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Concepts, Issues, and Applications

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Methodology for Business and Management

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Duncan/Duncan/Strycker/Li/Alpert An Introduction to Latent Variable Growth Curve Modeling: Concepts, Issues, and Applications

Marcoulides Modern Methods for Business Research

Heck/Thomas An Introduction to Multilevel Modeling Techniques

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An Introduction to Latent Variable Growth Curve Modeling  
 Concepts, Issues, and Applications

Terry E. Duncan  
 Susan C. Duncan  
 Lisa A. Strycker  
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1999

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## Preface

This volume presents a statistical method, known as Latent Variable Growth Curve Modeling, for analyzing repeated measures. Although a number of readers may be unfamiliar with Latent Growth Modeling (LGM), it is likely that most have already mastered many of the method's underpinnings, inasmuch as repeated measures analysis of variance (ANOVA) models are special cases of LGMs that focus only on the factor means. In contrast, a fully expanded latent growth curve analysis takes into account both factor means and variances. This combination of individual and group levels of analysis is unique to the LGM procedure. LGMs are also variants of the standard linear structural model. In addition to using regression coefficients and variances and covariances of the independent variables, they incorporate a mean structure into the model. LGMs strongly resemble the classic confirmatory factor analysis. However, because they use repeated measures raw-score data, the latent factors are interpreted as chronometric common factors representing individual differences over time. The book is written with two major themes: concepts and issues, and applications and is designed to take advantage of the reader's familiarity with ANOVA and standard structural equation modeling (SEM) procedures in introducing LGM techniques and presenting practical examples. Mathematically sophisticated readers may want to study more advanced treatments of this subject in Meredith and Tisak (1990) or Tisak and Meredith (1990). To estimate the LGM, it is necessary to use current standards in estimation and testing procedures found in SEM programs such as LISREL (Jöreskog & Sörbom, 1993), Mx (Neale, 1995), Amos (Arbuckle, 1995), and EQS (Bentler & Wu, 1995). Examples are provided using EQS, with supplemental notation for Amos and LISREL programs.

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## Chapter 1 Introduction

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. A variety of procedures have been developed to assist researchers in the analysis and quantification of change. Major analytic strategies for analyzing longitudinal data include autoregressive and growth curve models. These two approaches are, in general, quite different ways of modeling longitudinal data and can yield quite different results, although in some specific cases they are closely related. The choice of model depends on the nature of the phenomenon under study and the research question.

### Typical Approaches to Studying Change

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. Longitudinal panel models have a number of important advantages over cross-sectional models. Probably the most important advantage is the correspondence between panel models and the commonly stated conditions for inferring a causal connection between two variables. Methodologists generally agree that inferring causality requires demonstrating that three conditions are met: (1) the presumed cause and effect are related, (2) the presumed cause precedes the effect in time, and (3) other competing explanations for the observed effect can be ruled out (Bollen, 1989; Kessler & Greenberg, 1981). The second condition can never be met with cross-sectional data. Gollob and Reichardt (1987) have also argued that

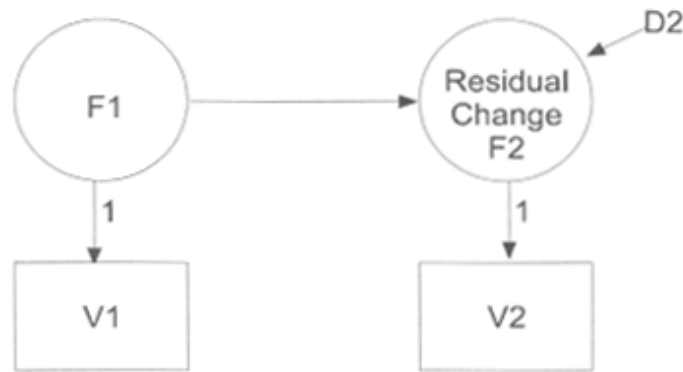


Fig. 1.1.  
Representation of an autoregressive or residual  
change model.

because causes take time to exert their effects and cross-sectional models fail to include these time lags, such models are inherently misspecified.

One traditional approach to studying change has been the use of an autoregressive or residual change model, such as that shown in Fig. 1.1. Gollob and Reichardt (1987) stated that the autoregressive effect (the effect of a Time 1 measure on the Time 2 measure of the same variable) is a legitimate competing explanation for an observed effect. Therefore, these authors have argued that time lags and autoregressive effects must be included in causal models before causal inferences can be made concerning the influence of additional predictor variables.

Other researchers have disputed the central role of autoregressive effects (residual change scores) and have focused instead on the simple difference score or on the analysis of growth curves when data are collected on more than two occasions (Rogosa, Brandt, & Zimowski, 1982; Stoolmiller & Bank, 1995). Such researchers have underscored serious shortcomings inherent in typical developmental models which incorporate autoregressive effects (i.e., panel models; Rogosa & Willett, 1985). The shortcomings they identify are fourfold:

1. In models depicting growth or developmental change, the sample means often carry useful statistical information. However, in a typical autoregressive covariance structural model, the parameters of interest are the variances and covariances of the independent variables. The means of the measured variables are implicitly assumed to be zero. Therefore, this common method of model estimation is inadequate because it fails to consider the influence of both inter- and intraindividual differences in development.

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2. The panel model fails to provide adequate generalization to more than two points in time. With more than two time points, it becomes less clear which autoregressive effect should be controlled for when evaluating the significance of other predictors in the model. The best that can be done, even in multiwave panel models, is to focus on change scores between any two points in time.

3. By controlling for initial levels (i.e., including the autoregressive effect), the panel model tends to eliminate all predictors except those that predict changes in the rank order of the observations over time. This is a disadvantage when studying monotonically stable phenomena (Meredith & Tisak, 1990), in which the rank order of the observations stays the same although significant change at the individual and group level can also be occurring.

4. The autoregressive effect is questionable as a true causal effect. Researchers such as Rogosa et al. (1982) and Rogosa and Willett (1985) provide a comprehensive discussion of the problems with panel models incorporating autoregressive effects.

#### Toward an Integrated Developmental Model

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, these 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. Latent variable growth curve methodology meets all of these criteria.

The recent resurgence of interest in time-ordered approaches that can incorporate information concerning the group or population, while conveying specific information about changes in the individual, has reintroduced the formative work of Rao (1958) and Tucker (1958). These researchers constructed a procedure that included unspecified longitudinal curves or functions. Rao and Tucker promoted the idea that, although everyone develops the same way, individual differences are both meaningful and important. Researchers such as Meredith and Tisak (1990) and McArdle (1988) have extended Rao and Tucker's basic model of growth curve analysis to permit the use of current standards in estimation and testing procedures found in structural equation modeling (SEM) programs such as LISREL (Jöreskog & Sörbom, 1993), EQS (Bentler & Wu, 1995), and Amos (Arbuckle, 1995). This methodology, which has gained recent popularity as the "latent growth curve" model, provides a means of

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modeling development as a factor of repeated observations over time. Within this approach, age is viewed as a dimension along which behavior changes are superimposed, forming part of the definition of the dependent variable in developmental studies.

Because Latent Growth Modeling (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 the capacity to test the adequacy of the hypothesized growth form, to incorporate time-varying covariates, and to develop from the data a common developmental trajectory, thus ruling out cohort effects. Some of the limitations of the LGM approach include the necessity for relatively large samples and the restrictive requirement of equal number and spacing of assessments for all individuals. Ware (1985) referred to this kind of data as "balanced-on-time." If the number of time points or the spacing between time points varies across individuals, other growth curve techniques are available (e.g., Bryk & Raudenbush, 1987; Hui & Berger, 1983; Kleinbaum, 1973). Clearly, a fundamental assumption of growth curve methodology is that change for each individual on the phenomena under study 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. In this case, a repeated measures regression approach, such as Generalized Estimating Equations (Liang & Zeger, 1986), would likely be more appropriate.

Modeling growth or development within the latent variable SEM framework is a potentially valuable methodology that many researchers believe is underused (e.g., Bryk & Raudenbush, 1987; Meredith & Tisak, 1990; Rogosa et al., 1982; Rogosa & Willett, 1985; Willett, Ayoub, & Robinson, 1991). It is likely that increased use of growth curve methodology, in any form, will bolster researchers' success in identifying important predictors and correlates of change.

## Organization of the Book

LGM concepts, issues, and applications are presented in the following chapters. Heuristically, growth curve methodology can be thought of as consisting of two stages. The first stage focuses on accurately describing and summarizing individual differences in growth trajectories, if they exist. Here, parameters of the growth curves, rather than the original variables, are of interest. In Stage 2, the parameters for an individual's growth curve become the focus of the analysis rather than the original measures.

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Chapter 2 presents an introduction to growth analyses using a simple two-factor LGM for two points in time. The chapter includes informal definitions and interpretations, as well as formal specifications for the various model parameters.

The ideas presented in chapter 2 are illustrated in chapter 3 within the more familiar analysis of variance (ANOVA) context. The first section of chapter 3 provides a simple comparison of a growth curve model analyzed by both repeated measures ANOVA and LGM methodologies. Having described individual differences in growth, the remaining sections of the chapter describe Stage 2 analyses. This second stage addresses hypotheses concerning determinants and sequelae of growth. Illustrations are provided to demonstrate how the basic growth curve model can be extended to include both predictors and sequelae of change.

Chapter 4 demonstrates the use of the basic LGM for analyzing multiple populations. Various LGMs can be generalized to the simultaneous analysis of data from multiple populations or groups. The multiple-sample approach is advantageous in that multiple groups are analyzed simultaneously rather than in separate analyses. Examples are provided for a typical multiple-sample LGM and for a useful alternative involving an added growth factor to capture normative growth that is common to both groups as well as differences in growth between groups.

When testing whether variables change together over time, multivariate LGM models can be used. Chapter 5 presents examples of associative and higher order multivariate LGMs. An important facet of multivariate LGMs, and an advantage over repeated measures polynomial ANOVA techniques, is that they enable associations to be made among the individual differences parameters. These associations, analogous to the synchronous model's correlation coefficient (Meredith & Tisak, 1990), are crucial to any investigation of development because they indicate the influences of development or correlates of change.

Chapter 6 presents models for the accelerated collection of longitudinal data. The method first introduced by Bell (1953) consists of limited repeated measurements of independent age cohorts with temporally overlapping measurements. This technique, which has gained recent popularity as the "cohort-sequential" design (Nesselrode & Baltes, 1979), provides a means by which adjacent segments of limited longitudinal data of different age cohorts can be linked to create a common developmental trend, or growth curve. This approach allows the researcher to approximate a long-term longitudinal study by conducting several short-term longitudinal studies of different age cohorts simultaneously.

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Building upon the approach to estimating nonlinear and interactive effects of latent variables proposed by Kenny and Judd (1984), chapter 7 demonstrates methods for including interaction effects in developmental models. Jöreskog and Yang's (1996) procedure for modeling interactions among latent variables is extended to LGMs. Examples of interactions among growth functions in single- (shape) and two-factor (level-shape) LGMs are provided.

Chapter 8 presents models for incorporating missing data. A taxonomy of missingness and a description of methods for use with partially missing data are presented. Model-based approaches to missingness, which include a multiple-group approach (Muthén, Kaplan, & Hollis, 1987) and a raw maximum likelihood approach (Arbuckle, 1996), are illustrated using LGM.

Combining procedures for missing data outlined in chapter 8, chapter 9 describes multilevel models for longitudinal data. Conventional LGM analyses are often applied to data that are obtained in a hierarchical fashion. However, such data are most frequently modeled as if the data were obtained as a simple random sample from a single population. Alternative LGM specifications are presented that use conventional SEM software for multilevel SEM. Full maximum likelihood estimation and a limited information approach are presented and compared using unbalanced data.

Chapter 10 illustrates the use of power estimation techniques pertaining to latent growth curve modeling. Although the issues raised in this chapter are not new, researchers are reminded of their importance. Exactly how these issues are handled will depend on the questions asked, the resources available, and other considerations. The chapter provides an overview of current power estimation methods available for latent variable approaches. These methods involve the estimation of power for single and multiple parameters and overall model fit. This is followed by applications of these methods with simulated data. Examples of power estimation for growth parameters in a single-sample LGM model and for treatment effects in a longitudinal experimental study are provided.

Finally, in chapter 11, the utility of latent growth curve methodology is re-emphasized with a discussion of the strengths and weaknesses of this approach for a variety of research domains.

This book provides a comprehensive introduction to LGM and its various methodological extensions, and incorporates a number of practical examples of its use. Space limitations do not allow illustrations of all LGM applications in all research domains.

To learn more about the possibilities of this methodology, readers are referred to a number of recent articles related to LGM, including such topics as: *general issues in LGM* (Aber & McArdle, 1991; McArdle & Epstein, 1987; Meredith & Tisak, 1990; Patterson, 1993; Raykov, 1992a; Stoolmiller, 1994, 1995; Walker, Acock, Bowman, & Li, 1996; Willett & Sayer, 1994); *LGM factor-of-curves and curve-of-factors approaches* (S.C. Duncan & T.E. Duncan, 1996; McArdle, 1988); *single-factor LGM or curve model* (Duncan & McAuley, 1993; McArdle, 1988; McArdle & Nesselroade, 1994; Raykov, 1991); *two-factor LGM* (Chassin, Curran, Hussong, & Colder, 1996; Patterson, 1993; Raykov, 1992b); *three-factor LGM* (T.E. Duncan, S.C. Duncan, & Hops, 1996; Stoolmiller, Duncan, Bank, & Patterson, 1993); *multiple-sample LGM* (Curran & Muthen, in press; S.C. Duncan, Alpert, T.E. Duncan, & Hops, 1997; McArdle, Hamagami, Elias, & Robbins, 1991; Muthen & Curran, 1997; J. Tisak & M. S. Tisak, 1996); *associative LGM* (Curran, Stice, & Chassin, 1997; Ge, Lorenz, Conger, & Elder, 1994; Raykov, 1994; Stoolmiller, 1994; Tisak & Meredith, 1990; Wickrama, Lorenz, & Conger, 1997); *multilevel LGM* (T. E. Duncan, S.C. Duncan, Alpert, Hops, Stoolmiller, & Muthen, 1997; Muthen, 1997; Schmidt & Wisenbaker, 1986); *LGM with missing data* (S. C. Duncan & T.E. Duncan, 1994; T.E. Duncan, S.C. Duncan, & Li, 1998); and *cohort-sequential designs* (Anderson, 1993, 1995; T.E. Duncan & S.C. Duncan, 1995; T.E. Duncan, S.C. Duncan, & Hops, 1994; S.C. Duncan, T.E. Duncan, & Hops, 1996; T.E. Duncan, S.C. Duncan, & Stoolmiller, 1994; T.E. Duncan, Tildesley, S.C. Duncan, & Hops, 1995; McArdle & Anderson, 1989; McArdle, Anderson, & Aber, 1987; McArdle & Hamagami, 1992; Tisak & Meredith, 1990).

## Software Implementation

Although currently available SEM software programs share many features, there are a number of distinctions among them. Given these idiosyncrasies, a text covering SEM methodology must devote considerable space to describing "the program" in addition to "the method." In choosing an SEM package, the user should weigh performance with convenience. Although any SEM software program will prove adequate for most of the user's requirements when estimating the models demonstrated in this book, the majority of the models in this book are presented using EQS (Bentler & Wu, 1995) notation, supplemented selectively with notation from two other SEM programs, LISREL (Jöreskog & Sörbom, 1993) and Amos (Arbuckle, 1995). Brief outlines of these programs and some of their distinctive features for

modeling growth and development within the SEM framework are presented next.

### Amos1

Amos accepts standard command line specifications. Amos does not have a matrix-oriented specification format. Instead, relations between variables may be specified with "arrows" formed from <and> signs, as in

Time 2 <-- Slope 1.1

or specified with equations as in

$V2 = (1)F2 + (1)EPS2,$  1.2

where  $F2$  = Slope,  $V2$  = Time 2, and  $EPS2$  = unique error associated with  $V2$ .

Amos also allows the user to specify models via path diagrams using Amos Graphics instead of the usual command lines. Beyond its usefulness as a command interface, Amos Graphics includes the tools necessary to produce publication-quality path diagrams. Moreover, beginning with release 3.5, all fit measures can be displayed on the path diagram.

Amos has a number of distinguishing features besides the usual capabilities found in competing SEM programs. Amos remains on the cutting edge of missing-data techniques, allowing for analyses based on full information maximum likelihood estimates in the presence of missing data (see also Mx [Neale, 1995] for a raw ML approach to missing data). Bootstrapped standard errors and confidence intervals are available for all parameter estimates, as well as for sample means, variances, and covariances. Amos provides a variety of methods for estimating parameters, including normal-theory maximum likelihood and generalized least squares methods. Amos also calculates an assortment of fit indices (see Table 1.1), and will compute modification indices and estimated parameter change statistics to aid in evaluating individual constraints on model fit.

Amos is limited to analysis of covariance matrices, which implies that it is not specifically designed for the analysis of ordinal data. However,

1 Amos 3.5. Written by James L. Arbuckle. Distributed by SmallWaters Corporation, 1507 East 53rd Street, Suite 452, Chicago, IL 60615. Internet smallwaters@acm.org, URL: <http://www.smallwaters.com>.

with the \$normalitycheck command, raw data files can be screened for univariate and multivariate normality. Another limitation is that Amos does not allow users to directly specify nonlinear or equality constraints on parameters, although comparable constraints can be implemented using the "phantom variable" techniques developed by Rindskopf (1984) and Hayduck (1987).

