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An Introduction to Latent Growth Curve Modeling

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Over the past 3 decades we have witnessed an increase in the complexity of theoretical models that attempt to explain development in a number of behavioral domains. The conceptual movement to examine behavior from both developmental and contextual perspectives parallels recent methodological advances in the analysis of change. These new analysis techniques have fundamentally altered how we conceptualize and study change, and have prompted researchers to identify larger frameworks to integrate knowledge. One such framework is latent growth modeling. This article presents a basic latent growth modeling approach for analyzing repeated measures data and delineates several of its extensions, including analyses for multiple populations, accelerated designs, multivariate associative models, and a framework for sample size selection and power estimation.

The representation and measurement of change is a fundamental concern to practically all scientific disciplines. Unfortunately, the study of change is not as straightforward as many researchers would like. The researcher interested in demonstrating change in behavior over time must use a longitudinal research design. Such a design, whether true, quasi-, or nonexperimental, poses several unique problems because it involves variables with correlated observations. There is no single statistical procedure for the analysis of longitudinal data, as different research questions dictate different data structures and, thus, different statistical models and methods.

Historically, the most prevalent type of longitudinal data in the behavioral and social sciences has been longitudinal panel data consisting of observations made on many individuals across pretest and posttest occasions. In the analysis of longitudinal data, of primary interest is the nature of change over time, which can not be assessed with only two repeated measurements unless development is known to be linear. Rogosa (1988) has demonstrated the

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hazards involved in using linear models when nonlinear growth processes are operative. Traditional approaches to studying change within this context have been ANOVA and multiple regression techniques.

These approaches, however, analyze only mean changes and consequently treat differences among individual subjects as error variance. Some of this "error variance" may contain valuable information about change. Recently a host of methodological contributions have extended researchers' ability to describe individual differences and the nature of change over time (e.g., random-effects ANOVA, random coefficient modeling, multilevel modeling, and hierarchical linear modeling). In these methodologies, individual differences in growth over time are captured by random coefficients. These random coefficient methods have both strengths and weaknesses. A strength is that they draw upon statistical procedures that have been rigorously examined over a number of years. A weakness is that the statistical modeling within these methods has been largely limited to a single response variable. As such, these methods do not fully accommodate the complexity and analytical needs of current developmental theories (Muthén & Curran, 1997).

A largely independent tradition to analysis of longitudinal data has been conducted within the latent variable structural equation modeling (SEM) framework. Although the estimation procedures are not yet well established for sufficiently general cases, the modeling framework has much more flexibility to fully examine the types of questions now posed by developmental and behavioral researchers. Once the random coefficient model has been placed within the latent variable framework, many general forms of longitudinal analyses can be studied. It has been suggested that the development of the latent variable modeling framework is perhaps the most important and influential statistical revolution to have occurred recently in the social and behavioral sciences (Cliff, 1983). Paralleling the growth in complexity of the theoretical models guiding behavioral research, methodologists have extended the latent variable framework to accommodate longitudinal models that include multivariate or higher-order specifications, multiple populations, the accelerated collection of longitudinal data, nonlinear and interactive effects, multilevel or hierarchical structures, and complex relations, including mediation, moderation, recursive and nonrecursive relationships, and reciprocal causation.

Toward an Integrated Developmental Framework

An appropriate developmental model is one that not only describes a single individual's developmental trajectory, but also captures individual differences in these trajectories over time. If, for example, trajectories produced a collection of straight lines for a sample of individuals, the developmental model should reflect individual differences in the slopes and intercepts of those lines. Another critical attribute of the developmental model is the ability to study predictors of individual differences to answer questions about which

variables exert important effects on the rate of development. At the same time, the model should be able to capture the vital group statistics in a way that allows the researcher to study development at the group level.

There has been a recent resurgence of interest in statistical models for time-ordered data utilizing structural equation methodology. Interest in models that have the ability to incorporate information concerning the group or population, and also information concerning changes in the individual, has reintroduced the formative work of Rao (1958) and Tucker (1958). The basic notion that Rao and Tucker promoted was the idea that while everyone develops the same way, individual differences are both meaningful and important. These researchers proposed a partial solution to this problem by constructing a procedure that included unspecified longitudinal growth curves or functions. One methodology that provides a means of modeling individual differences in growth curves has been termed a latent growth model or LGM.

Although strongly resembling the classic confirmatory factor analysis, the latent growth factors are actually interpreted as individual differences in attributes of growth trajectories over time (McArdle, 1988). For example, two potentially interesting attributes of growth trajectories are rates of change and initial status. For simple, straight line growth models, these are the slope and intercept, respectively. Meredith and Tisak (1990) note that repeated measures polynomial ANOVA models are actually special cases of latent growth models in which only the factor means are of interest. In contrast, a fully expanded latent growth analysis takes into account both factor means, which correspond to group level information, and variances, which correspond to individual differences. This combination of the individual and group levels of analysis is unique to the procedure. Heuristically, growth curve methodology can be thought of as consisting of two stages. In the first stage, a regression curve, not necessarily linear, is fit to the repeated measures of each individual in the sample. In the second stage, the parameters for an individual's curve become the focus of the analysis rather than the original measures.

Thus, the modeling task involves identifying an appropriate growth curve form which will accurately and parsimoniously describe individual development and allow for the study of individual differences in the parameters that control the pattern of growth over time. If, for example, the trajectories were well described by a collection of straight lines for a sample of individuals, the developmental model should reflect individual differences in the slopes and intercepts of those lines. Beyond describing and summarizing growth at the group and individual level, however, the model can also be used to study predictors of individual differences to answer questions about which variables exert important effects on the rate of development. Researchers such as Meredith and Tisak (1990) and McArdle (1988) have extended the basic model to permit the use of current standards in estimation and testing procedures found in SEM programs such as LISREL (Jöreskog & Sörbom, 1993), EQS (Bentler & Wu, 1995), Amos (Arbuckle, 1999), Mx (Neale, 2002), and

Mplus (Muthén & Muthén, 1998). Thus, statistical tests of overall model fit and the significance of individual model parameters are available. Although most of the models presented in the following sections can be estimated using any of the SEM programs cited earlier, we include Mplus (Muthén & Muthén, 1998) model specifications for selected examples in the appendices. Model specifications for comparable examples (see T. Duncan, Duncan, Strycker, Li, & Alpert, 1999) using LISREL (Jöreskog & Sörbom, 1984), EQS (Bentler & Wu, 1995), and Amos (Arbuckle, 1999) can be found at http://www.ori.org/methodology/index.html.

The latent growth curve approach is laid out in more technical detail in T. Duncan et al. (1999), T. Duncan, Duncan, and Stoolmiller (1994), Meredith and Tisak (1990), Muthén (1991), and Stoolmiller (1995).

Since LGM is carried out using SEM methodology, it shares many of the same strengths and weaknesses with regard to statistical methodology. Some of the strengths of the LGM approach include an ability to test the adequacy of the hypothesized growth form, to incorporate both fixed and time varying covariates, to correct for measurement error in observed indicators, to incorporate growth on several constructs simultaneously, and to develop from the data a common developmental trajectory, thus ruling out cohort effects. The more commonly cited limitations of SEM programs for estimating LGM models include the assumption of multinormally distributed variables and the necessity of large samples, although recent Monte Carlo simulations have demonstrated that basic LGMs hold up well with relatively small *N*s (e.g., Muthén & Muthén, 2002). Therefore, the requisite *N* largely depends on the specific empirical context (e.g., psychometric behavior of indicators, amount of missing data, size of effects, etc.) and design aspects such as the number of assessment points.

