factors model assumes a proportionality of pattern but orthogonal scores, whereas we assume proportionality of pattern and identity of scores. To wit, the one factor version of the biometric factors model actually includes three different factors, whereas the one factor version of the psychometric factors model has only one common factor. The greater parsimony entails more restrictions so psychometric factors are a testable alternative to biometric factors.

The alternative biometric and psychometric factors models have similar mathematical and statistical properties. Both multivariate models have advantages over the more traditional univariate models because they allow the examination of reliable covariation and the direct examination of hypotheses about independent environments $E$i. There are other advantages over univariate models as well.

The main differences arise because these two models represent restricted variations on particular first order and second order loading matrices. These may be considered by some to be subtle variations but they can be substantively important. In some cases the biometric structuring of individual differences can help the psychometrist define the important factors of interest, and this leads to devices for testing biometric ideas. We may, for example, desire factors to have "simple structure" in the biometric patterns, or more generally, we may desire factors that have "invariance over groups" in the biometric patterns. The two mathematical models emphasized here may be considered as extreme cases in the rotation of second order factors. In other substantive problems, alternative theoretical rotations may be more meaningful.

## Substantive Results

There are several conceptual differences in interpretation of our psychometric factors and those in the purely biometric case. For example, in our psychometric factors model the pattern of factor loadings can be said to be "pulled" toward values that allow the model organization of the genetic and environmental paths to fit as well as possible. In contrast, a single factor model with no biometric structuring has a different fitting function and, hence, a potentially different set of factor loadings. It follows that the numerical results of different latent factor organizations can be substantially different.

The empirical results of our PMA analyses offer only a limited view of these issues. We limited this investigation by starting with only five manifest variables. No doubt these five subscales are reliable indicators of primary abilities, but they may not provide the broad measurement basis needed for testing higher order hypotheses. Nevertheless, these illustrations suggested a psychometric model with two oblique measurement factors and second order biometric factors that fit about as well as the biometric model with three orthogonal biometric factors. The two psychometric factors obtained are highly correlated and some estimates are ill defined. Nevertheless, substantive interpretations can be easily described:

> The results of the present investigation also bear some relevance to Cattell's hypothesis of two kinds of intelligence, "fluid" and "crystallized" (Cattell, 1943, 1963). This hypothesis holds that two "general intelligence" factors exist, strongly correlated but functionally distinct, the one reflecting innate ability, the other the effects of educational and cultural processes. These factors are said to be best measured by nonverbal and verbal tests, respectively. In some ways the present study offers more direct support for such a notion than the data that Cattell himself presents, although it should be noted that the hereditary factor in this study is a quite general one, and by no means represented only or chiefly in nonverbal tests. (Loehlin and Vandenburg, 1968, p. 276)

In the original statements of *Gf*/*Gc* theory, *Gf* abilities, reflecting thinking, reasoning, and neurological efficiency, were assumed to be highly heritable. In contrast, *Gc* abilities, reflecting knowledge, learning, and acculturation, were considered less heritable. Our current results show that both *Gf* and *Gc* abilities have substantial heritability. These results are consistent with most recent theoretical and substantive treatments of this issue (Cattell, 1982; Horn, 1986; McArdle *et al.*, 1981). These limited empirical results also give direct evidence for the earlier implications of Loehlin and Vandenberg (1968) (also Goldberger, 1977; Royce, 1979; and others).

## Modeling Extensions

There are many other extensions of the psychometric factors model. In our initial presentation with twin data on childhood temperament, we proposed that

latent psychological constructs be derived in the same procedure in which genetic and environmental parameters were estimated, and we decomposed latent longitudinal paths biometically (McArdle *et al.*, 1980; see Goldsmith, 1984, p. 407). Next we applied the model to all 15 PMA subtests and demonstrated how the genetic and environmental paths could be estimated for latent psychometric factors of the first and second order (McArdle *et al.*, 1981). In this paper we estimated both biometric factors and psychometric factors models at different levels of measurement within the same model (cf. McArdle and Goldsmith, 1984; Horn, 1986). We also have shown how the basic ideas of the psychometric model organization allow for some dynamic growth models for longitudinal data, and we used this organization to fit twin models to both means and covariances (McArdle, 1986).