As a research tool, Amos provides all the functionality that many researchers need, with some special features not available in other packages. In addition to the version of Amos distributed by SmallWaters, a customized version is distributed by SPSS.2 SPSS Amos is functionally equivalent to the stand-alone version, except that it installs into the SPSS statistics menu and expects SPSS working files as default data input.

### Lisrel3

LISREL 8 accepts two different command languages in the input file, LISREL input and SIMPLIS input. The LISREL input is written in matrix notation whereas SIMPLIS input allows the user to avoid all matrix notation, requiring only the labeling of observed and latent variables in addition to the specification of the model. SIMPLIS may be used for specifying simple to moderately sophisticated models; the traditional LISREL command language is necessary for more complex procedures.

LISREL 8 offers a path diagram option. From a base model, paths can be added, deleted, or modified interactively from the path diagram, and the model re-estimated with the revised specifications. LISREL 8 also features a number of goodness-of-fit statistics (see Table 1.1), and the ability to impose linear and nonlinear equality constraints on any set of model parameters.

LISREL handles categorical (ordinal) data through PRELIS. PRELIS uses the marginal univariate distribution of the observed categorical variables to estimate thresholds for the underlying latent normal variable. These thresholds are used in the estimation of the polychoric correlation and the associated asymptotic weight matrix (Jöreskog & Sörbom, 1993). PRELIS estimates are identical to the estimates produced by Muthen's LISCOMP (Muthen, 1987) SEM program.

2 For more information on SPSS Amos contact Marketing Department, SPSS Inc., 44 North Michigan Avenue, Chicago, IL 60611. URL: <http://www.spss.com>.

3 LISREL 8. Written by Karl G. Jöreskog and Dag Sörbom. Distributed by Scientific Software International, Inc., 1525 East 53rd Street, Suite 530, Chicago, IL 60615. URL: <http://www.ssicentral.com/lisrel/mainlis.htm>.

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LISREL has no specific procedures for handling missing data, but is able to estimate growth models with missing data through the use of a model-based approach.

### EQS4

EQS uses a simple and straightforward specification language to describe the model to be analyzed, providing extensive syntax error checking to make use of the program relatively easy and error-free. In addition, using Diagrammer, a graphical interface, models may be specified without the need for EQS command language.

EQS implements Lagrange Multiplier (LM) and Wald tests, offers a number of fit indices, and can handle categorical variables. The Lagrange Multiplier evaluates the statistical appropriateness of one or more restrictions placed on a model, and is particularly useful in evaluating cross-group constraints in multiple population models. A discussion of the LM test, and its application in multiple population LGMs is given in chapter 4.

Although EQS has no specific procedures for handling missing data, like LISREL it can estimate growth models with missing data using a model-based approach. This approach to missingness is described in detail in chapter 8. Nonlinear restrictions are unavailable, but some can be handled by EQS through reparameterization (Wong & Long, 1987).

### Evaluation of Model Fit

A common approach to SEM has been to test the underlying structure of a hypothesized model and to report some index of the goodness of fit of that model to the data. A number of methods exist to evaluate the degree of data fit to the hypothesized model and to assess whether the fit can be improved as a function of testing alternative models. Commonly accepted indices of fit used to evaluate model fit are the chi-square test statistic and various goodness-of-fit indices. Two goodness-of-fit indices, the non-normed fit index (NNFI) and comparative fit index (CFI), based on the chi-square test statistic and the null model of uncorrelated or independent variables, are provided in the following chapters.

4 EQS 5 for Windows. Written by Peter M. Bentler and Eric J.C. Wu. Distributed by Multivariate Software, Inc., 4924 Balboa Blvd. #368, Encino, CA 91316. Internet eqs@netcom.com, URL: <http://www.mvsoft.com>.

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The NNFI takes into account the degrees of freedom ( $df$ ) of the model and is computed as

$$\frac{(f_i - f_k)}{(f_i - 1)}, \quad 1.3$$

where  $f_i = n \chi^2_i / df_i$  and  $f_k = n \chi^2_k / df_k$  are chi-square variates divided by the associated  $df$ . NNFI can be outside the 0 - 1 range.

The CFI (Bentler & Wu, 1995) is computed as

$$1 - \frac{\tau_k}{\tau_i}, \quad 1.4$$

where  $tk = \max [(n \chi^2k - dfk), 0]$  based on the model of interest and  $ti = \max [(n \chi^2i - dfi), (n \chi^2k - dfk), 0]$ . Both the NNFI and CFI reflect model fit well at various sample sizes.

Two parsimony-based indices which provide alternatives to assessing model fit are discussed in chapter 5. These are Akaike's (1974) information criterion (AIC) and Bozdogan's (1987) consistent version of this statistic (CAIC). These measures are intended for model comparisons and not for the evaluation of an isolated model. AIC is computed as

$$\text{Model } \chi^2 - 2d_k \quad 1.5$$

(Bentler & Wu, 1995). CAIC is given by the formula

$$\text{Model } \chi^2 - (\ln N + 1)d_k \quad 1.6$$

Both AIC and CAIC take into account the statistical goodness of fit and the number of parameters that must be estimated to achieve that degree of fit. The model that produces the minimum AIC or CAIC might be considered, in the absence of other substantive criteria, as the potentially more useful model. CAIC penalizes model complexity more than AIC.

Other approaches to model comparison can be found in Hu and Bentler (1995). For example, an additional measure to test the approximate fit of a given model is the root mean square error of approximation (RMSEA). This measure represents the discrepancy per degree of freedom for the model. The RMSEA is bounded below by zero and will be zero only if the model fits exactly. Browne and Cudeck (1993) indicated that a value of the RMSEA of about .05 or less suggests a close fit of the model in relation to the degrees of freedom.

A comparison of selected fit indices available in Amos, EQS, and LISREL is presented in Table 1.1

TABLE 1.1  
Selected Fit Indices Available in Amos, EQS, and LISREL

| <i>Fit Index</i>        | <i>Amos</i> | <i>EQS</i> | <i>LISREL</i> |
|-------------------------|-------------|------------|---------------|
| Model chi-square        | ✓           | ✓          | ✓             |
| Independence chi-square | ✓           | ✓          | ✓             |
| Robust chi-square       |             | ✓          |               |
| RMSR                    | ✓           | ✓          | ✓             |
| NNFI                    | ✓           | ✓          | ✓             |
| NFI                     | ✓           | ✓          | ✓             |
| CFI                     | ✓           | ✓          | ✓             |
| AIC                     | ✓           | ✓          | ✓             |
| CAIC                    | ✓           | ✓          | ✓             |
| RMSEA                   | ✓           | ✓          | ✓             |

## Chapter 2 Specification of the LGM

LGMs strongly resemble classic confirmatory factor analysis models. However, because they use repeated measures raw-score data, the latent factors are interpreted as chronometric common factors representing individual differences over time (McArdle, 1988). Meredith and Tisak (1990) noted that repeated measures polynomial ANOVA models are special cases of LGMs in which only the factor means are of interest. In contrast, a fully expanded latent growth analysis takes into account both factor means and variances. This combination of the individual and group levels of analysis is what makes the LGM procedure unique.

### Two-Factor LGM for Two Time Points

The simplest latent growth curve model involves one variable 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 provide information about change, they address some research questions poorly (Rogosa et al., 1982). For example, two temporally separated observations allow for estimating the amount of change, but it is impossible to study the shape of the developmental trajectory or the rate of change in the individual. The *shape* of individual development 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 is presented and diagrammed in Fig. 2.1 using the notation of Bentler and Wu (1995).

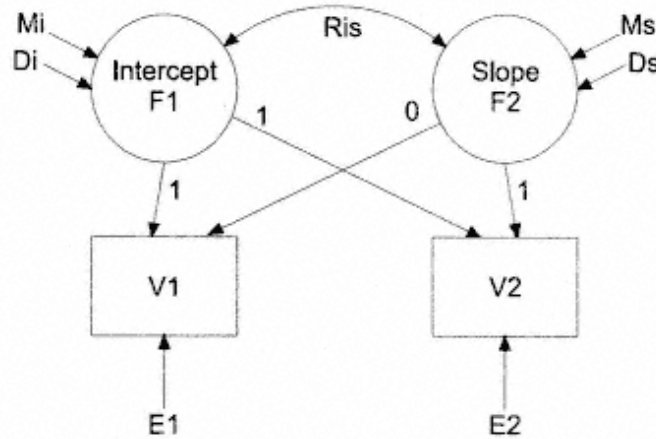


Fig. 2.1.  
Representation of a two-factor LGM for two time points.

**Intercept.** As can be seen from the diagram, the first factor is labeled "Intercept." The intercept is a constant for any given individual across time, hence the fixed values for factor loadings of 1 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 ( $M_i$ ) and variance ( $D_i$ ) of the collection of intercepts that characterize each individual's growth curve.

**Slope.** The second factor, labeled "Slope," represents the slope of an individual's trajectory. In this case, it is the slope of the straight line determined by the two repeated measures. The slope factor has a mean ( $M_s$ ) and variance ( $D_s$ ) across the whole sample that, like the intercept mean and variance, can be estimated from the data. The two factors, Slope and Intercept, are allowed to covary,  $R_{is}$ , which is represented by the double-headed arrow between the factors. The error variance terms ( $E_1$ ,  $E_2$ ) are shown in the diagram, but, to keep the presentation simple, error is assumed to be zero (i.e.,  $E_1 = E_2 = 0$ ).

To identify this model, two slope loadings must be fixed to two different values. Fixing the regression coefficient relating  $F_2$  and  $V_1$  at 0 and  $F_2$  and  $V_2$  at 1 has the effect of locating the intercept at the initial measurement,  $V_1$ . 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. With the careful choice of factor loadings, the model parameters have familiar and straightforward interpretations. The intercept factor represents initial status and the slope factor represents the difference scores ( $V_2 - V_1$ ) when  $V_1, F_2 = 0$  and  $V_2, F_2 = 1$  for the two points in time.

In this simple model there are not enough degrees of freedom to estimate the error variances from the data. The overall model has 5 estimated parameters, and there are 5 pieces of known information (3 variances and covariances, and 2 means) with which to estimate the model. If the model has more parameters than data, it can not be uniquely estimated, and is therefore not "identified." 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. If, however, the error variance is known either from prior research or from theoretical considerations, it could be fixed at that value and the model estimated. The error variances affect the interpretation of the model parameters by correcting the measured variances for random error. For example, the variance of  $F_2$  is now the variance of the difference scores corrected for measurement error, and the variance of the intercept factor is just the true score variance of  $V_1$ . 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.

#### LGM Parameters

To interpret some of the model parameters, it is necessary to review the basic equations for expectation, variance of difference scores, and covariances of difference scores with initial status. For readers unfamiliar with the expectation, variance, and covariance operators (symbolized  $E$ ,  $var$ , and  $cov$ , respectively), these operators can be construed as roughly equivalent to the mean, variance, and covariance statistics that might be computed for collected data. In this case, the operators are applied to hypothetical random variables instead of actual collected data. Stoolmiller (1995) provided an excellent introduction to LGM parameterization. The operators have algebraic rules governing their application to linear combinations of random variables that are found in most statistics texts

(e.g., Kirk, 1982), and these algebraic rules will be used to generate expressions that help in the interpretation of model parameters, beginning with the simple difference score.

The definition of the difference score of a variable from Time 1 to Time 2,  $V2$  minus  $V1$ , is given by the equation

$$\text{difference score} = \text{vdif} = V2 - V1. \quad 2.1$$

The expected value of the difference score is the difference of the expected values of  $V1$  and  $V2$ , as in

$$E(V2 - V1) = E(V2) - E(V1) = E(\text{vdif}). \quad 2.2$$

The variance for the difference score is a linear combination of the variances and covariances of  $V1$  and  $V2$ ,

$$\text{var}(\text{vdif}) = \text{var}(V1) + \text{var}(V2) - 2 \text{cov}(V1, V2). \quad 2.3$$

Finally, the covariance of the difference score with  $V1$  is the covariance of  $V2$  and  $V1$  minus the variance of  $V1$ , expressed as

$$\text{cov}(\text{vdif}, V1) = \text{cov}(V2, V1) - \text{var}(V1). \quad 2.4$$

As in the model diagram in Fig. 2.1,  $V1$  and  $V2$  can be expressed as linear functions of the latent factor scores (symbolized by  $F$ s), the factor loadings, and the latent factor means (symbolized by  $M$ s). The reason for using  $D$  as a symbol of the factor variance is that when a factor is a dependent variable, the  $D$  is interpreted as the disturbance variance, the variance not accounted for by the predictors of  $F$ . When the factor is an independent variable, the disturbance variance is equal to the entire factor variance. The same reasoning applies for the choice of  $M$  as a symbol for the factor mean. When a factor is a dependent variable,  $M$  is the regression intercept, that part of the mean of  $F$  that is not accounted for by the predictors of  $F$ . When the factor is an independent variable, the regression intercept is equal to the entire factor mean. Having clarified the notation, the equations for  $V1$ ,  $V2$ ,  $F1$ , and  $F2$  are

$$V1 = F1 + L1 F2 + E1, \quad 2.5$$

$$V2 = F1 + L2 F2 + E2, \quad 2.6$$

$$F1 = D1 + M1, \text{ and} \quad 2.7$$

$$F2 = D2 + M2, \quad 2.8$$

where  $L$  represents the regression coefficient relating the corresponding latent factor to the observed variables.

#### LGM Assumptions

Further standard assumptions are: (a) the means of all latent variables, error terms, and factors have zero variance, (b) the variances of all latent variables have zero means, (c) the means and variances of latent variables do not covary, and (d) the error variances do not covary with each other or with any variables except the measured variables they directly affect. These assumptions in equation form are

$$\text{var}(M1) = \text{var}(M2) = 0, \quad 2.9$$

$$E(D1) = E(D2) = E(E1) = E(E2) = 0, \text{ and} \quad 2.10$$

$$\begin{aligned} \text{cov}(M1, M2) &= \text{cov}(M1, D1) = \text{cov}(M1, D2) = \text{cov}(M2, D1) = \\ \text{cov}(M2, D2) &= \text{cov}(E1, E2) = \text{cov}(E1, D1) = \text{cov}(E1, D2) = \\ \text{cov}(E1, M1) &= \text{cov}(E1, M2) = \text{cov}(E2, D1) = \text{cov}(E2, D2) = \\ \text{cov}(E2, M1) &= \text{cov}(E2, M2) = 0. \end{aligned} \quad 2.11$$

Taken together, equations 2.9, 2.10, and 2.11 assert that a given individual's latent factor score can be expressed as the latent factor mean plus a latent deviation score from the mean. Inasmuch as the means for the factor scores have no variance, they are constants added to each individual's deviation scores. The deviation scores, on the other hand, have a mean of zero but vary across the sample. In more traditional SEM analyses, the mean of the factor is assumed to be zero so that only the deviation score remains. In LGM, this restriction is relaxed, allowing the factors to have non-zero means.

#### Expressing Model Parameters as Functions of Measured Means, Variances, and Covariances

All five of the model parameters can be expressed as functions of the measured means, variances, and covariances. Furthermore, the model parameters have familiar interpretations. Thus, researchers are provided with a familiar anchor from which to understand LGMs. With the preceding assumptions, the means, variances, and covariances of the measured variables can be expressed in terms of the model parameters

$$E(V1) = E(F1) + L1 E(F2) \text{ and } E(V2) = E(F1) + L2 E(F2), \quad 2.12$$

$$\text{var}(V1) = \text{var}(F1) + L1^2 \text{var}(F2) + 2 L1 \text{cov}(F1, F2) + \text{var}(E1), \quad 2.13$$

$$\text{var}(V2) = \text{var}(F1) + L2^2 \text{var}(F2) + 2 L2 \text{cov}(F1, F2) + \text{var}(E2), \text{ and} \quad 2.14$$

$$\text{cov}(V1, V2) = \text{var}(F1) + L1 L2 \text{var}(F2) + (L1 + L2) \text{cov}(F1, F2). \quad 2.15$$

Algebraic simplification shows that

$$E(V2) - E(V1) = E(F2) (L2 - L1) \text{ or } E(F2) = \frac{E(V2 - V1)}{L2 - L1}, \text{ and} \quad 2.16$$

$$E(F1) = \frac{L2 E(V1) - L1 E(V2)}{L2 - L1}. \quad 2.17$$

Further, for scaling purposes, let  $L2 = 1$  and  $L1 = 0$ , then  $E(F2) = E(V2 - V1)$  and  $E(F1) = E(V1)$ . This simplifies the factor means for the model into familiar quantities. The slope factor mean is the mean of the difference scores and the intercept factor mean is the mean of  $V1$ .

The same manipulations are used for the variances and covariances, taking advantage of the fixed values for the factor loadings. The strategy for solving for the variances and covariances of the factors is the same as for the factor means. For the sake of clarity the error variances are assumed to be zero and are dropped from the equations.

