

Using Covariance Structure Analysis to Detect Correlates and Predictors of Individual Change Over Time

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Recently, methodologists have shown how two disparate conceptual arenas—individual growth modeling and covariance structure analysis—can be integrated. The integration brings the flexibility of covariance analysis to bear on the investigation of systematic interindividual differences in change and provides another powerful data-analytic tool for answering questions about the relationship between individual true change and potential predictors of that change. The individual growth modeling framework uses a pair of hierarchical statistical models to represent (a) within-person true status as a function of time and (b) between-person differences in true change as a function of predictors. This article explains how these models can be reformatted to correspond, respectively, to the measurement and structural components of the general LISREL model with mean structures and illustrates, by means of worked example, how the new method can be applied to a sample of longitudinal panel data.

Questions about correlates and predictors of individual change over time are concerned with the detection of systematic interindividual differences in change, that is, whether individual change in a continuous outcome is related to selected characteristics of a person's background, environment, treatment, or training. Examples include the following: Do the rates at which students learn differ by attributes of the academic programs in which they are enrolled? Are longitudinal changes in children's psychosocial adjustment related to health status, gender, and home background?

Questions like these can be answered only when continuous data are available longitudinally on many individuals, that is, when both time points and individuals have been sampled representatively. Traditionally, researchers have sampled individual status at only two points in time, a strategy that has proven largely inadequate because two waves of data contain only min-

imal information on individual change (Rogosa, Brandt, & Zimowski, 1982; Willett, 1989). When true development follows an interesting trajectory over time, "snapshots" of status taken before and after are unlikely to reveal the intricacies of individual change.

In the last 15 years, the methods of *individual growth modeling* have capitalized on the richness of continuous multiwave data to provide better methods for answering questions about systematic interindividual differences in change (Bryk, 1977; Bryk & Raudenbush, 1987; Rogosa et al., 1982; Rogosa & Willett, 1985; Willett, 1988, 1994). Under this approach, an individual growth model is chosen to represent the change that each person experiences with time. This is often referred to as the within-person or Level 1 model. All members of a given population are assumed to have trajectories of the same functional form, but different members can have different values of the *individual growth parameters* present in the Level 1 model. For instance, if individual change is linear with time, interindividual differences in change may be due to heterogeneity in initial status (intercept) and rate of change (slope). Alternatively, if individual change is a quadratic function of time, then interindividual differences in change may also be due to between-person variation in the curvature parameter. Interindividual differences in change are said to be *systematic* when between-person variation in one or more individual growth parameters is related to variation in the selected predictors of change. The hypothesized link between the individual growth parameters and the predictors of change is described in a between-person or Level 2 statistical model.

A variety of methods have been proposed for estimating the parameters of the Level 1 and Level 2 models in the analysis of change. Rogosa and his colleagues (Rogosa et al., 1982; Rogosa & Willett, 1985; Willett, 1985, 1994; Williamson, 1986; Wil-

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liamson, Appelbaum, & Epanchin, 1991) described exploratory ordinary least squares regression-based methods to separately estimate the parameters of the Level 1 and Level 2 models, with reliability-based adjustments to the latter based on the marginal maximum likelihood methods of Blomqvist (1977). In an extension of the exploratory approach, Willett (1988, based on Hanushek, 1974) provided weighted least squares methods for obtaining asymptotically efficient estimates of the parameters of the Level 2 model. And, as part of their work on hierarchical linear modeling (HLM), Bryk and Raudenbush (1987, 1992) described strategies for simultaneously estimating the parameters of the Level 1 and Level 2 models using empirical Bayes estimation.

Recently, several pioneering authors have demonstrated how the analysis of change can be conducted very conveniently by the methods of covariance structure analysis. Meredith and Tisak (1984, 1990; see also Tisak & Meredith, 1990), for instance, have provided a technical framework for representing interindividual differences in intraindividual development and examples of how model parameters can be estimated by covariance structure analysis. Their work extends earlier research on longitudinal factor analysis (Rao, 1958; Tucker, 1958) and subsumes more traditional approaches to the analysis of panel data, such as repeated measures analysis of variance (ANOVA) and multivariate analysis of variance (MANOVA; see also Jöreskog & Sörbom, 1989). The Meredith-Tisak approach is very general. It permits the evaluation of the general shape of the individual growth trajectories and provides not only estimates of the individual growth parameters (through the estimation of factor scores) but estimates of the Level 2 means, variances, and covariances of the individual growth parameters across all members of the population. These latter statistics estimate the population average growth curve and provide evidence for the presence of interindividual differences in growth in the population.

In a linked body of applied work, McArdle and his colleagues have extended the covariance structure approach of Meredith and Tisak, demonstrating its flexibility by application to a wide variety of developmental problems in psychology and throughout the social sciences. For instance, they showed how covariance structure methods can be used to estimate average growth curves and to indicate the presence of interindividual differences in change in a single domain and simultaneously in many domains (McArdle, 1986a, 1986b, 1989, 1991; McArdle & Epstein, 1987). They also showed how average growth curves can be compared across groups (McArdle, 1989; McArdle & Epstein, 1987) and described how covariance structure methods can be used to conduct convergence analysis, in which segments of average growth curves estimated in overlapping cohorts are linked into a single continuous trajectory (McArdle & Anderson, 1989; McArdle, Anderson, & Aber, 1987; McArdle & Hamagami, 1991). Furthermore, in an extension that provided the impetus for this article, McArdle and Epstein (1987) demonstrated how the Level 2 relationship between slope and a single predictor of change can be modeled and estimated when individual change is represented by a restricted linear growth model that contains only a slope parameter (and no intercept).

Finally, in a separate but related stream of research, Muthén and his colleagues have also described the technical basis for,

and provided data-analytic examples of, the modeling of multilevel data using covariance structure methods (Muthén, 1989; Muthén & Satorra, 1989). Of particular interest are a pair of recent papers (Muthén, 1991, 1992) in which the parameters of a linear individual growth model were allowed to vary across individuals in ways systematically related to selected time-invariant predictors of change. The latter paper also presented an application of an interesting strategy based on multigroup analysis (see Bollen, 1989) for incorporating individuals with incomplete observed growth records into the analyses.

We are convinced that these new methods are another powerful data-analytic weapon in the armory of the empirical researcher. Questions about correlates and predictors of change pervade psychology and the social sciences. In this article, we present a careful exposition of the application of covariance structure methods to the investigation of systematic interindividual differences in change. Analytically, our article is closest to—and derivative of—the work of McArdle and Epstein (1987) and Muthén (1991, 1992). However, we intend our principal contribution to be the provision of a viewpoint that inverts that of our covariance modeling colleagues. Unlike them, we owe our principal allegiance to the field of individual growth modeling, and we have come to understand these recent innovations in the covariance structure analysis of longitudinal data from that perspective. Consequently, in this article, we have tried to link the pioneering contributions of McArdle, Muthén, and Meredith and Tisak directly to recent developments in the measurement of individual change (Bryk, 1977; Bryk & Raudenbush, 1987, 1992; Burchinall & Appelbaum, 1991; Rogosa et al., 1982; Rogosa & Willett, 1985; Willett, 1985, 1988, 1989, 1994; Williamson, 1986; Williamson et al., 1991).

The integration of the individual growth modeling and covariance structure approaches capitalizes on the fundamental mathematical equivalence of two alternative methods of representing the same data structure. The process of formulating population Level 1 and Level 2 models for individual change and for systematic interindividual differences in change is equivalent to postulating a specific structure for the matrix of population covariances among the multiple waves of observed data and the predictors of change. By using the general LISREL model with mean structures (Jöreskog & Sörbom, 1989) to explicitly articulate this latter covariance structure and to fit it to the matrix of sample covariances, we can obtain maximum likelihood estimates of the critical between-person parameters that were specified under the original growth modeling formulation and thereby answer our research questions about potential correlates and predictors of change.

This article has three sections and a concluding discussion. In the first section, we begin our presentation by introducing a simple Level 1 growth model to represent individual change over time. In this model, we hypothesize that true change is a linear function of time, and we assume that the occasion-by-occasion errors of measurement are both homoscedastic and mutually independent. Then we formulate a preliminary “no-predictor” Level 2 model for interindividual differences in change that describes heterogeneity in change across members of the population. In this latter model, the intercepts and slopes of the Level 1 individual growth model are permitted to vary

jointly across people, but interindividual heterogeneity in change is left unexplained by potential predictors of change. In the second section, we illustrate how the "baseline" individual growth modeling perspective maps onto the framework provided by the general LISREL model. Then we demonstrate how the respective Level 2 means, variances, and covariance of the individual growth parameters can be estimated straightforwardly by covariance structure analysis. To close out the section, we extend the baseline analysis to test and modify the critical assumptions made at Level 1 concerning (a) the linearity of the individual true growth trajectory and (b) the homoscedasticity and independence of the measurement error covariance structure. In the third section, we introduce potential predictors of change into the baseline Level 2 specification and describe how the methods of covariance structure analysis can be used to estimate the relationship between interindividual heterogeneity in the growth parameters and the predictors of change. Our rationale for this organization is both substantive and methodological because, logically, individual change must be described before interindividual differences in change can be examined, and interindividual differences in change must be present before one can ask whether any heterogeneity is related to predictors of change.

A data-based example is used to frame our presentation throughout the article, and we provide, in the Appendix, illustrative LISREL programs for conducting the proposed analyses. In our concluding discussion, we comment on the advantages and limitations of the covariance structure approach and note further extensions of the method that are made feasible by the flexibility of the general LISREL model.

Modeling Change Over Time: An Individual Growth Modeling Perspective

To answer research questions about individual change in a continuous variable, a representative sample of individuals must be observed systematically over time, with their status being measured on several temporally spaced occasions. To use the covariance structure approach described here, three or more waves of data must be available on each individual. In addition, the data must be balanced in a particular way. The occasions of measurement need not be equally spaced in time, but both the number and the spacing of assessments must be the same for all individuals, a pattern that Bock (1979) referred to as "time-structured" data.

Thus, the methods we describe here are appropriate for analyzing *panel* data, in which the number of individuals is large with respect to the number of occasions of measurement. The sample size must be large enough to enable the investigator to detect person-level effects. Other analytic methods are available for *time-series* data sets, which typically contain many repeated assessments on few individuals. In psychology, studies of physical growth, language development, and dyadic interaction are often of this latter form.

Introducing the Data Example

Throughout this article, we illustrate the covariance structure analysis of change using a data set that contains five waves of

data obtained from a sample of 168 adolescents on the continuous dependent variable *tolerance of deviant behavior*.¹ During each year of the study—at 11, 12, 13, 14, and 15 years of age—each participant completed a nine-item instrument that asked whether it was wrong for someone his or her age to cheat on tests, purposely destroy property of others, use marijuana, steal something worth less than \$5, hit or threaten someone without reason, use alcohol, break into a building or vehicle to steal, sell hard drugs, or steal something worth more than \$50 (Raudenbush & Chan, 1992). Responses to each item were registered on a 4-point scale ranging from *very wrong* (1) to *not wrong at all* (4), and responses were averaged across items to provide a scale score. In Table 1, for illustration, we list scores for 16 randomly selected cases. Inspection of the table—and the full data set—suggests that although there is considerable scatter in the observed scores over time and across individuals, adolescents appear to become gradually more tolerant of deviant behavior as they age.