In addition, a fundamental assumption of growth curve methodology is that change is systematically related to the passage of time, at least over the time interval of interest (Burchinal & Appelbaum, 1991). Evaluating the extent to which a particular growth model is capable of describing the observed pattern of change with respect to time is an important part of growth model testing. The application of LGM within the SEM framework depends, at least ideally, on data that are collected when subjects are observed at about the same time, and the spacing of assessments are the same for all individuals. Longitudinal panel data is typical of this design. LGM can be applied to circumstances where individuals are not measured at the same intervals of time; however, specific constraints need to be placed on the models for parameter identification. SEM methodology can still be applied if change on the variables of interest is not related to time. That is, any ordinal variable can be used as the index of the basis function. Time is only one useful possibility. If change is not systematically related to the passage of time, the models lose their growth curve interpretations and studying individual trajectories over time will not be very informative.

Specification of the LGM

The simplest latent growth curve model involves one variable (e.g., a measure of depression using the BDI) measured the same way at two time points. Two points in time are not ideal for studying development or for using growth curve methodology (Rogosa & Willett, 1985) as the collection of individual trajectories are limited to a collection of straight lines. Although two observations of depression provide information about change, they poorly address some research questions (Rogosa, Brandt, & Zimowski, 1982). For example, two temporally separated observations allow estimation of the amount of change, but it is impossible to study the shape of the developmental trajectory or the rate of change of depression in the individual. The *shape* of individual development of depression between two observations may be of theoretical interest either as a predictor or sequela. Unfortunately, two-wave panel designs preclude testing theories related to the shape of development. Two-wave designs are appropriate only if the intervening growth process is considered irrelevant or is known to be linear. In general, developmental studies should be planned to include more than two assessment points.

Multiwave data offer important advantages over two-wave data. With more than two observations the validity of the straight-line growth model for the trajectory can be evaluated (e.g., tests for nonlinearity can be performed). In addition, the precision of parameter estimates will tend to increase along with the number of observations for each individual. To introduce the LGM, a model with two time points, representing repeated measures of adolescent substance abuse, is presented in Figure 1.

Intercept

As can be seen from Figure 1, the first factor (*F1*) is labeled "Intercept." The intercept is a constant for any given individual across time, hence the

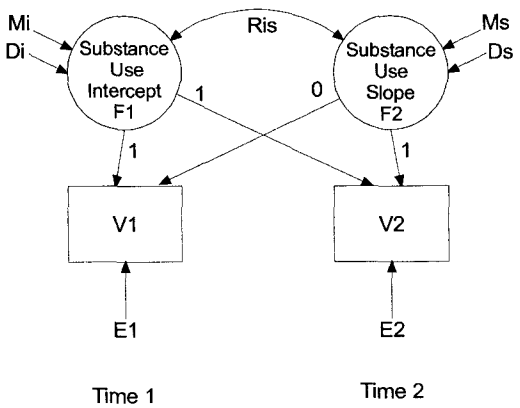

FIG. 1. LGM for two points in time.

fixed values of 1 for factor loadings on the repeated measures. The intercept in this model for a given individual has the same meaning as the intercept of a straight line on a two-dimensional coordinate system: It is the point where the line "intercepts" the vertical axis. The intercept factor presents information in the sample about the mean (*Mi*) and variance (*Di*) of the collection of intercepts that characterize each individual's substance abuse growth curve.

Slope

The second factor (*F2*), labeled "Slope," represents the slope of an individual's substance abuse trajectory. In this case, it is the slope of the straight line determined by the two repeated measures. The slope factor has a mean (*Ms*) and variance (*Ds*) across the whole sample which, like the intercept mean and variance, can be estimated from the data. The two factors, Slope and Intercept, are allowed to covary, *Ris*, which is represented by the double-headed arrow between the factors. The error variance terms (*E1*, *E2*) are shown in the diagram, but to keep the presentation simple, error is assumed to be zero (i.e., $E1 = E2 = 0$).

To identify this model, two slope loadings must be fixed to two different values. Although the choice of loadings is somewhat arbitrary, the intercept factor is bound to the time scale. Shifting the loadings on the slope factor alters the scale of time, which affects the interpretation of the intercept factor mean and variance.

The slope factor mean and variance differ from the intercept factor mean and variance in that changing the fixed loadings, and thereby changing the time scale, rescales the slope factor mean and variance, in this case by constants. Rescaling by constants does not change the fundamental meaning or affect significance tests of the parameters. It also does not affect the correlations between the slope factor and other predictors in the model.

In the simple two-points in time model there are not enough degrees of freedom to estimate the error variances from the data. The overall model has 5 estimated parameters (the Intercept mean and variance, the Slope mean and variance, and the covariance between the Intercept and Slope) and there are 5 pieces of known information (2 variances, 2 means, and 1 covariance) with which to estimate the model. Note that the error variances and the factor loadings for the Intercept and Slope are not included as estimated parameters in the model as they have been fixed to user-specified values. If the model has more parameters to estimate than pieces of information in the data — that is, if we attempted to estimate measurement error in our model — it can not be uniquely estimated, and is therefore not "identified." Having an unidentified model implies that it is impossible to compute a reasonable estimate for one or more of the model's parameters and that the model can not generally be relied on. If the model can be identified, then it is "just identified," meaning the model provides a perfect fit to the data using all the available degrees of freedom (as is the case with the model depicted in Figure 1).

Unfortunately, there is no way to test or confirm the plausibility of a saturated or "just identified" model because saturated models will always provide a perfect fit to the data. If, however, the error variance is known either from prior research or from theoretical considerations, it can be fixed at that value and the model estimated. This would result in positive degrees of freedom (e.g., more unique information in the data than parameters to be estimated) and the ability to provide an adequate test of the hypothesized model. The error variances affect the interpretation of the model parameters by correcting the measured variances for random error. For example, the variance of the substance abuse slope factor, *F2*, would be the variance of the difference scores corrected for measurement error, and the variance of the substance abuse intercept factor (*F1*) is just the true score variance of *V1*. By expanding the model to include error variance terms, the model parameters retain the same basic interpretations but are now corrected for random measurement error. Model identification is a complex issue which deserves careful consideration and handling.

Interpretation of the Growth Factors

Even with only two time points, the choice of loadings can affect the interpretation of both the intercept and slope factors. The models depicted in Figure 2

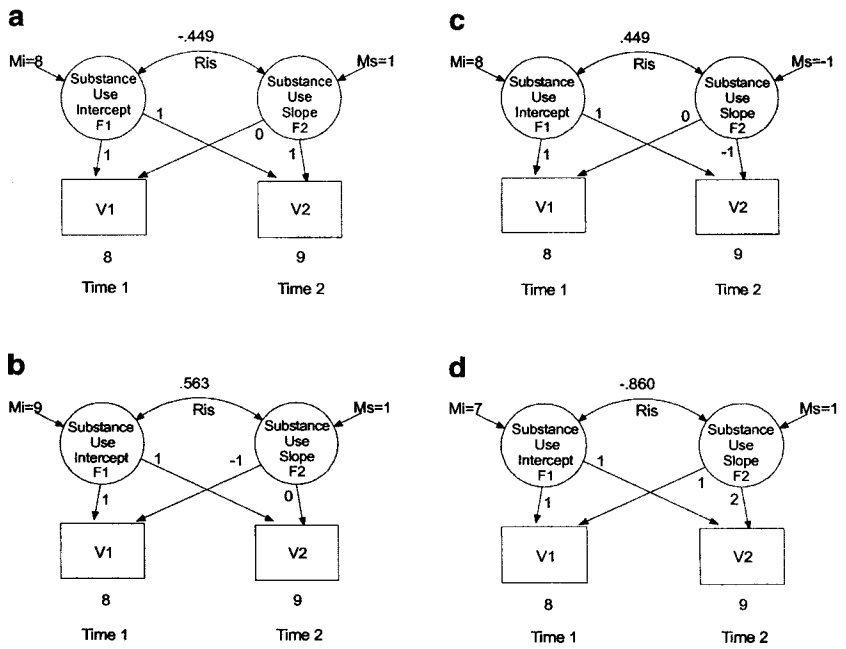

FIG. 2. LGM centering and factor interpretation.

each describe growth over two occasions, but vary the centering of time. For example, the model depicted in Figure 2a describes growth in substance abuse over two occasions (1 unit of time) where there is a 1-unit increase in mean levels of substance abuse (e.g., $M_{t2} - M_{t1} = 1$).