The second step is to rearrange equation 2.13 to isolate  $\text{var}(F1)$ ,

$$\text{var}(F1) = \text{var}(V1) - L1 \text{var}(F2) - 2 L1 \text{cov}(F1, F2). \quad 2.18$$

This expression is substituted into equation 2.14, isolating  $\text{cov}(F1, F2)$ . This expression is then substituted into equation 2.15 and simplified to yield

$$\text{var}(F2) = \text{var}(V2) + \text{var}(V1) - 2 \text{cov}(V1, V2). \quad 2.19$$

Expressions for  $\text{var}(F1)$  and  $\text{cov}(F1, F2)$  can also be generated:

$$\text{var}(F1) = \frac{L1^2 \text{var}(V2) + L2^2 \text{var}(V1) - 2 L2 L1 \text{cov}(V1, V2)}{(L2 - L1)^2}, \text{ and} \quad 2.20$$

$$\text{cov}(F1, F2) = \frac{L2 \text{cov}(V1, V2) - L2 \text{var}(V1) - L1 \text{var}(V2) + L1 \text{cov}(V1, V2)}{(L2 - L1)^2}. \quad 2.21$$

To identify this model, even with more than two time points, two slope loadings must be fixed to two different values. Fixing  $L1 = 0$  and  $L2 = 1$  has the effect of locating the intercept at the initial measurement,  $V1$ . Now, by fixing  $L2 = 1$  and  $L1 = 0$ , the expressions simplify to

$$\text{var}(F2) = \text{var}(V2) + \text{var}(V1) - 2 \text{cov}(V1, V2), \quad 2.22$$

$$\text{var}(F1) = \text{var}(V1), \text{ and} \quad 2.23$$

$$\text{cov}(F1, F2) = \text{cov}(V1, V2) - \text{var}(V1). \quad 2.24$$

Equation 2.22 states that the variance of the slope factor is equal to the variance of the difference scores. From equation 2.23, the intercept variance is the variance of  $V1$ . The covariance between intercept and slope factors, expressed in equation 2.24, is the covariance between initial status and the difference scores or change.

The choice of loadings is somewhat arbitrary, but it is important to note that the intercept factor is inextricably bound to the time scale. By shifting the factor loadings on the slope factor, the scale of time is altered and this in turn affects the meaning and interpretation of the intercept factor mean and variance. Similarly, the correlation and covariance between intercept and slope factors will vary depending on the choice of factor loadings.

Representing the Shape of Growth Over Time

Because of limited data for the latent growth curve model for two time points, the factor loadings have been of little interest thus far. However, with three points in time, 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. The most familiar approach to nonlinear trajectories is probably 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 2.2 represents a hypothetical growth model with a quadratic factor for three evenly spaced time points.

Example 2.1  
Three-Factor Polynomial LGM

Adolescent alcohol use data from a longitudinal study on tobacco reduction and cancer control (TRACC; Biglan, Duncan, Ary, & Smolkowski, 1995) were used to model the LGM depicted in Fig. 2.2. It was hypothesized that a

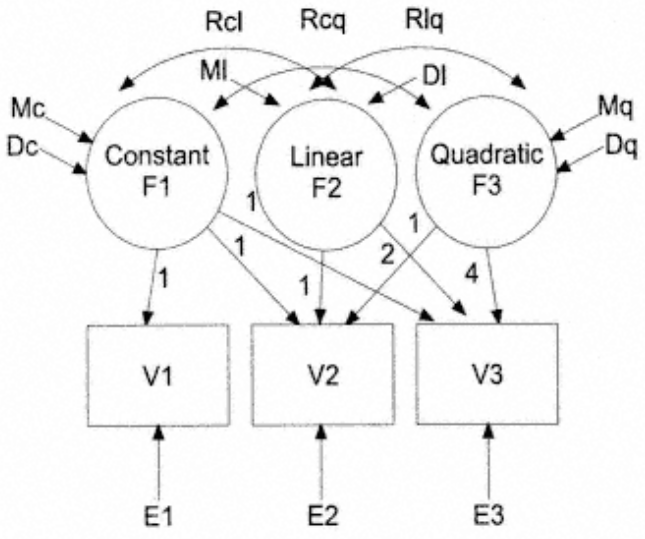


Fig 2.2.  
Representation of a three-factor polynomial LGM.

common developmental trajectory in alcohol consumption was tenable. The developmental model was tested on a sample of 343 adolescents ranging in age from 15 to 17 years. Each participant's level of alcohol consumption for the preceding 6 months was measured at three approximately equal time intervals over a 2-year period.

Descriptive statistics and the correlation matrix for the sample are presented in Table 2.1.

The input specifications necessary to estimate the model depicted in Fig. 2.2 are presented in Input 2.1. These commands and input data test the

TABLE 2.1  
Descriptive Statistics and Correlations for the Alcohol Use Variables

*Alcohol Consumption*

|      | V1    | V2    | V3    |
|------|-------|-------|-------|
| V1   | 1.000 |       |       |
| V2   | .4859 | 1.000 |       |
| V3   | .3988 | .5332 | 1.000 |
| Mean | 8.31  | 10.00 | 10.81 |
| SD   | 7.39  | 7.99  | 8.08  |



hypothesized model using the EQS SEM program. General specifications include number of cases (CAS = 343), number of variables in the input matrix (VAR = 3), the method of estimation (ME = ML or maximum likelihood: For LGM analyses maximum likelihood estimation is required), type of input data (MA = COR, a correlation matrix), and the type of analysis to be performed (ANAL = MOMENT: The analysis of a moment matrix includes information concerning the correlations, means, and standard deviations of the observed variables in the input program). Note that the number of equations equals the number of dependent variables, in this case the three repeated measures that have unidirectional arrows pointed toward them in Fig. 2.2.

An equation is specified for each observed variable,  $V$ , and for the latent or unobserved variables,  $F1$ ,  $F2$ , and  $F3$ . All other variables not having unidirectional arrows aimed toward them, the  $E$ s representing errors in measurement and  $D$ s representing disturbances in the latent variables, are independent variables; they do not have equations, but instead have variances and covariances as parameters. Each measured dependent  $V$  variable is a linear combination of the three common factors

#### INPUT 2.1 EQS Specifications for Latent Growth Analysis Using Data From Table 2.1

```

/TITLE
  INPUT 2.1 LATENT GROWTH ANALYSIS USING DATA FROM TABLE 2.1
/SPECIFICATIONS
  CAS=343; VAR=3; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
  V1=ALC_T1; V2=ALC_T2; V3=ALC_T3;
/EQUATIONS
  V1=F1+0F2+0F3+E1;
  V2=F1+1F2+1F3+E2;
  V3=F1+2F2+4F3+E3;
  F1=*V999+D1;
  F2=*V999+D2;
  F3=*V999+D3;
/VARIANCES
  E1 TO E3=0; D1 TO D3=*;
/COVARIANCES
  D1 TO D3=*;
/MATRIX
  1.000
   .4859    1.000
   .3988    .5332    1.000
/MEANS
  8.31    10.00    10.81
/STANDARD DEVIATIONS
  7.39    7.99    8.08
/PRINT
  EFFECTS=YES;
/LMTEST
/END

```

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and one independent  $E$ , or error, variable. The first factor,  $F1$ , is a linear combination of a constant,  $V999$ , representing the mean of the factor (and considered another observed variable in this notation), and an independent residual variable,  $D1$ . Similarly, the second factor,  $F2$ , is a linear combination of  $V999$  and an independent residual variable,  $D2$ . Each freely estimated parameter is designated by an asterisk.

As can be seen, all paths of the  $E$  and  $D$  variables on the  $V$  and  $F$  variables, respectively, are fixed at 1. In the case of the  $E$  and  $D$  variables, it is conventional to fix the path and estimate the variance. Hence the variances of the  $E$  and  $D$  variables appear as estimated parameters in the variance section. Here, the variances of the  $E$ s are not estimated, but fixed at zero because the model is saturated, lacking degrees of freedom. 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. Because the variables have no measurement error, the mean of the intercept factor ( $F1$ ) will equal the mean of the Time 1 alcohol use variable ( $M = 8.31$ ). The basic idea of identification is to impose sufficient constraints on model parameters to insure a unique solution. For a more complete discussion of mean and covariance structure analysis, see Bentler and Wu (1995).

Tests for overall model fit 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 information, to use in model estimation. The model estimates 3 variances, 3 covariances, and 3 means for the constant, linear, and quadratic latent factors, resulting in 0 degrees of freedom. In testing a more parsimonious model, such as a two-factor LGM (presented in subsequent sections), sufficient degrees of freedom are available for evaluation of model fit.

Output 2.1 shows the construct equations, standard errors, and test statistics for the three latent growth factors. The top row of each equation presents the latent mean estimates, the middle row presents the standard error, and the bottom row shows the test of significance ( $t$  value). Note that significant effects are found only for  $F1$  and  $F2$ , the intercept and linear effects, respectively.

OUTPUT 2.1  
Construct Equations From the Three-Factor Polynomial LGM

|    |   |        |       |   |       |    |
|----|---|--------|-------|---|-------|----|
| F1 | = | 8.310  | *√999 | + | 1.000 | D1 |
|    |   | .400   |       |   |       |    |
|    |   | 20.796 |       |   |       |    |
| F2 | = | 2.130  | *√999 | + | 1.000 | D2 |
|    |   | .744   |       |   |       |    |
|    |   | 2.863  |       |   |       |    |
| F3 | = | -.440  | *√999 | + | 1.000 | D3 |
|    |   | .353   |       |   |       |    |
|    |   | -1.247 |       |   |       |    |

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OUTPUT 2.2  
Variances of Independent Variables

|    |  |          |
|----|--|----------|
| D1 |  | 54.612*  |
|    |  | 4.176    |
|    |  | 13.077   |
| D2 |  | 189.290* |
|    |  | 14.475   |
|    |  | 13.077   |
| D3 |  | 42.608*  |
|    |  | 3.258    |
|    |  | 13.077   |

Output 2.2 presents the variances of the three independent variables.

As can be seen from the tests of significance, significant variation exists in all three growth functions. Correlations among the developmental parameters are presented in Output 2.3. All of the covariances are significant. Tests of significance are presented in parentheses.

OUTPUT 2.3  
Correlations Among the Developmental Parameters

|      | <i>CNST</i> | <i>LIN</i> | <i>QUAD</i> |
|------|-------------|------------|-------------|
| CNST | 1.000       |            |             |
| LIN  | -.358       | 1.000      |             |
|      | -36.444     |            |             |
|      | (-6.240)    |            |             |
| QUAD | .218        | -.951      | 1.000       |
|      | 10.522      | -85.413    |             |
|      | (3.941)     | (-12.745)  |             |

Output 2.4 presents the parameter indirect effects and reproduced means for the LGM, which, given the assumption of no measurement error, reproduce the observed means exactly. When measurement error is introduced, reproduced means will deviate from observed values.

OUTPUT 2.4  
Parameter Indirect Effects

|               |              |
|---------------|--------------|
| ALC_T1 = V1 = | 8.310 *√999  |
|               | .400         |
|               | 20.796       |
| ALC_T2 = V2 = | 10.000 *√999 |
|               | .432         |
|               | 23.145       |
| ALC_T3 = V3 = | 10.810 *√999 |
|               | .437         |
|               | 24.742       |

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Example 2.2  
Unspecified Two-Factor LGM

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 or unspecified (Tisak & Meredith, 1990). For example, the two-factor model can also be used to 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 2.3 represents a hypothetical two-factor growth model with an unspecified growth function factor for three evenly spaced time points. With the unspecified two-factor model, two loadings on the slope factor may be fixed at 0 and 1 as before, although 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 Fig. 2.3). The factor loadings plotted against the observed time metric suggest the shape of growth. If the model fits well, the factor loadings on the shape factor reflect the mean change in the observed variables.

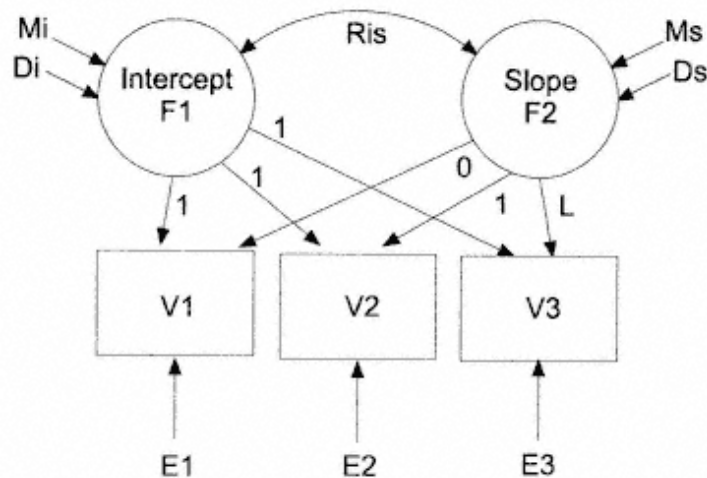


Fig. 2.3.  
Representation of a two-factor unspecified LGM.

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The mathematical model for the LGM depicted in Fig. 2.3 can be symbolized as

$$Y(t, n) = Mi(n) + B(t) Ms(n) + E(t, n), \quad 2.25$$

where  $Y(t, n)$  = observed score at Time  $t$ ,  $Mi(n)$  = unobserved score for the intercept,  $Ms(n)$  = unobserved score for the shape,  $E(t, n)$  = unobserved error, and  $B(t)$  = basis coefficient for Time  $t$ .

Observed scores are specified to be a weighted sum of two individual latent variables:  $Mi(n)$  is a variable representing individual differences in level of some attribute and is a constant for any individual across time;  $Ms(n)$  is a shape variable representing individual differences in the rate of change over time. Like the  $Mi(n)$  score,  $Ms(n)$  is a constant for any individual across time. The contribution of  $Ms(n)$  to  $Y(t, n)$ , however, changes as a function of the basis coefficient,  $B(t)$ .  $E(n)$  is an error variable representing an unobserved random score, with a mean of zero and no correlation with any other variable over time. Such errors are expected to change randomly over time for any individual.

The basis term,  $B(t)$ , is a mathematical function relating variable  $Y$  to variable  $t$ , specified in terms of linear departures from an origin, and may be of linear or nonlinear form. To illustrate, let  $B0(t) = [1, 1, 1]$  and  $B1(t) = [0, 1, 2]$  represent the function for the data at Times 1 through 3, respectively. In addition, let the mean intercept = 2 and mean slope = 1.

The equations for  $B0(t)$  and  $B1(t)$  become

$$Y(1) = Mi + 0Ms + E(1), \quad 2.26$$

$$Y(2) = Mi + 1Ms + E(2), \text{ and} \quad 2.27$$

$$Y(3) = Mi + 2Ms + E(3). \quad 2.28$$

With the assumption that  $E(t) = 0$ , then

$$Y(\text{Time 1}) = 2 + 0 = 2, \quad 2.29$$

where  $B(t) = 0$  at Time 1 simply starts the curve at this point by rescaling the intercept factor to represent initial status,

$$Y(\text{Time 2}) = 2 + 1 = 3, \quad 2.30$$

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where  $B(t) = 1$  at Time 2 indicates that from Time 1 to Time 2 there is one unit of change, and

$$Y(\text{Time 3}) = 2 + 2 = 4, \quad 2.31$$

where  $B(t) = 2$  indicates that from Time 1 to the third time point there are 2 units of change.

Therefore,  $B(t)$  describes change in terms of linear differences from initial status at Time 1. Given that  $B(t)$  represents the same relation for all individuals, it is likely that individual differences will not only exist in level,  $Mi(n)$ , but also in the estimated developmental trajectories,  $Ms(n)$  (McArdle & Hamagami, 1991).

Rather than fixing the basis terms, a developmental function reflecting an optimal pattern of change over the developmental period was specified by allowing the third basis term to be freely estimated. EQS input statements are presented in Input 2.2. LISREL program input for the model depicted in Fig. 2.3 is presented in Appendix 2.1.

#### INPUT 2.2

##### EQS Specifications for the Unspecified Two-Factor LGM

```

/TITLE
  INPUT 2.2
/SPECIFICATIONS
  CAS=343; VAR=3; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
  V1=ALC_T1; V2=ALC_T2; V3=ALC_T3;
/EQUATIONS
  V1=F1+0F2+E1;
  V2=F1+1F2+E2;
  V3=F1+*F2+E3;
  F1=*V999+D1;
  F2=*V999+D2;
/VARIANCES
  E1 TO E3=*; D1 TO D2=*;
/COVARIANCES
  D1 TO D2=*;
/CONSTRAINTS
  (E1, E1) = (E2, E2) = (E3, E3);

```

```

/MATRIX
1.000
.4859    1.000
.3988    .5332    1.000
/MEANS
8.31    10.00    10.81
/STANDARD DEVIATIONS
7.39    7.99    8.08
/PRINT
EFFECTS=YES;
/LMTEST
/END

```

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Fitting the LGM to the alcohol use data resulted in a mean intercept value of  $Mi = 8.314$ ,  $t = 20.609$ ,  $p < .001$ , and a mean slope value of  $Ms = 1.674$ ,  $t = 4.298$ ,  $p < .01$ . The unconstrained loading ( $L$  in Fig. 2.3) from the slope factor to the Time 3 alcohol use variable was estimated at a value of 1.496,  $t = 5.788$ ,  $p < .01$ . Applying the mean slope to the developmental curve ( $1.674 \times 1.496 = 2.50$ ), the average adolescent is expected to realize an approximate 30% increase ( $(2.50 \div 8.31) \times 100$ ) in alcohol use over a similar 3-year period.