To answer questions about systematic interindividual differences in change, information must also be available on potential predictors of change. Our data example provides the values of two potential predictors of change: (a) the gender of the adolescent (0 = male, 1 = female), and (b) the adolescent's reported exposure to deviant behavior in the 1st year of data collection (at age 11).² Values of these predictors are also presented for the 16 randomly selected cases in Table 1. In our illustrative data analyses, the broad research question is as follows: Are interindividual differences in change of tolerance toward deviance during adolescence related to respondent gender and initial exposure to deviant behavior?

Modeling Individual Change Over Time

As is well known, classical test theory describes the psychometric properties of scores on a single occasion, distinguishing *observed score* from *true score*, the former being a fallible operationalization of the latter. The observed score continues to be distinguished from the true score when change is investigated because change in underlying true score is the focus of research interest. Measurement error is an uninvited guest that randomly obscures the true growth trajectory from view. Consequently, when individual growth is represented by a statistical model, the model must contain a part describing a person's true growth trajectory over time and a part representing the stochastic effect of measurement error.

¹ We thank Stephen W. Raudenbush for providing these data.

² Adolescents' exposure to deviance was also self-reported on a nine-item instrument in each of the 5 years of the study. Participants were asked how many of their peers engaged in the same nine activities identified in the tolerance of deviant behavior instrument. For each item, ratings were obtained on a 5-point scale ranging from *none of them* (0) to *all of them* (4). Scale scores were computed by averaging across items. To simplify the presentation, we have chosen to use only the participant's initial scale score at age 11 as a predictor of change. Further analyses could capitalize on the potentially time-varying nature of the exposure data to answer more complex questions than we are asking here (e.g., Is change over time in adolescents' tolerance of deviant behavior related to change in their exposure to that behavior?).

Table 1
Data on a Subsample of 16 Drawn at Random From the 168 Adolescents in the Example

Subject ID number	Reported tolerance of deviant behavior ^a					Predictors of change	
	Age 11	Age 12	Age 13	Age 14	Age 15	Gender ^b	Exposure to deviant behavior at age 11
0009	2.23	1.79	1.90	2.12	2.66	0	1.60
0045	1.12	1.45	1.45	1.45	1.99	1	1.30
0268	1.45	1.34	1.99	1.79	1.34	1	0.76
0314	1.22	1.22	1.55	1.12	1.12	0	0.76
0442	1.45	1.99	1.45	1.67	1.90	0	0.84
0514	1.34	1.67	2.23	2.12	2.44	1	0.84
0569	1.79	1.90	1.90	1.99	1.99	0	2.29
0624	1.12	1.12	1.22	1.12	1.22	1	0.99
0723	1.22	1.34	1.12	1.00	1.12	0	0.99
0918	1.00	1.00	1.22	1.99	1.22	0	0.76
0949	1.99	1.55	1.12	1.45	1.55	1	0.84
0978	1.22	1.34	2.12	3.46	3.32	1	0.76
1105	1.34	1.90	1.99	1.90	2.12	1	1.12
1542	1.22	1.22	1.99	1.79	2.12	0	1.15
1552	1.00	1.12	2.23	1.55	1.55	0	0.84
1653	1.11	1.11	1.34	1.55	2.12	0	1.00

^a On a 4-point scale ranging from *very wrong* (1) to *not wrong at all* (4).

^b 0 = male, 1 = female.

Under the individual growth modeling framework, the “true” part of each person’s growth trajectory is represented by an algebraic function of time. Many possible mathematical functions are available, both those that depend linearly on time and those that do not. Choice of an appropriate mathematical function to represent true individual change is an important first step in any project.³

A responsible preliminary strategy for choosing a valid growth model is to inspect each person’s empirical growth record by plotting his or her observed status against time (see Willett, 1989). As an aid to inspection, we also find it useful to superimpose an observed growth trajectory (estimated through within-person ordinary least squares [OLS] regression analysis) on each individual’s plot. Such exploratory analyses permit the investigator to compare the appropriateness of alternative growth models through descriptive statistics that describe the fit of each model. In our data example, this process—along with examination of wave-by-wave univariate descriptive statistics on the dependent variable—suggested that the distribution of the natural logarithm of tolerance of deviance was less skewed and that, once transformed, a linear (straight-line) model was an appropriate representation of individual change in log tolerance of deviance over the adolescent years.⁴

As an evocative summary of our data exploration, Figure 1 presents OLS-fitted observed straight-line growth curves for the adolescents in Table 1. Notice that the observed (log) tolerance of deviance of most adolescents increases as time passes and that there is evidence of heterogeneity in observed change across people. This collection of trajectories must be interpreted carefully, however, because the trajectories summarize observed rather than true change. It is possible, for instance, that all differences among the slopes of the 16 fitted trajectories can be attributed to measurement error rather than to heterogeneity in

true rate of change. The methods described in this article can distinguish these two eventualities.

The methods described here do not explicitly demand the preliminary inspection of empirical growth records. In subsequent analysis, one can confirm earlier “eyeball” suspicions by testing whether higher order nonlinear terms must be added to the individual growth function. Nonetheless, we recommend that every analysis of change begin with individual-level data exploration. Sound data-analytic practice demands knowledge of the data at the lowest level of aggregation so that anomalous cases can be identified, outlying data points can be detected, and assumptions can be checked. Once data are summarized in a covariance matrix, all individual-level richness is lost.

As we have noted, in our data example, preliminary exploration suggested that a straight-line function was most appropriate for modeling change in log tolerance of deviance over the adolescent years. Therefore, we model true individual change in log tolerance as a linear function of time, with a stochastic term added to account for the influence of measurement error:

$$Y_{ip} = \pi_{0p} + \pi_{1p}t_i + \epsilon_{ip}, \quad (1)$$

³ Ideally, theory will guide the rational choice of model so that the specified individual growth parameters have meaningful substantive interpretations. Often, however, the mechanisms governing the change process are poorly understood and, thus, a well-fitting polynomial is used to approximate the trajectories. Also, in much research, only a restricted portion of the life span is observed with few waves of data collected, and so the selected growth model must contain a small number of individual growth parameters if the model is to be fitted successfully. Thus, the most popular growth model is often a linear or a quadratic function of time.

⁴ Details are available on request. Raudenbush and Chan (1992) also transformed the dependent variable logarithmically.

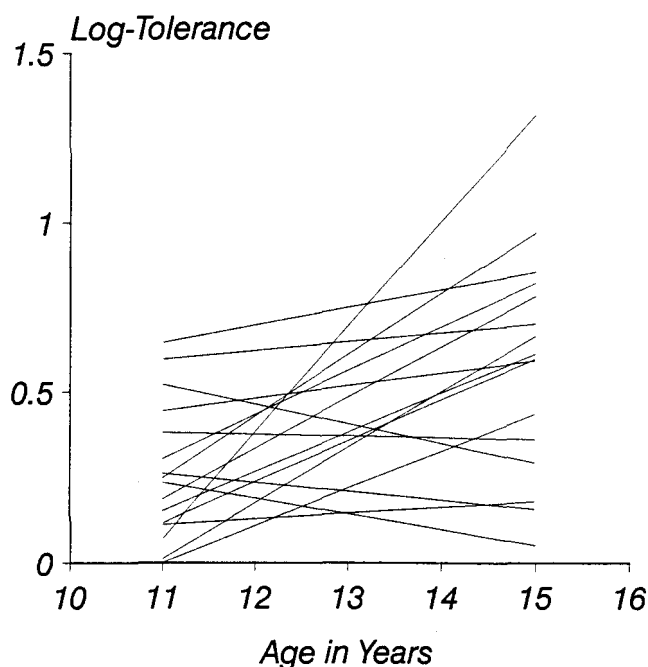


Figure 1. A collection of ordinary least squares (OLS) fitted trajectories summarizing observed linear growth in (log) tolerance for deviant behavior between ages 11 and 15 for the subsample of 16 randomly selected youths whose empirical growth records are displayed in Table 1.

where Y_{ip} is the observed value of log tolerance of deviance and ϵ_{ip} is the measurement error for the p th person ($p = 1, 2, \dots, 168$) at known times t_i ($i = 1, 2, \dots, 5$).

The shape of the trajectory for a particular person depends on the way in which time is parameterized in the model and on the values of the constants—the individual growth parameters—that appear on the right-hand side of the model. The straight-line individual growth model in Equation 1 contains a linear parameterization of time and a pair of individual growth parameters representing the intercept and slope of the true trajectory. The slope parameter π_{1p} is easy to interpret. It represents rate of change in true status over time for the p th person. In our example, with time measured in years, π_{1p} represents the yearly rate of true change in log tolerance of deviance. Adolescents whose tolerance increased rapidly with time will have large positive values of this parameter; those whose tolerance increased less rapidly will possess correspondingly smaller values.

Mathematically, the intercept parameter π_{0p} is also easy to interpret: It is the true status of person p when t_i is equal to zero. However, in many research projects there is no natural or convenient origin for time; thus, the investigator can control the interpretation of the intercept parameter by defining Time 0 at some interesting or important point in the life course. In our example, for instance, although we possess measurements on each person at 11, 12, 13, 14, and 15 years of age, we chose to define the third occasion of measurement as the origin of time (i.e., we set $t_3 = 0$). Our measurement times are thus $t_1 = -2$, $t_2 = -1$, $t_3 = 0$, $t_4 = 1$, and $t_5 = 2$ years, and the intercept parameter

π_{0p} represents the true value of log tolerance of deviance for the p th adolescent at 13 years of age.⁵

A word of caution: Like many other common forms of statistical analysis, the individual growth modeling approach is applicable only if it is intuitively sensible to measure change in the outcome variable. At the very least, this means that the outcome variable must have three properties. First, it must be a continuous variable at either the interval or ratio level. Second, it must be equatable from occasion to occasion (i.e., each scale point on the measure must retain an identical meaning as time passes). Finally, it must remain construct valid for the entire period of observation. If any of these conditions are violated, the methods that we describe here are being inappropriately applied.

A Matrix Representation of the Empirical Growth Record

In our data example, five waves of longitudinal data were collected. Therefore, each person's empirical growth record contains five measurements of observed status: Y_{1p} , Y_{2p} , Y_{3p} , Y_{4p} , and Y_{5p} . Under the individual growth model in Equation 1, these measurements can be represented conveniently as

$$\begin{bmatrix} Y_{1p} \\ Y_{2p} \\ Y_{3p} \\ Y_{4p} \\ Y_{5p} \end{bmatrix} = \begin{bmatrix} 1 & t_1 \\ 1 & t_2 \\ 1 & t_3 \\ 1 & t_4 \\ 1 & t_5 \end{bmatrix} \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix} + \begin{bmatrix} \epsilon_{1p} \\ \epsilon_{2p} \\ \epsilon_{3p} \\ \epsilon_{4p} \\ \epsilon_{5p} \end{bmatrix}. \quad (2)$$

For pedagogical reasons, in Equation 2 and throughout the text, we have retained symbols t_1 through t_5 to represent the times at which the panel data were obtained. In any particular research project, each of these symbols will have a known constant value. For instance, in our data example, because of our earlier centering of the time axis at age 13, t_1 through t_5 have the values -2 , -1 , 0 , 1 , and 2 years, respectively.

Note that, by algebraic manipulation, we have shown that the observed growth record for person p can be written as a combination of three parts: (a) a matrix of known times and constants identical across all individuals, multiplied by (b) an individual-specific vector of unknown individual growth parameters (which we refer to henceforth as the *latent growth vector*), and added to (c) an individual-specific vector of unknown errors of measurement. This representation provides a critical conceptual emphasis showing that, for each person, one can view the empirical growth record (the observed score vector on the left of Equation 2) as a weighted linear combination of the elements of an unobserved latent growth vector added to a measurement error vector. It is the latent growth vector that is the focus of a study of interindividual differences in change. In our data example, the two elements of the latent growth vector represent the within-person signal: the individual growth parameters that describe true change over time for person p . The elements of the error vector, on the other hand, describe the within-person noise: the forces that disturb measurement of person p 's

⁵ Making the middle of the occasions of measurement, the origin of time ensures that the intercept parameter is estimated most precisely and facilitates the convergence of the iterative model-fitting process.

true change over time. If the latter are large and erratic, one may not be able to detect the former.