The factor loadings are fixed at values that represent polynomial contrasts used to identify the scale of the F variables. To further explain the nature of the contrasts used, consider the equation for a growth curve for a single individual with two data points:

$$V_i = b_1 + t_i b_2 + e_i \tag{1}$$

where b_1 is the intercept, b_2 is the slope (amount of vertical increase per unit of horizontal run of the growth curve), t_i is the ith value of time, e_i represents the time-specific errors of prediction, and i is the value of time. For this hypothetical individual, therefore, the set of equations is:

$$V_1 = b_1 + 0\, b_2 + e_1 \tag{2}$$

$$V_2 = b_1 + 1\, b_2 + e_2 \tag{3}$$

Relating these equations back to Figure 2a, for any given individual, b_1 corresponds to the intercept factor score ($F1$), b_2 corresponds to the slope factor score ($F2$), and e_i corresponds to the time-specific errors of prediction. If $F1 = 8$, $F2 = 1$ and Et = 0, t = 1, 2, then the model for this individual implies the following trajectory:

$$V_1 = 8 + 0(1) + 0 = 8$$

$$V_2 = 8 + 1(1) + 0 = 9,$$

where L1 = 0 at Time 1 (T1) simply starts the curve at this point by rescaling the intercept factor to represent initial status, and L2 = 1 at Time 2 (T2) indicates that from T1 to T2 there is one unit of change. Thus, Lt describes a linear relation of change in terms of linear differences from initial status at T1. The selected contrasts rescale the intercept factor to represent initial status at T1. Because the variables have no measurement error, the mean of the intercept factor ($F1$) will equal the mean of the T1 variable ($Mi = 8$). The mean of the slope factor ($F2$) will equal the change in terms of differences between T2 and T1 means per 1 unit of time [$(9_{mean\ at\ t2} - 8_{mean\ at\ t1})/1_{\ unit\ of\ time}$] or ($Ms = 1$). Because the factor loadings represent a positively increasing trend, the slope factor is interpreted as positive growth where higher scores on the factor (i.e., factor scores) represent more positive, or greater increases in substance abuse. The correlation between the intercept and slope factors (−.449) is negative, suggesting that those with greater values on substance abuse at T1 tend to have lower slope scores or less positive growth in substance abuse over time. Mplus (Muthén & Muthén , 1998) program specifications for the two-factor LGM depicted in Figure 2a are presented in Appendix A. A

summary of the Mplus language can be found at http://www.statmodel.com/mplus/language.html.

Figure 2b depicts factor loadings set at values of −1 and 0. Note that the mean for the intercept factor is no longer initial status at T1, but is now interpreted as status at T2 (e.g., $Mi = 9$). (Note that the variable mean associated with the time point where the factor loading on the slope factor is fixed at a value of 0 defines the intercept factor mean.) The loadings still represent a positively increasing trend, thus the slope factor mean is again positive, and higher scores on the factor represent greater increases in substance abuse. Because the interpretation of the intercept factor has changed, the correlation between the intercept and slope factors has also changed ($r = .563$).

Figure 2c depicts the same model where the factor loadings are now fixed at values of 0 and −1. Note that the zero loading for the first variable of the slope factor allows for the intercept factor to be once again interpreted as initial status at T1. However, because the loadings on the slope factor represent a negative trend from T1, the slope mean is negative (e.g., $Ms = -1$) and higher scores on the slope factor now represent more negative or greater decreases in substance abuse. Compared to Figure 2a, the correlation between the intercept and slope is of the same magnitude, but now of opposite sign (positive vs. negative).

As might be expected, the choice of factor loadings also allows the researcher to express the intercept factor as representing a point prior to or following the time frame encompassed by the data collection. For example, the model depicted in Figure 2d represents linear growth emanating from a time point (T1-1) prior to that expressed by the substance abuse data. Here, the zero loading on the slope factor originates from a T1-1 data point and T1 and T2 are fixed at values of 1 and 2, respectively. Extrapolating the linear trend backwards 1 unit in time yields an intercept factor mean of $Mi = 7$. Note that the slope factor mean is still 1 since the model now represents substance abuse change from T1 minus 1 to T2 or two units of time, and mean growth in substance abuse from $M = 7$ to $M = 9$ or two units of change (note that the change in the interpretation of the intercept factor again changes the correlation between intercept and slope, $r = -.860$). Although the specification of factor loadings offers the researcher a wide range of modeling possibilities, extrapolation beyond the range of scores used in the estimation of the growth trajectory is not advisable as it assumes that the trajectory continues to be linear when in fact it may be curvilinear.

The ability to center growth around various time points affords the researcher great latitude when specifying conditional LGMs involving various predictors of the growth sequence. For example, in the course of a naturalistic longitudinal study on the course of risk factors and substance abuse outcomes over three time points, the researcher can alternately specify predictors of initial status (T1), average growth (the constant), or the ending or terminal status (T3), in addition to predictors of the growth trend.

Representing the Shape of Growth Over Time

Polynomial Growth Functions

Factor loadings have been of little interest thus far in the two time points LGM. With three time points, however, the factor loadings carry information about the *shape* of growth over time. Three or more time points provide an opportunity to test for nonlinear trajectories in various behaviors. Perhaps the most familiar approach to nonlinear trajectories is the use of polynomials. The inclusion of quadratic or cubic effects is easily accomplished by including another factor or two. The factor loadings can then be fixed to represent a quadratic or cubic function of the observed time metric. Figure 3 represents a hypothetical growth model with a quadratic factor for three evenly spaced time points. The factor loadings are fixed at values which represent polynomial contrasts and are used to identify the scale of the *F* variables. The selected contrasts rescale the intercept factor to represent initial status. The polynomials depicted are only one possibility for modeling the three-factor LGM. The use of orthogonal polynomials with loadings of 1,1,1; −1,0,1; and 1,−2,1 for the intercept, linear, and quadratic factors, respectively, would rescale the intercept mean to represent a constant or the average level over time. Therefore, the linear and quadratic functions would not be centered around the initial time point, but would be centered around the constant or average level over time influencing their variances and covariances with other variables in the model. Mplus program specifications for the three-factor LGM are presented in Appendix B.

Tests for overall model fit of the three-factor LGM suggest a perfect fit of the model to the data given the saturated nature of the hypothesized model. With three repeated measures there are 3 variances, 3 covariances, and 3 observed means, or 9 pieces of known information, to use in model estimation.

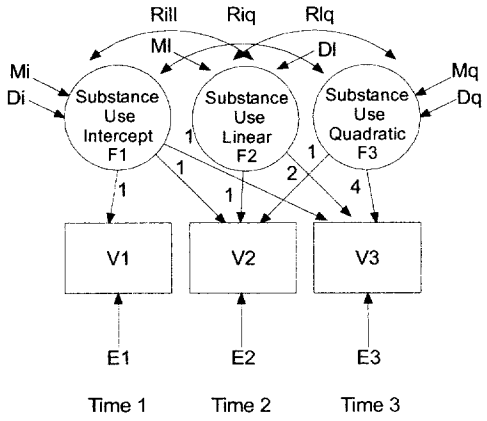

FIG. 3. Three-factor polynomial LGM.

The model estimates 3 variances, 3 covariances, and 3 means for the constant, linear, and quadratic latent factors, resulting in 0 degrees of freedom. Note that there are not enough degrees of freedom to estimate random error in the observed variables and that these are constrained to zero. In testing a more parsimonious model, such as a two-factor LGM (see section on Unspecified Growth Functions), sufficient degrees of freedom are available for evaluation of model fit.

Table 1 shows the construct equations, standard errors, and test statistics for the three latent growth factors shown in Figure 3.

Column 1 displays the parameter estimate, column 2 the standard error of the estimate, and column 3 the test of significance where values greater than 1.96 indicate estimates that are significantly different from zero. Note that the only significant Mean effects are found for *CNST* and *LIN*, the constant and linear effects, respectively. Covariances are also estimated with significant relationships existing between the constant and linear factors, and between the linear and quadratic factors.