The latent variances are also estimated. The intercept variance for adolescent alcohol use,  $Di = 27.777$ ,  $t = 6.002$ ,  $p < .001$ , and the variance of the latent slope scores,  $Ds = 6.318$ ,  $t = 1.778$ ,  $p < .05$ , indicate substantial variation among individuals in initial status and growth of alcohol use. Error variance, constrained to be equal across the three time points, was significant,  $E = 28.602$ ,  $t = 13.077$ ,  $p < .001$ . The estimated correlation between the intercept and shape scores was not significant,  $Ris = -.089$ ,  $t = -.393$ ,  $p > .05$ . Reported values for the various fit indices, NNFI = .997, CFI = .998, and the chi-square test statistic,  $\chi^2(2, N = 343) = 2.461$ ,  $p = .292$ , indicated an adequate fit of the model to 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 how many factors are 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).

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 adequate to describe the data. Figure 2.4 illustrates a series of simple growth plots, each of which is nested within the general, unspecified two-factor growth model (Tisak & Meredith, 1990). In general, the various growth curves illustrated in Fig. 2.4 represent various simplifications that might adequately represent the actual collection of growth curves.

For example, when individuals develop linearly but individual differences do not vary across time, there is *parallel stability*. When straight line growth occurs and the differences among individuals vary longitudinally, *linear stability* exists. Some particular cases are interesting enough to warrant special attention. For example, consider what would happen to the latent growth curve model if all the straight lines in the sample were parallel and flat, but passed through different intercepts. In this case, one might say that *strict stability* exists, and the slope factor mean and variance would not differ significantly from zero. Or consider the case where all the lines emanate from zero at the intercept with different slopes.

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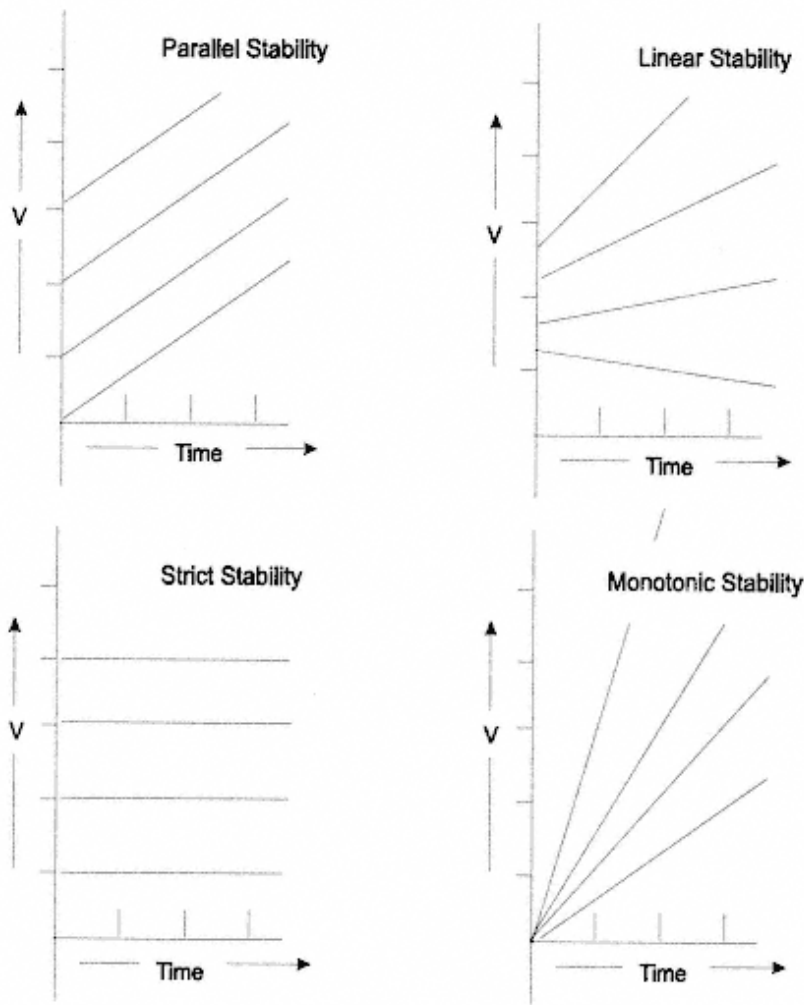


Fig. 2.4.  
Representation of a collection of simple growth curve trajectories.

Under these conditions the intercept mean and variance would not be significantly different from zero. One may define this situation as *monotonic stability*. In each of these latter cases of strict and monotonic stability, because of the structure of the data, a single factor is adequate.

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### Example 2.3 The Single-Factor LGM

The single-factor latent growth curve model presented in Fig. 2.5, which has been presented and used by Duncan and McAuley (1993), McArdle (1988), and McArdle and Epstein, (1987), is probably more familiar to developmentalists than the two-factor approach outlined earlier. McArdle has termed the univariate single-factor LGM a *curve* model. McArdle's model is actually a special case of the two-factor model. Meredith and Tisak (1990) indicate that the curve model is nested within the two-factor model and have termed this a *monotonic stability* model, implying that, although significant changes in mean levels may be occurring, the rank order of the observations stays the same over the repeated measures.

One way of demonstrating that the curve model is nested within the two-factor model is to derive the curve model from the more general model through a series of constraints on the more general model's parameters. According to Meredith and Tisak (1990), the intercept factor can be eliminated if it is zero (i.e., its mean and variance are zero) or if it

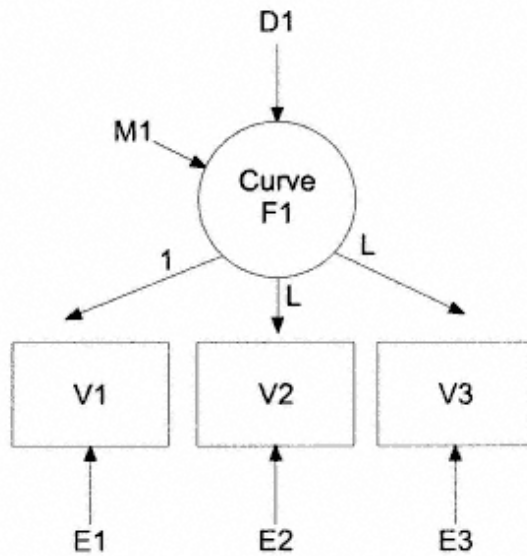


Fig. 2.5.  
Representation of the single-factor LGM

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is strictly proportional to the slope. The first of these two conditions is obvious when it happens. The second condition, strict proportionality, can be tested by changing the basic two-factor model so that the intercept factor is a linear function of the slope factor, and the residual variance (disturbance term) and the regression intercept (residual factor mean) for the intercept factor are constrained to zero. If these constraints are acceptable, the one-factor curve model could be considered the more parsimonious and preferred model. The EQS input statements for the single-factor curve model are presented in Input 2.3.

Fitting the curve model to the alcohol use data resulted in a curve factor mean value of  $M1 = 8.314$ ,  $t = 22.025$ ,  $p < .001$ . The unconstrained loadings from the curve factor to the Time 2 and Time 3 alcohol use variables were estimated at values of 1.215 and 1.288, respectively. The variance of the curve factor,  $D1 = 21.285$ ,  $t = 8.282$ ,  $p < .001$ , indicated that substantial individual variation existed in the single-factor model. Error variance, constrained to be equal across the three time points, was significant,  $E = 31.911$ ,  $t = 18.493$ ,  $p < .001$ . Reported values for the various fit indices, NNFI = .993, CFI = .991, and the chi-square test statistic,  $\chi^2(4, N$

INPUT 2.3  
EQS Specifications for the Single-Factor LGM

```

/TITLE
  INPUT 2.3
/SPECIFICATIONS
  CAS=343; VAR=3; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
  V1=ALC_T1; V2=ALC_T2; V3=ALC_T3;
/EQUATIONS
  V1=1F1+E1;
  V2=*F1+E2;
  V3=*F1+E3;
  F1=*V999+D1;
/VARIANCES
  E1 TO E3=*; D1=*;
/CONSTRAINTS
  (E1,E1)=(E2,E2)=(E3,E3);
/MATRIX
  1.000
  .4859      1.000
  .3988      .5332      1.000
/MEANS
  8.31      10.00      10.81
/STANDARD DEVIATIONS
  7.39      7.99      8.08
/PRINT
  EFFECTS=YES;
/LMTEST
/END

```

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$= 343) = 6.030, p = .196$ , indicated an adequate fit of the single-factor curve model to the data. A chi-square difference test between the two- and single-factor models,  $\chi^2(2, N = 343) = 3.569, p > .05$ , revealed no significant statistical differences between the two competing models.

Premature adoption of a single-factor model can result in erroneous conclusions about the covariation between some predictor variable (e.g.,  $X$ ) and the growth parameters. If monotonic stability holds, the rank order of the observations stays the same over time. Therefore, the correlation of  $X$  with change will be the same as the correlation of  $X$  with initial status because initial status is strictly proportional, or perfectly correlated, to change. Because monotonic stability puts severe demands on the structure of the means, variances, and covariances of the observed variables, the model should be adopted only when it makes sense theoretically and the data warrant it. Such would be the case when the rank ordering of individuals does not vary across time despite mean level changes.

## Summary

It is crucial to recognize the limitations of trying to build an adequate model of social behavior with just two points in time. Many important assumptions must be made that can fundamentally affect the conclusions drawn about the nature of change over time on the constructs of interest. Rogosa (1988) has clearly demonstrated the hazards involved in using linear panel models when nonlinear growth processes are operative. This assumption cannot be tested with only two repeated assessments.

Linear panel models are not optimal for studying linear growth processes, either. The best that can be done, even in multiwave panel models, is to focus on simple change scores between any two points in time. If one believes that change is systematically related to the passage of time (i.e., growth processes are at work), then growth models should be used. A number of recent papers have demonstrated how standard structural equation techniques and software can be used to fit linear and nonlinear growth models (e.g., T.E. Duncan & S.C. Duncan, 1995; Meredith & Tisak, 1990).

If growth processes can be ruled out, linear panel models may be useful. Kessler and Greenberg (1981) pointed out, however, that the two-wave panel model is still limited in that identification constraints preclude the simultaneous estimation of all potential lagged and synchronous effects. For example, a mistaken assumption that synchronous effects are negligible runs the risk of obtaining severely biased estimates of lagged effects. Kessler and Greenberg outlined several strategies for circumventing

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this problem, including collection of more than two waves of data and use of additional control or instrumental variables.

With the development of SEM, researchers have a powerful tool for the construction, estimation, and testing of complex developmental models. However, theory testing within the SEM paradigm requires clearly specified hypotheses and adequate measurement strategies. The study of longitudinal samples permits more stringent hypothesis testing, inasmuch as the data can be analyzed synchronously and models can be specified to account for the effects of independent variables on the dependent variables over time. With each test of the hypothesized model, relationships can be examined between the theoretical constructs of interest, enabling the researcher to discard some hypotheses while clarifying others. Promising hypotheses can be more rigorously tested with experimental manipulation of the variables thought to be causally related.

The general two-factor LGM approach outlined in this chapter has many advantages for use in the testing and evaluation of developmental models. With the careful choice of factor loadings to identify the model, the intercept and shape 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. In cases where growth is structured in the sample so that simpler, one-factor models are adequate and theoretically appropriate, parsimony dictates their use. However, the decision to move to a simpler model should be supported by the data. Premature adoption of single-factor models can confound initial status with change and lead to misleading conclusions about the role of predictor variables.

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## Chapter 3 LGM and Repeated Measures ANOVA

The procedures covered in the last chapter can be easily expressed in terms of the general linear modeling ANOVA techniques typically used in repeated measures analyses. In a simple repeated measures analysis, all dependent variables represent different measurements of the same variable for different values or levels of a within-subjects factor. The within-subjects factor distinguishes measurements made on the same individual, rather than between different individuals. In models capturing growth or development over time, the within-subject factor is time of measurement. Between-subjects factors and covariates can also be included in the model, just as in models not involving repeated measures data. The ideas presented in the previous chapter, and some extensions of them, are illustrated here within the more familiar ANOVA context. Repeated measures ANOVAs are, in fact, special cases of latent growth curve models (Meredith & Tisak, 1990), and the two methods share some similarities and differences, as will be seen. The first section of this chapter provides a simple comparison of a growth curve model analyzed by both repeated measures ANOVA and LGM. The remaining sections of the chapter illustrate how the growth curve model is extended to include both predictors and sequelae of change.

### Example 3.1 The Unconditional Growth Curve Model

The data presented in Table 2.1 were analyzed twice, once using the MANOVA (multivariate analysis of variance) procedure in SPSS (SPSS 7.0, 1996) and once using the EQS (Bentler & Wu, 1995) SEM program. SPSS MANOVA performs a polynomial transformation of the dependent variables in a repeated measures design. For comparison's sake, therefore, the second analysis is a three-factor fully saturated LGM procedure using an orthogonal polynomial transformation matrix to represent the regression coefficients relating the latent factors to the observed variables, rather than the unspecified two-factor specification presented in chapter 2.

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INPUT 3.1  
SPSS Input Statements for ANOVA Model

```
MATRIX DATA VARIABLES=ROWTYPE_ ALC1 ALC2 ALC3.
BEGIN DATA.
MEAN 8.31 10.00 10.81
STDDEV 7.39 7.99 8.08
N 343 343 343
COR 1.000
COR .4859 1.000
COR .3988 .5332 1.000
END DATA.
MANOVA ALC1 ALC2 ALC3
/TRANSFORM(ALC1 ALC2 ALC3)=POLYNOMIAL
/RENAME=CNST LIN QUAD
/PRINT=CELLINFO(ALL) ERROR TRANSFORM PARAM(ALL)
SIGNIF(MULTIV UNIV)
/MATRIX=IN(*)
/DESIGN.
```

*The Analysis of Variance Growth Model.* For the first analysis using SPSS MANOVA, the input program is given in Input 3.1. The MANOVA procedure allows for the inclusion of raw matrix materials. The matrix data statement defines variable names and their order in the raw data file. The data can include various vector statistics, such as means and standard deviations, as well as matrices such as correlations. The specification, ROWTYPE\_, is a string variable which defines the data type for each record. Here it defines rows of values corresponding to the means, standard deviations, number of observations for  $p$  measurements, and the  $p \times p$  correlation matrix as shown in Table 2.1. In this example, the variables *ALC1*, *ALC2*, and *ALC3* represent the repeated measures alcohol use variable at Times 1, 2, and 3, respectively.

Output 3.1 presents the transformation matrix transposed. Column 1 is the constant effect, column 2 the linear effect, and column 3 the quadratic effect. This matrix will be used in the LGM replication to represent the regression coefficients relating the corresponding latent factors to the observed variables.

OUTPUT 3.1  
Transformation Matrix (Transpose)

|      | <i>CNST</i> | <i>LIN</i> | <i>QUAD</i> |
|------|-------------|------------|-------------|
| ALC1 | .577        | -.707      | .408        |
| ALC2 | .577        | .000       | -.816       |
| ALC3 | .577        | .707       | .408        |

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OUTPUT 3.2  
Analysis of Variance Parameter Estimates

| <i>Variable</i> | <i>Error MS</i> | <i>Coeff.</i> | <i>SE</i> | <i>t Value</i> |
|-----------------|-----------------|---------------|-----------|----------------|
| CNST            | 119.19706       | 16.8124398    | .58950    | 28.51971       |
| LIN             | 36.13642        | 1.7677669     | .32458    | 5.44627        |
| QUAD            | 28.40512        | -.3592585     | -.3592585 | -1.24841       |

Output 3.2 presents the results from the SPSS MANOVA procedure with data presented in Table 2.1. Tests of significance are shown for the transformed variables. Of particular interest are the parameter coefficients from the individual univariate tests (i.e.,  $CNST = 16.81$ ,  $SE = .589$ ,  $t = 28.52$ ) and the values for the mean square error (the unexplained or residual variance) for each of the variables (i.e.,  $Error MS = 119.19$  for the constant,  $Error MS = 36.13$  for the linear trend, and  $Error MS = 28.40$  for the quadratic trend). These values are noted here as they are the parameters of interest in the subsequent LGM procedure.

Output 3.3 presents the within cells correlations representing the associations among the transformed variables. These can be thought of as associations among the individual differences parameters. The correlation between the constant and linear trend,  $r = .102$ , has a similar meaning as the relationship between the intercept and slope,  $R_{is}$ , from chapter 2.

*The Latent Growth Curve Model.* The diagrammatic representation of the three-factor saturated latent growth curve model is presented in Fig. 3.1. Specific restrictions must be placed on this model to correspond with the assumptions from the general linear modeling procedure (MANOVA) previously presented.

First, the orthogonal polynomial transformation matrix generated from the MANOVA procedure is used to represent the regression coefficients relating the latent factors to the observed variables, rather than the unspecified coefficients presented in chapter 2. Second, because variables are assumed to be measured without error in the MANOVA procedure, the  $Es$

OUTPUT 3.3  
Within Cells Correlations

|      | <i>CNST</i> | <i>LIN</i> | <i>QUAD</i> |
|------|-------------|------------|-------------|
| CNST | 10.918      |            |             |
| LIN  | .102        | 6.011      |             |
| QUAD | -.094       | -.007      | 5.330       |

Note. Standard deviations are presented on the diagonal.