Distribution of the Measurement Errors

In Equations 1 and 2, we stated that error ϵ_{1p} disturbs the true status of the p th person on the first occasion of measurement, ϵ_{2p} does so on the second occasion, and so forth. However, we have made no claims about the shape of the error distribution; the errors may be homoscedastic and independent over time within individuals, they may be heteroscedastic, or they may be autocorrelated. We usually begin by assuming that the errors of measurement obey stringent "classical" assumptions; that is, they are distributed independently and homoscedastically over time with mean zero and homogeneous variance σ_ϵ^2 . In other words, person p draws his or her measurement error vector from the following distribution:

$$\begin{bmatrix} \epsilon_{1p} \\ \epsilon_{2p} \\ \epsilon_{3p} \\ \epsilon_{4p} \\ \epsilon_{5p} \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_\epsilon^2 & 0 & 0 & 0 & 0 \\ 0 & \sigma_\epsilon^2 & 0 & 0 & 0 \\ 0 & 0 & \sigma_\epsilon^2 & 0 & 0 \\ 0 & 0 & 0 & \sigma_\epsilon^2 & 0 \\ 0 & 0 & 0 & 0 & \sigma_\epsilon^2 \end{bmatrix} \right), \quad (3)$$

where the mean vector and covariance matrix on the right-hand side are assumed to be identical across people.

A major advantage of the covariance structure approach described here lies in the flexibility with which the error covariance structure can be modeled. Under the method, we assume that each person draws his or her measurement error vector at random from a distribution with mean vector zero and an unknown covariance matrix whose shape can be specified as necessary. This permits us to test the fit of the classical error structure against other, more liberal hypotheses, and we can modify the error covariance structure as necessary. And regardless of the final structure adopted, we can estimate the components of the hypothesized error covariance matrix.⁶ This facility is important in a study of change because knowledge of the magnitudes of the error variances and covariances underpins the estimation of measurement reliability and error autocorrelation. We provide examples of this later.

Modeling Interindividual Differences in Change

Even though all people share a common functional form for their change, the true growth trajectories may still differ across people because of interindividual variation in the values of the individual growth parameters. Thus, formerly ill-specified questions about vaguely defined interindividual differences in change can be reframed as specific questions about the distribution of individual growth parameters across people in the population. In our data example (in which we believe that straight-line growth is occurring), for instance, we can ask questions about (a) the population mean vector of the individual growth parameters (e.g., Across all members of the population, what is the average value of the true intercept? Of the true slope?) and (b) the population covariance matrix of the individual growth parameters (e.g., Across all members of the population, what is the variance of the true intercept? Of the true slope? What is the population covariance of the true intercept and slope?).

Thus, when one studies interindividual differences in change, one expresses an interest in the population between-person distribution of the individual growth parameters. In our data example, for instance, we assume that each person in the population draws his or her latent growth vector independently from a multivariate normal distribution of the following form:

$$\begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix} \sim N \left(\begin{bmatrix} \mu_{\pi_0} \\ \mu_{\pi_1} \end{bmatrix}, \begin{bmatrix} \sigma_{\pi_0}^2 & \sigma_{\pi_0\pi_1} \\ \sigma_{\pi_1\pi_0} & \sigma_{\pi_1}^2 \end{bmatrix} \right). \quad (4)$$

The hypothesized distribution in Equation 4 is our first between-person, or Level 2, model for interindividual differences in true change. Later we extend this model by introducing predictors of change into the formulation. Even in this simple model, however, there are several between-person parameters worthy of estimation: the population means, variances, and covariance on the right-hand side of Equation 4. These parameters provide baseline information on the average trajectory of true change, the variation of true intercept and slope, and the covariation of true intercept and slope in the population, thereby answering the preliminary questions cited earlier in this subsection.

Adopting a Covariance-Structure Perspective

In Table 2, we present the sample mean vector and covariance matrix for the variables introduced in Table 1, estimated with data on all 168 adolescents in the illustrative data set. What statements about change over time do these statistics readily support? Focus, first, on the statistics describing the five waves of observed log tolerance of deviance. Examining the wave-by-wave means shows that observed (log) tolerance tends to increase steadily, on average, over the 5-year period of observation in the sample as a whole. In addition, the magnitudes of the variances along the leading diagonal of the sample covariance matrix suggest that observed log tolerance of deviance becomes more variable over time, perhaps as adolescents' scores "fan out" with age. Finally, inspection of the sample between-wave covariances suggests a generally positive association among observed log tolerance of deviance over the five occasions of measurement.

However, even ignoring the distinction between observed and true scores, it is not easy to reach informed conclusions about interindividual differences in change by inspecting between-wave summary statistics (Rogosa et al., 1982; Rogosa & Willett, 1985; Willett, 1989). Between-wave statistics do not provide an optimal view for easy inference about differences in individual change. To answer questions about change, one must adopt a perspective that emphasizes change. Rather than summarizing data as between-wave variances and covariances, one must use individual growth trajectories. For instance, it is easier to see from Figure 1 that observed change is generally positive, individuals are fanning out over time, and there is heterogeneity in level and rate of change across people. The data are identical in both cases, but the view offered by the summary statistics differs; each view supports a qualitatively different kind of interpretation.

⁶ Provided the hypothesized covariance structure model is identified.

Table 2
Sample Mean Vector and Covariance Matrix for the Five Waves of Log Tolerance of Deviant Behavior and Two Predictors of Change

Statistic	Log tolerance of deviant behavior					Predictors of change	
	Age 11	Age 12	Age 13	Age 14	Age 15	Gender (G _p)	Log exposure to deviant behavior (E _p)
Mean vector	.2008	.2263	.3255	.4168	.4460	.4762	-.0788
Covariance matrix							
Age 11	.0317						
Age 12	.0133	.0395					
Age 13	.0175	.0256	.0724				
Age 14	.0213	.0236	.0531	.0857			
Age 15	.0230	.0233	.0479	.0663	.0873		
Gender	-.0108	-.0143	-.0225	-.0299	-.0270	.2509	
Log exposure	.0115	.0133	.0089	.0091	.0186	-.0498	.0693

Note. $N = 168$.

Does this mean that one cannot recover information about change once data have been collapsed into between-wave means and covariances? No, it does not. One must simply "match up" the between-wave and change perspectives explicitly. If we could, for instance, determine the between-wave implications of the individual growth modeling perspective adopted in Equations 1–4, we could check whether they compared favorably with the data summaries in Table 2. For instance, in Equations 4 and 3, we proposed what we believe are reasonable models for interindividual variation in the individual growth parameters and errors of measurement. If we are correct, then these models must underwrite the between-wave mean and covariance structure evident in Table 2. In other words, although we are dealing with two different perspectives on the problem—a between-wave perspective in Table 2 and a growth perspective in Equations 1–4—the between-wave covariance structure implied by the growth models must resemble the between-wave covariance structure observed in our data if our parameterization of change is correct.

Fortunately, well-developed methods are available for testing our suspicions: the methods of covariance structure analysis. Starting with the sample mean vector and covariance matrix in Table 2 as input we can claim that our hypothesized growth models fit when, having estimated the parameters of Equations 3 and 4, we can accurately predict the between-wave covariance structure of the observed data. As Meredith, Tisak, McArdle, and Muthén have pointed out, the growth formulation that we have posited—the within-person models of Equations 2 and 3 and the between-person model of Equation 4—falls naturally into the framework offered by the LISREL model with mean structures (Jöreskog & Sörbom, 1989). Thus, maximum likelihood estimates of the important parameters in Equations 3 and 4 can be obtained by covariance structure analysis, as we now demonstrate.

Rewriting the Individual Growth Model as the LISREL Measurement Model for Y

When covariance structure analysis is used to examine change over time, the hypothesized individual growth model

plays the role of the LISREL measurement model for the vector of endogenous variables Y . For instance, we can rewrite the empirical growth record of the p th person in our illustrative example as

$$\begin{bmatrix} Y_{1p} \\ Y_{2p} \\ Y_{3p} \\ Y_{4p} \\ Y_{5p} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 & t_1 \\ 1 & t_2 \\ 1 & t_3 \\ 1 & t_4 \\ 1 & t_5 \end{bmatrix} \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix} + \begin{bmatrix} \epsilon_{1p} \\ \epsilon_{2p} \\ \epsilon_{3p} \\ \epsilon_{4p} \\ \epsilon_{5p} \end{bmatrix}, \quad (5)$$

which has the format of the LISREL measurement model for endogenous variables Y :

$$Y = \tau_y + \Lambda_y \eta + \epsilon, \quad (6)$$

with LISREL score vectors that contain the empirical growth record, the individual growth parameters, and the errors of measurement, respectively:

$$Y = \begin{bmatrix} Y_{1p} \\ Y_{2p} \\ Y_{3p} \\ Y_{4p} \\ Y_{5p} \end{bmatrix}, \eta = \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix}, \epsilon = \begin{bmatrix} \epsilon_{1p} \\ \epsilon_{2p} \\ \epsilon_{3p} \\ \epsilon_{4p} \\ \epsilon_{5p} \end{bmatrix}. \quad (7)$$

Furthermore, unlike the usual practice of covariance structure analysis, the elements of the LISREL τ_y and Λ_y parameter matrices are entirely constrained to contain only known values,

$$\tau_y = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \Lambda_y = \begin{bmatrix} 1 & t_1 \\ 1 & t_2 \\ 1 & t_3 \\ 1 & t_4 \\ 1 & t_5 \end{bmatrix}, \quad (8)$$

and the error vector ϵ is distributed with zero mean vector and covariance matrix Θ_ϵ , which, under the classical assumptions of Equation 3, is given by

$$\Theta_\epsilon = \text{Cov}(\epsilon) = \begin{bmatrix} \sigma_\epsilon^2 & 0 & 0 & 0 & 0 \\ 0 & \sigma_\epsilon^2 & 0 & 0 & 0 \\ 0 & 0 & \sigma_\epsilon^2 & 0 & 0 \\ 0 & 0 & 0 & \sigma_\epsilon^2 & 0 \\ 0 & 0 & 0 & 0 & \sigma_\epsilon^2 \end{bmatrix}. \quad (9)$$

Rewriting the Model for Interindividual Differences in Change as the LISREL Structural Model

Note that, unlike in more familiar standard covariance structure analyses, we have chosen to specify the entire LISREL Λ_y parameter matrix in Equation 8 as a matrix of known times and constants rather than as a collection of unknown parameters to be estimated. This specification acts to "pass" the critical Level 1 individual growth parameters (π_{0p} and π_{1p}) from the Level 1 growth model into the LISREL endogenous construct vector η , which we have then referred to as the latent growth vector. In other words, our fully constrained specification for Λ_y has forced the η vector to contain the very individual-level parameters whose Level 2 distribution is to become the focus of our subsequent between-person analyses.

