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LATENT CURVE ANALYSIS

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As a method for representing development, latent trait theory is presented in terms of a statistical model containing individual parameters and a structure on both the first and second moments of the random variables reflecting growth. Maximum likelihood parameter estimates and associated asymptotic tests follow directly. These procedures may be viewed as an alternative to standard repeated measures ANOVA and to first-order auto-regressive methods. As formulated, the model encompasses cohort sequential designs and allow for period or practice effects. A numerical illustration using data initially collected by Nesselroade and Baltes is presented.

Key words: longitudinal analysis, individual growth curves, structural equation modeling.

Introduction

Tucker (1958) developed the idea of determining parameters of a functional relation by factor analysis. Concurrently, Rao (1958) sketched out similar procedures. Scher, Young and Meredith (1960) also have discussed the technique, while Anderson (1963) approached the same problem from a time series perspective. In general, however, these procedures have been rarely used, merit wider recognition by behavioral and biological scientists, and deserve review in the broader context provided by recent research on individual growth curves (Bock & Thissen, 1980; Rogosa, Brandt & Zimowski, 1982; Rogosa & Willett, 1985a) and curves in general (Ramsey, 1982). We will show that such techniques provide generalizations of and alternatives to the usual repeated measures ANOVA procedures or first-order auto-regressive models.

Suppose we are interested in some univariate random variable, $X(t)$, with possible realizations, $x_i(t)$, where i denotes an individual subject or entity in an experiment or study. The random variable, X, and the nonrandom variable, t, may be continuous or discrete. In practice we will always assume t to be discrete and X continuous. We regard $X(t)$ as functionally related to t, where t may, for example, denote time, age, grade, trial number, degree of arousal, experimental condition, test form or stimulus intensity, and might even be unordered and multivariate, as in the dummy coding of unordered experimental conditions.

The realizations, $x_i(t)$, will be assumed decomposable into a sum of elementary (generally unknown) basis functions and error. Explicitly,

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$$x_i(t) = \sum_{k=1}^{r} w_{ik} g_k(t) + e_i(t), \tag{1}$$

where $g_k(t)$ denotes a basis function, implying that every $x_i(t)$ can be expressed, apart from measurement error, as a linear combination of the vector basis furnished by the $g_k(t), k = 1, \ldots, r$. Generally, for basis functions to be useful and interpretable, r must be relatively small. This formulation will be shown to be unlike various Markovian models for growth (see Jöreskog, 1970) in that the increments are not independent. As we will demonstrate in the subsequent development, the functions, $g_k(t)$, can be assumed partially or completely known.

The random variable, $E(t)$, with realizations, $e_i(t)$, is an error of measurement as a function of t, although we may think of it as comprising errors of approximation as well. The additional assumptions we will make, confine $E(t)$ to bring measurement error although in the sequel we will indicate how these assumptions may be relaxed. The random variables, W_k, have realizations, w_{ik}, which are the weights or saliences that characterize the i-th individual and represent the degree to which the i-th subject utilizes the single basis, $g_k(t)$. Thus, the collection of realizations, $\{x_i(t)\}$, for all subjects relate to the common set of basis functions, $\{g_k(t)\}$, with individual differences, represented by the weights, $\{w_{ik}\}$. If w_{ik} were classificatory (i.e., multinomial), then $g_k(t)$ would represent a type of development and w_{ik} would indicate class membership. This sort of model will not be explored in this paper but will be pursued subsequently.

Since continuous observation is impractical or impossible in most situations, we suppose that $X(t)$ is observed at values $t_1, t_2, \ldots, t_p$ of t. If t is inherently discrete, these would be all, or a selection from, the possibly finite or countable infinite set of values of t. If t is continuous, the values $t_1, t_2, \ldots, t_p$ would represent a chosen set of values that span the space of interest. We suppose that all subjects will be observed at all chosen values of t, but the sequel will show how this assumption may be relaxed to some degree.

As notation, let $x_{ij} = x_i(t_j)$, $\gamma_{jk} = g_k(t_j)$, and $e_{ij} = e_i(t_j)$, and define the vectors, $\mathbf{x}_i' = [x_{i1}, x_{i2}, \ldots, x_{ip}]$, $\mathbf{w}_i' = [w_{i1}, w_{i2}, \ldots, w_{ir}]$, and $\mathbf{e}_i' = [e_{i1}, e_{i2}, \ldots, e_{ip}]$ as realizations of the vector-valued random variables $\mathbf{x}$, $\mathbf{w}$, and $\mathbf{e}$, respectively. Further, let Γ be a $p \times r$ matrix whose jk-th element is given by γ_{jk}. Using the foregoing, (1) may be re-expressed as

$$\mathbf{x} = \Gamma \mathbf{w} + \mathbf{e}. \tag{2}$$

Now, if $\mathscr{E}[\mathbf{w}] \equiv \boldsymbol{\nu}$, $\mathscr{E}[\mathbf{ww}'] \equiv \Upsilon$, and $\mathscr{E}[\mathbf{ee}'] \equiv \Psi$, where $\mathscr{E}[\cdot]$ denotes the expectation operator, and assuming $\mathscr{E}[\mathbf{e}] = \mathbf{0}$ and $\mathscr{E}[\mathbf{we}'] = \mathbf{0}$, then

$$\mathscr{E}[\mathbf{x}] \equiv \boldsymbol{\mu} = \Gamma \boldsymbol{\nu} \tag{3}$$

and

$$\mathscr{E}[\mathbf{xx}'] \equiv \Omega = \Gamma \Upsilon \Gamma' + \Psi. \tag{4}$$

If we change the assumption $\mathscr{E}[\mathbf{we}'] = 0$ to independence of $\mathbf{w}$ and $\mathbf{e}$ and assume mutual independence for the components of $\mathbf{e}$ (hence, Ψ is a diagonal matrix), we are essentially interpreting $\Gamma\mathbf{w}$ to be a vector-valued true score for $\mathbf{x}$ (Lord & Novick, 1968). If time is continuous, it is impossible to require that $e_i(t)$ and $e_i(t + s)$ be independent as $s \rightarrow 0$, $s > 0$, but we shall ignore this problem created by independence assumptions. If time is discrete, no inherent difficulty exists insofar as the assumption of independence is concerned. The model we shall generally appeal to throughout this paper will assume mutual independence of the components of $\mathbf{e}$, but it will become clear in the development that some relaxation of this assumption is possible.

The model in (2) has the general factor analytic form. The differences lie in that $\mathscr{E}[\mathbf{x}] \neq \mathbf{0}$ and $\mathscr{E}[\mathbf{w}] \neq \mathbf{0}$, although the usual factor analysis model has been expressed in this fashion (Jöreskog & Sörbom, 1985). If $\Upsilon = \Pi\Pi'$ and $\Theta = \Gamma\Pi$, we can express (4) in terms of orthogonal factors as

$$\Omega = \Theta\Theta' + \Psi \quad \text{and} \quad \Omega - \Psi = \Theta\Theta'. \tag{5}$$

The matrix, Θ, could then be composed of the r eigenvectors of $\Omega - \Psi$ corresponding to the nonzero eigenvalues with rescaling by the square roots of the corresponding eigenvalues.