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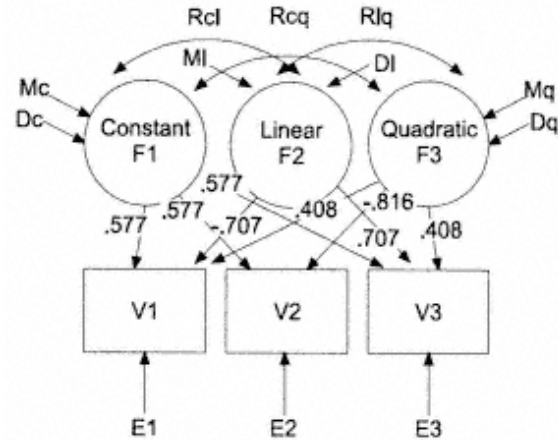


Fig. 3.1.  
Representation of the three-factor LGM.

representing errors in measurement must be fixed at a value of zero for this comparison. The EQS commands necessary to process the data to correspond to Table 2.1 are presented in Input 3.2.

INPUT 3.2  
EQS Specifications for Latent Growth Analysis Using Data From Table 2.1

```

/TITLE
LATENT GROWTH ANALYSIS USING DATA FROM TABLE 2.1
/SPECIFICATIONS
CAS=343; VAR=3; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
V1=ALC1; V2=ALC2; V3=ALC3;
/EQUATIONS
V1=.577F1-.707F2+.408F3+E1;
V2=.577F1+.000F2-.816F3+E2;
V3=.577F1+.707F2+.408F3+E3;
F1=*V999+D1;
F2=*V999+D2;
F3=*V999+D3;
/VARIANCES
E1 TO E3=0;
D1 TO D3=*;
/COVARIANCES
D1 TO D3=*;
/MATRIX
1.000
.4859 1.000
.3988 .5332 1.000
/MEANS
8.31 10.00 10.81
/STANDARD DEVIATIONS
7.39 7.99 8.08
/PRINT
EFFECTS=YES;
/LMTEST
/END

```

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OUTPUT 3.4  
Construct Equations From the Latent Growth Curve Model

|    |   |        |       |   |  |       |    |
|----|---|--------|-------|---|--|-------|----|
| F1 | = | 16.823 | *V999 | + |  | 1.000 | D1 |
|    |   | .591   |       |   |  |       |    |
|    |   | 28.478 |       |   |  |       |    |
| F2 | = | 1.768  | *V999 | + |  | 1.000 | D2 |
|    |   | .325   |       |   |  |       |    |
|    |   | 5.438  |       |   |  |       |    |
| F3 | = | -.359  | *V999 | + |  | 1.000 | D3 |
|    |   | .288   |       |   |  |       |    |
|    |   | -1.247 |       |   |  |       |    |

Tests for overall model fit suggested 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. The model estimates 3 variances, 3 covariances, and 3 means for the constant, linear, and quadratic latent factors, resulting in 0 degrees of freedom. In testing a more parsimonious model, such as a two-factor LGM, sufficient degrees of freedom are available for evaluation of model fit.

Output 3.4 shows the construct equations, standard errors, and test statistics for the three latent growth factors shown in Fig. 3.1. Note that these parameter estimates, their standard errors, and test statistics are comparable to those generated from the ANOVA procedure (e.g.,  $F1$  (constant) = 16.823,  $SE = .591$ ,  $t = 28.478$  from the LGM analyses compared to  $CNST = 16.81$ ,  $SE = .589$ ,  $t = 28.52$  for the constant in the MANOVA). Note that the only significant effects are found for  $F1$  and  $F2$ , the constant and linear effects, respectively.

Output 3.5 presents the variances of the three independent variables (i.e., the mean square error in ANOVA terms). Note that the parameter estimates are similar to those presented in Output 3.2 (e.g.,  $D1 = 119.342$ ,  $SE = 9.126$ ,  $t = 13.077$  compared to the  $Error MS$  of 119.197 generated for the constant in the MANOVA procedure).

OUTPUT 3.5  
Variances of Independent Variables

|         |  |          |
|---------|--|----------|
| D1 - F1 |  | 119.342* |
|         |  | 9.126    |
|         |  | 13.077   |
| D2 - F2 |  | 36.147*  |
|         |  | 2.764    |
|         |  | 13.077   |
| D3 - F3 |  | 28.440*  |
|         |  | 2.175    |
|         |  | 13.077   |

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OUTPUT 3.6  
Correlations Among the Growth Parameters

|             | <i>CNST</i> | <i>LIN</i> | <i>QUAD</i> |
|-------------|-------------|------------|-------------|
| <i>CNST</i> | 1.000       |            |             |
| <i>LIN</i>  | .102        | 1.000      |             |
|             | 1.878       |            |             |
| <i>QUAD</i> | -.094       | -.007      | 1.000       |
|             | -1.735      | -.132      |             |

Correlations among the growth parameters are presented in Output 3.6. Note that none of the covariances are significant (this information is not available from the MANOVA procedure). The values for the correlations are identical to those from the MANOVA procedure (e.g.,  $CNST/LIN = .102$ ,  $CNST/QUAD = -.094$ , and  $LIN/QUAD = -.007$ ).

These analyses show that the two procedures can produce identical growth parameter estimates (mean levels and variation) given a set of common constraints (i.e., regression weights, zero measurement error) imposed across methods. LGM, however, allows variations and extensions of the general repeated measures ANOVA approach. For example, LGM has the advantage of allowing for a test of the adequacy of the hypothesized growth form and measurement error distributions of either a homoscedastic or heteroscedastic nature.

#### Including Predictors and Sequelae of Change in Growth Curve Models

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

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.

In previous LGM examples, the means of the growth factors (*Ms*) were 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.

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 remaining sections of this chapter demonstrate the comparability of repeated measures ANOVA and LGM in analyzing models with static predictors and sequelae of individual differences in change parameters. Longitudinal data involving adolescent alcohol use development and subsequent problem behavior (TRACC; Biglan et al., 1995) is used for this purpose. The descriptive statistics and the correlation matrix for the sample are presented in Table 3.1.

The model hypotheses concern the form of growth in alcohol use, the extent of individual differences in the common trajectory over time, and covariates influencing both chronicity and development. This section focuses on a growth curve model involving one static predictor, age. The model is estimated using both repeated measures ANOVA and the LGM procedure.

TABLE 3.1  
Descriptive Statistics for the Alcohol Use Variables

*Alcohol Consumption*

|                         | <i>V1</i> | <i>V2</i> | <i>V3</i> | <i>Age</i> | <i>Problem Behavior</i> |
|-------------------------|-----------|-----------|-----------|------------|-------------------------|
| <i>V1</i>               | 1.000     |           |           |            |                         |
| <i>V2</i>               | .4859     | 1.000     |           |            |                         |
| <i>V3</i>               | .3988     | .5332     | 1.000     |            |                         |
| <i>Age</i>              | -.1454    | -.0178    | -.0966    | 1.000      |                         |
| <i>Problem behavior</i> | .3102     | .3428     | .5156     | .0398      | 1.000                   |
| Mean                    | 8.31      | 10.00     | 10.81     | 21.94      | .03                     |
| SD                      | 7.39      | 7.99      | 8.08      | 1.42       | .38                     |

#### INPUT 3.3 SPSS Specifications for MANOVA for Repeated Measures

```

MATRIX DATA VARIABLES=ROWTYPE_ ALC1 ALC2 ALC3 AGE.
BEGIN DATA.
MEAN      8.31    10.00    10.81    21.94
STDDEV    7.39    7.99     8.08     1.42
N 343 343 343 343
COR       1.000
COR       .4859    1.000
COR       .3988    .5332    1.000
COR       -.1454   -.0178   -.0966    1.000
END DATA.
MANOVA ALC1 ALC2 ALC3 WITH AGE
  /TRANSFORM(ALC1 ALC2 ALC3)=POLYNOMIAL
  /RENAME=CNST LIN QUAD AGE
  /PRINT=CELLINFO(ALL)
        ERROR TRANSFORM
        PARAM(ALL)
        SIGNIF(MULTIV UNIV)
  /MATRIX=IN(*)
  /DESIGN.

```

### Example 3.2 Growth Curve Models Involving Predictors of Change

Input 3.3 presents the model specifications necessary to estimate the effect of the covariate age on the developmental functions using SPSS MANOVA for repeated measures.

The analysis allows a subset of continuous variables (covariates) to be used in estimating factor-by-covariate interaction terms. Output 3.7 presents the results from the ANOVA procedure.

#### OUTPUT 3.7 Parameter Estimates From the ANOVA Procedure

| COVARIATE          | B        | SE   | t Value | Sig. of t |
|--------------------|----------|------|---------|-----------|
| Dependent variable | .. CNST  |      |         |           |
| Age                | -. 81205 | .414 | -1.961  | .051      |
| Dependent variable | .. LIN   |      |         |           |
| Age                | .14639   | .229 | .639    | .523      |
| Dependent variable | .. QUAD  |      |         |           |
| Age                | -.45154  | .202 | -2.238  | .026      |

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### INPUT 3.4 EQS Specifications for the Predictors of Change Model

```

/TITLE
  PREDICTORS OF CHANGE
/SPECIFICATIONS
  CAS=343; VAR=4; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
  V1=ALC1; V2=ALC2; V3=ALC3; V4=AGE;
/EQUATIONS
  V1=.577F1-.707F2+.408F3+E1;
  V2=.577F1+.000F2-.816F3+E2;
  V3=.577F1+.707F2+.408F3+E3;
  V4=*V999+ E4;
  F2=*V999+*V4+D2;
  F1=*V999+*V4+D1;
  F3=*V999+*V4+D3;
/VARIANCES
  E1 TO E3=0; E4=*;
  D1 TO D3=*;
/COVARIANCES
  D1 TO D3=*;
/MATRIX
  1.000
  .4859    1.000
  .3988    .5332    1.000
  -.1454   -.0178   -.0966    1.000
/MEANS
  8.31    10.00    10.81    21.94
/STANDARD DEVIATIONS
  7.39    7.99     8.08     1.42
/PRINT
  EFFECTS=YES;

```

/LMTEST  
/END

Input 3.4 presents the EQS specifications for the predictors of change model in which age ( $V4$ ) is a predictor of change ( $F1$ ,  $F2$ , and  $F3$ ) in alcohol use.

Results of model fitting procedures yielded a perfect fit to the data,  $\chi^2(0, N = 343) = 0.000$ , reflecting the saturated nature of the hypothesized model. Output 3.8 shows the construct equations, standard errors, and test statistics for the three latent growth factors.

OUTPUT 3.8  
Construct Equations From the Predictors of Change LGM

|    |   |           |   |       |    |
|----|---|-----------|---|-------|----|
| F1 | = | -.813 *V4 | + | 1.000 | D1 |
|    |   | .414      |   |       |    |
|    |   | -1.964    |   |       |    |
| F2 | = | .146 *V4  | + | 1.000 | D2 |
|    |   | .229      |   |       |    |
|    |   | .640      |   |       |    |
| F3 | = | -.452 *V4 | + | 1.000 | D3 |
|    |   | .202      |   |       |    |
|    |   | -2.241    |   |       |    |

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Note that these parameter estimates, their standard errors, and test statistics are comparable to those generated from the MANOVA procedure (e.g., the effect of age on  $F1$  is  $-.813$ ,  $SE = .414$ ,  $t = -1.964$  from the LGM compared to  $-.812$ ,  $.414$ , and  $-1.961$ , respectively, for the MANOVA).

Example 3.3  
Growth Curve Models Involving Sequelae of Change

This section presents analyses of growth as a predictor of subsequent static outcomes. In this example the static criterion is adolescent problem behavior. In testing sequelae of change, the analysis subcommand of SPSS MANOVA also allows the user to switch the roles of the dependent variables and a covariate. Input 3.5 details the MANOVA syntax necessary to test the effect of growth in alcohol use consumption on subsequent problem behavior.

Output 3.9 presents results from the MANOVA procedure. Note that problem behavior is significantly affected by the intercept of alcohol, as well as by both linear and quadratic trends in alcohol use (i.e.,  $CNST = .016$ ,  $SE = .002$ ,  $t = 10.326$ ;  $LIN = .010$ ,  $SE = .003$ ,  $t = 3.720$ ;  $QUAD = .008$ ,  $SE = .003$ ,  $t = 2.628$ ).

INPUT 3.5  
SPSS Specifications for the Sequelae of Change MANOVA

```
MATRIX DATA VARIABLES=ROWTYPE_ ALC1 ALC2 ALC3 PROBBEH.  
BEGIN DATA.  
MEAN 8.31 10.00 10.81 .03  
STDDEV 7.39 7.99 8.08 .38  
N 343 343 343 343  
COR 1.000  
COR .4859 1.000  
COR .3988 .5332 1.000  
COR .3102 .3428 .5156 1.000  
END DATA.  
MANOVA ALC1 ALC2 ALC3 WITH PROBBEH  
/TRANSFORM(ALC1 ALC2 ALC3)=POLYNOMIAL  
/RENAME=CNST LIN QUAD PROBBEH  
/ANALYSIS=PROBBEH WITH CNST LIN QUAD  
/PRINT=CELLINFO(ALL)  
ERROR TRANSFORM  
PARAM(ALL)  
SIGNIF(MULTIV UNIV)  
/MATRIX=IN(*)  
/DESIGN=.
```

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OUTPUT 3.9  
Regression Analysis for the Sequelae of Change MANOVA

Dependent variable .. Problem Behavior

| COVARIATE | B      | SE   | t Value | Sig. of t |
|-----------|--------|------|---------|-----------|
| CNST      | .01672 | .002 | 10.326  | .000      |
| LIN       | .01089 | .003 | 3.720   | .000      |
| QUAD      | .00867 | .003 | 2.628   | .009      |

Input 3.6 presents the EQS specifications for the sequelae of change model in which the latent growth factors of alcohol are seen to predict problem behavior (V5). Age (V4) is included in the data set, but is not specified in the equations and is therefore not part of the model.

INPUT 3.6  
EQS Specifications for the Sequelae of Change Model

```

/TITLE
  SEQUELAE OF CHANGE
/SPECIFICATIONS
  CAS=343; VAR=5; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
  V1=ALC1; V2=ALC2; V3=ALC3; V4=AGE; V5=PROBBEH;
/EQUATIONS
  V1=.577F1-.707F2+.408F3+E1;
  V2=.577F1+.000F2-.816F3+E2;
  V3=.577F1+.707F2+.408F3+E3;
  V5=*V999+*F1+*F2+*F3+E5;
  F2=*V999+D2;
  F1=*V999+D1;
  F3=*V999+D3;
/VARIANCES
  E1 TO E3=0; E5=*;
  D1 TO D3=*;
/COVARIANCES
  D1 TO D3=*;
/MATRIX
  1.000
  .4859    1.000
  .3988    .5332    1.000
  -.1454   -.0178   -.0966    1.000
  .3102    .3428    .5156    .0398    1.000
/MEANS
  8.31    10.00    10.81    21.94    .03
/STANDARD DEVIATIONS
  7.39    7.99    8.08    1.42    .38
/PRINT
  EFFECTS=YES;
/END

```

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OUTPUT 3.10  
Measurement Equations for the Sequelae of Change LGM

| V5 = | .017 *F1 | .011 *F2 | .009 *F3 |
|------|----------|----------|----------|
|      | .002     | .003     | .003     |
|      | 10.371   | 3.736    | 2.640    |

Output 3.10 presents the measurement equations for this model. The output shows the effects of each of the growth factors on V5, the problem behavior variable, along with standard errors and tests of significance. Note that V5 is significantly predicted by all growth factors as in the MANOVA procedure results ( $t$  values greater than 1.96 are significant at  $\alpha = .05$ ).

Example 3.4  
The Full Growth Curve Model Involving Predictors and Sequelae of Change

A full model which includes both static predictors of the developmental parameters as well as sequelae of the developmental parameters can not be analyzed in the repeated measures ANOVA format because the transformed variables must be either independent or dependent variables, not both. In contrast, the LGM framework allows for latent and measured variables to be used as both predictors and criteria. The full model is depicted in Fig. 3.2. In this model, age (V4) is specified as a covariate and problem behavior (V5) is predicted by the developmental trends in alcohol use.

Input 3.7 presents the EQS specifications for the full model.

The parameters of the model depicted in Fig. 3.2 are the coefficients in the equations and the variances and covariances of the independent variables, and the means of the independent variables and the intercepts of the dependent variables. Although these parameters are directly specified, they may not be the only aspects of interest in the model. In Fig. 3.2, the variables  $V4$  and  $V5$  are connected by paths as follows:  $V4 \rightarrow F1 \rightarrow V5$ ;  $V4 \rightarrow F2 \rightarrow V5$ ; and  $V4 \rightarrow F3 \rightarrow V5$ . Thus, although the exogenous predictor,  $V4$ , has no specified direct effect on the criterion variable,  $V5$ , it may influence  $V5$  indirectly through its effect on the growth parameters. A measure of this indirect effect is given by the product of the coefficients represented by the arrows. If there are many sequences by which a variable like  $V4$  can influence  $V5$ , the total indirect effect is a number indicating the size of this effect. Total indirect effects summarize how one variable in the model influences another regardless of the particular paths chosen.