We have not dealt here with several issues of practical concern. For example, the efficiency of structural equation specification, the often unwieldy behavior of the numerical fitting algorithms, and the use of formal hypothesis testing. These topics all deserve further consideration. These concerns are even more apparent when working with higher-order latent variable structures, and these issues may be easier to study using algorithms other than LISREL (e.g., Fraser, 1979). We also think our basic model, and our representation of it using LISREL (in the Appendix), can be valuable for further biometric investigations (Carey, 1986; Neale and McArdle, 1990). In any form, formal models help us understand the "hidden" complexity of "simple" correlational approaches (Eaves *et al.*, 1978; McArdle and Gottesman, 1987), and in this sense, further research on structural equation models is a practical necessity for biometrics.

Multivariate structural equation techniques allow us to define latent factors by both psychometric measurement patterns and by biometric patterns. These models allow new combinations of psychometric and biometric principles. Psychological substance or well-defined research goals may formally prescribe one organizing principle over the other. In one experiment the psychometric factors measurement model may be useful, while in another experiment the biometric factors model may be better. We think that a diversity of models is necessary for the long-term fitness of both biometrics and psychometrics.

## ACKNOWLEDGMENTS

This research was initiated in 1979 while both authors were engaged in post-doctoral work at the Psychology Department of the University of Denver. The basic ideas discussed here were originally presented at the *Behavioral Genetics Association Annual Meetings* in 1980, 1981, 1984, and 1986. We thank the editors and reviewers of this paper, Ray Cattell, Jim Connell, John Horn, Carol Prescott, and Steve Vandenberg for their constructive comments on earlier

## APPENDIX

**Table [A1]:** A LISREL-7 Program Input for General Multiple Factors Models

```
Multivariate PMA Data: Simple I Psychometric Factors: Group 1 = MZ Between
DA NG=4 NI=5 NO=123 MA=CM
LA
'mzb-n','mzb-v','mzb-s','mzb-w','mzb-r'
CM SYM
3603.41
1521.73  2047.49
1449.47  712.91  4059.80
 889.60  837.76   304.36  1161.32
1034.20  959.43   453.67   937.22
Model NY=5 NE=13 BE=FU,FI PS=SY,FI LY=IZ TE=ZE
LE
'mzb-Un','mzb-Uv','mzb-Us','mzb-Uw','mzb-Ur'
'F1','F2','Ga-1','Es-1','Ei-1','Ga-2','Es-2','Ei-2'
MA BE[effects-or-arrows]
0 0 0 0 0 1 1 0 0 0 0 0 0
0 0 0 0 0 0 1 0 0 0 0 0 0
0 0 0 0 0 1 0 0 0 0 0 0 0
0 0 0 0 0 0 1 0 0 0 0 0 0
0 0 0 0 0 1 0 0 0 0 0 0 0
0 0 0 0 0 0 0 1 1 1 0 0 0
0 0 0 0 0 0 0 1 1 1 1 1 1
0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0
MA PS[proportions-or-slings]
1
0 1
0 0 1
0 0 0 1
0 0 0 0 1
0 0 0 0 0 0
0 0 0 0 0 0 0
0 0 0 0 0 0 0 1
0 0 0 0 0 0 0 0 1
0 0 0 0 0 0 0 0 0 1
0 0 0 0 0 0 0 0 0 0 1
0 0 0 0 0 0 0 0 0 0 0 1
0 0 0 0 0 0 0 0 0 0 0 0 1
ST 1 AL[simple-structure-first-order-loadings]
FR BE 1 6 BE 3 6 BE 5 6
FR BE 1 7 BE 2 7 BE 4 7
ST 1 AL[identifiable-second-order-loadings]
FR BE 6 9 BE 6 10
FR BE 7 12 BE 7 13
FR BE 7 9 BE 7 10 BE 7 11
ST 1 AL[unstructured-zero-order-uniqueness]
FR PS 1 1 PS 2 2 PS 3 3 PS 4 4 PS 5 5
ST 50 PS 1 1 PS 2 2 PS 3 3 PS 4 4 PS 5 5
ST 1 AL[biometric-second-order-proportions]
ST 1.0 PS 8 8 PS 11 11
ST 2.0 PS 9 9 PS 12 12
ST 1.0 PS 10 10 PS 13 13
OU ND=3 NS TO ALL add=off
```