If $\mathbf{X}$ denotes a $n \times p$ matrix whose rows represent n independent realizations of $\mathbf{x}'$ and $\mathbf{1}$ denotes a column vector of ones, Tucker (1966) suggested that one could factor analyze the sample second moment matrix $\hat{\Omega} = (1/n)\mathbf{X}'\mathbf{X}$ to obtain an estimate $\hat{\Theta}$ of Θ using an Eckart-Young decomposition. Rao (1958) proposed first removing an estimate of the average growth curve, $\hat{\boldsymbol{\mu}}' = (1/n)\mathbf{1}'\mathbf{X}$, and factoring $\hat{\Sigma} = \hat{\Omega} - \hat{\boldsymbol{\mu}}\hat{\boldsymbol{\mu}}'$ by the method of maximum likelihood to estimate Θ. In our notation, the first column of $\hat{\Theta}$ would then be $\hat{\boldsymbol{\mu}}$. Although Rao was not explicit about rotation, Tucker (1966) does suggest rotational criteria and recommends against simple structure in this situation.

Maximum Likelihood Estimation and Hypothesis Testing

In addition to our earlier assumptions (i.e., the representation in (2); independence of $\mathbf{w}$ and $\mathbf{e}$; and the independence of the components of $\mathbf{e}$), joint multivariate normality of $\mathbf{w}$ and $\mathbf{e}$ is imposed, which in turn implies multivariate normality for $\mathbf{x}$. Maximum likelihood estimation and hypothesis testing will then be possible.

Consider the following definitions of partitioned matrices:

$$\mathbf{M} = \begin{bmatrix} \Omega & \boldsymbol{\mu} \\ \boldsymbol{\mu}' & 1 \end{bmatrix}, \tag{6}$$

and

$$\hat{\mathbf{M}} = \begin{bmatrix} \hat{\Omega} & \hat{\boldsymbol{\mu}} \\ \hat{\boldsymbol{\mu}}' & 1 \end{bmatrix}. \tag{7}$$

Using standard theorems on partitioned matrices (Graybill, 1969), where $\Sigma = \Omega - \boldsymbol{\mu}\boldsymbol{\mu}'$, we have

$$|\Sigma| = |\Omega - \boldsymbol{\mu}\boldsymbol{\mu}'| = \begin{vmatrix} \Omega & \boldsymbol{\mu} \\ \boldsymbol{\mu}' & 1 \end{vmatrix} = |\mathbf{M}|. \tag{8}$$

Similarly

$$|\hat{\Sigma}| = |\hat{\mathbf{M}}|, \tag{9}$$

and

$$\operatorname{tr} \mathbf{M}^{-1}\hat{\mathbf{M}} = \operatorname{tr} \Sigma^{-1}\hat{\Sigma} + (\hat{\boldsymbol{\mu}} - \boldsymbol{\mu})'\Sigma^{-1}(\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}) + 1. \tag{10}$$

Consequently, we can write, apart from an additive constant, the logarithm of the likelihood function of $\mathbf{X}$ as

$$\ln L = -\frac{n}{2}\,[\ln |\mathbf{M}| + \mathrm{tr}\,\mathbf{M}^{-1}\hat{\mathbf{M}} - 1]. \tag{11}$$

Using the model provided by (3) and (4), we obtain

$$\mathbf{M} = \Lambda\Phi\Lambda' + \begin{bmatrix} \Psi & \mathbf{0} \\ \mathbf{0}' & 0 \end{bmatrix}, \tag{12}$$

where

$$\Lambda = \begin{bmatrix} \Gamma & \mathbf{0} \\ \mathbf{0}' & 1 \end{bmatrix} \quad \text{and} \quad \Phi = \begin{bmatrix} \Upsilon & \boldsymbol{\nu} \\ \boldsymbol{\nu}' & 1 \end{bmatrix}. \tag{13}$$

The logarithm of the likelihood ratio can be expressed as

$$\ln LR = -\frac{n}{2}\left[\ln \frac{|\mathbf{M}|}{|\hat{\mathbf{M}}|} + \mathrm{tr}\,\mathbf{M}^{-1}\hat{\mathbf{M}} - (p+1)\right], \tag{14}$$

and $-2 \ln LR$ is distributed asymptotically as a chi-square random variable if the model in (12) and (13) allows fewer than $[(p + 2)(p + 1)/2] - 1$ free elements. Estimates of the parameters and a goodness-of-fit test can be obtained by analyzing $\hat{\mathbf{M}}$ as a covariance matrix in any maximum likelihood confirmatory factor analysis program [e.g., LISREL 7 (Jöreskog & Sörbom, 1989), COSAN (McDonald, 1978), or EQS (Bentler, 1989)], identifying some of the elements in Λ and Φ to insure a unique solution, and constraining the matrices as indicated in (12) and (13). Note that the fitting function, (14), is not affected by the -1 in (11) when an identified model derived from (12) and (13) characterize $\mathbf{M}$, although the calculation of the degrees of freedom require care; one more degree of freedom is lost from the value given by such programs if $\mathbf{M}$ is treated as a covariance matrix. We are used to regarding sample means and covariance matrices as independent, but this is not the case for the model in (2).

Beyond identification, which requires specification of at least r^2 elements in Γ, Υ and $\boldsymbol{\nu}$, other constraints could be added. For example, the first column of Γ could be set equal to 1; the second could correspond to $t_1, t_2, \ldots, t_p$; the third to $t_1^2, t_2^2, \ldots, t_p^2$; and so on. Such a specification would force the basis curves to be simple polynomials. We could orthogonalize the completely specified columns of Γ with respect to some $r \times r$ positive definite matrix to facilitate interpretation (e.g., orthogonal polynomials).

Still other models could provide all elements of Γ. In such cases we may regard the procedure proposed as a fixed empirical Bayes procedure in the sense that the moments of $\mathbf{w}$ are estimated under normality assumptions and then empirical Bayes estimates of $\mathbf{w}_i$, given $\mathbf{x}_i$, can be constructed by regression. It can be shown that $\mathscr{E}[\mathbf{w}|\mathbf{x} = \mathbf{x}_0] = [\Upsilon^{-1} + \Gamma'\Psi^{-1}\Gamma]^{-1}[\Gamma'\Psi^{-1}(\mathbf{x}_0 - \Gamma\boldsymbol{\nu}) + \boldsymbol{\nu}]$. This is a variation on the usual factor scores regression procedure in which means are explicitly modeled. Hence, these procedures lead to Bayes estimates of $\mathbf{w}$ if Ψ, Γ, Υ, and $\boldsymbol{\nu}$ are known and to empirical Bayes estimates if some or all of the parameters are estimated (Maritz, 1970). Note that in this situation, Ψ need not be diagonal. Even if most elements of Γ are free, the method leads to such empirical Bayes procedures.

Since Ψ denotes a diagonal matrix of error variances, one might naturally require that $\Psi = \psi\mathbf{I}$, where ψ is a scalar (i.e., equality of error variance over all values of t). Such a condition can be easily imposed. We could also allow some degree of correlation between errors by supposing Ψ to be tri-diagonal ($\psi_{ij} \neq 0$ for $i = j$, $i = j + 1$, and $j = i + 1$), for example; or by imposing some other structure (e.g., block diagonal) on Ψ. It is also possible to build an auto-regressive into the Ψ matrix.