These Level 2 analyses are conducted within the structural component of the general LISREL model, which permits the distribution of the η vector to be modeled explicitly in terms of selected population means, variances, and covariances. And, of course, the particular population means, variances, and covariances that we have selected as parameters of the structural model are those that we have hypothesized are the important parameters in the joint distribution of the individual growth parameters in Equation 4. All that is required is to write the latent growth vector as

$$\begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix} = \begin{bmatrix} \mu_{\pi_0} \\ \mu_{\pi_1} \end{bmatrix} + \begin{bmatrix} 0 & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix} + \begin{bmatrix} \pi_{0p} - \mu_{\pi_0} \\ \pi_{1p} - \mu_{\pi_1} \end{bmatrix}, \quad (10)$$

which has the form of the reduced LISREL structural model

$$\eta = \alpha + B\eta + \zeta \quad (11)$$

with a latent residual vector ζ that contains the deviations of the individual growth parameters from their respective population means,

$$\zeta = \begin{bmatrix} \pi_{0p} - \mu_{\pi_0} \\ \pi_{1p} - \mu_{\pi_1} \end{bmatrix}, \quad (12)$$

and parameter matrices,

$$\alpha = \begin{bmatrix} \mu_{\pi_0} \\ \mu_{\pi_1} \end{bmatrix}, B = \begin{bmatrix} 0 & 0 \\ 0 & 0 \end{bmatrix}. \quad (13)$$

Note that we have moved the population averages of the individual growth parameters—true intercept and slope, in this case—into the LISREL α vector. This permits these important mean parameters to be estimated explicitly. The elements of the LISREL latent residual vector, ζ , in Equations 11 and 12 contain deviations of π_{0p} and π_{1p} from their respective population means. The ζ vector of latent residuals is of special interest here because it is distributed with zero mean vector and covariance matrix Ψ , the matrix containing the very variance and covariance parameters in which one is most interested in an investigation of interindividual differences in change:

$$\Psi = \text{Cov}(\zeta) = \begin{bmatrix} \sigma_{\pi_0}^2 & \sigma_{\pi_0\pi_1} \\ \sigma_{\pi_1\pi_0} & \sigma_{\pi_1}^2 \end{bmatrix}. \quad (14)$$

To summarize, in Equations 1–4, the individual growth mod-

eling framework provides baseline Level 1 (within-person) and Level 2 (between-person) models that represent our initial hypotheses about the growth structure underlying the five waves of panel data in our data example. Then, in Equations 5–14, we have shown that these models can be rewritten, without loss of generality, in the format and notation of the general LISREL model with mean structures. By carefully choosing our specification of the various standard LISREL parameter matrices, we have forced the LISREL Y -measurement model to become our original Level 1 individual growth model (including all existing assumptions on the distribution of the measurement errors), and we have forced a reduced form of the LISREL structural model to become our Level 2 model for interindividual differences in true change.

Because of this direct and explicit mapping of one model into the other, we can test whether our hypothesized growth formulation underpins the matrix of observed between-wave variances and covariances in Table 2 using the LISREL program. If the implied covariance structure fits the data, then we also obtain, and can interpret, LISREL-provided maximum likelihood estimates of the unknown parameters in our growth models that now reside in the α vector, the Θ matrix, and the Ψ matrix. In the Appendix, we provide an annotated LISREL program for this analysis (Model 1). The program specifies the τ_y , Λ_y , Θ , α , B , and Ψ parameter matrices as defined in Equations 8, 9, 13, and 14. All hypothesized zero entries in these parameter matrices are fixed at zero in the program; the values of measurement times t_1 through t_5 are set to -2 , -1 , 0 , 1 , and 2 in accordance with our earlier centering decision; and all unknown parameters are free to be estimated.

This baseline "no predictors of change" model fits moderately well (see Bollen, 1989, pp. 256–289, for a discussion of the use of summary statistics in model evaluation). Although the model chi-square statistic (49.74) is slightly large, given its degrees of freedom (14), the values of other goodness-of-fit indices are heartening: Both LISREL goodness-of-fit statistics are greater than .9 (goodness of fit index [GFI] = .918, adjusted goodness of fit index [AGFI] = .912), and the root mean-square residual (RMSR) is small relative to the absolute magnitude of the elements of the sample covariance matrix in Table 2 (RMSR = .008). Maximum likelihood estimates of the unknown parameters are listed under Model 1 in Table 3, along with approximate p values.⁷

The entries in the first two rows of Table 3 for Model 1 estimate the population means of true intercept (.3231, $p < .001$) and true slope (.0681, $p < .001$) and describe the average trajectory of true change in the dependent variable. On average, ado-

⁷ The approximate p value tests the null hypothesis that the value of a parameter is zero in the population using a test statistic that is the ratio of the parameter estimate to its asymptotic standard error (see Bollen, 1989, p. 286). The investigator should be cautious in interpreting p values associated with these tests of the variance components, however, because they are sensitive to failures of the assumption of multivariate normality. As Miller (1986) noted, when commenting generally on parametric tests of variance, "the effects of nonnormality on the distribution theories for the [variance component] test statistics . . . are catastrophic. For each test the actual significance level can be considerably different from the nominally stated level" (p. 264).

Table 3
Fitted Models Demonstrating Interindividual Differences in
Change in Log Tolerance in the Full Sample

Parameter	Maximum likelihood estimates		
	Model 1	Model 2	Model 3
μ_{π_0}	.3231***	.3235***	.3197***
μ_{π_1}	.0681***	.0664***	.0643***
$\sigma_{\pi_0}^2$	.0328***	.0326***	.0295***
$\sigma_{\pi_1}^2$	.0026***	.0029***	.0023*
$\sigma_{\pi_0\pi_1}$	.0081***	.0079***	.0070***
$\sigma_{\epsilon_1}^2$	.0254***	.0186***	.0195**
$\sigma_{\epsilon_2}^2$	.0254***	.0269***	.0275***
$\sigma_{\epsilon_3}^2$	.0254***	.0340***	.0382***
$\sigma_{\epsilon_4}^2$	.0254***	.0242***	.0350***
$\sigma_{\epsilon_5}^2$	.0254***	.0178***	.0212*
$\sigma_{\epsilon_1\epsilon_2}$			.0010
$\sigma_{\epsilon_2\epsilon_3}$			.0052†
$\sigma_{\epsilon_3\epsilon_4}$			.0113***
$\sigma_{\epsilon_4\epsilon_5}$			.0084
χ^2	49.74	39.82	20.83
df	14	10	6
Goodness of fit index (GFI)	.918	.941	.981
Adjusted goodness of fit index (AGFI)	.912	.912	.951
Root mean-square residual (RMSR)	.008	.006	.004

Note. $N = 168$. See text for descriptions of models.

† $p < .10$. * $p < .05$. ** $p < .01$. *** $p < .001$ (approximate values).

lescents' true log tolerance of deviance increases by .0681 per year, having a value of .3231 in Year 3 (13 years of age).

The entries in the third and fourth rows for Model 1—the fitted variances of true intercept (.0328, $p < .001$) and true slope (.0026, $p < .001$)—estimate population interindividual heterogeneity in true change. Because both of these variances are nonzero, we know that between-person heterogeneity in the age 13 level and rate of change in true log tolerance exist in the population. The fifth table entry under Model 1 provides an estimate of the covariance of the true intercept and true rate of change in log tolerance of deviance across people in the population (.0081, $p < .001$). Combining this covariance estimate with the estimated variances suggests that the true rate of change has a correlation of .887 with the true intercept; this large value indicates that participants with higher age 13 levels of true log tolerance also have the most rapid rates of increase.

Entries in the 6th through 10th rows for Model 1 provide an estimate of the homoscedastic measurement error variance (.0254, $p < .001$), which—together with the variances of observed score along the leading diagonal of the sample covariance matrix in Table 2—indicates that, except for the first and second panels, the within-wave reliability of measurement was moderate (.198, .357, .649, .703, and .709, respectively, in Years 1 through 5). Finally, substituting the estimated variances of measurement error and true slope into Equation 29 of Willett (1989), we find that the rate of true change in log tolerance has been measured with a reliability of .502. This is higher than

usually anticipated in the measurement of change and higher than the reliability with which log tolerance itself was measured on two of the occasions. It illustrates that, if sufficient waves of longitudinal data are collected, the measurement of change can be more reliable than the measurement of status on a single occasion despite the prognostications of Bereiter (1963), Lord (1963), and others.

Testing for Evidence of Nonlinear Individual Change

So far, we have hypothesized that individual change over time in log tolerance is linear. However, in practice, individual change may be curvilinear (e.g., see the research on vocabulary growth in children conducted by Huttenlocher, Haight, Bryk, & Seltzer, 1991).

The covariance structure approach that we have described can easily be modified to include any Level 1 growth model that is linear in the individual growth parameters. Keats (1983) defined such models as having the property of dynamic consistency; for such models, the curve of the averages (obtained by taking the population of true growth curves and plotting the average of the true scores at each value of time) is identical to the average of the curves (obtained by averaging the individual growth parameters over the population and plotting a curve with parameters equal to these averages). Many common growth functions, including segmented growth curves and polynomial growth of any order, are dynamically consistent. Other, more specialized growth functions (such as the Gompertz, Jenss, and logistic functions) are not; therefore, the character of the individual curves is distorted by group averaging, making it difficult to infer the shape of individual growth from a group growth curve (Boas, 1892; Estes, 1956).

If true individual change is hypothesized to be a quadratic function of time, for instance, the observed status of the p th person at time t_i can be represented by

$$Y_{ip} = \pi_{0p} + \pi_{1p}t_i + \pi_{2p}t_i^2 + \epsilon_{ip}, \quad (15)$$

where the presence of the quadratic parameter π_{2p} permits the trajectory to be curvilinear. If π_{2p} is negative, the trajectory is concave to the time axis; if it is positive, the trajectory is convex to the time axis. Because time was centered on the third occasion of measurement, π_{0p} represents the p th person's true log tolerance of deviance at age 13, and π_{1p} is the instantaneous rate of true change in log tolerance of deviance at age 13.

Again, following Equation 5, we can write the empirical growth record for the p th person as the product of a matrix of known times and constants and an individual-specific latent growth vector containing the unknown individual growth parameters, added to a measurement error vector. As before, this provides the LISREL measurement model for the endogenous variables Y , but now the quadratic individual growth parameter is forced into the latent growth vector η along with true intercept and slope by suitable redefinition of the earlier Δ_y parameter matrix, as follows:

$$\begin{bmatrix} Y_{1p} \\ Y_{2p} \\ Y_{3p} \\ Y_{4p} \\ Y_{5p} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 & t_1 & t_1^2 \\ 1 & t_2 & t_2^2 \\ 1 & t_3 & t_3^2 \\ 1 & t_4 & t_4^2 \\ 1 & t_5 & t_5^2 \end{bmatrix} \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \\ \pi_{2p} \end{bmatrix} + \begin{bmatrix} \epsilon_{1p} \\ \epsilon_{2p} \\ \epsilon_{3p} \\ \epsilon_{4p} \\ \epsilon_{5p} \end{bmatrix}. \quad (16)$$

This matrix again has the format of the LISREL Y -measurement model in Equation 6 with constituent score vectors,

$$Y = \begin{bmatrix} Y_{1p} \\ Y_{2p} \\ Y_{3p} \\ Y_{4p} \\ Y_{5p} \end{bmatrix}, \eta = \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \\ \pi_{2p} \end{bmatrix}, \epsilon = \begin{bmatrix} \epsilon_{1p} \\ \epsilon_{2p} \\ \epsilon_{3p} \\ \epsilon_{4p} \\ \epsilon_{5p} \end{bmatrix}, \quad (17)$$

and parameter matrices,

$$\tau_y = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \Lambda_y = \begin{bmatrix} 1 & t_1 & t_1^2 \\ 1 & t_2 & t_2^2 \\ 1 & t_3 & t_3^2 \\ 1 & t_4 & t_4^2 \\ 1 & t_5 & t_5^2 \end{bmatrix}, \quad (18)$$

$$\Theta_\epsilon = \begin{bmatrix} \sigma_\epsilon^2 & 0 & 0 & 0 & 0 \\ 0 & \sigma_\epsilon^2 & 0 & 0 & 0 \\ 0 & 0 & \sigma_\epsilon^2 & 0 & 0 \\ 0 & 0 & 0 & \sigma_\epsilon^2 & 0 \\ 0 & 0 & 0 & 0 & \sigma_\epsilon^2 \end{bmatrix},$$

where the times t_1 through t_5 have known numeric value (as before).