**Table [A1] (Continued)** A LISREL Program Input for General Multiple Factors Models

```
%%%%% Group 2 = DZB
DA NO=75
LA
'dzb-n','dzb-v','dzb-s','dzb-w','dzb-r'
CM SYM
3942.48
2160.52  2161.06
2248.69  1683.94  4595.79
1282.17  1062.12   877.62  1064.25
1425.28  1199.44  1084.55   682.36  1064.74
MOdel BE=IN PS=PS LY=IZ TE=ZE
LE
'dzb-Un','dzb-Uv','dzb-Us','dzb-Uw','dzb-Ur'
'F1','F2','Ga-1','Es-1','Ei-1','Ga-2','Es-2','Ei-2'
ST 1.5 PS 8 8 PS 11 11
ST 2.0 PS 9 9 PS 12 12
ST 1.0 PS 10 10 PS 13 13
OU
Group 3 = MZW
DA NO=124
LA
'mzw-n','mzw-v','mzw-s','mzw-w','mzw-r'
CM SYM
  372.74
 -1.48  161.25
  1.36   18.13  449.28
 -2.57   58.41   28.26  196.90
 30.04   69.88   13.66   43.60  126.89
Model BE=IN PS=PS LY=IZ TE=ZE
LE
'mzw-Un','mzw-Uv','mzw-Us','mzw-Uw','mzw-Ur'
'F1','F2','Ga-1','Es-1','Ei-1','Ga-2','Es-2','Ei-2'
ST  .0 PS 8 8 PS 11 11
ST  .0 PS 9 9 PS 12 12
ST 1.0 PS 10 10 PS 13 13
OU
Group 4 = DZW
DA NO=76
LA
'dzw-n','dzw-v','dzw-s','dzw-w','dzw-r'
CM SYM
1183.74
 242.25  325.00
 464.66  111.14  1110.50
 307.51  198.69   313.88  478.80
 226.77  132.65   183.25  114.34  177.84
Model BE=IN PS=PS LY=PS TE=ZE
LE
'dzw-Un','dzw-Uv','dzw-Us','dzw-Uw','dzw-Ur'
'F1','F2','Ga-1','Es-1','Ei-1','Ga-2','Es-2','Ei-2'
ST  .5 PS 8 8 PS 11 11
ST  .0 PS 9 9 PS 12 12
ST 1.0 PS 10 10 PS 13 13
OU
```

reports of this research. We especially thank John Loehlin and Nick Martin for their corrections and encouragements.

## REFERENCES

Behrman, J., Taubman, P., and Wales, T. (1977). Controlling for and measuring the effects of genetics and family environment in equations for schooling and labor market success. In Taubman, P. (ed.), *Kinometrics: Determinants of Socioeconomic Success Within and Between Families*, North-Holland, Amsterdam.

Bock, R. D. (1989). *Multilevel Analysis of Educational Data*, Academic Press, San Diego.

Bock, R. D., and Vandenberg, S. G. (1968). Components of heritable variation in mental test scores. In Vandenberg, S. G. (ed.), *Progress in Human Behavior Genetics*, Johns Hopkins Press, Baltimore.

Boomsma, D.I., and Gabrielli, W. F. (1985). Behavioral genetic approaches to psychophysiology data. *Psychophysiology* **22**:249–260.

Boomsma, D. I., and Molenaar, P. C. M. (1986). Using LISREL to analyze genetic and environmental covariance structure. *Behav. Genet.* **16**:237–250.

Cantor, R. M., Nance, W. E., Eaves, L. J., Winter, P. M., and Blanchard, M. M. (1983). Analysis of the covariance structure of digital ridge counts in the offspring of monozygotic twins. *Genetics* **103**:495–512.

Carey, G. (1986). A general multivariate approach to linear modeling in human genetics. *Am. J. Hum. Genet.* **39**:775–786.

Cattell, R. B. (1960). The multiple abstract variance analysis equations and solutions: For nature-nuture research on continuous variables. *Psychol. Rev.* **67**:353–372.

Cattell, R. B. (1982). *The Inheritance of Personality and Ability: Research Methods and Findings*, Academic Press, New York.

Chamberlain, G., and Grilliches, Z. (1977). More on brothers. In Taubman, P. (ed.), *Kinometrics: Determinants of Socioeconomic Success Within and Between Families*, North-Holland, Amsterdam.

Crawford, C. B., and DeFries, J. C. (1978). Factor analysis of genetic and environmental correlation matrices. *Multivar. Behav. Res.* **13**:297–318.

DeFries, J. C. (1979). Comment on Fulker's "Some implications of biometrical genetical analysis for psychological research." In Royce, J. R., and Mos, L. P. (eds.), *Theoretical Advances in Behavior Genetics*, Sijthoff & Noordhoff, Alphen aan den Rijn, The Netherlands, pp. 381–383.

Eaves, L. J., Martin, N. B., and Eysenck, S. B. G. (1977). An application of the analysis of covariance structures to the psychogenetical study of impulsiveness. *Br. J. Math. Stat. Psychol.* **30**:1–42.