Given a solution for Γ, estimates of the basis functions, $g_k(t)$, can be plotted at the observed points $t_1, t_2, \ldots, t_p$ by choosing the appropriate elements of $\hat{\Gamma}$. By drawing a horizontal line at height, $\hat{\gamma}_{jk}$, over the interval t_j to t_{j+1}, we would form a step function approximation to $g_k(t)$. By connecting the heights, $\hat{\gamma}_{jk}$, with straight lines, a linear spline (piece-wise linear) approximation to $g_k(t)$ is formed. A quadratic spline approximation could in principle be created by fitting a quadratic function through sets of three adjacent values $\hat{\gamma}_{j-1,k}$, $\hat{\gamma}_{jk}$, $\hat{\gamma}_{j+1,k}$ (Schumaker, 1981). Or, using a regression approach to splines (Smith, 1979), various spline models might be parameterized and tested by placing appropriate constraints on Γ.

Various nested hypotheses about the means and second moments of $\mathbf{w}$, and about the elements of Γ and Ψ can be easily tested utilizing subtractive chi-square tests, given an overall good fit of the model. For example, if the elements of Γ were quadratically specified, one could easily test for no quadratic trend by the deletion of a column of Γ; or the absence of linear trend could be tested by a second column deletion. Similarly, equality of error variance can easily be assessed or free elements in Γ compared to a succession of fixed models by subtractive chi-square tests. The possibilities are, in fact, only limited by the dimensions of $\mathbf{x}$, $\mathbf{w}$ and $\mathbf{e}$.

Cohort Sequential Design

The cohort sequential design (Schaie, 1965) furnishes a method for studying development and change in which a long span of ages may be studied longitudinally in relatively short time periods. Each subject is observed on each of $j = 1, \ldots, p$ occasions (years of measurement). Subjects are grouped according to cohorts defined by birth year, $b = 1, \ldots, q$. Within-cell age is the difference between year of measurement and year of birth, that is, age $= j - b$. We assume that both birth year and occasion of measurement are naturally ordered. Cohorts may be further broken down by demographic variables, such as gender, social class, or experimental manipulation, yielding multiples of the foregoing scheme. The design of data collection may also yield "corner triangles" by which we mean "new young" subjects from cohorts observed on occasions $j = 2, \ldots, p$; $j = 3, \ldots, p$; and so on, and "old dropouts" from cohorts observed on occasions $j = 1, \ldots, p - 1$; $j = 1, \ldots, p - 2$; and so on. Simple random sampling is assumed and longitudinal attrition will be ignored in our presentation. Also, we will not deal with corner triangles, although they can be handled by the introduction of dummy variates.

Confining ourselves to the simple cohort sequential design, we superscript matrices and vectors with b to denote cohort. The model becomes

$$\mathbf{x}^{(b)} = \Gamma^{(b)}\mathbf{w}^{(b)} + \mathbf{e}^{(b)}, \tag{15}$$

and consequently

$$\mathbf{M}^{(b)} = \begin{bmatrix} \Gamma^{(b)} & \mathbf{0} \\ \mathbf{0}' & 1 \end{bmatrix} \begin{bmatrix} \Upsilon^{(b)} & \boldsymbol{\nu}^{(b)} \\ \boldsymbol{\nu}^{(b)\prime} & 1 \end{bmatrix} \begin{bmatrix} \Gamma^{(b)\prime} & \mathbf{0} \\ \mathbf{0}' & 1 \end{bmatrix} + \begin{bmatrix} \Psi^{(b)} & \mathbf{0} \\ \mathbf{0}' & 0 \end{bmatrix}. \tag{16}$$

In practice, the foregoing is of interest only if some elements of $\mathbf{M}$ are equated over cohorts, and in the most interesting special case, the elements of Γ are lagged, for example,

$$\Gamma^{(1)} = \begin{bmatrix} \gamma_{11} & \gamma_{12} \\ \gamma_{21} & \gamma_{22} \\ \gamma_{31} & \gamma_{32} \\ \cdot & \cdot \\ \cdot & \cdot \\ \cdot & \cdot \\ \gamma_{p1} & \gamma_{p2} \end{bmatrix}, \quad \Gamma^{(2)} = \begin{bmatrix} \gamma_{21} & \gamma_{22} \\ \gamma_{31} & \gamma_{32} \\ \cdot & \cdot \\ \cdot & \cdot \\ \cdot & \cdot \\ \gamma_{p1} & \gamma_{p2} \\ \gamma_{p+1,1} & \gamma_{p+1,2} \end{bmatrix}, \text{ and so forth.} \tag{17}$$

In the balanced setup described,

$$\gamma_{j-1,k}^{(b+1)} = \gamma_{jk}^{(b)}, \quad \text{for} \quad b = 1, \ldots, q-1, j = 2, \ldots, p, \quad \text{and} \quad k = 1, \ldots, r. \tag{18}$$

For this observational scheme and given the lagged model, if sufficient identification conditions are imposed on the first cohort (i.e., on $\Gamma^{(1)}$, $\Upsilon^{(1)}$, and $\boldsymbol{\nu}^{(1)}$), the identification will carry over into other cohorts. Identification in unbalanced situations would have to be dealt with on a case by case basis. In any event, we can supply $\hat{\mathbf{M}}^{(b)}$ as covariance matrices to any algorithm that will carry out confirmatory factor analysis in multiple groups along with the provision for identification conditions. If there are q cohorts, q would have to be subtracted from the degrees of freedom as calculated by such programs. A variety of hypotheses can be addressed via subtractive chi-square tests, for example, equality of error variances over age or over cohort or both; equality of means for $\mathbf{w}^{(b)}$ ($\boldsymbol{\nu}^{(b)}$) over cohorts or subsets of cohorts; equality of second moments over cohorts; the column dimensionality of the $\Gamma^{(b)}$, and so on. Calculation of subtractive chi-square tests requires the sequential fitting of appropriately constrained models to the data.

We have assumed that cohort differences will appear in $\boldsymbol{\nu}^{(b)}$ and $\Upsilon^{(b)}$ but not in $\Gamma^{(b)}$, where the $\Gamma^{(b)}$s overlap. Differences in overlapping elements of the $\Gamma^{(b)}$s would indicate a cohort by growth interaction. The essential feature of (17) and (18) is that, referring to (1), we are postulating that

$$x_i^{(b)}(t) = \sum_{k=1}^{r} w_{ik}^{(b)} g_k(t-b) + e_i^{(b)}(t, b), \tag{19}$$

where t denotes calendar time and b denotes calendar time of birth. This model asserts that the basis functions characterizing development do not change in number or form over cohorts, although the distribution of $\mathbf{w}^{(k)}$ may alter as a function of cohort effects. Under such a constrained model, a few observations per subject within each cohort can provide insight into the form of growth and development over a long range of ages.