In this example, the means of the growth factors (*Ms*) are characterized as latent means, or the beta weights for the regression of the latent factors on a unit constant (a vector of 1s). When the only predictor in a regression equation is the constant 1, the beta weight for the regression of the latent factors on the constant is equal to the means of the dependent variables, *Ms*. The *Ds*, representing deviation-from-the-mean variables, are the variances of the latent factors.

As noted earlier, growth curve methodology consists of two stages. First, a regression curve, not necessarily linear, is fit to the repeated measures of each individual in the sample. Second, the parameters for an individual's curve become the focus of the analysis rather than the original measures. In growth

TABLE 1
PARAMETER ESTIMATES FROM THE THREE-FACTOR LGM

	Estimate	S.E.	Est./S.E.
Means			
CNST	4.176	.183	22.836
LIN	.822	.263	3.131
QUAD	.034	.122	.280
Variances			
CNST	3.344	.473	7.071
LIN	6.893	.975	7.071
QUAD	1.477	.209	7.071
Covariances			
CNST WITH LIN	−1.608	.506	−3.175
QUAD	.222	.223	.993
LIN WITH QUAD	−3.054	.442	−6.915

models, between-subjects factors and covariates can be included in the model, just as in models not involving repeated measures data.

When the means and variances of the latent factors are significantly different than zero, the researcher may choose to add important explanatory variables to their models. With the addition of predictor variables, however, these parameters have different interpretations. Specifically, the *Ms* now represent the regression intercept, or that part of the dependent variable mean that is not explained by the additional predictor variables, and the *Ds* are deviation-from-predicted-value variables, generally referred to as disturbance terms, representing unexplained or residual variation.

The basic latent variable growth curve method illustrated here also allows for an integrated approach to modeling development that includes sequelae of change where the growth parameters are used as predictors of subsequent outcomes (for example, substance abuse development predicts subsequent criminal activity or clinically relevant deviant behavior). As such, LGM provides more flexibility in the measurement of change than the more traditional approach, in its ability to model development that includes both predictors and sequelae of change, allowing for complex representations of growth and correlates of change.

Because the quadratic mean is not significantly different from zero, the researcher may wish to respecify the model as a two factor polynomial model specifying only the constant and linear terms. In doing so, four degrees of freedom are obtained, 2 covariances, 1 variance, and 1 mean, allowing for the estimation of measurement error (e.g., y1* y2* y3*;) and a formal evaluation of model fit. Model fitting tests for the respecified model resulted in a χ^2 value of .078 with 1 degree of freedom and a p value of .78. Note that p values greater than .05 suggest that the model adequately represents the relationships observed in the data.

The characteristics of the collection of developmental trajectories that comprise the sample not only determine the magnitude of the estimated model parameters, but also the number of factors needed to adequately describe the data. Although it is possible to add factors until a satisfactory fit to the data is obtained, LGM is most powerful with a small number of factors describing the data. Questions about the number of factors needed for a given growth form, or how well a small number of factors approximates a particular nonlinear trajectory, are covered in detail in Tucker (1958), Tisak and Meredith (1990), and Burchinal and Appelbaum (1991).

Unspecified Growth Functions

Polynomials with squared or higher-order terms are not the only way to model nonlinear growth. Other plausible nonlinear growth curves can be modeled with fewer than three factors. One advantage of LGM is that the developmental curves may be specified (as in Figure 3) or unspecified (Tisak & Meredith, 1990). For example, the two-factor model can also be used to

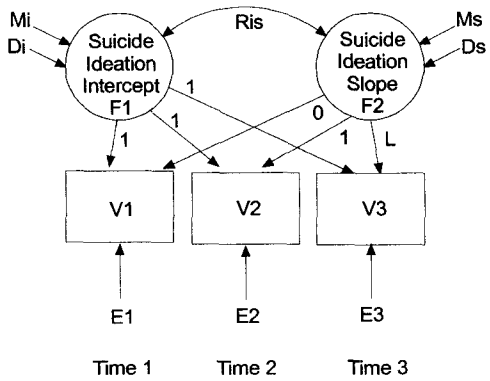

FIG. 4. Two-factor unspecified LGM.

model unspecified trajectories. If the shape of the trajectories is not known, the data can determine the shape. This could be a starting point from which more specific types of trajectories are tested. When there are enough points in time to freely estimate factor loadings beyond the two required for identification of the model, the slope factor is better interpreted as a general shape factor. If linear (i.e., straight line) growth turns out to be a good model for the data, then the shape factor is more appropriately called a slope factor.

Figure 4 represents a hypothetical two-factor growth model, where the repeated observations represent, for example, suicide ideation, with an unspecified growth function factor (*F2*) for three evenly spaced time points. With the unspecified two-factor model, two loadings on the slope factor are fixed at 0 and 1 as before (in theory any two fixed values should work equally well; McArdle & Hamagami, 1991). With the two loadings fixed, the rest of the factor loadings are allowed to be freely estimated (*L* in Figure 4). The factor loadings plotted against the observed time metric indicate the shape of growth. If the model fits well, the factor loadings on the shape factor reflect mean change in the observed variables.

Piecewise Growth Functions

Occasionally, interest centers on changes during distinct time periods (e.g., transitions from middle to high school or changes observed during treatment and follow-up phases of a treatment outcome trial). As such, factors related to differences in change in one segment of the overall growth period may differ substantially from those in a different segment. Moreover, rates of change during one period may vary substantially among individuals, whereas in another period they may be fairly homogeneous. Piecewise growth models provide a means to subdivide a series of measurements into meaningful segments and to summarize important aspects of change in each segment (Bryk

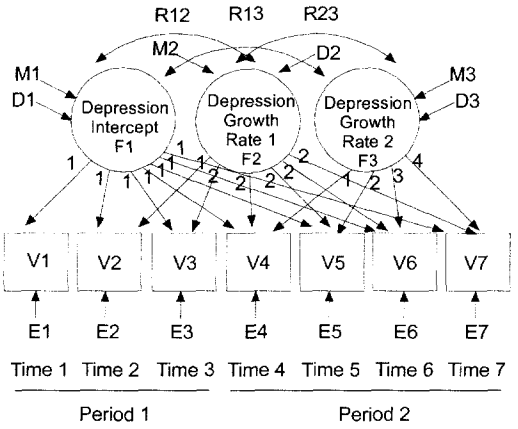

FIG. 5. Piece-wise LGM.

& Raudenbush, 1992). For example, in a treatment outcome trial involving psychiatric disorders, the piecewise model would be useful in reflecting different treatment trajectories across the active treatment and follow-up phases of the study.

Figure 5 depicts a two-piece growth model for growth covering two distinct developmental periods, Period 1 (V1, V2, and V3) and Period 2 (V4, V5, V6, and V7). The first piece (growth rate 1) might represent development of depressive symptoms during the middle school years (grades 6 through 8) and the second piece (growth rate 2) might represent development in depressive symptoms during high school (grades 9 through 12). Here, initial status is defined as status in grade 6 (V1) and all coefficients of the intercept are constrained at values of 1 [1, 1, 1, 1, 1, 1, 1]. Basis coefficients for the first and second slope factors are constrained at values of [0, 1, 2, 2, 2, 2, 2], and [0, 0, 0, 1, 2, 3, 4], respectively. These values represent linear growth in Periods 1 (middle school) and 2 (high school). By subdividing a series of repeated measurements into meaningful segments and summarizing growth in each segment, piecewise growth models provide a means of examining (a) whether rates of change in depressive symptoms differ as a function of growth period, (b) whether individual variability in rates of change in depressive symptoms differ between periods of interest, and (c) important predictors of change in depressive symptoms unique to a particular developmental period. The piecewise growth model can also be specified to capture curvilinear growth (as previously discussed in the growth models using unspecified growth functions) by specifying values of [0, 0, 0, 1, 2, *, *], where * indicates a loading that is freely estimated to reflect the shape of the depressive symptoms trajectory observed in the data. Applications of piecewise LGMs may be found in Sayer and Willet (1998) and Wang et al. (1999).