Although all members of the population share a common quadratic growth function, their true change trajectories may differ when the values of the individual growth parameters differ from person to person. Thus, when studying interindividual differences in quadratic change, one remains interested in the population distribution of the latent growth vector, which can again be modeled within the LISREL structural model:

$$\begin{bmatrix} \pi_{0p} \\ \pi_{1p} \\ \pi_{2p} \end{bmatrix} = \begin{bmatrix} \mu_{\pi_0} \\ \mu_{\pi_1} \\ \mu_{\pi_2} \end{bmatrix} + \begin{bmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \\ \pi_{2p} \end{bmatrix} + \begin{bmatrix} \pi_{0p} - \mu_{\pi_0} \\ \pi_{1p} - \mu_{\pi_1} \\ \pi_{2p} - \mu_{\pi_2} \end{bmatrix}. \quad (19)$$

Again, this model has the form of the reduced structural model in Equation 11 but with an expanded definition of the LISREL latent residual vector,

$$\zeta = \begin{bmatrix} \pi_{0p} - \mu_{\pi_0} \\ \pi_{1p} - \mu_{\pi_1} \\ \pi_{2p} - \mu_{\pi_2} \end{bmatrix}, \quad (20)$$

and parameter matrices modified to account for the presence of the quadratic individual growth parameter in the latent growth vector η ,

$$\alpha = \begin{bmatrix} \mu_{\pi_0} \\ \mu_{\pi_1} \\ \mu_{\pi_2} \end{bmatrix}, B = \begin{bmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, \quad (21)$$

$$\Psi = \begin{bmatrix} \sigma_{\pi_0}^2 & \sigma_{\pi_0\pi_1} & \sigma_{\pi_0\pi_2} \\ \sigma_{\pi_1\pi_0} & \sigma_{\pi_1}^2 & \sigma_{\pi_1\pi_2} \\ \sigma_{\pi_2\pi_0} & \sigma_{\pi_2\pi_1} & \sigma_{\pi_2}^2 \end{bmatrix}.$$

This expanded model for interindividual differences in true quadratic change (Equations 15–21) can be fitted by straightforward modification of the LISREL program for Model 1 in the Appendix. The respective fits of the linear and quadratic

formulations can then be compared directly because the linear formulation is nested within the quadratic formulation (setting π_{2p} to zero in Equations 15–21 leads to Equations 5–14). Specifically, the null hypothesis that the addition of a quadratic term to the linear individual growth model does not improve the fit of the simpler representation can be evaluated by performing a standard “decrement-to-chi-square” test in which the respective goodness of fits (and degrees of freedom) of the linear and quadratic representations are differenced. In our data example, this test indicates that the addition of the quadratic parameter does not improve global goodness of fit (change in $\chi^2 = 49.74 - 44.18 = 5.56$, change in $df = 14 - 10 = 4$). We conclude, therefore, that the straight-line individual growth model in Equation 1 is an appropriate representation of change over time in this particular case.

Note, however, that we refer to this comparison of the two nested models as a global test. Its purpose is analogous to the usual inspection of the global F statistic associated with a complex main effect in an ANOVA before conducting multiple comparisons or follow-up contrast analyses. With the addition of the quadratic term to the individual straight-line growth model, four new parameters have been added to the Level 2 model: μ_{π_2} , the population mean of the quadratic parameter; $\sigma_{\pi_2}^2$, the population variance of π_{2p} , and $\sigma_{\pi_2\pi_0}$ and $\sigma_{\pi_2\pi_1}$, the population covariances of π_{2p} with π_{0p} and π_{1p} . Therefore, a comparison of the fits of the linear and quadratic formulations is actually a simultaneous test of the jointly null values of these Level 2 quadratic mean, variance, and covariance parameters, holding Type I error at some manageable level (e.g., an alpha level of .05). Broadly speaking, the global test evaluates whether there is any interest in including a quadratic term in the individual growth model; in our case, there is no such interest.⁸

Of course, the flexibility of the covariance structure approach permits a sequence of more subtle and restrictive hypotheses to be tested. If we had rejected the null hypothesis under the global test, for instance, we would have been entitled to follow up with tests of subhypotheses in which the four Level 2 parameters were constrained to be zero, either singly or in interesting combinations. For example, we could test whether everyone does, in fact, experience quadratic growth but with a curvature identical for all, that is, the case in which the value of the quadratic growth parameter π_{2p} is fixed at its population average for all individuals (i.e., $\pi_{2p} = \mu_{\pi_2}$ for all p). This hypothesis is easily tested by comparing the fit of the full quadratic model, as described earlier, with that of a reduced quadratic model in which the population average of the curvature term μ_{π_2} is estimated but the population variance of π_{2p} and its covariances with true intercept and slope are constrained to be zero (in other words, everyone is hypothesized to possess an identical nonzero curvature coefficient equal to μ_{π_2}). On the other hand, if we wished to test whether the population average of the quadratic growth parameter was, in fact, zero but that individual quadratic terms

⁸ A reviewer pointed out that the results of a global test may be misleading if the variance components associated with the quadratic parameter are small. The power to detect a nonzero mean coefficient may be lower for the global test than for a specific test of the quadratic mean parameter. Therefore, the prudent strategy is always to conduct separate tests of each hypothesis in lieu of the omnibus test.

were distributed (randomly) about this value, we would compare the full quadratic model with one in which μ_{π_2} was set to zero and $\sigma_{\pi_2\pi_0}$, $\sigma_{\pi_2\pi_1}$, and $\sigma_{\pi_2}^2$ are free to be estimated. The comparison of nested models within the general LISREL framework provides a very flexible strategy for testing the effectiveness of reasoned modifications to the basic measurement (within-person) and structural (between-person) models.

Testing Whether Measurement Errors Are Heteroscedastic and Nonindependent

Investigators often assume that measurement errors are homoscedastic and independent within individuals over time, as we have done so far in this article. Such assumptions are common in the psychometric literature, in which they are central to classical test theory, and in the growth literature (e.g., see Berkley, 1982a, 1982b). However, with consecutive measurements on an individual changing over time, these assumptions may be untenable. There is no reason to believe a priori that the precision with which an attribute can be measured is identical at all ages, and so the measurement errors may be heteroscedastic. And when measurements are closely spaced in time, there may be inadvertent links among their errors.

The covariance structure approach affords great flexibility in modeling the error covariance structure; one can easily relax the stringent assumptions of homoscedasticity and zero autocorrelation on the measurement errors. At present, this facility is not available under the HLM approach of Bryk and Raudenbush (1992); neither has it been demonstrated in other applications of covariance structure analysis to the measurement of individual change (McArdle & Epstein, 1987; Muthén, 1991).

When distributional assumptions on the measurement errors are relaxed, the basic covariance structure approach is unchanged. The error covariance structure associated with the Level 1 (Y-measurement) model is simply modified to contain whatever parameters permit the hypothesized heteroscedasticity or autocorrelation among the errors. The Level 2 (structural) model for the distribution of the latent growth vector remains the same. The modified model can then be fit by means of the approach already described once the LISREL Θ_ϵ matrix—in which the newly hypothesized error structure resides—has been reparameterized appropriately, with suitable constraints on the equality of parameters being imposed or omitted as required.

For instance, one can hypothesize that the measurement errors are independent but heteroscedastic. Then, Θ_ϵ in Equation 9 becomes

$$\Theta_\epsilon = \begin{bmatrix} \sigma_{\epsilon_1}^2 & 0 & 0 & 0 & 0 \\ 0 & \sigma_{\epsilon_2}^2 & 0 & 0 & 0 \\ 0 & 0 & \sigma_{\epsilon_3}^2 & 0 & 0 \\ 0 & 0 & 0 & \sigma_{\epsilon_4}^2 & 0 \\ 0 & 0 & 0 & 0 & \sigma_{\epsilon_5}^2 \end{bmatrix}. \quad (22)$$

A program suitable for fitting the modified model is provided in the Appendix. When the new linear-change heteroscedastic-error model is fitted (Model 2 in Table 3), there is a statistically significant improvement in fit over Model 1 (change in $\chi^2 = 49.74 - 39.82 = 9.92$, change in $df = 14 - 10 = 4$). Now, rather than remaining constant at .0254 on all occasions, the estimated

measurement error variance is lower on the first and last occasions of measurement and peaks at .0340 when the adolescent is 13 years old. This, of course, modifies our earlier yearly estimates of the reliability of the dependent variable, which now becomes .413, .320, .531, .718, and .797, respectively. Other parameter estimates remain relatively stable from those obtained when Model 1 was fitted.

We can also relax the assumption of independence across time that we imposed on the wave-by-wave measurement errors by further respecifying the Θ_ϵ matrix. The LISREL program permits considerable flexibility in this regard. For instance, we can retain the heteroscedasticity that we detected earlier but also allow temporally adjacent pairs of measurement errors to be mutually autocorrelated:

$$\Theta_\epsilon = \begin{bmatrix} \sigma_{\epsilon_1}^2 & \sigma_{\epsilon_1\epsilon_2} & 0 & 0 & 0 \\ \sigma_{\epsilon_2\epsilon_1} & \sigma_{\epsilon_2}^2 & \sigma_{\epsilon_2\epsilon_3} & 0 & 0 \\ 0 & \sigma_{\epsilon_3\epsilon_2} & \sigma_{\epsilon_3}^2 & \sigma_{\epsilon_3\epsilon_4} & 0 \\ 0 & 0 & \sigma_{\epsilon_4\epsilon_3} & \sigma_{\epsilon_4}^2 & \sigma_{\epsilon_4\epsilon_5} \\ 0 & 0 & 0 & \sigma_{\epsilon_5\epsilon_4} & \sigma_{\epsilon_5}^2 \end{bmatrix}. \quad (23)$$

Model 3, in Table 3 (see the Appendix for the associated LISREL program), contains this pairwise autocorrelated error covariance structure. It improves successfully on the fit of Model 2 (see Table 3; change in $\chi^2 = 18.99$, change in $df = 4$), with estimated autocorrelations between adjacent pairs of measurement errors of .044, .159, .309, and .307, respectively. Note that, despite major changes in the hypothesized links among the measurement errors across the models in Table 3, the shape of the average trend line, the heterogeneity in linear growth, and the correlation between intercept and slope remain relatively stable. We use Model 3 as the foundation for subsequent investigations of systematic interindividual differences in change.

A Comment on the Requirement for Time-Structured Data

As we noted earlier, covariance structure methods for the analysis of change require that all sample members be observed on the same set of occasions. If the available data are not time structured, then the method cannot be used. This requirement is a potentially serious limitation not shared by other analytic approaches, such as those of Bryk and Raudenbush (1987) and Willett and Ayoub (1991).

In longitudinal research, investigators often intend at the outset to collect time-structured data; however, reality intervenes, and observations on some individuals on some occasions are omitted as a result of forces beyond the researcher's control. This introduces missing values into the data set and destroys the intended time structuring, leading to difficulties in the estimation of the sample covariance matrix on which subsequent analyses are based.