Period/Practice Effects

Suppose that instead of $x_{ij}^{(b)}$, we observe

$$x_{ij}^{(b)*} = \delta_j \left[\sum_{k=1}^{r} w_{ik}^{(b)} \gamma_{kj}^{(b)} + \alpha_j \right] + e_{ij}^{(b)}. \tag{20}$$

There is only a period or time of measurement subscript on δ and α (i.e., no cohort superscript). This model retains the general linear approach. Period or time of measurement effects may be due to sociological factors, to practice, or to fatigue, and different types of effects cannot be discriminated. If $\mathbf{x}^{(b)}$ is personological, we might assume that period effects are due to social change, not practice. If $\mathbf{x}^{(b)}$ is cognitive, we would probably prefer to regard period effects as due to practice (or fatigue depending on the time scale; Vinsonhaler & Meredith, 1966). Given (20),

$$\mathbf{M}^{(b)} = \Delta\begin{bmatrix}\Gamma^{(b)} & \boldsymbol{\alpha} \\ \mathbf{0}' & 1\end{bmatrix}\begin{bmatrix}\Gamma^{(b)} & \boldsymbol{\nu}^{(b)} \\ \boldsymbol{\nu}^{(b)\prime} & 1\end{bmatrix}\begin{bmatrix}\Gamma^{(b)\prime} & \mathbf{0} \\ \boldsymbol{\alpha}' & 1\end{bmatrix}\Delta + \begin{bmatrix}\Psi^{(b)} & \mathbf{0} \\ \mathbf{0}' & 0\end{bmatrix}, \tag{21}$$

where

$$\boldsymbol{\alpha}' = \{\alpha_1, \alpha_2, \ldots, \alpha_p\} \tag{22}$$

and

$$\Delta = \begin{bmatrix}\text{diag}\,\{\delta_j\} & \mathbf{0} \\ \mathbf{0}' & 1\end{bmatrix}. \tag{23}$$

One set of identification conditions is $\delta_1 = 1$ and $\alpha_1 = 0$.

Treating $\hat{\mathbf{M}}^{(b)}$ as covariance matrices in any program that will do simultaneous higher order (ACOVS) factor analysis in multiple groups, we can proceed to evaluate a variety of hypotheses (e.g., no period/practice effects, etc.) by the sequential fitting of a series of constrained models. For a single cohort, we must have $\delta_j = 1$, since in this case Δ can be absorbed into Λ; given proper identification, the elements of $\boldsymbol{\alpha}$ could be variable. This topic will be taken up in the next section. We could also permit some cohort variation in the elements of $\Delta (= \Delta^{(b)})$ and $\boldsymbol{\alpha} (= \alpha^{(b)})$ consistent with full identification of the model; such variation would imply cohort by period/practice interaction.

Relation to ANOVA and MANOVA Models

We return again to (1) and make the following suppositions: (i) $r = 2$; (ii) $w_{i2} \equiv 1$; (iii) $g_1(t) \equiv 1$; (iv) mutual independence and constant variance for $e_i(t)$.

Using (i) through (iv), we can rewrite (1) as

$$x_i(t) = w_{i1} + g_2(t) + e_i(t). \tag{24}$$

As usual, treating t as discrete, we are lead to a version of (2):

$$\mathbf{x} = w_1\mathbf{1} + \boldsymbol{\alpha} + \mathbf{e}, \tag{25}$$

where $\boldsymbol{\alpha}' = \{g_2(t_1), g_2(t_2), \ldots, g_2(t_p)\}$, $\mathbf{e}$ is as previously defined, and $\mathbf{1}$ denotes a column vector of ones. The additive effect vector $\boldsymbol{\alpha}$ is similar to that introduced in (20) and (21). The inclusion of $\boldsymbol{\alpha}$, corresponding to strictly additive effects, allows us to assume, without loss of generality, that $\mathscr{E}[W_1] = 0$ by absorbing $\nu_1\mathbf{1}$ into $\boldsymbol{\alpha}$, that is,

$$\mathscr{E}[\mathbf{x}] = \boldsymbol{\mu} = \boldsymbol{\alpha} \quad \text{and} \quad \mathscr{E}[(\mathbf{x} - \boldsymbol{\alpha})(\mathbf{x} - \boldsymbol{\alpha})'] = \sigma^2\mathbf{1}\mathbf{1}' + \psi\mathrm{I}. \tag{26}$$

With the addition of normality, these are the assumptions of the usual repeated measures ANOVA frequently applied to this kind of data. The random variable, W_1, becomes the subject random effect usually introduced in such models. Some hypotheses about $\boldsymbol{\alpha}$ are frequently addressed by way of orthogonal polynomials. If $r > 2$, $g_1(t) \neq 1$, $\Psi \neq \psi\mathrm{I}$, or some combination of these hold, MANOVA alternatives would usually be employed since (26) cannot then be justified.

We can extend the foregoing discussion to mixed models by introducing cohort notation from the previous section. Now, cohort might refer to a non-tested experimental condition. As developed in the previous section, the notion of lag would not usually apply although it could be utilized in some form if different subsets (cohorts) of subjects were measured under different subsets of t (e.g., stimuli, condition, etc.). Generalizing (20) with $\delta_j = 1$, we have in the additive case with $\boldsymbol{\alpha}^{(b)}$ analogous to the additive effect introduced in (20) and (25),

$$\mathbf{x}^{(b)} = W_1^{(b)}\mathbf{1} + \boldsymbol{\alpha}^{(b)} + \mathbf{e}^{(b)}. \tag{27}$$

The vector, $\boldsymbol{\alpha}^{(b)}$, would denote an average. This equation, along with the usual normality assumptions and the like, lead to the full panoply of mixed model ANOVAs depending on the design. Hypotheses about the $\boldsymbol{\alpha}^{(b)}$ can be evaluated by standard methods. Again, if $r > 2$, $g_1(t) \neq 1$, $\Psi \neq \psi I$, or some combination of these characterize the situation, MANOVA techniques would be preferred. However, ANOVA and MANOVA can only inform us about $\boldsymbol{\alpha}^{(b)}$. Every ANOVA or MANOVA repeated measures analysis involving a univariate dependent variable can be viewed as a special case of our general models.

As special cases, the usual ANOVA and MANOVA models can be performed with LISREL-like analyses by utilizing an equation similar to (21) in which $\Delta = I$, the last column of Λ corresponds to the additive component, $\boldsymbol{\alpha}^{(b)}$, and the only column of $\Gamma = \mathbf{1}$. Depending on the formulation, one might also relax the diagonality assumption for Ψ. With imagination and careful attention to detail, given suitable identification, every form of repeated measures ANOVA or MANOVA can be built up as a special case.

The genuinely interesting cases arise from the models, generalized from (27), as

$$\mathbf{x}^{(b)} = \Gamma\mathbf{w}^{(b)} + \boldsymbol{\alpha}^{(b)} + \mathbf{e}^{(b)}, \tag{28}$$

where $\boldsymbol{\alpha}^{(b)}$ represents a common growth curve or effect within groups. Individual differences appear in $\mathbf{w}^{(b)}$ as mediated through Γ. When the column dimensionality of Γ is one, but $\Gamma \neq \mathbf{1}$, we have a case in which there is a location and a scale parameter without individual differences in the location parameter and with individual differences in scale. Individual differences in both can be treated by employing (28) in which the column dimension of Γ is 2, $\boldsymbol{\alpha}^{(b)}$ is set equal to zero, and one column of Γ is set equal to $\mathbf{1}$. What is far more important is that individual differences can be explicitly built into such models by appropriate definitions of the $\mathbf{w}^{(b)}$ vectors as random variables and permitting appropriate free elements in $\Gamma^{(b)}$, $\boldsymbol{\alpha}^{(b)}$, $\boldsymbol{\nu}^{(b)}$, $\Gamma^{(b)}$, and $\Psi^{(b)}$. A variety of hypotheses can be tested by suitably constraining elements of the previous matrices. Observe that the general forms of latent curve analysis (e.g., (2), (15) and (21)) provides multiplicative alternatives to the usual additive ANOVA/MANOVA models regularly employed in analyzing repeated measures data in the sense that subject effects (W) multiply treatment effects (Γ, etc.).