Modeling Between-Subjects Effects

Multiple Sample Growth Models

In the typical LGM application it is assumed that individuals whose data are being analyzed represent a random sample of observations from a single population. This assumption implies that data from different individuals provide comparable information concerning a hypothesized developmental process operationalized by the model. However, in practice, this assumption is not always reasonable. For example, individuals may be identified as belonging to certain groups, such as males and females, age cohorts, ethnicities, treatment or control conditions, and so forth. In these cases it may be appropriate to examine whether there are multiple populations rather than a single population, and multiple developmental pathways rather than a single underlying trajectory for all individuals. Many studies involving multiple populations have examined separate models for each group and compared the results. Unfortunately, such procedures do not allow a test of whether a common developmental model exists and whether there are multiple developmental pathways across groups.

Developmental hypotheses involving multiple populations can be evaluated simultaneously provided that data on the same variables over the same developmental period are available in multiple samples. For example, the multiple sample growth model has clear relevance to randomized control trials where one group might involve a wait-list control or an alternative treatment condition. In many cases, populations may be indistinguishable as far as the measured variables are concerned. When this occurs, the same population moment matrix describes all populations, and different sample moment matrices obtained from the various samples would simply be estimates of the same single population moment matrix. Growth models generated from the different samples should describe the same underlying developmental process for the population, and the separate models should be identical except for chance variations.

In other cases, the populations may share the same population covariance matrix but differ in the means obtained from the various samples. Growth models generated from these different samples would not be expected to describe the same underlying developmental process for the population, and the separate models would carry unique information concerning the growth trajectories for that population despite identical covariance structures (except for chance variations).

In practice, multiple-sample growth curve analyses are performed by fitting an ordinary growth curve model in each sample (e.g., treatment and control conditions), doing so simultaneously for all groups. The analysis can specify that some parameters are the same in each of the samples (using equality constraints across groups) and allow others to differ (no equality constraints are imposed). Substantively, the question of interest concerns the extent to which parameters of interest are the same across m groups. If a model having identical parameters in all groups fits acceptably, then the various samples

can be treated as arising from the same population. If, however, the models of the various groups have different parameters, the resulting model moment matrices will be different and the various samples must be treated as arising from different populations. These differences can be interpreted as evidence of an interaction between population membership and the particular structural model under investigation.

A variety of growth models can be generalized to the simultaneous analysis of data from multiple populations. To some extent, population differences can be captured in single-population analyses by representing the different groups as dummy vectors used as time-invariant covariates. However, to achieve more generality in modeling as well as specificity in the examination of population differences, it is necessary to use the multiple-population approach. Collapsing across different populations may mask potential group differences (e.g., age, gender, ethnicity) that are important to the study of change. Multiple-sample LGM has the potential to test for similarities and differences in developmental processes across different populations, including differences in levels of behaviors, developmental trajectories, rates of change, and effects of predictors and outcomes. Thus, when data from multiple populations are available, a multiple-sample LGM is likely to be advantageous in the study of numerous behavioral processes.

Added Growth Models

Conventional longitudinal multiple-population latent variable analyses specify a common growth model in multiple groups, testing for equality of parameters across the different populations. An alternative approach (Muthén & Curran, 1997) is shown in Figure 6. Here, an additional growth factor is introduced for one population (for example, the treatment condition in a program to reduce family conflict). Muthén and Curran call this the "added growth" factor (Muthén & Curran, 1997, p. 378). Whereas the first two factors (i.e., intercept and slope) are the same in both groups, the added growth factor, specified in one group (treatment condition), represents incremental/decremental growth in family conflict that is specific to that group.

In Figure 6, the added growth factor is specified to capture linear differences between the two groups. In this case the linear slope factor captures normative growth in family conflict that is common to both groups. For all factors except the initial status factor, one may specify an added growth factor. For example, one group may have a linear and quadratic growth factor beyond the intercept or initial status factor, and the remaining group may have added factors for both the linear and quadratic trajectories. Mplus program specifications for the added growth LGM are presented in Appendix C.

Alternative Approaches to Analyzing Treatment Effects: Interrupted Time Series Models

Although randomized control trial designs are generally preferred in intervention settings and analyzed in a multiple population framework (e.g.,

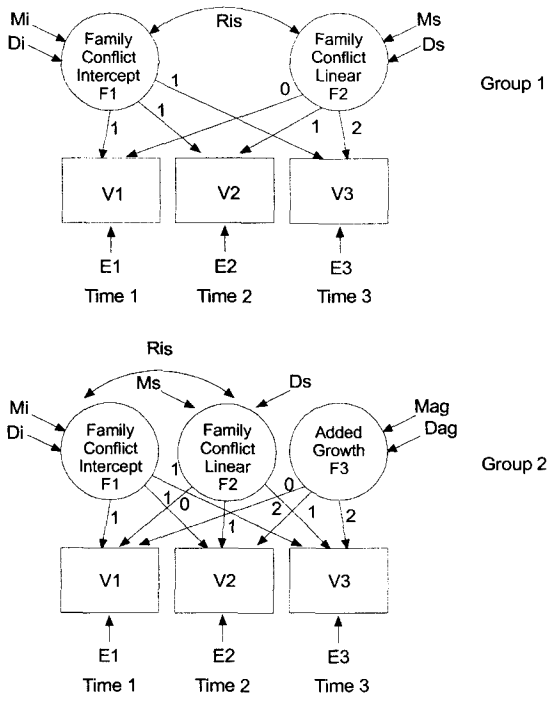

FIG. 6. Multiple-sample added-growth LGM.

Muthén & Curran, 1997), interrupted time series (ITS) designs, although less common in treatment research, have been widely used in prevention, intervention, and services research, especially in applied settings where randomized experiments are not feasible or indicated. Although considered quasi-experimental, the ITS design has been noted as representing one of the strongest alternatives to the randomized experiment (West, Biesanz, & Pitts, 2000). In the basic ITS design, measurements of the outcome variable are collected at equally spaced intervals over an extended period of time, with an intervention implemented at a specific point within that period. ITS designs allow for assessments of the onset (i.e., abrupt, gradual) and duration (i.e., permanent, temporary) of change in response to the implementation of an intervention whose effects may be cumulative. These advantages make the ITS design highly appropriate for use in pilot studies, where the goal is to document the presence of effects (and obtain a preliminary estimate of their size) that might warrant further evaluation in a large-scale randomized trial. Of particular relevance here is the fact that ITS designs permit assessment of the onset and duration of change in response to an intervention.

As can be seen from Figure 7, the ITS LGM is similar to the added growth

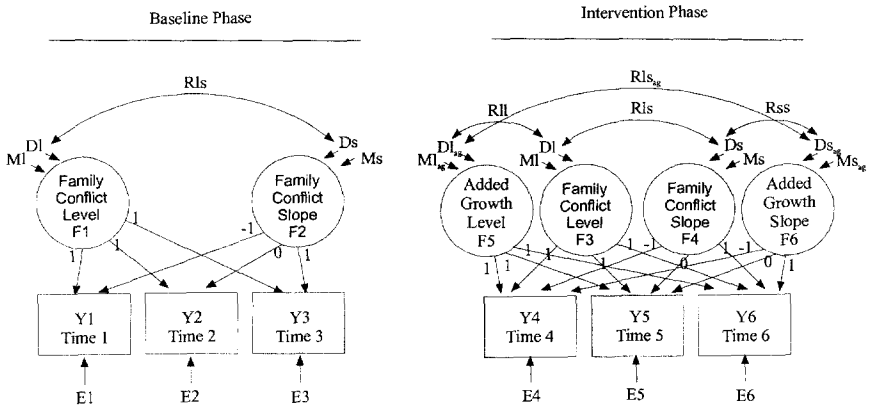

FIG. 7. Interrupted time series LGM.

model, except that the ITS LGM model captures both intercept and slope differences over baseline and treatment intervention periods in a single sample. This allows researchers to specifically examine changes in level and slope over the intervention implementation phase compared to the baseline phase. Basis terms for the slope factors were fixed at values of -1, 0, and 1, allowing for interpretation of the slope factors as linear change, and the level factors as average levels over time. The model specifies that common parameters (e.g., means, variances, and covariances) are the same in each of the different study phases (using equality constraints).