Eaves, L. J., Last, K. A., Young, P. A., and Martin, N. G. (1978). Model-fitting approaches to the analysis of human behavior. *Heredity* **41**:249–320.

Fraser, C. (1979). *COSAN User's Guide*, Ontarior Institute for Studies in Education, Toronto (Note: Center for Behavioral Studies, University of New England, Armidale, N.S.W., Australia).

Fulker, D. W. (1978). Multivariate extensions of a biometrical model of twin data. In Nance, W. E., *et al.*, (eds.). *Twin Research: Psychology and Methodology*, Liss, New York, pp. 217–236.

Fulker, D. W. (1979). Some implications of biometrical genetical analysis for psychological research. In Royce, J. R., Mos, L. P. (eds.), *Theoretical Advances in Behavior Genetics*, Sitjhoff & Noordhoff, Alphen aan den Rijn, The Netherlands.

Fulker, D. W., Baker, L. A., and Bock, R. D. (1983). Estimating components of covariance using LISREL. *Data Anal. Commun. Comp. Data Anal.* **14**:261–281.

Goldberger, A. S. (1978). Pitfalls in the resolution of intelligence inheritance. In Morton, N. E., and Chang, C. S. (eds.), *Genetic Epidemiology*, Academic Press, New York, pp. 30–45.

Goldsmith, H. H. (1984). Continuity of personality: A genetic perspective. In Emde, R. M., and Harmon, R. J. (eds.), *Continuities and Discontinuities in Development*, Plenum, New York.

Goldsmith, H. H. (1983). Genetic influences on personality from infancy to adulthood. *Child Dev.* **54**:331–355.

Henderson, N. D. (1982). Human behavior genetics. *Annu. Rev. Psychol.* **33**:403–440.

Horn, J. L. (1986). Intellectual ability concepts. In Sternberg, R. J. (ed.), *Advances in the Psychology of Human Intelligence*, Erlbaum, Hillsdale, N. J.

Horn, J. L., and McArdle, J. J. (1980). Perspectives on mathematical and statistical model building (MASMOB) in aging research. In Poon, L. W. (ed.), *Aging in the 1980s: Contemporary Perspectives*, American Psychological Association, Washington, D.C.

Jaspars, J. M. F., and deLeeuw, J. A. (1980). Genetic-environment covariation in human behaviour genetics. In van der Kamp, L. J. Th., Langerak, W. F., and de Gruijter, D. N. M. (eds.), *Psychometrics for Educational Debates*, Wiley, New York.

Jinks, J. L., and Fulker, D. W. (1970). Comparison of the biometrical genetical, MAVA, and classical approaches to the analysis of human behavior. *Psychol.* Bull. **73**:311–349.

Jöreskog, K. G. (1969). A general approach to confirmatory maximum likelihood factor analysis. *Psychometrika* **34**:183–202.

Jöreskog, K. G. (1970). A general model for the analysis of covariance structures. *Biometrika* **57**:239–251.

Jöreskog, K. G., and Sörbom, D. (1979). In Magidson, J. (ed.), *Advances in Factor Analysis and Structural Equation Models*, Abt Books, Cambridge, Mass.

Kempthorne, O., and Osborne, R. H. (1961). The interpretation of twin data. *Am. J. Hum. Genet.* **13**:320–329.

Lange, K., and Boehnke, M. (1983). Extensions to pedigree analysis. IV. Covariance component models for multivariate traits. *Am. J. Med. Genet.* **14**:513–524.

Loehlin, J. C. (1987). *Latent Variable Models: An Introduction to Factor, Path, and Structural Analysis*, Erlbaum, Hillsdale, N.J.

Loehlin, J. C. (1978). Heredity-environment analyses of Jenck's IQ correlations. *Behav. Genet.* **8**:(5):415–435.

Loehlin, J. C. (1979). Combining data from different groups in human behavior genetics. In Royce, J. R., and Mos, L. P. (eds.), *Theoretical Advances in Behavior Genetics*, Sijthoff & Noordhoff, Germantown, Md.

Loehlin, J. C., and Vandenberg, S. G. (1968). Genetic and environmental components in the covariation of cognitive abilities: An additive model. In Vandenberg, S. G. (ed.), *Progress in Human Behavior Genetics*, Johns Hopkins Press, Baltimore.

Martin, N. G., and Eaves, L. G. (1977). The genetical analysis of covariance structure. *Heredity* **138**:(1):79–95.

Martin, N. G., Eaves, L. J., and Fulker, D. W. (1979). The genetical relationship of impulsiveness and sensation seeking to Eysenck's personality dimensions. *Acta Genet. Med. Gemellol.* **28**:197–210.