Relation to Simplex Models

Wiener and Markov simplex models (Jöreskog, 1970; Jöreskog & Sörbom, 1985) are discussed next. If one examines Table 2 in Jöreskog (p. 122), we see that every case discussed can be treated as a special case of the cohort formulation with period/practice effects. Let the $p \times p$ matrix

$$\Gamma = \begin{bmatrix} 1 & 0 & \cdots & 0 & 0 \\ 1 & 1 & \cdots & 0 & 0 \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ 1 & 1 & \cdots & 1 & 0 \\ 1 & 1 & \cdots & 1 & 1 \end{bmatrix}, \tag{29}$$

then

$$\mathbf{M} = \Delta\begin{bmatrix}\Gamma & \boldsymbol{\alpha}\\ \mathbf{0}' & 1\end{bmatrix}\begin{bmatrix}\Upsilon & \boldsymbol{\nu}\\ \boldsymbol{\nu}' & 1\end{bmatrix}\begin{bmatrix}\Gamma' & \mathbf{0}\\ \boldsymbol{\alpha}' & 1\end{bmatrix}\Delta + \begin{bmatrix}\Psi & \mathbf{0}\\ \mathbf{0}' & 0\end{bmatrix}. \tag{30}$$

We further require that both $\Upsilon - \boldsymbol{\nu}\boldsymbol{\nu}'$ and Ψ be diagonal. With suitable modifications and restrictions leading to identification and over-identification, the foregoing characterizes all models proposed by Jöreskog in the single cohort case. Multiple cohorts can be dealt with by superscripting matrices and vectors as in (21). A variety of hypotheses about $\boldsymbol{\nu}^{(b)}$ and $\Upsilon^{(b)}$, and the like, can then be addressed by the sequential fitting of constrained models. A problem arises in connection with the requirement that the p elements of $\mathbf{w}$ be mutually independent (uncorrelated); that is, $\Upsilon^{(b)} - \boldsymbol{\nu}^{(b)}\boldsymbol{\nu}^{(b)\prime} = \text{diag}$, which cannot be readily formulated in the format we have employed. It can, however, be implemented by utilizing the full power of LISREL-like programs. Our point is not to suggest how to carry out simplex type analysis by way of latent curve analysis. Rather we wish to point out that when the random vector $\mathbf{w}$ is thought of as comprising mutually independent elements, and Γ is given by (29), the model for the data, as random vectors, can be expressed with fully generality, disregarding identification, as

$$\begin{bmatrix}\mathbf{x}^{(b)}\\ 1\end{bmatrix} = \Delta^{(b)}\begin{bmatrix}\Gamma & \boldsymbol{\alpha}^{(b)}\\ \mathbf{0}' & 1\end{bmatrix}\begin{bmatrix}\mathbf{w}^{(b)}\\ 1\end{bmatrix} + \begin{bmatrix}\mathbf{e}^{(b)}\\ 0\end{bmatrix}. \tag{31}$$

Equation (31) is a generalization of (20) leading to an equation like (21). In other words, simplex models are generalizations of the models provided by (1) and (20). The key issues are the independence of the components of $\mathbf{w}$ and the square form of Γ given in (29), which imply independent increments, versus reduced dimension curve fitting without independent increments when r is substantially less than p. In practice, it may be difficult to distinguish between such models when the number of free parameters to be estimated are similar (Rogosa & Willett, 1985b). It should be noted that, as developed, simplex models can not easily handle period/practice effects which, as we have shown, can be treated linearly in the latent curve framework extended to the cohort sequential design. Further work on simplex models in this connection is required.

A Simple Example

This example employs artificial data[1] which were analyzed blind, that is, without knowledge of how the data were constructed or knowledge of the values of t_j other than their rank order. These data consist of 75 curves each observed at 14 points in time. The lower triangular moment matrix is presented in Table 1; the last row contains the means. LISREL 7 (Jöreskog & Sörbom, 1989) was used to perform the analysis.

A simple one curve model, $x_i(t_j) = w_i g(t_j) + e_i(t_j)$, with $\sigma^2_{e_i}(t_j) = \psi$ and $\sigma_{e_i}(t_j)e_i(t_{j'}) = 0$ for $t_j \neq t_{j'}$, was tested first. The analysis yielded $\chi^2(103) = 2057.38$. Parenthetically, the root mean square residual is only 1.45 and the Q-plot of normalized residuals looks reasonable.

A simple two curve model is $x_i(t_j) = w_{i1} + w_{i2}g_2(t_j) + e_i(t_j)$ with $\sigma^2_{e_i}(t_j) = \psi$ and $\sigma_{e_i}(t_j)e_i(t_{j'}) = 0$ for $t_j \neq t_{j'}$. In this model, the first column of Γ from (2) consists of a vector of ones. The analysis yielded a $\chi^2(101) = 90.24, p = .770$. Hence, we believe that this model best fits the data. The parameter estimates are $(\hat{\nu}_1, \hat{\nu}_2) = (10.111, 4.127)$, $(\hat{\sigma}^2_{W_1}, \hat{\sigma}^2_{W_2}, \hat{\sigma}_{W_1W_2}) = (9.828, 0.726, -2.616)$, $\hat{\rho}_{W_1W_2} = -.979$, and $\hat{\psi} = .160$; the estimated values for $g_2(t_j)$ (i.e., $\hat{\gamma}_{j2}$) are plotted in Figure 1.

[1] The authors wish to thank David Rogosa and John Willett for furnishing us these data.

TABLE 1

The augmented moment matrix of the simulated data

112.1288										
151.0116	208.0034									
182.0271	252.7919	308.9195								
204.8107	286.0187	350.2101	398.0287							
225.2741	315.7227	387.1415	440.1612	487.3850						
241.0956	338.6745	415.7779	473.0214	523.8347	563.4994					
253.4796	356.5985	438.0767	498.5768	552.2259	594.0168	626.5312				
262.4238	369.8594	454.6013	517.6537	573.4898	616.9781	650.7060	676.1360			
270.3683	381.3613	468.9517	534.0884	591.7720	636.7196	671.5296	697.7036	720.2900		
276.8108	390.6987	480.5759	547.4397	606.6458	652.7802	688.4866	715.3244	738.3818	757.2411	
281.1356	397.0443	488.5256	556.6130	616.7899	663.7106	700.0468	727.3935	750.8594	769.8849	783.1000
286.6480	404.9506	498.2938	567.7779	629.1942	677.1243	714.2042	742.1564	766.0935	785.4807	798.8190
815.1647										
288.0999	407.1844	501.2264	571.1909	633.0530	681.3083	718.6778	746.7500	770.8830	790.4473	803.7990
820.1553	825.4742									
291.0291	411.3030	506.1871	576.8893	639.3093	688.0465	725.7664	754.1241	778.5012	798.2249	811.7502
828.2364	833.4532	841.8151								
10.1084	14.2339	17.4899	19.9101	22.0555	23.7240	25.0193	25.9902	26.8245	27.5027	27.9659
28.5329	28.7100	28.9928	1.0000							

The first two values are set equal to zero and one, respectively, for identification. The above model with $\hat{\rho}_{W_1 W_2} = -1$ was rejected by $\chi^2(102) = 1032.64$.