As in the general LGM framework, ITS LGM allows the researcher to predict changes in treatment outcomes from time-invariant and time-varying covariates and to use changes in treatment outcomes as predictors of subsequent outcomes.

Accelerated Designs

Although a true longitudinal design is ideal for modeling the development of behavior, alternative approaches are needed to reduce study time, subject attrition, and the cost of continual assessment. The recent resurgence of interest in time-ordered or dynamic approaches for accelerating the collection of longitudinal information has rekindled the seminal work of Bell (1953), who advocated the method of "convergence" as a means for meeting research needs not satisfied by either longitudinal or cross-sectional methods. This method consists of limited, temporally overlapping repeated measurements of independent age cohorts. Figure 8 represents a cohort-sequential model in which limited longitudinal information from three different age cohorts are linked together to form a common developmental trajectory in a variable of interest (e.g., deviance) spanning a 5-year period.

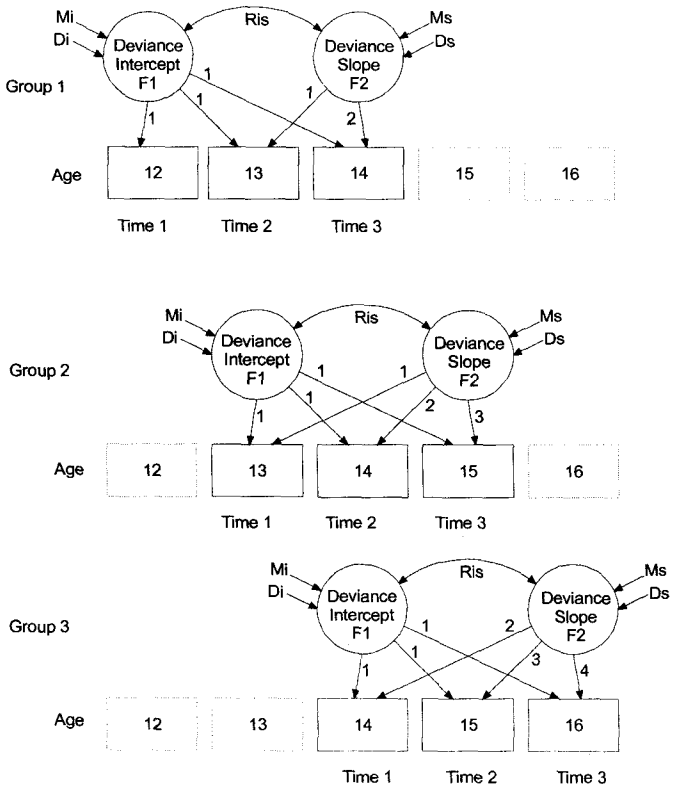

FIG. 8. Accelerated or cohort-sequential LGM.

This technique, which has gained recent popularity as the "cohort-sequential" design (Nesselroade & Baltes, 1979), links adjacent segments consisting of limited longitudinal data to determine the existence of a common developmental trend, or growth curve. This technique also allows the researcher to determine whether those trends observed in the repeated observations are corroborated within short time periods for each age cohort. This design approximates a long-term longitudinal study by conducting several short-term longitudinal studies of different age cohorts simultaneously. Although Bell (1953) described the technique as an ad hoc statistical procedure, S. Duncan, Duncan, and Hops (1996) demonstrated how it approximated a full longitudinal curve. Recently, a number of researchers (e.g., T. Duncan & Duncan, 1995; Duncan et al., 1994; McArdle & Anderson, 1989; McArdle & Hamagami, 1991; Meredith & Tisak, 1990) have demonstrated the usefulness of the accelerated longitudinal design. Mplus program specifications for the accelerated or "cohort-sequential" growth LGM are presented in Appendix D.

Multivariate LGM Extensions

The previous sections have described how LGMs can be used to model growth as a factor of repeated observations of one variable. Although development in a single behavior is often of interest, in longitudinal studies it might be important to examine a number of behaviors simultaneously (e.g., various types of substance use or problem behaviors) to determine the extent to which their development is interrelated. To this end, a multivariate longitudinal model may be considered. With multivariate LGMs it is possible to determine whether development in one behavior covaries with other behaviors.

The univariate longitudinal model is actually a special case of the general multivariate growth curve model. Multivariate LGMs provide a more dynamic view of the correlates of change, as development in one variable can be associated with development in another variable. The multivariate generalization of the growth curve model was originally conceptualized by Tucker (1966) as a descriptive technique. Multivariate, or associative, LGMs can be specified to model development of a multiple series of outcomes over time (see Figure 9). The associative model relates multiple behaviors (e.g., different substance use behaviors) simultaneously over time, and estimates the extent of covariation in the development of pairs of behaviors.

McArdle (1988) proposed two alternative methods, the *factor-of-curves* and *curve-of-factors* models, for conducting a *multivariate* analysis of the relations among numerous behaviors. In the factor-of-curves model, one examines whether a higher-order factor (e.g., substance use) adequately describes relationships among lower-order (e.g., alcohol, cigarettes, marijuana) developmental functions. The curve-of-factors model fits a growth curve to factor scores representing what the different behaviors have in common at each time

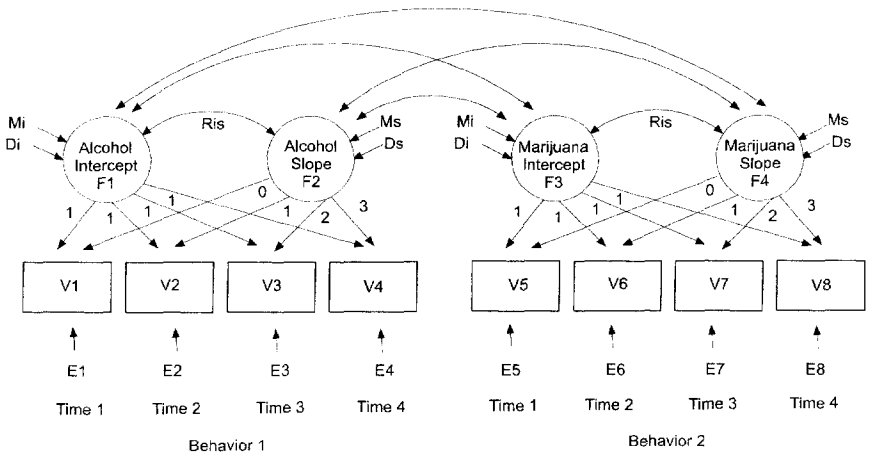

FIG. 9. Associative LGM.

point. The observed variables at each time point are factor analyzed to produce factor scores, which are then used for modeling growth curves. In practical terms, these multivariate extensions offer differing opportunities for evaluating the dynamic structure of both intra- and interindividual change, and represents a logical progression in testing the adequacy of latent growth curve representations of behavioral dynamics. Mplus program specifications for the multivariate LGM are presented in Appendix E.

Discussion

Advantages of the LGM Framework

LGM methodology provides a number of advantages to both epidemiological and prevention-oriented researchers studying behavioral change and development over time. The LGM describes a single individual's developmental trajectory and also captures individual differences in these trajectories over time. It is able to study predictors of those individual differences to answer questions about which variables exert important effects on the rate of development. At the same time, the model is able to capture the important group statistics in a way that allows the researcher to study development at the group level.