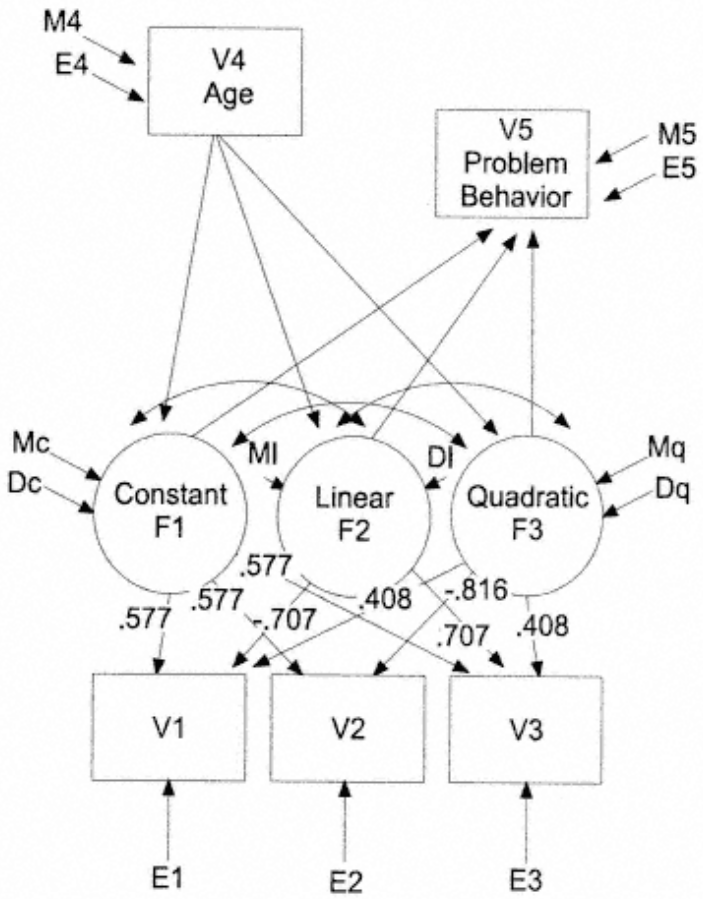


Fig. 3.2. Representation of the LGM involving sequelae and predictors of change.

While specific indirect effects (e.g.,  $V4 \rightarrow F1 \rightarrow V5$ ) may be of interest, EQS computes only the total indirect effects. A total effect for a particular variable's influence in the model is the sum of both direct and total indirect effects. Because indirect effects are sample statistics, they, like direct effects, have sampling variability. A test of significance for the unstandardized total effect, based on the work of Sobel (1982, 1986, 1987), is implemented in EQS.



INPUT 3.7  
EQS Specifications for the Full Model

```

/TITLE
  PREDICTORS AND SEQUELAE OF CHANGE
/SPECIFICATIONS
  CAS=343; VAR=5; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
  V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=AGE; V5=PROBBEH;
/EQUATIONS
  V1=.577F1-.707F2+.408F3+E1;
  V2=.577F1+.000F2-.816F3+E2;
  V3=.577F1+.707F2+.408F3+E3;
  V5=*V999+*F1+*F2+*F3+E5;
  F1=*V999+*V4+D1;
  F2=*V999+*V4+D2;
  F3=*V999+*V4+D3;
  V4=*V999+E4;
/VARIANCES
  E1 TO E3=0; E4 to E5=*;
  D1 TO D3=*;
/COVARIANCES
  D1 TO D3=*;
/MATRIX
  1.000
  .4859      1.000
  .3988      .5332      1.000
 -.1454     -.0178     -.0966      1.000
  .3102      .3428      .5156      .0398      1.000
/MEANS
  8.31      10.00      10.81      21.94      .03
/STANDARD DEVIATIONS
  7.39      7.99      8.08      1.42      .38
/PRINT
  EFFECTS=YES;
/LMTEST
  SET=BFV;
/END

```

Model fitting procedures resulted in the following indices of fit:  $\chi^2(1, N = 343) = 4.858$ , NNFI = 0.886, and CFI = 0.989. There is no direct effect of age on subsequent problem behavior, thus the model results in a test with 1 degree of freedom. Because the model no longer provides a perfect fit to the data, a substantive model fit for the hypothesized model is achieved.

Output 3.11 shows the measurement equations corresponding to the full model. The standard errors and test statistics for V5, the problem behavior variable, are shown here. All three latent growth factors are significant predictors of V5.

OUTPUT 3.11  
Measurement Equations From the Full LGM

|           |          |          |          |
|-----------|----------|----------|----------|
| PB = V5 = | .017 *F1 | .011 *F2 | .009 *F3 |
|           | .002     | .003     | .003     |
|           | 10.371   | 3.736    | 2.640    |

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OUTPUT 3.12  
Construct Equations From the Full LGM

|      |           |
|------|-----------|
| F1 = | -.813 *V4 |
|      | .414      |
|      | -1.964    |
|      | .146 *V4  |
| F2 = | .229      |
|      | .640      |
|      | -.452 *V4 |
|      | .202      |
| F3 = | -2.241    |

Output 3.12 shows the construct equations, standard errors, and test statistics for the effect of age on the three latent growth factors. The only significant effects for age were found for  $F1$  and  $F3$ , the constant and quadratic trends, respectively. Parameter estimates for the effect of age on the growth factors ( $V4 \rightarrow F1$ ,  $V4 \rightarrow F2$ , and  $V4 \rightarrow F3$ ) are similar to those reported earlier in the separate growth curve analyses.

Although the exogenous predictor,  $V4$ , has no specified direct effect on the criterion variable,  $V5$ , it may influence  $V5$  indirectly through its effect on the growth parameters. Output 3.13 presents this indirect effect.

OUTPUT 3.13  
Parameter Indirect Effects From the Full LGM

|    |   |    |   |  |            |
|----|---|----|---|--|------------|
| PB | = | V5 | = |  | - .016 *V4 |
|    |   |    |   |  | .008       |
|    |   |    |   |  | -2.009     |

The significant effect suggests that age predicts subsequent problem behavior through its effect on the developmental parameters. However, examination of the Lagrange Multipliers suggested that the inclusion of a direct effect of age on problem behavior ( $V4 \rightarrow V5$ ) would significantly improve the fit of the model ( $LM=4.825$ ,  $p = .028$ ). Output 3.14 presents the measurement equations and Output 3.15 presents the parameter indirect effects when the model is re-estimated to include the direct effect of  $V4$  on  $V5$ , resulting in a saturated model.

OUTPUT 3.14  
Measurement Equations From the Respecified LGM

|           |          |          |          |          |
|-----------|----------|----------|----------|----------|
| PB = V5 = | .027 *V4 | .017 *F1 | .011 *F2 | .010 *F3 |
|           | .012     | .002     | .003     | .003     |
|           | 2.212    | 10.637   | 3.656    | 2.927    |

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OUTPUT 3.15  
Parameter Indirect Effects From the Respecified LGM

|           |  |  |  |  |            |
|-----------|--|--|--|--|------------|
| PB = V5 = |  |  |  |  | - .017 *V4 |
|           |  |  |  |  | .008       |
|           |  |  |  |  | -2.071     |

As can be seen from Outputs 3.14 and 3.15,  $V4$  (age) has both direct (.027,  $t = 2.212$ ; Output 3.14), and indirect (-.017,  $t = -2.071$ ; Output 3.15) effects on the criterion variable,  $V5$  (problem behavior).

Summary

Examples from this chapter demonstrate that both repeated measures ANOVA and LGM address salient issues in the measurement of change, and that growth is represented by a constant base of initial levels and changes in these levels as a function of time. Using statistical techniques such as LGM affords an opportunity to extend and refine investigations of the development of behavioral outcomes, the context in which they occur, and the antecedents and sequelae of change in such behaviors across the life course. 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.

Another closely related method not presented here, but directly applicable to LGMs, are random effects models. Unlike traditional fixed effects analytical methods (e.g., ANOVA), random effects models are more suited to the hierarchical data structure in repeated measures data, making use of within-cluster differences in parameter estimates rather than treating these differences as within-group error (Kreft, 1994). The LGMs presented in chapters 2 and 3 can be considered two-level random effects models with repeated measures (Level 1) nested within individuals (Level 2). See chapter 9 for a detailed discussion of more complex random effects models.

LGM provides more flexibility in the measurement of change than the more traditional ANOVA approach, the most notable being LGM's ability to approximate random changes in measurement error. Another 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. Other advantages of the LGM approach, as demonstrated in subsequent chapters, include its capacity to (a) analyze interindividual differences in change simultaneously in cross-domain latent

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variable associative growth models, (b) include time-varying as well as time-invariant covariates as demonstrated here, (c) develop from the data a common developmental trajectory in overlapping cohorts, and (d) model multilevel longitudinal data.

Although researchers have been encouraged to adopt growth curve methodology in one form or another (e.g., Rogosa et al., 1982; Rogosa & Willett, 1985), these techniques have not been widely used in the study of development. The approach makes available to a wide audience of researchers the possibility for a variety of analyses of growth and developmental processes. By integrating typical causal model features found in a majority of SEM applications and the dynamic features of LGM, researchers may disentangle some of the cause-and-effect relationships inherent in the study of development.

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## Chapter 4 Analyzing Growth in Multiple Populations

This chapter addresses covariance and mean structure models for longitudinal designs in multiple populations. 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, as well as multiple developmental pathways rather than a single underlying trajectory for all individuals.

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. 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 terms of the means obtained from the various samples. Growth models generated from the different samples would not be expected to describe the same underlying developmental process for the population, and the separate models would carry unique

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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, but 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). The chi-square test statistic can be used to describe the adequacy of the model.

Let  $u$  and  $\sigma$  be the sample mean vector and covariance matrix for the observed variables, respectively. Given an LGM that specifies  $u = u(\gamma)$  and  $\sigma = \sigma(\gamma)$  as a function of some parameter vector,  $\gamma$ , the simultaneous hypothesis of equality of growth across multiple groups,  $m$ , to be tested is

$$(u(\gamma), \sigma(\gamma))_i, \dots, (u(\gamma), \sigma(\gamma))_m. \quad 4.1$$

Substantively, the question of interest concerns the extent to which the parameters in  $(u(\gamma), \sigma(\gamma))$  are the same across  $m$  groups. Therefore, different applications of expression 4.1 will represent different constraints placed on the parameters  $(u(\gamma), \sigma(\gamma))$  of the  $i$ th group ( $i = 1, 2, \dots, m$ ). The appropriateness of the imposed constraints can be evaluated using the chi-square test statistic.

The hypothesis conveyed in expression 4.1 has the same form whether all of the parameters of a given group,  $i$ , are the same in all groups or, alternatively, vary across 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.

The general models given in expression 4.1 can be used in practice to evaluate several popular hypotheses about multiple populations. These concern the invariance of key parameters across populations (Alwin & Jackson, 1981; Bentler & Wu, 1995; Jöreskog, 1971). Although any free parameter, or set of free parameters, can be evaluated for invariance or equality across populations, various parameters tend to be evaluated together.

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### Equality of Sets of Parameters of an LGM

A number of invariance hypotheses may be tested within the multiple-population LGM framework. These include:

- 1. Equality of Factor Loadings or Growth Functions.** If the same underlying growth factors exist in each of the groups, then the regression of the variables on these factors, the factor loadings, should be equivalent in all groups.
- 2. Equality of Residual Factor Variances or Individual Difference Parameters.** In models with latent dependent factors such as latent variable growth models, the equality of these variances, representing individual differences in the hypothesized growth trajectory, is an important hypothesis to evaluate.
- 3. Equality of Factor Means.** SEMs which incorporate a mean structure introduce the possibility of testing the equivalency of both the means of the independent variables and the intercepts of the dependent variables: the mean and deviation-from-the-mean, respectively. In LGM applications, the equivalency of means, rather than deviations-from-the-mean, is more generally the hypothesis of interest.
- 4. Equality of Unique, or Error, Variances and Covariances.** Equality of unique error variances and covariances is generally the least important hypothesis to test. Typically, it is the last hypothesis in a sequence of tests on nested hypotheses. Assuming no predictors in the model and following the sequence of tests outlined in (1) to (3), acceptance of this hypothesis implies that all of the parameters in the model are equal across groups.

5. *Equality of Regression Coefficients.* If path coefficients representing antecedents or sequelae of the various growth functions are included in a structural model and are the same across groups, then the causal process hypothesized to exist is similar across groups. Equivalency of regression coefficients can be tested even when variances, covariances, and means of the residual factors are not equal.

6. *Equality of Covariance Matrices.* The hypothesis that covariance matrices,  $(\sigma(\gamma))_i$ , are identical may be true even when the underlying model is unknown.

7. *Equality of all Parameters in the Model.* Although very restrictive, this hypothesis implies not only that both the first moments of the data, namely the means, as well as the second moments of the data about the means, namely the variances and covariances, are equal, but also that the LGM generating those matrices is identical in all respects across samples. Here, the models may be essentially equivalent except for a few nuisance parameters that vary trivially across samples. The test of equivalence of moment matrices is of interest in model-based analyses of growth models that incorporate missingness (see chap. 8).

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.

A good first step is to perform separate growth analyses for each group. Previous research may suggest a priori hypotheses about the form of the growth trajectories. Inspection of individual and overall growth patterns may also guide the choice of growth forms to be tested in the analyses. In the second step, a multiple-group analysis is conducted in which the growth factors found in the single-sample analyses are simultaneously fit to all populations.

Example 4.1  
Multiple-Sample Analysis of Change in Adolescent Alcohol Use

Longitudinal data of adolescent alcohol use (TRACC; Biglan et al., 1995) were used to show how LGM techniques can be extended to analyses involving multiple populations (males and females). The developmental model was based on a sample of 291 adolescents (196 females and 95 males) ranging in age from 15 to 17 years. Each participant's level of alcohol consumption for the preceding 6 months was measured at three approximately equal intervals over a 2-year period.

Descriptive statistics and the covariance matrices for the separate samples are presented in Table 4.1.

TABLE 4.1  
Descriptive Statistics for the Multiple-Sample LGM

|                        | <i>Alcohol Consumption</i> |           |           |
|------------------------|----------------------------|-----------|-----------|
|                        | <i>V1</i>                  | <i>V2</i> | <i>V3</i> |
| Females <i>N</i> = 196 | 1.764                      |           |           |
|                        | .933                       | 2.291     |           |
|                        | .856                       | 1.304     | 2.355     |
| Mean                   | 1.443                      | 1.723     | 1.831     |
| Males <i>N</i> = 95    | 1.941                      |           |           |
|                        | .978                       | 2.223     |           |
|                        | .901                       | 1.645     | 2.729     |
| Mean                   | 1.554                      | 1.864     | 2.280     |

*Note.* Variances and covariances are in the triangle; means for the observed variables are presented in the bottom rows of the matrix.

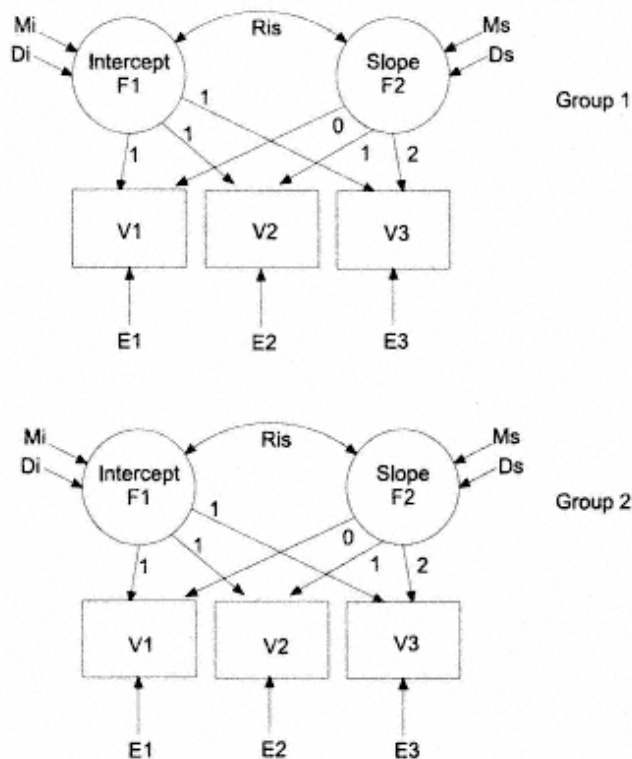


Fig. 4.1.  
Representation of the multiple-sample LGM.

The multiple-sample model tested is depicted in Fig. 4.1. The EQS input for this model is presented in Appendix 4.1. As can be seen in Fig. 4.1, the LGM includes a test of a linear trend in the data (loadings set at values of 0, 1, and 2 on the slope factor).

Model fitting procedures for the model presented in Fig. 4.1, with parameters constrained to be equal across groups, resulted in the following fit indices:  $\chi^2(10, N = 291) = 9.476, p = .487, NNFI = 1.001,$  and  $CFI = 1.000.$

Intercept and slope means and variances, correlations, and reproduced means for this model are shown in Table 4.2.

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TABLE 4.2  
Parameter Estimates From the Multiple-Sample LGM

| <i>Parameter</i>   | <i>Coefficient</i> | <i>t Value</i> |
|--------------------|--------------------|----------------|
| Mean intercept     | 1.493              | 19.536         |
| Mean slope         | .243               | 5.247          |
| Intercept variance | 1.020              | 5.446          |
| Slope variance     | .423               | 4.277          |
| Covariance         | -.069              | -.714          |
| Error variances    |                    |                |
| E1                 | .805               | 4.475          |
| E2                 | .970               | 8.626          |
| E3                 | .085               | .416           |

The significant slope means indicated that linear growth in adolescent alcohol use occurred over the time period measured. In addition, the significant variances indicated that substantial variation existed in individual differences regarding initial status and trajectories of alcohol use.