Assuming equal time intervals, we did attempt to fit a linear model for $g_2(t_j)$ and a quadratic model for $g_3(t_j)$. Orthogonal polynomials were used for $g_2(t_j)$ and $g_3(t_j)$; again, equal error variance was assumed. Both the linear and quadratic models were clearly rejected, that is, $\chi^2(113) = 3219.49$ and $\chi^2(109) = 1048.06$, respectively.

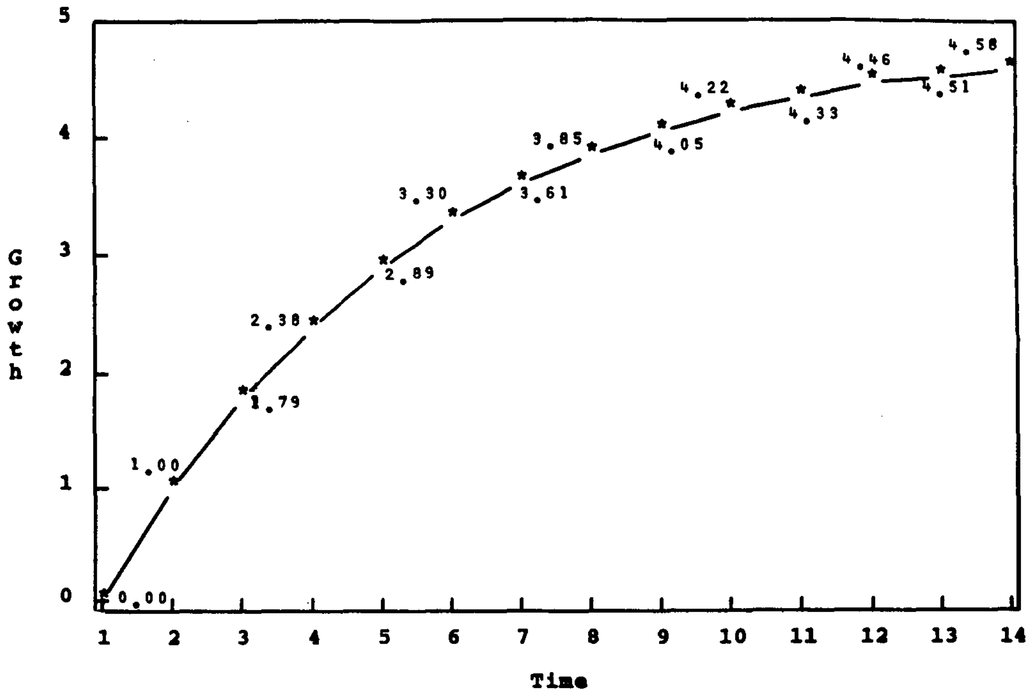

FIGURE 1.
The Growth Curve, $g_2(t_j)$, for the Artificial Data.

If one assumes that $t_1 = a$, $t_2 = a + b$, $t_3 = a + 2b, \ldots, t_{14} = a + 13b$, where a and b are any numbers ($b > 0$), the plot in Figure 1 resembles a negatively accelerated exponential growth curve which we will refer to as a negative exponential curve. Further, if the individual curves are negative exponential, an average curve can be negative exponential if and only if the rate parameter does not vary over individuals. The intercept and asymptote may vary. This suggests that the data were generated by $x_i(t) = v_{i1}^* + v_{i2}^*[1 - \exp(-\beta t)] + e_i(t)$, or, equivalently, by $x_i(t) = v_{i2} - [v_{i2} - v_{i1}] \exp(-\beta t)] + e_i(t)$. To investigate this possibility further, we note that given equally spaced t_j, we can scale t (and β) so that $t_j - t_{j-1} = 1$. With the identification restrictions employed, $\hat{g}_2(t_j) = \hat{\gamma}_{j2} = [1 - \exp(-\hat{\beta}[j - 1])]/[1 - \exp(-\hat{\beta})]$, where $\hat{\beta}$ is as yet unknown. It can be shown that $\ln(\hat{\gamma}_{j2} - \hat{\gamma}_{j-1,2}) \approx -\hat{\beta}[j - 2]$ for $j = 3, 4, \ldots, 14$. A plot of the logarithm of the differences against the values $j - 2$ is nearly linear. A least squares line through the origin has slope $-.235$, hence $\hat{\beta} = .235$, and the coefficient of congruence (correlation with zero intercept) is $-.98$. Rewriting, $x_{ij} = v_{i2} - [v_{i2} - v_{i1}] \exp(-\beta[t_0 + j]) + e_{ij}$ in terms of our identification yields

$$x_{ij} = v_{i2} - [v_{i2} - v_{i1}]\left[[1 - e^{-\beta}][e^{-\beta}][e^{-\beta t_0}]\left[\left[\frac{1}{1 - e^{-\beta}}\right] - \left[\frac{1 - e^{-\beta[j-1]}}{1 - e^{-\beta}}\right]\right]\right] + e_{ij}$$

$$= v_{i2} - [v_{i2} - v_{i1}]k_0 k_1 + [v_{i2} - v_{i1}]k_0 \gamma_{j2} + e_{ij},$$

where $k_0 = [1 - \exp(-\beta)] \exp(-\beta) \exp(-\beta t_0)$, $k_1 = [1 - \exp(-\beta)]^{-1}$, $\gamma_{j2} = [1 - \exp(-\beta[j - 1])]/[1 - \exp(-\beta)]$, and t_0 is an additive or shift constant. Equating this curve to the latent curve, yields

$$x_{ij} = v_{i2} - [v_{i2}k_1 - v_{i1}]k_0 k_1 + [v_{i2} - v_{i1}]k_0 \gamma_{j2} + e_{ij} = w_{i1} + w_{i2}\gamma_{j2} + e_{ij},$$

where $w_{i1} = v_{i2} - [v_{i2} - v_{i1}]k_0 k_1$ and $w_{i2} = [v_{i2}k_2 - v_{i1}]k_0$. Or

$$v_{i1} = w_{i1} - w_{i2}\frac{1 - k_0 k_1}{k_0} \quad \text{and} \quad v_{i2} = w_{i1} + w_{i2}k_1.$$

We note that in the general expression, $x_i(t) = y_i + z_i[1 - \exp(-\beta t)] + e_i(t)$, the value for the origin for t is indeterminate. Arbitrarily, we define $\rho_{V_1 V_2} = 0$ (alternatively, we could have set $t_0 = 0$ or -1), and conclude that the data were generated by the following negative exponential function,

$$x_{ij} = v_{i2} - [v_{i2} - v_{i1}] \exp(-\beta[t_0 + j]) + e_{ij},$$

with constant rate parameter, $\hat{\beta} = .235$ and additive constant, $\hat{t}_0 = -6$ (rounded to integer time). The intercept, v_{i1}, and the asymptote, v_{i2}, may vary with the observations, that is, individual differences parameters; their means and variances are, respectively, $(\hat{\mu}_{V_1}, \hat{\mu}_{V_2}) = (23.729, 29.814)$ and $(\hat{\sigma}^2_{V_1}, \hat{\sigma}^2_{V_2}) = (.474, 1.412)$. The errors of measurement have mean, $\hat{\mu}_E = 0$, and variance, $\hat{\sigma}^2_E = .160$. The assumption of normality for these variates (V_1, V_2, E) is consistent with the normality assumptions placed on the manifest variables.