Bollen (1989) described two general approaches for dealing with missing data in covariance structure analysis. The first uses either listwise or pairwise deletion of incomplete cases, or the imputation of missing data points, to construct an alternative estimator of the sample covariance matrix. Estimators obtained in the reduced sample created by listwise deletion retain the

important property of consistency when data are missing completely at random. The second approach uses all available data by treating individuals with similar patterns of missing data as subgroups of the original sample so that multigroup analysis (Jöreskog & Sörbom, 1989) can be used to obtain estimates of model parameters, which are again consistent providing that data are missing completely at random. Both approaches are potentially applicable in the investigation of change, although the second may be preferable to the first. Muthén (1992) has described ways of applying this latter approach to the covariance structure analysis of incomplete longitudinal data. Recent advances in the handling of missing data may also lead to further innovations in this area (Graham, Hofer, & Piccinin, in press; Little & Rubin, 1987).

Of course, great caution must be exercised if there are individuals in the data set with incomplete or missing data. Data may not be missing completely at random; people with particular values of the predictors may have experienced unique patterns of change over time. Any such systematicity in the pattern of missing values will necessarily undermine the investigator's ability to make inferences back to the population as originally defined and may lead to bias in the interpretation of the findings. For this reason, we recommend that preliminary exploratory data analysis be conducted to examine whether cases with missing or incomplete data are atypical so that any interpretation of study findings can be circumscribed appropriately.

Modeling Systematic Interindividual Differences in Change

A baseline investigation of the no predictor of change model informs the subsequent analysis. If baseline analyses confirm the existence of heterogeneity in true change in the population, then we can ask whether this heterogeneity is related to selected characteristics of the people being observed. In other words, once interindividual differences in true change have been detected, we can ask about the systematic nature of that variation. And, because we have distinguished among the true change of different people in terms of their individual growth parameters, questions about systematic heterogeneity in true change naturally translate into questions about relationships between the individual growth parameters and predictors (Rogosa & Willett, 1985).

In our data example, we know that heterogeneity in true change exists in the population (Table 3), and we have two potential predictors of change to investigate: adolescent gender (G_p) and initial (log) exposure to deviant behavior at age 11 (E_p). Therefore, we can ask whether the individual growth parameters—intercept and slope—are related to this pair of predictors: Does the age 13 level of true (log) tolerance of deviance differ for boys and girls? Does it differ by initial exposure to deviance at age 11? Does the rate at which true (log) tolerance changes over time also depend on gender and exposure? The methods described here generalize immediately to the case of more than two predictors.

As we stated earlier, such questions are concerned with between-person differences in change. To answer them, we must incorporate potential predictors of change into the Level 2 model (i.e., into the LISREL structural model in which interin-

dividual differences in change are described). Within the general LISREL framework, predictors can be inserted into the structural model indirectly by taking advantage of the LISREL measurement model for exogenous predictors, X . This last component of the general LISREL model permits us to pass predictors of change into the LISREL vector of exogenous constructs ξ , which is a natural and so-far unused constituent of the LISREL structural model.

In the current case, in which we have single indicators of each predictor, we set up the X -measurement model in the following way:

$$\begin{bmatrix} G_p \\ E_p \end{bmatrix} = \begin{bmatrix} \mu_G \\ \mu_E \end{bmatrix} + \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} G_p - \mu_G \\ E_p - \mu_E \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix}. \quad (24)$$

This model has the format of the LISREL measurement model for exogenous variables X :

$$X = \tau_x + \Lambda_x \xi + \delta. \quad (25)$$

With constituent predictor, latent exogenous score, and error vectors,

$$X = \begin{bmatrix} G_p \\ E_p \end{bmatrix}, \xi = \begin{bmatrix} G_p - \mu_G \\ E_p - \mu_E \end{bmatrix}, \delta = \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \quad (26)$$

and constituent τ_x and Λ_x parameter matrices,

$$\tau_x = \begin{bmatrix} \mu_G \\ \mu_E \end{bmatrix}, \Lambda_x = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}. \quad (27)$$

The measurement model for exogenous variables X in Equation 24 can easily be modified in the usual way (Jöreskog & Sörbom, 1989) to accommodate multiple indicators of each predictor construct (if they are available). The parameter matrix Λ_x is simply expanded to include the requisite loadings (under the usual requirements for identification; see Bollen, 1989).

In a regular covariance structure analysis, there is typically an explicit statistical purpose for including multiple indicators of a particular construct in any measurement model. Multiple indicators are present so that their covariation can reveal the true variance of the underlying construct that they represent. This ensures that the fallibility with which each indicator has been measured is accounted for in the measurement model and ultimately leads to estimates of their associated error variances and reliabilities. In the case of exogenous variables X , this is achieved by permitting the error vector δ to contain nonzero entries and by estimating the elements of its associated error covariance matrix Θ_δ (Jöreskog & Sörbom, 1989). This same strategy is, of course, available to the investigator when covariance structure analysis is being used to examine systematic interindividual differences in change and is tantamount to applying a maximum likelihood correction for errors in the predictors to the fitted relationship between individual growth parameters and predictors of change (cf. Fuller, 1987). No other currently available software for the analysis of change permits such a correction.

Note that we have defined the LISREL τ_x parameter vector and Λ_x parameter matrix so that the predictors of change, G_p and E_p , are centered at their population averages and passed as deviations from their means into the LISREL latent exogenous

construct vector ξ . The standard LISREL covariance matrix Φ —which is intended to represent interrelationships among the elements of the latent exogenous vector ξ —is used to account for potential intercorrelations among the predictors of change:

$$\Phi = \text{Cov}(\xi) = \begin{bmatrix} \sigma_G^2 & \sigma_{GE} \\ \sigma_{EG} & \sigma_E^2 \end{bmatrix}. \quad (28)$$

The centering of the predictors of change forces the LISREL α vector in the forthcoming structural model to contain the population values of true intercept and slope at the population average values of G_p and E_p rather than at $G_p = 0$ and $E_p = 0$, respectively. In other words, the centering of the predictors of change in Equation 24 ensures that the LISREL α vector will continue to contain the population means of the individual growth parameters π_{0p} and π_{1p} , as it did in the earlier Equations 10 and 19. This has some convenience for later interpretation.⁹

The general LISREL model permits us to represent the relationship between all individual growth parameters and all predictors of change simultaneously. The Level 1 individual growth model in Equations 5–9 is unchanged. However, to express the interrelationships among the growth parameters and predictors of change, we must modify the existing LISREL structural model in Equations 10–14 so that the newly defined vector of latent exogenous predictors (which now contains the predictors of change as deviations from their means) is introduced on the right-hand side. We can do this by taking advantage of the so-far unused LISREL latent regression-weight matrix Γ that is present in the general LISREL model for the specific purpose of modeling the relationship between the η and ξ vectors. We simply free those elements of the Γ matrix that represent the simultaneous linear regression of true intercept and slope on the predictors of change.

A model that includes all possible linear relationships among the individual growth parameters and the predictors of change is

$$\begin{aligned} \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix} &= \begin{bmatrix} \mu_{\pi_0} \\ \mu_{\pi_1} \end{bmatrix} + \begin{bmatrix} \gamma_{\pi_0 G} & \gamma_{\pi_0 E} \\ \gamma_{\pi_1 G} & \gamma_{\pi_1 E} \end{bmatrix} \begin{bmatrix} G_p - \mu_G \\ E_p - \mu_E \end{bmatrix} \\ &+ \begin{bmatrix} 0 & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \pi_{0p} \\ \pi_{1p} \end{bmatrix} \\ &+ \begin{bmatrix} \pi_{0p} - [\mu_{\pi_0} + \gamma_{\pi_0 G}(G_p - \mu_G) + \gamma_{\pi_0 E}(E_p - \mu_E)] \\ \pi_{1p} - [\mu_{\pi_1} + \gamma_{\pi_1 G}(G_p - \mu_G) + \gamma_{\pi_1 E}(E_p - \mu_E)] \end{bmatrix}. \end{aligned} \quad (29)$$

This model is the general LISREL structural model

$$\eta = \alpha + \Gamma\xi + B\eta + \zeta \quad (30)$$

with constituent parameter matrices,

$$\alpha = \begin{bmatrix} \mu_{\pi_0} \\ \mu_{\pi_1} \end{bmatrix}, \Gamma = \begin{bmatrix} \gamma_{\pi_0 G} & \gamma_{\pi_0 E} \\ \gamma_{\pi_1 G} & \gamma_{\pi_1 E} \end{bmatrix}, B = \begin{bmatrix} 0 & 0 \\ 0 & 0 \end{bmatrix}, \quad (31)$$

and latent residual vector

$$\begin{aligned} Z &= \begin{bmatrix} \pi_{0p} | G, E \\ \pi_{1p} | G, E \end{bmatrix} \\ &= \begin{bmatrix} \pi_{0p} - [\mu_{\pi_0} + \gamma_{\pi_0 G}(G_p - \mu_G) + \gamma_{\pi_0 E}(E_p - \mu_E)] \\ \pi_{1p} - [\mu_{\pi_1} + \gamma_{\pi_1 G}(G_p - \mu_G) + \gamma_{\pi_1 E}(E_p - \mu_E)] \end{bmatrix}. \end{aligned} \quad (32)$$

The two elements of the latent residual vector ζ in Equation 32 contain the values of true intercept and slope deviated from their conditional means, based on their linear relationships with the predictors of change. These are the “adjusted” values of true intercept and slope, partialing out the linear effects of the predictors of change (those parts of the true intercept and slope, respectively, that are not linearly related to G_p and E_p). The latent residual vector ζ in Equation 32 is therefore distributed with zero mean vector and covariance matrix Ψ :

$$\Psi = \begin{bmatrix} \sigma_{\pi_0}^2 | X=[G, E]' & \sigma_{\pi_0 \pi_1} | X=[G, E]' \\ \sigma_{\pi_1 \pi_0} | X=[G, E]' & \sigma_{\pi_1}^2 | X=[G, E]' \end{bmatrix}. \quad (33)$$

Unlike Equation 14, the Ψ matrix in Equation 33 contains the partial variances and covariances of true intercept and slope, controlling for the linear effects of the predictors of change. If we successfully predict true intercept and slope by G_p and E_p , then we would expect these partial variances to be markedly smaller than their unconditional cousins in Equation 14. In fact, the proportional declines in the variances of true intercept and slope on inclusion of G_p and E_p as predictors of change provide pseudo- R^2 statistics that can be used to summarize the magnitude of the systematic heterogeneity in change.

Maximum likelihood estimates of the new parameters in regression-weight matrix Γ , along with estimates of the other unknown parameters in τ_x , Φ , α , and Ψ —which together characterize our hypotheses about the nature of any systematic inter-individual differences in change in the population—can again be estimated straightforwardly with LISREL. In the Appendix (Model 4), we again provide a LISREL program that does so, specifying the Δ_y , Θ_1 , τ_x , Λ_x , Φ , α , B , Γ , and Ψ matrices as defined in Equations 8, 23, 27, 28, 31, and 33. Fit statistics and maximum likelihood estimates of the unknown parameters in the model are listed under Model 4 in Table 4 with the exception of the measurement error variances and covariances, which have been omitted to conserve space.