Given more than two assessment points, LGMs are able to test both linear and nonlinear growth functions. With the judicious choice of factor loadings, the general two-factor latent growth model can be parameterized so that the intercept and slope factors have straightforward interpretations as initial status and change, respectively. Using this parameterization, investigators can study predictors of change separately from correlates of initial status. When appropriate, the LGM also allows the flexibility of including more than two factors to capture developmental trends through the use of specified growth functions and additional factors (e.g., quadratic, cubic growth).

LGM methodology can also accommodate time-varying covariates. Both static and time-varying variables can be included in models as predictors of growth functions, as well as outcomes of growth functions, thus allowing the researcher to address questions related to the antecedents and consequences of development.

Another advantage of the LGM compared to more traditional approaches is the ability to use variables simultaneously as both independent and dependent variables in the model, allowing for complex representations of growth and correlates of change. Most general linear modeling software packages (e.g., SPSS) will automatically compute the desired polynomial contrasts necessary for the analysis of growth curves and allow the contrast variates to be used as either independent or dependent variables. Continuous covariates accommodated in an analysis of covariance allow for tests of both continuous predictors of change and change as a predictor. This method does not, however, allow for the simultaneous inclusion of change as both an independent and dependent variable. The basic latent variable growth curve method illustrated

here allows for an integrated approach to modeling development that includes both predictors and sequelae of change. In practical terms, LGMs offer differing opportunities for evaluating the dynamic structure of both intra- and interindividual change, and represent a logical progression in the paradigm of representing behavioral dynamics.

In addition to the special cases of the LGM presented in previous sections, several other noteworthy extensions are possible.

Incorporating missing data in LGMs. Because nearly all longitudinal data sets suffer from various forms of missing data, it is important that analytic techniques be able to appropriately handle missing data that might result from attrition and omissions, as well as from planned missingness. From a statistical point of view, the best missing data procedures do several things. First, they take into consideration all available causes of missingness. Second, they employ the same statistical model to handle the missing data that is used to perform the desired analysis. For example, if the final model of interest is a latent variable model, the best approach would also use a latent variable model to handle the missing data. Finally, the best procedures provide consistent and efficient parameter estimates. Within LGM, model-based procedures can be used to analyze incomplete data using either multiple-sample SEM or raw maximum likelihood (ML) procedures. Both approaches allow the researcher to take into consideration all available causes of missingness, employ the same statistical model to handle the missing data that is used to perform the desired analysis, and provide consistent and efficient parameter estimates. Applications of missing data methods within the LGM framework can be found in S. Duncan and Duncan (1994), T. Duncan, Duncan, and Li (1998), and Muthén, Kaplan, and Hollis (1987).

Design issues: Sample size selection and power estimation. The latent variable method described in this article also provides a power estimation framework to aid researchers in making design decisions for a variety of intervention studies. From a statistical point of view, the best procedures for power estimation should (a) employ the same statistical model for power and sample size estimation as used for the desired analysis (for example, if the final model of interest is an LGM, the best approach for power estimation would also use an LGM); (b) cover the situations most commonly encountered by researchers; (c) be flexible enough to deal with new or unusual situations; (d) allow easy exploration of multiple values of input parameters; and (e) allow estimation of sampling variance from pilot data and from the statistics commonly reported in the literature.

Within the latent variable growth modeling framework, power estimation is directly related to the parameter values of a specified model. The relations among values of the level of significance (α), measures of effect size (χ^2), the sample size (n), and the degrees of freedom are identical to those in more traditional techniques. However, LGM has the added advantage of accounting for measurement error, thus disattenuating the relationships among the variables of interest, which increases reliability and power and reduces sample

size requirements. This simple relationship between reliability and power underscores the advantages of the statistical reduction of attenuation due to the unreliability of a study's measures within the SEM framework. In the context of testing and interpreting treatment effects, questions of statistical power naturally arise. Researchers need to know whether they have any realistic chance of rejecting a null hypothesis or discriminating between one model and another. Suppose, for example, we wanted to evaluate, post hoc, the power of detecting a treatment effect as significantly different from zero at the 5% level of significance. Or prospectively, we assumed an expected treatment effect was reasonable and we wanted to design an intervention to detect the effect, maximizing power while minimizing cost. There are numerous ways to approach this, and power calculations such as these in growth modeling contexts can be accommodated using the method outlined by Satorra and Saris (1985). A description of this method can be found in T. Duncan et al. (1999) and T. Duncan, Duncan, and Strycker (2002).

Satorra and Saris (1985) show that power can be approximated using a two-step procedure that involves two models, one that is assumed to be correctly specified and the other, more restrictive, assumed to be misspecified. Because the two models are nested, the discrepancy index between the correct and incorrectly specified models is reflected in the likelihood ratio (LR) chi-square estimate, except that the value corresponds to the noncentrality parameter (NCP) in a statistical power analysis. Given the value of the NCP obtained, the degrees of freedom, and the probability level of the test chosen, the power of the test can be determined using tables (e.g., Haynam, Govindarajulu, & Leone, 1973) for the noncentral chi-square distribution.

All parameter values for the hypothesized model must be explicitly stated and may come from previous theory, previous experimentation, or some other rationale. However, this aspect of power estimation within the SEM framework often poses the most difficult challenges to the researcher who may not have access to multiple time point data from pilot studies or extant published research (e.g., often the best available data are treatment group pre- and posttest means and standard deviations, and ANOVA results from a few published studies). In these cases, combining information from multiple sources may provide the researcher with enough information to adequately specify the model's parameters. Often it is easier to generate an input matrix of means, standard deviations, and correlations than it is to generate parameter estimates for a fully specified LGM. For example, treatment studies can provide information regarding pre- and posttest means and standard deviations and epidemiological studies may provide information regarding a plausible correlational structure for the observed variables. Once this input matrix is generated, it can be used to estimate the desired LGM and obtain the necessary parameter estimates.

Because the Satorra and Saris (1985) method computes power from a model's population values, it is not suitable for analyses requiring information beyond the second-order moments, such as those involving missing or

nonnormal data. Muthén and Muthén (2002) outline the use of Monte Carlo simulations for determining sample sizes needed to obtain acceptable estimates and power to reject zero effects. Using the mixture approach available in Mplus, a very flexible Monte Carlo procedure is available. In Monte Carlo studies, data are generated from a population with hypothesized parameter values. A large number of samples are drawn, and a model is estimated for each sample. Parameter values and standard errors are averaged over the samples. In the Monte Carlo procedure available in Mplus, parameter estimate bias, standard error bias, coverage (the proportion of replications for which the 95% confidence interval contains the true parameter value), and power are also evaluated. Like the Satorra and Saris (1985) method, the Monte Carlo procedure also requires specification of population values for each parameter of the model. Mplus syntax for the Monte Carlo power estimation procedure is provided in Appendix F.

Limitations of the LGM

Despite numerous attractions, LGM is not always the appropriate analytical choice. The LGM approach involves the fundamental assumption that change for each individual is systematically related to the passage of time, at least over the time interval of interest (Burchinal & Appelbaum, 1991). If change is not related to the passage of time, studying individual trajectories over time will not be very informative. Other situations in which LGM methods would not be apt include randomly varying within-subjects designs, including unequal intervals of observations, varied within-person distributions of time-varying covariates having random effects, the incorporation of clustered designs, and data missing at random. Although the latent variable framework accommodates treatments of missing data (e.g., Muthén et al., 1987) and growth modeling with clustered data (e.g., Muthén, 1997), the analyses do not yet allow the flexibility of the random coefficient approach.

Concluding Remarks

The search for the best methods to address complex issues in studies of behavioral change has been a major focus of recent developmental research (e.g., Collins & Horn, 1991; Collins & Sayer, 2001; T. Duncan et al., 1999; Gottman, 1995). It has prompted a movement away from analyses of homogeneous populations and interindividual variability to a focus on both inter- and intraindividual variability and heterogeneity in growth trajectories over time. The ultimate purpose of these new statistical methods is to provide a means for drawing conclusions from the data. At their best these statistical methods enjoy a symbiotic relationship with substantive research. The need to answer substantive questions inspires the development of new statistical methods, and subsequently, these methods prompt substantive researchers to view their data in new ways and to pose new substantive questions. Just as there are a plethora of substantive questions posed by researchers, so too

are there a broad and varied assortment of newly developed statistical methods available to answer these substantive questions. Although these techniques have fundamentally changed how researchers think of and study change, the application of these methods in practice has been slowly implemented. The LGM approach is particularly beneficial as it allows for a more comprehensive and flexible approach to research design and data analysis than any other single statistical model for longitudinal data in standard use by social and behavioral researchers, making available to a wide audience of researchers an analytical framework for a variety of analyses of growth and behavioral processes.