The data were actually generated by a negative exponential function (J. Willett, personal communication, May 25, 1988) with constant rate parameter, $\beta = .23$ and integer time points, j, ranging from -6 to 7. The intercept, $V_1 \sim N(25, .437)$ and the asymptote, $V_2 \sim N(30, 1.5)$; their correlation, $\rho_{V_1 V_2} = 0$. Errors of measurement, $E \sim N(0, .15)$. By comparison, we conclude that the latent curve analysis recovered the data structure in this situation remarkably well.

TABLE 2

The cohort sequential design of the Nesselroade-Baltes data

		Year of measurement		
		1970	1971	1972
	1	7	8	9
Cohort	2	8	9	10
	3	9	10	11
	4	10	11	12

A Cohort Sequential Example

To provide a nonartificial example, we employ data[2] from Nesselroade and Baltes (1974), involving the raw scale scores of the Number Series subtest of the Primary Mental Abilities Test (Thurstone & Thurstone, 1962). For further information the reader can refer to both publications. The data collection scheme can be described by the following table, in which the elements correspond to grade in school.

Defining Cohort 1 through 4 as females, and Cohort 5 through 8 as males, we deal with 8 cohorts by treating the two genders separately, replicating Table 2 for each gender.

The eight **M** matrices are presented in Table 3 with females above the diagonal and males below.

The last rows and columns of the matrices in Table 3 contain the means for each grade-by-gender subset of data within cohorts. Also, note that each subject is observed on each of three occasions (1970, 1971, 1972). These data has been edited by subjective elimination of *extreme* outliers, and all analyses reported were performed with LISREL 7 (Jöreskog & Sörbom, 1989), employing LISREL's ability to handle multiple groups (our 8 cohorts) as well as the options for constraining parameters (e.g., those in $\Gamma^{(b)}$).

The first model is described by (21). Since $\Psi^{(b)}$ is assumed to be ψI, we are requiring equivalence of error of measurement over both occasions and cohorts. With $\delta_1 = 1$ and $\alpha_1 = 0$, we consider lag

$$\Gamma^{(1)} = \Gamma^{(5)} = \begin{bmatrix} 1 \\ \gamma_2 \\ \gamma_3 \end{bmatrix}, \quad \Gamma^{(2)} = \Gamma^{(6)} = \begin{bmatrix} \gamma_2 \\ \gamma_3 \\ \gamma_4 \end{bmatrix}, \quad \Gamma^{(3)} = \Gamma^{(7)} = \begin{bmatrix} \gamma_3 \\ \gamma_4 \\ \gamma_5 \end{bmatrix},$$

and

$$\Gamma^{(4)} = \Gamma^{(8)} = \begin{bmatrix} \gamma_4 \\ \gamma_5 \\ \gamma_6 \end{bmatrix}. \tag{32}$$

Gender-by-cohort differences are presumed to be represented in $\boldsymbol{\nu}^{(b)}$ and $\Upsilon^{(b)}$, that is, no interactions are assumed. This model yields $\chi^2(46) = 57.35$, $p = .12$. We call this Model 1 for comparative purposes. Given a reasonable fit of the overall model, in Model 2 we test the hypothesis of no growth by requiring $\Gamma^{(b)} = 1$. The resulting $\chi^2(51) = 73.88$, $p = .02$. The subtractive or restrictive chi-square comparing Model 2 to 1 is $\chi^2_R(5) = 16.53$, $p = .005$, and clearly model 2 is rejected.

[2] The authors wish to thank John Nesselroade for permitting us to use these data.

TABLE 3

The augmented moment matrices of Number Series scale

		Cohort 1 females (N = 116)						Cohort 2 females (N = 121)			
		34.1	36.5	43.4	5.4			43.9	48.9	52.9	6.0
	37.0		45.1	51.2	6.2		46.7		63.3	65.5	7.5
Cohort 5	41.4	54.0		65.1	7.5	Cohort 6	51.4	65.3		74.1	8.0
males	48.8	59.7	73.5		1.0	males	56.7	69.3	79.9		1.0
(N = 98)	5.6	6.7	8.0	1.0		(N = 93)	6.2	7.4	8.2	1.0	
		Cohort 3 females (N = 117)						Cohort 4 females (N = 62)			
		50.9	55.1	58.1	6.5			51.0	54.6	61.2	6.7
	53.8		67.1	69.0	7.7		58.0		63.9	68.6	7.5
Cohort 7	57.4	70.4		76.3	8.2	Cohort 8	66.7	87.2		78.9	8.3
males	61.1	70.6	78.1		1.0	males	71.0	88.4	97.2		1.0
(N = 96)	6.7	7.8	8.3	1.0		(N = 79)	7.0	8.7	9.3	1.0	

In model 3, we revert to the form of model 1, but require $\underline{\Delta} = \mathrm{I}$ and obtain $\chi^2(48) = 60.24$, $p = .11$. The subtractive chi-square for comparing model 3 to 1 is $\chi^2_R(2) = 2.89$, $p = .24$. Model 4 is conceptually similar to Model 3, although we now assume $\boldsymbol{\alpha} = 0$. This requires the period/practice effects to be multiplicative, whereas in Model 3 they were additive. The fit of this model is $\chi^2(48) = 58.51$, $p = .14$. The subtractive chi-square for comparing Model 4 to 1 is $\chi^2_R(2) = 1.16$, $p = .56$. In Model 5, we require $\underline{\Delta} = \mathrm{I}$ and $\boldsymbol{\alpha} = \mathbf{0}$, no period/practice effects. This yields $\chi^2(50) = 67.02$, $p = .05$. The subtractive chi-square which compares Model 5 to Model 1 is $\chi^2_R(4) = 9.67$, $p = .05$, and we conclude that some period/practice effect is worthy of inclusion although it may not matter whether this effect is regarded as multiplicative in $\underline{\Delta}$ or additive in $\boldsymbol{\alpha}$. In subsequent analysis, we set $\boldsymbol{\alpha} = \mathbf{0}$ (or assume Model 4).