Focus first on the column in Table 4 titled Model 4. The first five rows present maximum likelihood estimates of the population means and the unconditional variances and covariances of the individual growth parameters.¹⁰ These estimates are very similar in magnitude to those already examined in the investigation of interindividual differences in Model 3 of Table 3; the inclusion of predictors of change has not seriously disturbed our estimates of the heterogeneity in change present in the population. Rows 6 through 8 of Table 4 contain the estimated partial variances and covariances of true intercept and true slope, con-

⁹ Because gender is a dichotomous variable, its introduction into X appears to violate the assumption of multivariate normality on which the maximum likelihood estimation is based. Bollen (1989) examined the consequences of the nonnormality of X on the estimation and concluded that the estimator retains desirable statistical properties of consistency and efficiency when the predictor is measured infallibly and is truly exogenous. The gender variable meets both of these criteria in our model.

¹⁰ Even though these unconditional variances and covariances are not an explicit part of the model for systematic interindividual differences in change, they are output automatically by the LISREL program as part of the default Covariance Matrix of Eta and Ksi.

Table 4
Fitted Models Demonstrating Systematic Interindividual Differences in Change in Log Tolerance in the Full Sample, With Gender and Log Exposure to Deviant Behavior at Age 11 as Predictors of Change

Parameter	Maximum likelihood estimates		
	Model 4	Model 5	Model 6
μ_{π_0}	.3192***	.3198***	.3190***
μ_{π_1}	.0644***	.0643***	.0643***
$\sigma^2_{\pi_0}$	.0299	.0294	.0301
$\sigma^2_{\pi_1}$	.0026	.0023	.0027
$\sigma_{\pi_0\pi_1}$	.0068	.0069	.0069
$\sigma^2_{\pi_0 X}$	.0267***	.0278***	.0273***
$\sigma^2_{\pi_1 X}$	.0025**	.0022**	.0026**
$\sigma_{\pi_0\pi_1 X}$	.0064***	.0066***	.0066***
γ_{π_0G}	-.0457	-.0793***	
γ_{π_1G}	-.0148	-.0171†	
γ_{π_0E}	.1664***		.2003***
γ_{π_1E}	.0112		.0223
χ^2	31.54	41.31	34.01
df	12	14	14
Goodness of fit index (GFI)	.970	.958	.965
Adjusted goodness of fit index (AGFI)	.930	.916	.930
Root mean-square residual (RMSR)	.003	.005	.006

Note. $N = 168$. See text for descriptions of models. It was assumed that individual change is linear over time and that measurement errors are pairwise autocorrelated and heteroscedastic.

† $p < .10$. * $p < .05$. ** $p < .01$. *** $p < .001$ (approximate values).

trolling for the linear effects of adolescent gender and initial exposure to deviant behavior. Comparing the estimated conditional variances with their unadjusted cousins in rows 3 and 4 shows that the simultaneous inclusion of the predictors of change successfully reduced the unexplained variance in true intercept and slope by 11% and 4%, respectively, suggesting that these two variables are of moderate to small importance in the prediction of interindividual differences in true change in the population.

The coefficients in rows 9 through 12 estimate the linear regression of true intercept and slope on the predictors of change. Focus on the coefficients in rows 11 and 12 that summarize the linear relationship between the individual growth parameters and initial exposure, controlling for the linear effect of gender. They suggest that children who are exposed to greater levels of deviant behavior initially are more tolerant of deviant behavior at midadolescence ($\hat{\gamma}_{\pi_0E} = .1664, p < .001$) but that their rate of true change in tolerance over the adolescent period is not distinguishable from that of children who are less exposed ($\hat{\gamma}_{\pi_1E} = .0112, p > .10$). Interestingly, on the basis of the approximate p values displayed in rows 9 and 10 under Model 4, we cannot reject the null hypothesis that true intercept and slope are unrelated to adolescent gender, once (log) exposure to deviant behavior is controlled.

To clarify the joint influence of gender and initial exposure on change in tolerance, we refit Model 4 twice. Constraining

γ_{π_0E} and γ_{π_1E} to zero in Model 5 allowed us to investigate the uncontrolled effect of gender, and constraining γ_{π_0G} and γ_{π_1G} to zero in Model 6 permitted us to explore the uncontrolled effect of (log) exposure. The fit statistics and parameter estimates for these additional models are presented in Table 4. Most important are the entries in rows 9 and 10 under Model 5, which indicate that the gender of the adolescent is related to true intercept, and, more weakly, to true slope. Boys are generally more tolerant of deviant behavior at age 13 than are girls, and they become increasingly more tolerant over their adolescence. The difference in findings between Models 4 and 5 is accounted for by the implicit relationship between the two predictors of change themselves (i.e., collinearity). Moderate collinearity exists between the predictors ($r = -.378, p < .001$),¹¹ suggesting that boys were more exposed to deviant behavior initially, and it is this difference in exposure that forges a spurious bivariate relationship between true intercept and gender. Once exposure is controlled, however, there are no statistically significant differences in the way that boys and girls differ in true tolerance at age 13 or in the way that their true tolerance of deviant behavior changes over adolescence. This suggests that the more parsimonious representation in Model 6 is more appropriate for summarizing our findings.

Using fitted coefficients from Model 6, along with the estimated means of true intercept, true slope, and of the predictors of change, we can specify a pair of simultaneously fitted Level 2 models that explicitly describe the linear association between true change and the remaining predictor of interest, log exposure. Substituting parameter estimates from Model 6 in Table 4 into the structural model in Equation 29, we have

$$\begin{aligned}\hat{\pi}_{0p} &= .3190 + .2003[E_p - (-.0788)] \\ \hat{\pi}_{1p} &= .0643 + .0223[E_p - (-.0788)].\end{aligned}\quad (34)$$

For interpretive purposes, these fitted models can be reported explicitly in a research account or used to construct fitted true growth trajectories for prototypical adolescents at substantively interesting values of the predictors. We favor this latter approach and illustrate it in Figure 2.

The particular prototypical fitted trajectories that we have plotted in Figure 2 were selected to provide a substantively interesting display of statistically important effects, in this case, the impact of exposure on growth in tolerance. However, recall that we have also detected collinearity between gender and exposure—boys have greater initial exposure to deviant behavior than girls—suggesting that, even though gender no longer predicts growth in tolerance once exposure is controlled, fitted trajectories for prototypical boys and girls will differ because of the underlying difference in exposure. We have captured these linked differences in Figure 2 by plotting prototypical trajectories for boys and girls at the lower and upper quartile values of log exposure, with the requisite quartiles being estimated separately in subsamples of boys and girls. The four values of log exposure that we have used are as follows: (a) girls, $Q1 \approx -.32$,

¹¹ The correlation coefficient was computed from relevant estimated variances and covariances listed in the Covariance Matrix of Eta and Ksi on the standard LISREL output, which contains, by default, bivariate covariances among all elements of the η and ξ vectors.

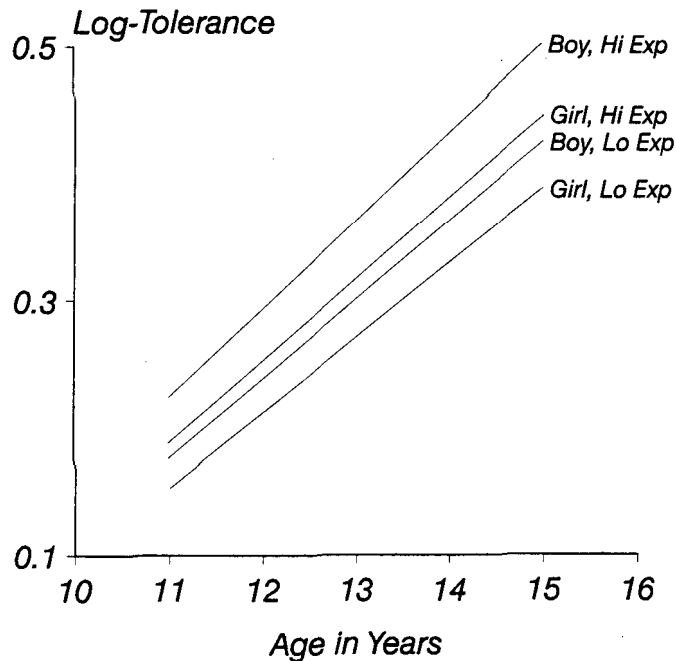


Figure 2. Fitted true growth trajectories in log tolerance of deviant behavior from 11 to 15 years of age for four prototypical adolescents at varying combinations of gender and initial exposure to deviance.

Q3 = $-.09$; and (b) boys, Q1 = $-.17$, Q3 = $.14$. Thus, Figure 2 displays fitted true growth trajectories for four prototypical adolescents. The two extreme trajectories represent a high-exposure boy and a low-exposure girl. The slopes of all of the trajectories are approximately parallel (exposure is not a statistically significant predictor of rate of change in Equation 34), illustrating that adolescents who were more exposed to deviant behavior at age 11 do not differ in the rate at which they become more tolerant of deviance than those adolescents who were less exposed.

Figure 2 also displays important differences in elevation, illustrating that the level of tolerance during adolescence differs by initial exposure to deviant behavior and, because of the background link between gender and exposure, also by gender. The main effect of initial exposure is indicated by the vertical displacement of the fitted trajectories within gender; for both genders, higher levels of initial exposure to deviance are related to higher levels of tolerance throughout adolescence. The effect of gender is illustrated by the vertical displacement of the trajectories within exposure; for adolescents at the same level of initial exposure, boys display higher tolerance for deviant behavior than girls at all ages.

Discussion

In recent years, pioneering authors (McArdle & Epstein, 1987; Meredith & Tisak, 1990; Muthén, 1991) have demonstrated how notions of individual growth modeling can be accommodated within the general framework offered by covariance structure analysis. Their work has illustrated how the methods of covariance structure analysis—here in the guise of

the LISREL program—can provide a straightforward and convenient technique for answering important research questions about the relationship between attributes of individual true change and selected characteristics of the person.

Here, we have explored and reviewed the links between these two formerly distinct conceptual arenas, carefully laying out in detail the mapping of the one onto the other. Specifically, we have reviewed and illustrated how the Level 1 (within-person) and Level 2 (between-person) models of the individual growth modeling framework can be reformatted to correspond, respectively, to the measurement and structural components of the general LISREL model with mean structures. The direct correspondence between these two pairs of models permits the population covariance matrix of the errors of measurement and the relationships among the individual growth parameters and potential predictors of change to be modeled explicitly within a covariance structure framework. Consequently, critical parameters in the investigation of systematic interindividual differences in change can readily be estimated. This innovative application of covariance structure analysis offers several important features to data analysts.

1. The method can accommodate any number of waves of longitudinal data. Willett (1988, 1989) has shown that the collection of additional waves of data leads naturally to higher precision for the estimation of the individual growth trajectory and greater reliability for the measurement of change. In the case of covariance structure analyses of change, extra waves of data act to extend the length of the empirical growth record and expand the dimensions of the sample between-wave covariance matrix (thereby increasing the number of degrees of freedom

available for fitting the model) but do not change the fundamental parameterization of the Level 1 and Level 2 models themselves. In this article, for instance, we have provided an example in which 5 waves of longitudinal data were analyzed; the method serves equally well with 3 waves or 30.

2. Occasions of measurement need not be equally spaced. In our example, measures of adolescents' tolerance of deviant behavior were each separated by 1 year throughout the entire period of data collection. However, equal spacing of the occasions of measurement is not a requirement of the method. Individual change data may be collected at irregular intervals either for convenience (at the beginning and end of each of several school years, perhaps) or because the investigator wishes to estimate certain features of the trajectory more precisely (by clustering data collection points more closely at times of greater research interest). Such irregularly spaced data are easily accommodated by the method, provided everyone is measured on the same set of irregularly spaced occasions.