The Lagrange Multiplier (LM) test evaluates the effect of adding free parameters to a restricted model (i.e., reducing restrictions placed on the model). A test equivalent to the LM test in a maximum likelihood context, called the score test, was first introduced by Rao (1958). Aitchison and Silvey (1958) rationalized Rao's score test by the use of Lagrange Multipliers. The LM principle was adopted by Lee and Bentler (1980) for covariance structure analysis under normality assumptions, and is available in EQS for all distributional assumptions as well as for evaluation of cross-group equality constraints in multiple-sample models.

The LM test and the chi-square difference test (D), which is based on separate estimation of two nested models, are asymptotically equivalent chi-square tests (Bentler & Dijkstra, 1985). This equivalence means that the LM test can be interpreted as if a D test had been conducted, and represents an approximate decrease in model goodness-of-fit chi-square resulting from freeing previously fixed parameters and from eliminating equality restrictions. However, in contrast to the D test, there is no need to actually estimate the alternative models to obtain statistics for the D test because these statistics are conveniently obtained in a single computer run. Therefore, the LM test can be implemented with relative ease in an exploratory model to provide guidance on modifications to yield an improved fit to the data (Bentler & Chou, 1986). Output 4.1 presents the EQS LM test results for the multiple-sample model depicted in Fig. 4.1.

OUTPUT 4.1  
Lagrange Multiplier Test (For Releasing Constraints)

CONSTRAINTS FROM GROUP 2

|         |   |                                    |
|---------|---|------------------------------------|
| CONSTR: | 1 | (1, F1, V999) - (2, F1, V999) = 0; |
| CONSTR: | 2 | (1, F2, V999) - (2, F2, V999) = 0; |
| CONSTR: | 3 | (1, D1, D1) - (2, D1, D1) = 0;     |
| CONSTR: | 4 | (1, D2, D2) - (2, D2, D2) = 0;     |
| CONSTR: | 5 | (1, D1, D2) - (2, D1, D2) = 0;     |
| CONSTR: | 6 | (1, E1, E1) - (2, E1, E1) = 0;     |
| CONSTR: | 7 | (1, E2, E2) - (2, E2, E2) = 0;     |
| CONSTR: | 8 | (1, E3, E3) - (2, E3, E3) = 0;     |

UNIVARIATE TEST STATISTICS:

| NO | CONSTRAINT | CHI-SQUARE | PROBABILITY |
|----|------------|------------|-------------|
| 1  | CONSTR: 1  | 1.631      | 0.202       |
| 2  | CONSTR: 2  | 5.190      | 0.023       |
| 3  | CONSTR: 3  | 0.164      | 0.686       |
| 4  | CONSTR: 4  | 1.725      | 0.189       |
| 5  | CONSTR: 5  | 0.137      | 0.711       |
| 6  | CONSTR: 6  | 0.304      | 0.581       |
| 7  | CONSTR: 7  | 0.073      | 0.787       |
| 8  | CONSTR: 8  | 2.599      | 0.107       |

Examination of the univariate LM statistics revealed that significant cross-group (in this case cross-gender) differences existed for Constraint 2, the slope mean, ((1, F2, V999) - (2, F2, V999) = 0;), with an expected drop in the model chi-square of approximately 5.190,  $p < .023$  if this constraint were relaxed across groups. Re-estimation of the model without this constraint resulted in fit indices of  $\chi^2(9, N = 291) = 4.235, p = .895, NNFI = 1.01,$  and  $CFI = 1.000$ . The chi-square difference between the two competing models,  $\chi^2(1, N = 291) = 5.241, p < .022,$  indicated that accounting for group differences in the rate of change significantly improved the fit of the model.

Intercept and slope means and variances, correlations, and reproduced means for the respecified model are shown in Table 4.3.

TABLE 4.3  
Parameter Estimates for the Respecified Multiple-Sample LGM

| Parameter          | Coefficient | t Value |
|--------------------|-------------|---------|
| Mean intercept     | 1.493       | 19.536  |
| Mean slope         |             |         |
| Females (Group 1)  | .175        | 3.221   |
| Males (Group 2)    | .382        | 5.028   |
| Intercept variance | 1.020       | 5.446   |
| Slope variance     | .423        | 4.312   |

|                 |       |       |
|-----------------|-------|-------|
| Covariance      |       |       |
|                 | -.074 | -.771 |
| Error variances |       |       |
| E1              | .805  | 4.475 |
| E2              | .976  | 8.673 |
| E3              | .060  | .295  |

The difference in slope means shows that growth in alcohol use occurred more rapidly for males (Group 2),  $M_s = .382$ , than for females (Group 1),  $M_s = .175$ . The difference in the rate of growth,  $.382 - .175 = .207$ , is significant, as noted by the significant chi-square difference test,  $\chi^2(1, N = 291) = 5.241, p < .022$ , for this parameter. Note that all other parameters remained constrained across the two groups.

An examination of the univariate LM statistics for the respecified model revealed that none of the remaining constraints, if released, would significantly improve overall model fit.

Example 4.2  
Alternative Multiple-Sample Analysis of "Added Growth" LGM

As in conventional multiple-population latent variable analyses, the preceding analyses specified a two-factor growth model in both groups, testing for equality of parameters across the two populations. An alternative approach (Muthén & Curran, 1997) is shown in Fig. 4.2.

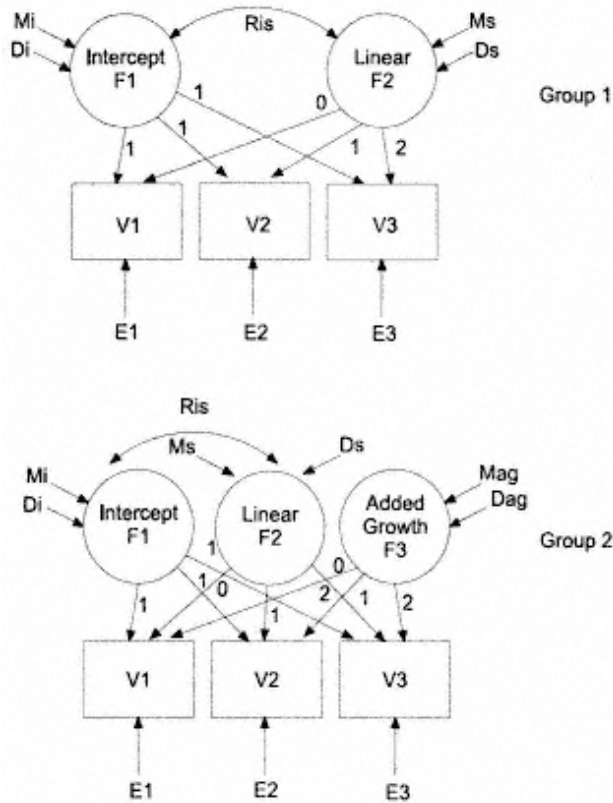


Fig. 4.2.  
Representation of the added growth LGM.

Here, an additional growth factor is introduced for one population. Muthén and Curran call this the added growth factor. Whereas the first two factors (i.e., intercept and slope) are the same in both groups, the added growth factor, specified in one group, represents incremental/decremental growth that is specific to that group.

As can be seen in Fig. 4.2, the added growth factor is specified to capture linear differences between the two groups. In this case, the linear slope factor captures normative growth that is common to both groups. The added growth factor approach provides a test of the difference in growth rate between the two groups without having to resort to the use of LM or other model modification tests.

Appendix 4.2 presents the EQS program specifications necessary to estimate the model presented in Fig. 4.2. Intercept and slope means, variances, and covariances for this model are shown in Table 4.4.

Model fitting procedures for the model presented in Fig. 4.2, with parameters constrained to be equal across groups for all common parameters, resulted in the following fit indices:  $\chi^2(8, N = 291) = 2.891, p = .941, NNFI = 1.015,$  and  $CFI = 1.000.$

The difference in the rate of growth as indicated by the mean for the added growth factor,  $Mag = .207, t = 2.228,$  was significant. The positive mean value for the added growth factor indicated that when compared to the mean slope value for both groups ( $Ms = .175$ ), the group with the added growth factor (Group 2: males) had a mean growth rate that was approximately twice as large as that for the first group (females) ( $.175 + .207 = .382$  for males compared to  $.175$  for females). Note that the added growth model uses 1 fewer degree of freedom when compared to the

TABLE 4.4  
Parameter Estimates for the Added Growth LGM

| <i>Parameter</i>         | <i>Coefficient</i> | <i>t Value</i> |
|--------------------------|--------------------|----------------|
| Mean intercept           | 1.493              | 19.536         |
| Mean slope-F2            | .175               | 3.321          |
| Mean added growth-F3     | .207               | 2.228          |
| Intercept variance       | 1.020              | 5.446          |
| Slope variance-D2        | .393               | 3.903          |
| Added growth variance-D3 | .107               | 1.102          |
| Covariance-D1, D2        | -.073              | -.767          |
| Error variances          |                    |                |
| E1                       | .805               | 4.475          |
| E2                       | .980               | 8.692          |
| E3                       | .043               | .215           |

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comparable model depicted in Fig. 4.1. However, the difference in chi-square values for the two competing models,  $\chi^2(1, N = 291) = 1.344, p = .246,$  indicated that there were no statistical differences between the two models in terms of overall model fit. An advantage of the added growth model to the more standard multiple-sample LGM is that it affords a statistical test of the mean differences between the two groups in a single run without having to resort to the use of LMs or other post hoc procedures.

For all factors except the initial status factor, one may specify an added growth factor. For example, one group may have both 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.

## Summary

The present chapter demonstrates the use of the basic LGM for analyzing multiple populations. Various LGMs can be generalized to the simultaneous analysis of data from multiple populations or groups. Although group differences can be captured in single-population analyses to some extent, by representing the different groups as dummy vectors used as time-invariant covariates, the multiple-sample approach is advantageous in that multiple groups are analyzed simultaneously rather than in separate analyses.

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 model exists and whether there are *significant* differences in parameters of interest between populations. Because models from several groups are analyzed at the same time in a multiple-sample LGM, this approach allows the researcher to determine whether a common developmental model exists, or whether there are multiple developmental pathways across groups.

Hypotheses involving growth for multiple populations can be examined simultaneously as long as data on the same variables over the same developmental period are available in the different populations. As a first step in a multiple-sample LGM, growth can be studied by a separate analysis of each group. Prior research may direct a priori hypotheses about the form of the growth trajectories. Inspection of individual and overall growth patterns may also help in the selection of growth forms to be tested in the analyses. In the second step, a multiple-group analysis can be performed in which the growth factors established in the single-sample analyses are simultaneously fit to multiple populations.





|     |       |       |       |       |       |       |       |       |       |       |       |       |
|-----|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| V4  | .566  | .624  | .706  | 1.000 |       |       |       |       |       |       |       |       |
| V5  | .419  | .281  | .303  | .283  | 1.000 |       |       |       |       |       |       |       |
| V6  | .344  | .362  | .350  | .367  | .671  | 1.000 |       |       |       |       |       |       |
| V7  | .224  | .281  | .353  | .360  | .548  | .783  | 1.000 |       |       |       |       |       |
| V8  | .183  | .234  | .300  | .384  | .458  | .696  | .823  | 1.000 |       |       |       |       |
| V9  | .579  | .482  | .410  | .303  | .455  | .333  | .244  | .179  | 1.000 |       |       |       |
| V10 | .532  | .571  | .501  | .440  | .347  | .444  | .352  | .272  | .663  | 1.000 |       |       |
| V11 | .439  | .507  | .648  | .496  | .378  | .419  | .430  | .345  | .551  | .709  | 1.000 |       |
| V12 | .431  | .469  | .527  | .571  | .345  | .424  | .427  | .412  | .499  | .682  | .736  | 1.000 |
| M   | 1.338 | 1.591 | 2.019 | 2.364 | .862  | 1.218 | 1.445 | 1.756 | .554  | .890  | 1.033 | 1.123 |
| SD  | 1.260 | 1.334 | 1.440 | 1.376 | 1.709 | 1.948 | 2.117 | 2.265 | 1.199 | 1.432 | 1.496 | 1.503 |

Note. Correlation matrix is in the triangle; means and standard deviations are presented in the bottom rows of the matrix.

#### Example 5.1 Associative LGM

Associative LGMs allow researchers to examine the correlations among development parameters for pairs of behaviors. The first step in developing an associative model is to model each repeated measure separately to determine whether it increases, decreases, or remains constant over time. Plots of the longitudinal functions representing mean changes over time can show change at the group, or interindividual, level. Before formulating the associative model, it is essential to determine from the univariate models (in this case, alcohol, tobacco, and marijuana use) whether there is sufficient interindividual variation in initial status and growth (i.e., whether intercept factor and slope factor variances are significantly different from zero) to warrant conducting an LGM. At the intraindividual level, change may be estimated from individual saliences.

Once the repeated measures have been successfully modeled independently, they may be modeled simultaneously. The associative model depicted in Fig. 5.1 describes the form of growth and the pattern of associations among the growth parameters of adolescent alcohol, tobacco, and marijuana use. In this model the slope factor loadings are constrained at 0, 1, 2, and 3 to represent linear growth in use of each substance over time. The EQS input specification for the model is shown in Appendix 5.1.

The associative extension of the basic LGM allows for the assessment of relationships among the individual difference parameters for alcohol, tobacco, and marijuana use, and for the estimation of means, variances, and covariances for the growth factors of each substance. Model fitting procedures for the associative LGM,  $\chi^2(51, N = 357) = 224.395, p < .001, NNFI = .928, CFI = .944, AIC = 122.395, \text{ and } CAIC = -126.369$ , indicated that an associative multivariate representation of the various substances was tenable. Parameter estimates indicated significant average mean levels in alcohol,  $M_i = 1.310, t = 19.777$ , tobacco,  $M_i = .884, t = 9.726$ , and marijuana use,  $M_i = .608, t = 9.531$ , and significant growth in alcohol,  $M_s = .347, t = 15.928$ , tobacco,  $M_s = .291, t = 7.862$ , and marijuana use,  $M_s = .187, t = 7.822$ , at the group level. Variances of the intercepts of alcohol,  $D_i = 1.283, t = 10.484$ , tobacco,  $D_i = 2.324, t = 10.124$ , and marijuana use,  $D_i = 1.125, t = 9.732$ , and the slopes of alcohol,  $D_s = .084, t = 5.160$ , tobacco,  $D_s = .326, t = 7.901$ , and marijuana use,  $D_s = .113, t = 6.015$ , were significant, an indication that significant individual variation existed in the development of the three substances.

Table 5.2 presents the relationships among the intercepts and slopes for adolescent alcohol, tobacco, and marijuana use in this model. The intercepts

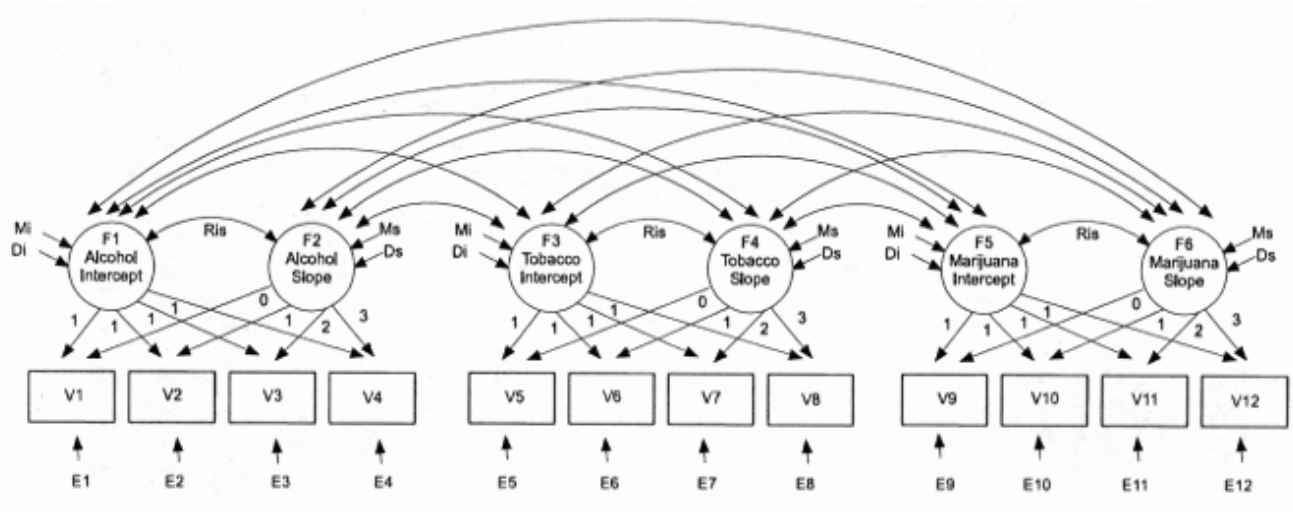


Fig. 5.1.  
Representation of the associative LGM.

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TABLE 5.2  
Correlations Among Alcohol, Tobacco, and Marijuana Use

|           | <i>Alcohol</i> |              | <i>Tobacco</i> |              | <i>Marijuana</i> |              |
|-----------|----------------|--------------|----------------|--------------|------------------|--------------|
|           | <i>Int</i>     | <i>Slope</i> | <i>Int</i>     | <i>Slope</i> | <i>Int</i>       | <i>Slope</i> |
| Alcohol   |                |              |                |              |                  |              |
| Intercept | 1.000          |              |                |              |                  |              |
| Slope     | -.260*         | 1.000        |                |              |                  |              |
| Tobacco   |                |              |                |              |                  |              |
| Intercept | .520*          | -.129        | 1.000          |              |                  |              |
| Slope     | -.194*         | .602*        | -.083          | 1.000        |                  |              |
| Marijuana |                |              |                |              |                  |              |
| Intercept | .783*          | -.369*       | .596*          | -.230*       | 1.000            |              |
| Slope     | -.074          | .881*        | .037*          | .534*        | -.082            | 1.000        |

\* denotes correlations significant at  $p < .05$  or greater.

and slopes of the three substances were all significantly related. Thus, the relationships support the hypothesis of common developmental trends and hypothesized associations among the individual difference parameters for the various substances.