Appendix A
Two-Factor LGM

```
data:
      file is basis.dat;
      format is free;
      type is means std corr;
      nobservations = 100;
variable:
      names are y1 y2;
      usevar = y1-y2;
analysis: type = general meanstructure;
      iterations = 100;
model:
      int by y1-y2@1;
      slp by y1@0 y2@1;
      [int*8 slp*1];
      [y1-y2@0];
      y1@0 y2@0;
      int*54.066 slp*60.460;
      int with slp-25.662;
output: tech1;
```

```
basis.dat
8 9
7.39  7.99
1.00
.4859 1.00
```

```
Note: The model statement (model:) for the LGM consists of the following commands
    BY                    Short for measured by - defines latent variables.
                            Example: int by y1-y2
    WITH                  Short for correlated with - defines correlational relationships.
                            Example: int WITH slp
    list of variables;    Refers to variances and residual variances;
                            Example: y1 y2
    [list of variables];  Refers to means or regression intercepts
                            Example: [int*8 slp*1]
    *                     Freely estimated parameter at specific starting value
                            Example: int*54.066 slp*60.460
    @                     Fixed parameter at a specific value
                            Example: [y1-y2@0];
```

Appendix B
Three-Factor Polynomial Growth Model

```
data:
      file is lgm.dat;
      format is free;
      type is means covariance;
      nobservations = 100;
variable:
      names are y1 y2 y3;
      usevar = y1-y3;
analysis: type = general meanstructure;
      iterations = 100;
model:
      [cnst* lin* quad];
      cnst by y1-y3@1;
      lin by y1@0 y2@1 y3@2;
      quad by y1@0 y2@1 y3@4;
      [y1-y3@0];
      y1@0 y2@0 y3@0;
      cnst* lin* quad*;
      cnst with lin*;
      cnst with quad*;
      lin with quad*;
output: tech1;
```

```
lgm.dat
4.176         5.032         5.956
3.378
1.978         2.863
1.026         1.010         1.037
```

Appendix C
LGM Multisample Analysis

```
data:
      file is mltgrp.dat;
      format is free;
      type is means covariance;
      ngroups = 2;
      nobservations = 100 100;
variable:
      names are y1 y2 y3;
      usevar = y1-y3;
analysis: type = general mgroup meanstructure;
      iterations = 100;
model:
      int by y1-y3@1;
      slp by y1@0 y2@1 y3@2;
      add by y1@0 y2@1 y3@2;
      [y1-y3@0];
      [int@0 slp@0];
      [int*1.493](m1);
      [slp*.175](m2);
      [add*.207];
      add with slp@0 int@0;
      int with slp-.069(d12);
      int*1.020(d1);
      slp*.393(d2);
      add*.107(d3);
      y1*.805(e1);
      y2*.970(e2);
      y3*.085(e3);
```

```
model g1:
       add by y1@0 y2@0 y3@0;
       [y1-y3@0];
       [int*1.493](m1);
       [slp*.175](m2);
       int with slp-.069(d12);
       int*1.020(d1);
       slp*.393(d2);
       y1*.805(e1);
       y2*.970(e2);
       y3*.085(e3);
output: samp standardized;
```

```
mltgrp.dat
4.176      5.032      5.956              model g1 data
3.378
1.978      2.863
1.026      1.010      1.037
4.176      4.032      4.056              model: data
2.378
1.078      2.263
1.026      1.010      2.037
```

Appendix D
LGM Accelerated Design

```
Data:
      File is accel.dat;
      format is free;
      type is means covariance;
      ngroups = 3;
      nobservations = 200 200 200;
Variable:
      Names are y1 y2 y3;
      usevar = y1-y3;
Analysis: type = general mgroup meanstructure;
      Iterations = 100;
Model:
      int by y1-y3@1;
      slp by y1@2 y2@3 y3@4;
      [y1-y3@0];
      [int*.310](m1);
      [slp*.384](m2);
      int with slp-.140(r1);
      int*.314(d1);
      slp*.077(d2);
      y1*.590(e3);
      y2*.460(e4);
      y3*.760(e5);
Model g1:
      int by y1-y3@1;
      slp by y1@0 y2@1 y3@2;
      [y1-y3@0];
      [int*];(m1);
      [slp*];(m2);
      int with slp*(r1);
      int*(d1);
      slp*(d2);
      y1*.178(e1);
      y2*.479(e2);
      y3*.590(e3);
```

```
Model g2:
      int by y1-y3@1;
      slp by y1@1 y2@2 y3@3;
      [y1-y3@0];
      [int*];(m1);
      [slp*];(m2);
      int with slp*(r1);
      int*(d1);
      slp*(d2);
      y1*.479(e2);
      y2*.590(e3);
      y3*.460(e4);
Output: samp standardized;
```

```
accel.dat
 0.335 0.774 0.964            model g1 data
 0.483
 0.303 .899
 0.271 0.488 1.258
 0.764 0.992 1.384            model g2 data
 0.759
 0.400 0.988
 0.412 0.683 1.315
 0.939 1.541 2.170            model data
 1.170
 0.711 1.371
 0.662 0.936 1.709
```

Appendix E
Associative Model

```
data:
      file is assoc.dat;
      format is free;
      type is means stdeviations correlation;
      nobservations = 100;
variable:
      names are y1-y9;
      usevar = y1-y9;
analysis: type = general meanstructure;
iterations = 100;
model:
      int1 by y1-y3@1;
      slp1 by y1@0 y2@1 y3@2;
      int2 by y4-y6@1;
      slp2 by y4@0 y5@1 y6@2;
      int3 by y7-y9@1;
      slp3 by y7@0 y8@1 y9@2;
      [y1-y9@0];
      [int1* slp1* int2* slp2* int3* slp3];
      int1 with int2* int3* slp1* slp2* slp3*;
      int2 with int3* slp1* slp2* slp3*;
      int3 with slp1* slp2* slp3*;
      slp1 with slp2* slp3*;
      slp2 with slp3*;
```

```
output: standardized;
```

```
assoc.dat
4.106  5.032  5.956  4.096  4.939  5.782  4.496  4.539  5.282
1.510  1.702  2.118  1.669  1.985  1.979  1.976  2.240  2.126
1.000
 .468  1.000
 .366   .482  1.000
 .525   .458   .395  1.000
 .397   .452   .432   .683  1.000
 .399   .395   .523   .666   .710  1.000
 .479   .392   .402   .552   .387   .321  1.000
 .374   .489   .391   .322   .439   .362   .598  1.000
 .273   .366   .429   .301   .378   .498   .389   .659  1.000
```

Appendix F
Montecarlo Power Analysis (No Missingness)

```
Montecarlo: Names are y1 y2 y3 y4;
Nobservations = 206;
Nreps = 10000;
Seed = 53487;
Analysis: Type = random;
Estimator = ML;
Model Montecarlo:
      [int*4.096 slp*.843];
      int by y1-y4@1;
      slp by y1@0 y2@1 y3@2 y4@3;
      [y1-y4@0];
      y1*1.143 y2*1.428 y3*.454 y4*.182;
      int*1.986 slp*.160;
      int with slp*-.531;
Model:
      [int*4.096 slp*.843];
      int by y1-y4@1;
      slp by y1@0 y2@1 y3@2 y4@3;
      [y1-y4@0];
      y1*1.143 y2*1.428 y3*.454 y4*.182;
      int*1.986 slp*.160;
      int with slp*-.531;
Output: tech9;
```

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