3. Individual change can be represented by either a straight-line or a curvilinear trajectory. In this article, for convenience, we have used a straight-line growth model to represent individual change over time, but we have demonstrated briefly how this decision can be modified to include a quadratic curvature term if required. In fact, the covariance structure approach can accommodate not only polynomial growth of any order but also any type of curvilinear growth model in which status is linear in the individual growth parameters. An example of such a model is the negative exponential growth model with instantaneous rate parameter fixed across population members (see Meredith & Tisak, 1990; Rogosa & Willett, 1985). In addition, because goodness of fits of nested models can be compared directly under the covariance structure approach, one is able to systematically evaluate the adequacy of contrasting individual growth models in any particular empirical setting.

4. The covariance structure of the occasion-by-occasion measurement errors can be modeled explicitly and its parameters estimated. Unlike other popular methods for the analysis of longitudinal data, the approach we have described does not restrict the population measurement error covariance matrix to a particular shape or pattern. The investigator need not accept unchecked the Level 1 independence and homoscedasticity assumptions of classical and HLM analyses nor the band-diagonal configuration required by repeated measures ANOVA. Indeed, under the covariance structure approach, the researcher is completely in charge. The effectiveness of a variety of reasonable error structures can be systematically compared and the structure most appropriate for the particular empirical problem adopted. In our data example, for instance, we compared growth formulations in which the occasion-by-occasion measurement errors were assumed to be, respectively, (a) independent and homoscedastic, (b) independent and heteroscedastic, and (c) pairwise autocorrelated and heteroscedastic. We found the latter configuration to be the most appealing in this particular example.

5. Multiple predictors of change can be included in the Level 2 model. The analysis of systematic interindividual differences in change is not usually limited to the examination of the effect of a single predictor of change. Within the normal constraints imposed by the requirements of statistical power and the tenets

of common sense, multiple predictors of change can be included under the covariance structure approach; the specifications that we have described extend straightforwardly to these more complex situations. Predictors can represent the main effects of important correlates of change, or, by suitable preprocessing of the data set to create crossproducts among interesting combinations of predictors, statistical interactions among potential correlates can be included in the Level 2 model. In our example, we described the configuration of the LISREL parameter matrices for the case in which interindividual differences in change are related to the main effects of two predictors.

6. The method of maximum likelihood is used to provide overall goodness-of-fit statistics, parameter estimates, and asymptotic standard errors for each hypothesized model, including estimates of all Level 2 variance and covariance parameters that are central to the detection of systematic interindividual differences in change. By using the covariance structure method, the investigator benefits from all of the flexibility and utility of a well-documented, popular, and widely disseminated statistical technique. Appropriate computer software is available on many systems, both mainframe and personal computer based. In this article, we have relied on the well-known LISREL computer package, but the techniques that we have reviewed can easily be implemented with other well-known packages such as EQS (Bentler, 1985), LISCOMP (Muthén, 1987), and PROC CALIS (SAS Institute, 1991).

7. By comparing the goodness of fit of explicitly specified nested models, the investigator can test complex hypotheses about the nature of interindividual differences in true change. An additional benefit of fitting an explicitly parameterized covariance structure to data using a well-tested and flexible software package such as LISREL is that selected parameters in the model specification can be individually or jointly constrained during analysis to particular values. This allows the investigator to conduct a variety of nested tests on the specific shape of the average growth trajectory and on the variability of the individual growth parameters across people. As with other common analytic approaches such as HLM (Bryk & Raudenbush, 1992), for instance, we can "fix" the value of one growth parameter (e.g., the slope) to a value common across individuals but permit another parameter (the intercept) to be random.

8. The flexibility of the general LISREL model permits the covariance structure analysis of longitudinal data to be extended in several statistically and substantively interesting ways. There are several potential extensions of the covariance structure approach that are facilitated by the flexibility of the general LISREL model. First, multiple indicators can be used to represent each predictor of change, providing a ready maximum likelihood adjustment for errors in the predictors (cf. Fuller, 1987). Second, individual change can be modeled simultaneously in more than one domain (Willett & Sayer, 1993), engendering investigation of profiles of change (see Williamson, 1986; Williamson et al., 1991). This includes the investigation of (a) interrelationships among the several types of change and (b) the simultaneous and joint association of these several changes and selected predictors of change. Third, the method enables the modeling of intervening effects, whereby a predictor may not act directly on change but indirectly through the influence of intervening variables.

Of course, other analytic methods are available for fitting these hierarchical models that describe individual change and interindividual differences in change. Each method has its own strengths.¹² Nevertheless, one particular method may offer benefits over another in a specific research setting. For instance, the HLM approach of Bryk and Raudenbush (1992) is also well documented and flexible, and software suitable for conducting the analyses is widely available. And, like the covariance structure approach, HLM can handle any number of unequally spaced waves of longitudinal data; individual growth trajectories can be linear or curvilinear; multiple predictors of change can be included in the Level 2 model; a variety of goodness-of-fit statistics, parameter estimates, and standard errors are provided; and complex hypotheses about change over time can be tested through the analysis of contrasts and the program's ability to restrict individual growth parameter variances to zero at the investigator's behest. In addition, HLM offers an advantage that cannot be matched by the covariance structure method as we have described it here: It does not require time-structured data; each individual in the data set can possess an empirical growth record containing different numbers of waves of data with randomly assigned temporal spacing (but see Muthén, 1992).

Nevertheless, we believe that there is no single analytic method that can be declared unilaterally the best, nor have we written this article to declare such a winner. Different empirical settings demand different analytic decisions. When the data are not time structured, either by accident or design, then the investigator may have to set aside the analytic methods that we have described here. However, when equal numbers of waves of data are available on each subject, the covariance structure approach offers great flexibility in the investigation of systematic interindividual differences in change and an unparalleled opportunity to model error covariance structure explicitly. That a variety of analytic tools are available for such an important task is a boon rather than a hindrance, leading us to conclude—to paraphrase Cronbach and Furby (1970)—that we *can* measure “change”—and we *should*!

¹² Within the limits posed by their methods of estimation, most of the available analytic methods for the measurement of change—including the covariance structure approach described here—produce convergent answers. However, other popular methods of analysis, including the exploratory methods of Rogosa and his colleagues (Rogosa, Brandt, & Zimowski, 1982; Rogosa & Willett, 1985; Willett, 1985; Williamson, 1986), the weighted least squares methods of Willett (1989), and the empirical Bayes methods of Bryk and Raudenbush (1987, 1988, 1992), are unable to model error covariance structure explicitly because of the assumptions built into their statistical models (and, consequently, their associated software). The heteroscedastic, autocorrelated measurement errors that are a feature of our analyses are a direct result of parameterizing the model specifically to allow for such structure on the errors and then locating appropriate software to estimate these parameters. General covariance structure programs such as LISREL and EQS provide the required flexibility, as compared with menu-driven programs such as BMDP-5V or SAS PROC MIXED. For this reason, we have not included comparison tables of parameter estimates obtained under different methods of estimation, as a reviewer suggested. However, when models could be fitted by multiple methods (Model 1, for instance, is identical to the unconditional model of Bryk & Raudenbush, 1987), parameter estimates and standard errors obtained under the covariance structure approach and by other methods were either identical or almost identical. A computer printout of these comparison analyses is available on request.

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Appendix

Sample LISREL VII Programs

In this appendix, we present the LISREL VII programs that were used to fit Models 1 through 4. All have a similar structure. We present the program used to fit Model 1 in its entirety. For the remaining models, we present the title lines and then highlight the code that differentiates each from the other.

In the first part of any complete program, we list several title lines to distinguish the particular model being fitted. Following the title lines is the data definition (DA) line, in which we specify a single group rather than multisample analysis ($NG = 1$), the number of input variables (NI), and the sample size (NO). The next line identifies the file that contains the input data. Then we label the input variables (LA) and, when necessary, select those that are to be analyzed in the current run (SE).

The model definition (MO) line describes the basic shape of the various hypothesized LISREL variable and parameter matrices. The $\mathbf{Y}$, η , $\mathbf{X}$, and ξ score vectors are dimensioned (NY, NE, NX, NE), and the shape and initial contents of the τ_y , τ_x , Φ , α , $\mathbf{B}$, Γ , and Ψ parameter matrices are specified (TY, TX, PH, AL, BE, GA, PS) according to their definitions in text. Afterward, the contents of the latent growth record and the vector of latent exogenous predictors are labeled (LE, LK).

Then, in several lines, we specify the various fixed and free parameters that constitute the particular measurement and structural models listed in the text. We completely fix the contents of the Λ_y and Λ_x matrices (in the matrix of stated values following the MA LY and MA LX lines). We free appropriate elements of the Θ , vector (FR TE) according to the hypothesized error covariance structure and elements of the Γ matrix (FR GA) according to the hypothesized structural model. Occasionally, parameter groups are constrained to be equal. For instance, when the errors of measurement are assumed to be homoscedastic, selected diagonal elements of the Θ , matrix are set equal (EQ TE). Similar constraints could be used to test specific hypotheses in a nested sequence of models.

Finally, in the "output" line (OU), we indicate that we require the estimation and printing of standard errors (SE) and t values (TV), as well as the printing of a residual analysis (RS), all to six decimal places ($ND = 6$). We limit the maximum number of iterations during estimation ($IT = 10,000$).

Model 1: Linear individual growth in log deviance

```
Origin of time is age 13
No predictors
Independent homoscedastic errors
DA NG = 1 NI = 11 NO = 168
RA FI = A:\TOLERANC.DAT
LA
'ID' 'Y1' 'Y2' 'Y3' 'Y4' 'Y5' 'LnE' 'SEX'
SE
2 3 4 5 6/
```

```
MO NY = 5 TY = ZE NE = 2 TE = SY, FI AL = FR BE = ZE PS =
SY, FR
```

```
LE
'Pi0' 'Pi1'
MA LY
```

```
1 -2
1 -1
1 0
1 1
1 2
```

```
FR TE(1,1) TE(2,2) TE(3,3) TE(4,4) TE(5,5)
```

```
EQ TE(1,1) TE(2,2) TE(3,3) TE(4,4) TE(5,5)
```

```
OU SE TV RS ND = 6 IT = 10000
```

Model 2: Linear individual growth in log deviance

Origin of time is age 13

No predictors

Independent heteroscedastic errors

Eliminate the line in the Model 1 program that constrains the error variances to equality, i.e.,

```
EQ TE(1,1) TE(2,2) TE(3,3) TE(4,4) TE(5,5)
```

Model 3: Linear individual growth in log deviance

Origin of time is age 13

No predictors

Pairwise autocorrelated heteroscedastic errors

Add the following line to the Model 2 program to free selected error covariances for estimation:

```
FR TE(2,1) TE(3,2) TE(4,3) TE(5,4)
```

Model 4: Linear individual growth in log deviance

Origin of time is age 13

Predictors are gender and initial log exposure to deviance at age 11

Pairwise autocorrelated heteroscedastic errors

Modify the select line in the Model 3 program to select the predictors:

```
SE
2 3 4 5 6 8 7/
```

Modify the model specification to include predictors of change:

```
MO NY = 5 TY = ZE NE = 2 TE = SY, FI NX = 2 TX = FR NK = 2
```

```
TD = ZE PH = SY, FR AL = FR BE = ZE
```

```
GA = FU, FI PS = SY, FR
```

Add lines to label the predictors and specify the Λ_x matrix:

```
LK
'Sex' 'LnE'
MA LX
```

```
1 0
```

```
0 1
```

Add lines to free the appropriate elements of the Γ matrix:

```
FR GA(1,1) GA(1,2) GA(2,1) GA(2,2)
```

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