Martin, N. G., Jardine, R., and Eaves, L. J. (1984). Is there only one set of genes for different abilities? *Behav. Genet.* **14**:355–370.

Martin, N. G., Boomsma, D. I. and Neale, M. C. (1989). Forward. *Behav. Genet.* **19**:5–7.

McArdle, J. J. (1980). Causal modeling applied to psychonomic systems simulation. *Behav. Res. Methods Instrument.* **12**:193–209.

McArdle, J. J. (1986). Latent growth within behavior genetic models. *Behav. Genet.* **16**:163–200.

McArdle, J. J. (1988). Dynamic but structural equation modeling of repeated measures data. In Nesselroade, J. R., and Cattell, R. B. (eds.), *Handbook of Multivariate Experimental Psychology, Vol. II*, Plenum Press, New York pp. 561–614.

McArdle, J. J. and Boker, S. M. (1990). *RAMpath: Computer software for path diagrams and path analysis*. Denver, CO: Data Transforms.

McArdle, J. J., and Goldsmith, H. H. (1984). Structural equation modeling applied to the twin design: Comparative multivariate models of the WAIS. *Behav. Genet.* **14**:609 (abstract).

McArdle, J. J., Goldsmith, H. H., and Horn, J. L. (1981). Genetic structural equation models of fluid and crystallized intelligence. *Behav. Genet.* **11**:607 (abstract).

McArdle, J. J., and Gottesman, I. I. (1987). Some models where independent ≠ different: A response to Plomin & Daniels. *Behav. Brain Sci.* **10**(1):31–32.

McArdle, J. J., and Horn, J. L. (1990). An effective graphic representation for linear structural equation models. *Multivar. Behav. Res.* (in press).
McArdle, J. J., and McDonald, R. P. (1984). Some algebraic properties of the Reticular Action Model for moment structures. *Br. J. Math. Stat. Psychol.* **37**:234–251.
McArdle, J. J., Connell, J. P., and Goldsmith, H. H. (1980). Structural modeling of stability and genetic influence: Some results from a longitudinal study of behavioral style. *Behav. Genet.* **10**:487.
McDonald, R. P. (1985). *Factor Analysis and Related Methods*, N.J. Erlbaum, Hillsdale.
McDonald, R. P., and Krane, W. R. (1979). A Monte Carlo study of local identifiability and degrees of freedom in the asymptotic likelihood ratio test. *Br. J. Math. Stat. Psychol* **32**:121–132.
Meredith, W. (1968). Factor analysis and the use of inbred strains. In Vandenberg, S. G. (ed.), *Progress in Human Behavior Genetics*, Johns Hopkins Press, Baltimore.
Neale, M. C. and McArdle, J. J. (1990). The analysis of assortative mating: A LISREL model. *Behavior Genetics*, **20**(2):287–293.
Plomin, R., and Daniels, D. (1987) Why are children in the same family so different? *Behav. Brain Sci.* **10**:37.
Roudabush, G. (1968), Analyzing dyadic relationships. In Vandenberg, S. G. (ed.), *Progress in Human Behavior Genetics*, Johns Hopkins Press, Baltimore.
Royce, J. R. (1979). The factor-gene basis of individuality. In Royce, J. R., and Mos, L. P. (eds.), *Theoretical Advances in Behavior Genetics*, Sijthoff & Noordhoff, Alphen aan den Rijn, The Netherlands.
Spearman, D. (1904). General intelligence objectively determined and measured. *Am. J. Psychol.* **15**:201–293.
Tambs, K., Sundet, J. M., and Magnus, P. (1984). Heritability analysis of the WAIS subtests. A study of twins. *Intelligence* **8**:283–293.
Taubman, P. (1978). Determinants of socioeconomic success: Regression and latent variable analysis in samples of twins. In Nance, W. E., *et al*, (eds.), *Twin Research: Psychology and Methodology*, Liss, New York.
Thurstone, L. L. (1947). *Multiple Factor Analysis*, University of Chicago Press, Chicago.
Vandenberg, S. G. (ed.), (1968). *Progress in Human Behavior Genetics: Recent Reports on Genetic Syndromes, Twin Studies, and Statistical Advances,* Johns Hopkins Press, Baltimore.
Wright, S. (1921). Correlation and causation. *J. Agr. Res.* **20**:557–585.
Wright, S. (1982). On "Path analysis in genetic epidemiology: A critique." *Am. J. Hum. Genet.* **35**:757–762.

Edited by N. G. Martin