The next parameterization, Model 6, requires $\boldsymbol{\nu}^{(b)}$ to be equal over grade cohort within gender; $\chi^2(54) = 60.99$, $p = .24$. The subtractive chi-square of Model 6 versus Model 4 is $\chi^2_R(6) = 2.48$, $p = .87$, suggesting that there are no cohort differences in the factor means within gender. In Model 7, we test for equality of factor means for both cohorts and gender; $\chi^2(55) = 63.93$, $p = .19$. The subtractive chi-square between Models 7 and 6 is $\chi^2_R(1) = 2.94$, $p = .09$. Finally, we test for no cohort and gender differences in factor means and variances, Model 8; $\chi^2(62) = 71.33$, $p = .20$. The Model 8 versus 7 subtractive chi-square is $\chi^2_R(7) = 7.40$, $p = .39$. Implementing Model 8 equates the matrices whose free elements are $\Upsilon^{(b)}$ and $\boldsymbol{\nu}^{(b)}$ in (21) over cohorts.

We conclude: (a) there is growth; (b) period/practice effects cannot be ignored; (c) average errors of measurement do not vary over gender and cohort; and (d) there are no gender or cohort differences or interactions in development with respect to the Number Series test.

All numerical estimates of parameters presented are taken from the solution for Model 8. Since the variation in parameter estimates is minimal (and nonsignificant), these are not presented for the other models. The multiplicative practice effects, $\{\delta_j\}$, are equal to 1.11 from Occasion 1 to 2, 1.16 from Occasion 1 to 3, and consequently, 1.05 from Occasion 2 to 3. The values of the true growth curve at the Points (Grades) 7 through 12 are represented in Figure 2.

These values were obtained from the elements of the $\Gamma^{(b)}$ matrices as described in (32); the first value is set equal to one for identification purposes. A linear spline approximation can be obtained by plotting the points and connecting them with straight line segments.

Since $g(t)$ is monotone as estimated, the individual growth curves when multiplied

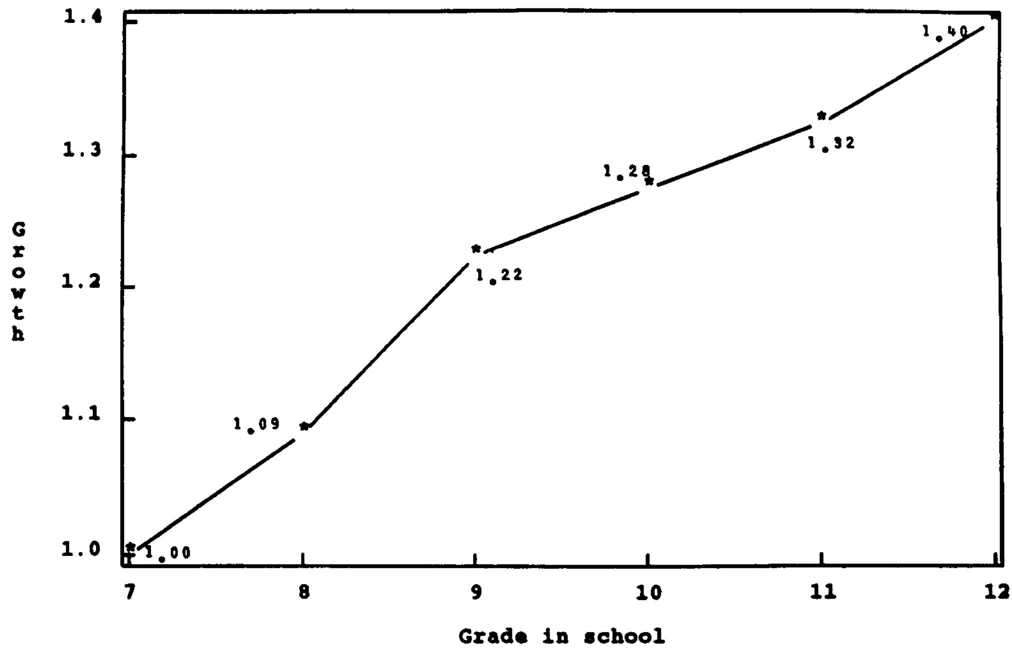

FIGURE 2.
The Growth Curve, $g(t)$, for Model 8.

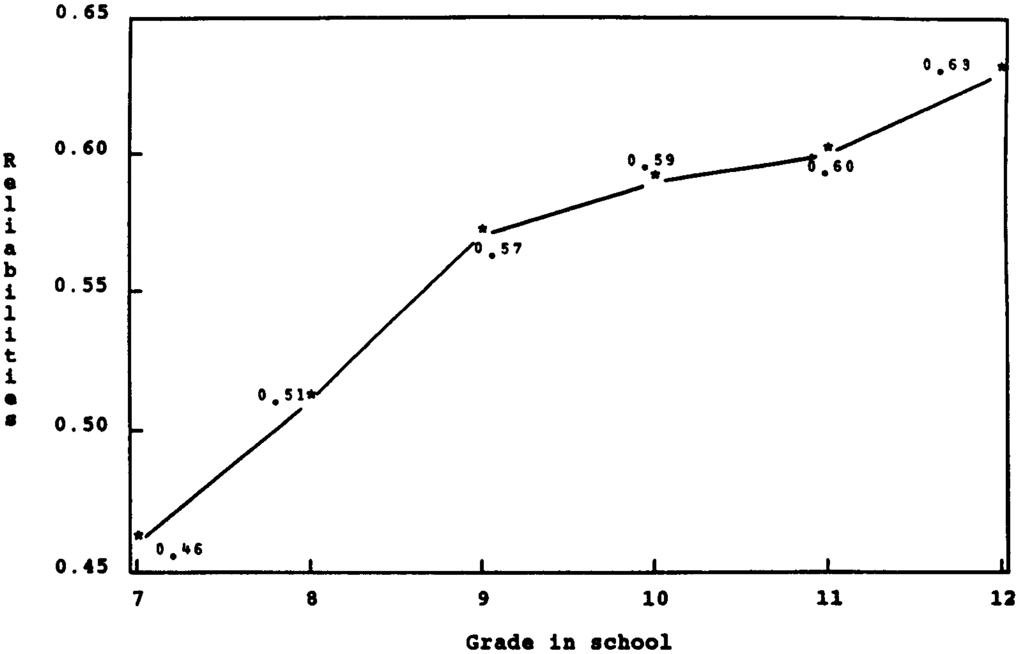

FIGURE 3.
The Reliability Estimates for Model 8.

by W would appear to be a fan over Grades 7 to 12, that is, the growth curves do not cross. Such a result is not a necessary consequence if either the curve is not monotone or more than one basis curve is needed, or both. The mean of the sole individual differences variable, W, is 5.46 and its standard deviation is 1.71. For this kind of data, negative values of W would be problematic. Given the normality assumptions made, and our estimates, we find that the probability that $W \leq 0$ is approximately .0007. Using the error variance, 3.38, and variance estimate multiplied by the squares of the appropriate elements in the growth curve, we can calculate the reliability for each grade. Notice $g(t)$ is monotonic and the true variance increases over grade; consequently, the reliabilities increase. The reliabilities estimates based on this procedure are contained in Figure 3.

We believe this is a much better way of estimating reliabilities than those conventionally used, and discuss this in a subsequent paper. Thurstone and Thurstone (1962) combined the Number Series test with other measures to get a reasoning ability test. This suggests that the Number Series test is not a very reliable measure when used alone. Both the median test-retest reliability, which is .625, and the reliabilities in Figure 3 concur on this point.

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