#### Higher Order LGMS

Although associative models are useful in determining the extent to which *pairs* of behaviors covary over time, McArdle (1988) has suggested two alternative methods for conducting a *multivariate* analysis of the relations among numerous behaviors. These two approaches are termed the factor-of-curves model and the curve-of-factors model.

In the factor-of-curves model, one examines whether a higher order factor adequately describes relationships among lower order developmental functions. The second method suggested by McArdle (1988), the curve-of-factors model, fits a growth curve to factor scores representing what the three substance use behaviors have in common at each time point. The observed variables at each time point are factor analyzed to produce substance use factor scores, which are then used for modeling growth curves. In the example presented in this chapter, higher order factors were examined for two developmental functions of interest, namely, the intercept of adolescent substance use and the slope, or rate of development, of adolescent substance use over time, using repeated measures adolescent alcohol, tobacco, and marijuana use data over four assessments.

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As discussed earlier, it is not possible to statistically compare the two higher order models. Although well-defined research goals may formally prescribe a particular perspective, a clear substantive choice between the factor-of-curves and curve-of-factors models may be difficult to justify in practice. In these cases, it might be useful to view the problem not as one of testing a given hypothesis, but rather of fitting both alternatives and comparing them in the context of various common model parameters.

When considering the use of a factor-of-curves or curve-of-factors LGM, it is important to first test an associative model for the behaviors of interest to determine whether the behaviors are related. Because the results of the associative two-factor LGM shown in Fig. 5.1 demonstrated significant relations between the intercepts and slopes for each of the three substances, it was reasonable to extend this model to higher order models of substance use.

#### Example 5.2 Factor-of-Curves LGM

To test whether a higher order substance use construct could describe the relations among the growth factors of alcohol, tobacco, and marijuana use, the associative LGM was reparameterized as a factor-of-curves LGM. The higher order model follows a structure similar to the first-order associative LGM, except that the covariances among the first-order factors are hypothesized to be explained by the higher order factors. Note that even if the higher order model can account for all of the covariation among the first-order factors, the goodness-of-fit indices cannot exceed those of the corresponding first-order model. However, if the fit indices for the higher order model approach those of the corresponding first-order model, then the higher order model is more parsimonious (Marsh, 1985).

The model depicted in Fig. 5.2 represents the factor-of-curves LGM. Here, as in the associative model, the growth curves are applied to each substance separately. Therefore, each first-order LGM describes individual differences within each univariate series, and the second-order common factor model describes individual differences among the first-order LGMs. In the factor-of-curves LGM, the covariances among the first-order latent growth curve disturbances are fixed at zero, and factor loadings between the first- and second-order factors are restricted to be equal over time for each substance, imposing a form of factorial invariance that ensures the same units of scaling for the second-order factor scores. Thus, in Fig. 5.2 tobacco is used as the reference scaling for the second-order structure for substance use, and the factor loadings between the first- and second-order factors are restricted to be equal over

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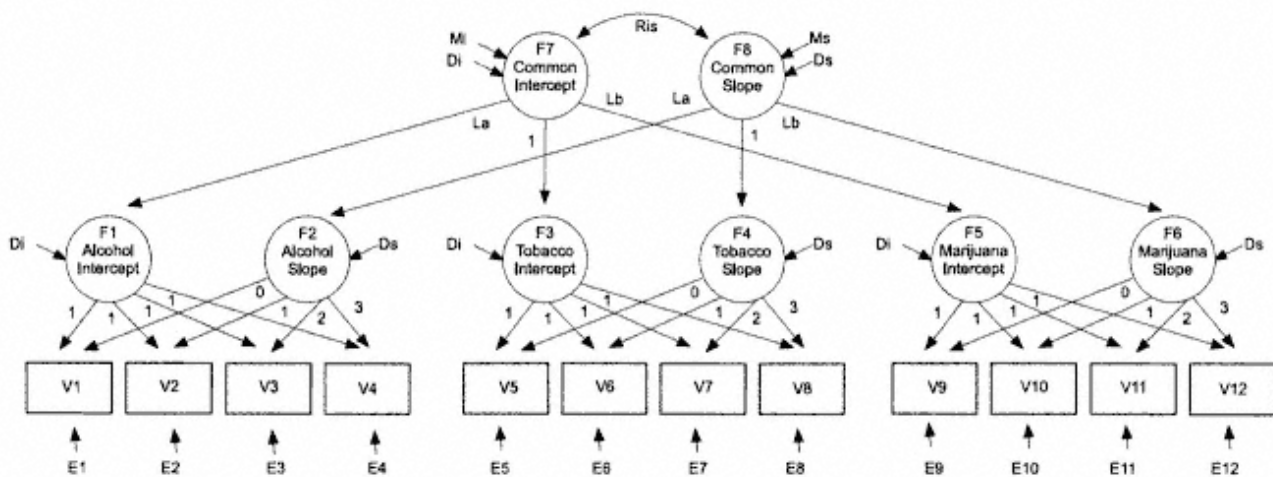


Fig. 5.2.  
Representation of the factor-of-curves LGM.

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time for alcohol ( $La$ ) and for marijuana use ( $Lb$ ). A more formal discussion of the mathematical representation of the factor-of-curves model is given by McArdle (1988). Program specifications for the factor-of-curves model are provided in Appendix 5.2.

Model fitting procedures for the factor-of-curves LGM,  $\chi^2(61, N = 357) = 242.472, p < .001, NNFI = .937, CFI = .941, AIC = 120.472,$  and  $CAIC = -177.07,$  indicated that a higher order common factor representation of the three substances was tenable. Parameter estimates for the factor-of-curves model resulted in significant mean levels in the common intercepts,  $Mi = .884, t = 9.633,$  and trajectories,  $Ms = .291, t = 7.957,$  for substance use. Individual differences in the higher order factors were significant, with estimated variances of  $Di = 1.031, t = 6.170,$  and  $Ds = .096, t = 5.709.$  In addition, all common factor-of-curve loadings were significant,  $La = .901, t = 11.684,$  and  $Lb = 1.000, t = 11.415.$  The higher order factors accounted for approximately 67%, 43%, and 85% of the variation in the first-order intercepts for alcohol, tobacco, and marijuana use, respectively. Approximately 95%, 30%, and 76% of the variation in the first-order trajectories for alcohol, tobacco, and marijuana use was accounted for by the higher order structure. On average, 73%, 79%, and 72% of the variation in observed alcohol, tobacco, and marijuana use variables was accounted for by the factor-of-curves LGM.

#### Example 5.3 Curve-of-Factors LGM

Although the factor-of-curves LGM appeared to provide an adequate fit of the model to the data, the alternative curve-of-factors LGM was also tested. Recall that the curve-of-factors model fits a growth curve to factor scores representing what the three substance use behaviors have in common at each time point. The observed variables at each time point are factor analyzed to compute substance use factor scores for use in modeling growth curves. McArdle (1988) suggested that such nonnested model comparisons form a basic requirement for any serious study of multivariate dynamics. Figure 5.3 represents the curve-of-factors LGM. In fitting the curve-of-factors LGM, unique factor covariances for each variable over time are allowed to covary, and are included mainly to improve model fit. The curve-of-factors LGM explicitly requires a condition of factor pattern invariance where common factor pattern elements must be equal over time.

In Fig. 5.3, tobacco use ( $V5$  to  $V8$ ) is again used as the scaling reference, this time for the first-order common factors ( $F1$ ,  $F2$ ,  $F3$ , and  $F4$ ), and the loadings for alcohol ( $La$ ) and marijuana use ( $Lb$ ) are constrained to be equal across time. Detailed rationales for the metric invariance assumptions are provided by Nesselroade (1983) and Meredith and Tisak (1982).

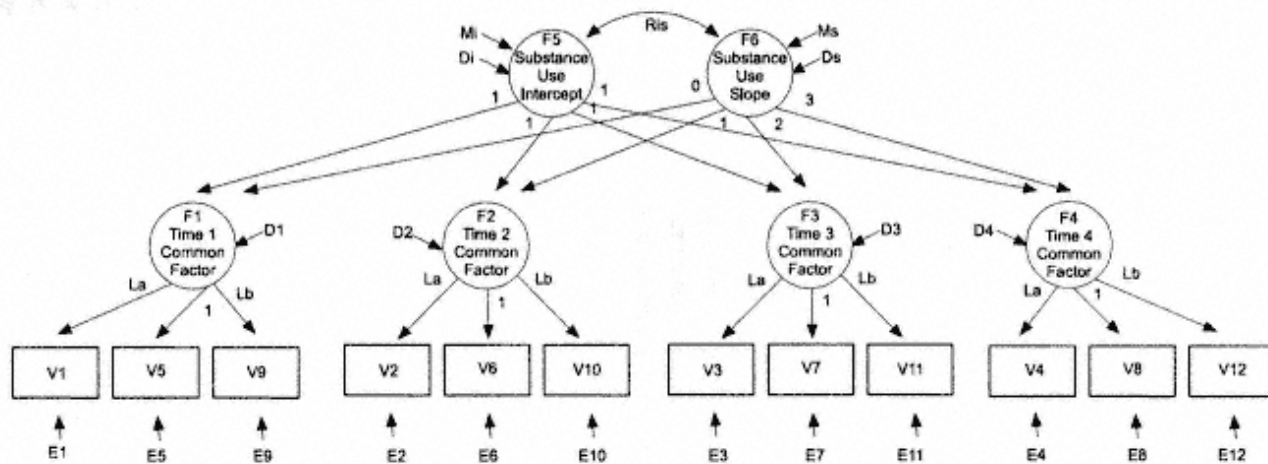


Fig. 5.3.  
Representation of the curve-of-factors LGM.

There are a variety of ways to ensure mathematical identification of the latent variable parameters, each having slightly different implications. The possibility of the factor pattern elements changing over time is discussed by Nesselroade (1977) and Horn, McArdle, and Mason (1983). Program information for the curve-of-factors model is shown in Appendix 5.3.

Fitting the curve-of-factors LGM resulted in the following indices of fit:  $\chi^2(41, N = 357) = 76.001, p < .001$ , NNFI = .982, CFI = .989, AIC = -5.999, and CAIC = -205.986. Parameter estimates for the curve-of-factors model indicated significant mean levels in the intercept,  $Mi = .874, t = 9.815$ , and trajectory,  $Ms = .292, t = 8.073$ , of the common factors. Individual differences in each higher order growth factor were significant with estimated variances of  $Di = .812, t = 5.912$ , and  $Ds = .072, t = 4.684$ . Common factor loadings were all significant,  $La = .972, t = 12.210$ , and  $Lb = 1.109, t = 11.614$ . The higher order factors accounted for approximately 91%, 86%, 80%, and 99% of the variation in the first-order  $F1$ ,  $F2$ ,  $F3$ , and  $F4$  substance use factors, respectively. Approximately 52%, 26%, and 64% of the variation in observed alcohol, tobacco, and marijuana use variables, respectively, was accounted for by the curve-of-factors LGM.

In comparing the fit of the competing models, the AIC indicated a better fit for the curve-of-factors model than the factor-of-curves model (-5.999 and 120.472, respectively) whereas the CAIC indicated a better fit for the factor-of-curves model (-177.07 vs. -205.986). However, the factor-of-curves model must be viewed as more parsimonious, with 20 fewer parameters estimated, compared to the curve-of-factors model. Based solely on these statistical comparisons, selecting a superior model is difficult.

Although model fitting procedures revealed similarities between the factor-of-curves and curve-of-factors approaches with these data, this will not always be the case for different selections of measures or occasions. Because both empirical and substantive differences may be critical for correct interpretation of the dynamics and influences of change, studies that apply these approaches should be pursued.

### Summary

The multivariate latent growth curve methods demonstrated in this chapter allow for an integrated approach to modeling development that includes both multiple measures and multiple occasions. The associative model relates multiple behaviors simultaneously over time, and estimates the extent of covariation in the development of pairs of behaviors. The higher

order LGMs extend the test of dynamic associations of behaviors over time by describing growth factors in terms of common higher order constructs.

One of the higher order extensions of the LGM, the curve-of-factors model, merges a psychometric common factor model for the multiple measures within a specific occasion and a growth curve model of the common factor scores over time. An entirely different approach, the factor-of-curves model, examines individual differences within separate univariate series and forms common factors to describe differences among these basic growth curves. In practical terms, these two multivariate extensions offer differing opportunities for evaluating the dynamic structure of both intra- and interindividual change, and represent a logical progression in testing the adequacy of latent growth curve representations of behavioral dynamics.

Following procedures demonstrated in chapter 3, it is possible to include predictors of development, as well as the developmental trends as predictors of numerous outcomes, in all three multivariate models. Factor-of-curves and curve-of-factors models can test for the common effects of predictors on the intercept and slope, as well as effects of predictors specific to a single substance (S.C. Duncan & T.E. Duncan, 1996). This capability makes the higher order approach particularly appealing because, while testing for the amount of commonality among certain behaviors, it is also possible to identify effects that are unique to a specific behavior.

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## Chapter 6 Accelerated Designs

This chapter presents models for the accelerated collection of longitudinal data. As a means of understanding human development, the single longitudinal design has many advantages over comparable cross-sectional methods. Perhaps its greatest advantage is the ability to examine the same person at different times, permitting within-individual analyses of change. Cross-sectional designs, on the other hand, allow only for the study of variations between individuals. Although desirable, true longitudinal designs present some practical problems. Given time constraints, concerns about subject attrition, and the cost of multiple assessments, researchers have long sought alternative approaches that maintain the advantages and minimize the disadvantages of the longitudinal design.

Bell (1953) introduced the idea of "convergence" as a means of meeting research needs not satisfied by either longitudinal or cross-sectional methods. This method calls for limited repeated measurements of independent age cohorts, resulting in temporally overlapping measurements of the various groups. The technique, which has gained popularity as the "cohort-sequential" design (Nesselroade & Baltes, 1979), provides a way to link adjacent segments of limited longitudinal data from different age cohorts to determine the existence of a common developmental trend, or growth curve. In this way, the researcher approximates a long-term longitudinal study by simultaneously conducting and connecting several short-term longitudinal studies of different age cohorts.

An obvious advantage of the accelerated design over the single-cohort longitudinal design is the shorter follow-up period. This reduces the problems of cumulative testing effects and attrition, and produces quicker results. Another advantage is that tracking several cohorts, rather than one, allows the researcher to determine whether those trends observed in the repeated observations are corroborated within short time periods for each age cohort.

The main disadvantage of the accelerated design, compared to the single-cohort longitudinal design, is that within-individual developmental sequences are followed, and behavioral continuity and prediction are studied, over shorter periods. As a result, it may be that the accelerated or

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cohort-sequential approach inadequately recovers information concerning the full longitudinal curve from different cohort segments. In addition, questions remain about the ability of the cohort-sequential approach to assess the impact of important events and intervening variables on the course of development (Raudenbush & Chan, 1992).

### Cohort-Sequential LGM

The following sections provide a test of the cohort-sequential LGM and a comparison of findings from the cohort-sequential LGM to a "true longitudinal" growth curve model using data assessed from a single age cohort. The cohort-sequential technique was used to model the development of adolescent alcohol use from 12 to 16 years of age over a 3-year period and a true longitudinal model was used over a 5-year period. Previous research has demonstrated that a cohort-sequential design can adequately approximate adolescent alcohol use (T.E. Duncan, S.C. Duncan, & Hops, 1994) as well as the development of other substances (T. E. Duncan, Tildesley, S. C. Duncan, & Hops, 1995) and, as such, may represent an efficient method for analyzing development. For example, a comparison of a cohort-sequential design and a true longitudinal design with alcohol use data (S.C. Duncan, T.E. Duncan, & Hops, 1996) yielded similar results spanning a 6-year period.

Data for the model examples were from the National Youth Survey (Elliott, 1976). For the accelerated longitudinal model, data were used from three different age cohorts (12, 13, and 14 years of age at the initial assessment). The 12- through 14-year-old cohorts were each measured three times at approximately 1-year intervals (Time 1 to Time 3), thus representing an overall age range of 12 to 16 years. These age cohorts were chosen so that the time of measurement and age of testing were "approximately staggered" (McArdle & Anderson, 1989), meaning that the average age of the first cohort at the second measurement period was about the same as the average age of the second cohort at the initial measurement, and so forth. The sample sizes for the three cohorts were 248, 250, and 231, respectively ( $N = 729$ ). An additional 11-year-old cohort ( $N = 215$ ) was included to represent data from a true longitudinal design. This 11-year-old cohort was measured over five assessments (Time 2 to Time 6; 12 to 16 years of age), allowing a comparison of the developmental trends for similar age spans from two differing design methodologies.

Groups 1, 2, and 3 in the model depicted in Fig. 6.1 represent a cohort-sequential LGM in which the basic parameters describe a systematic pattern of individual differences in change over time. The same developmental

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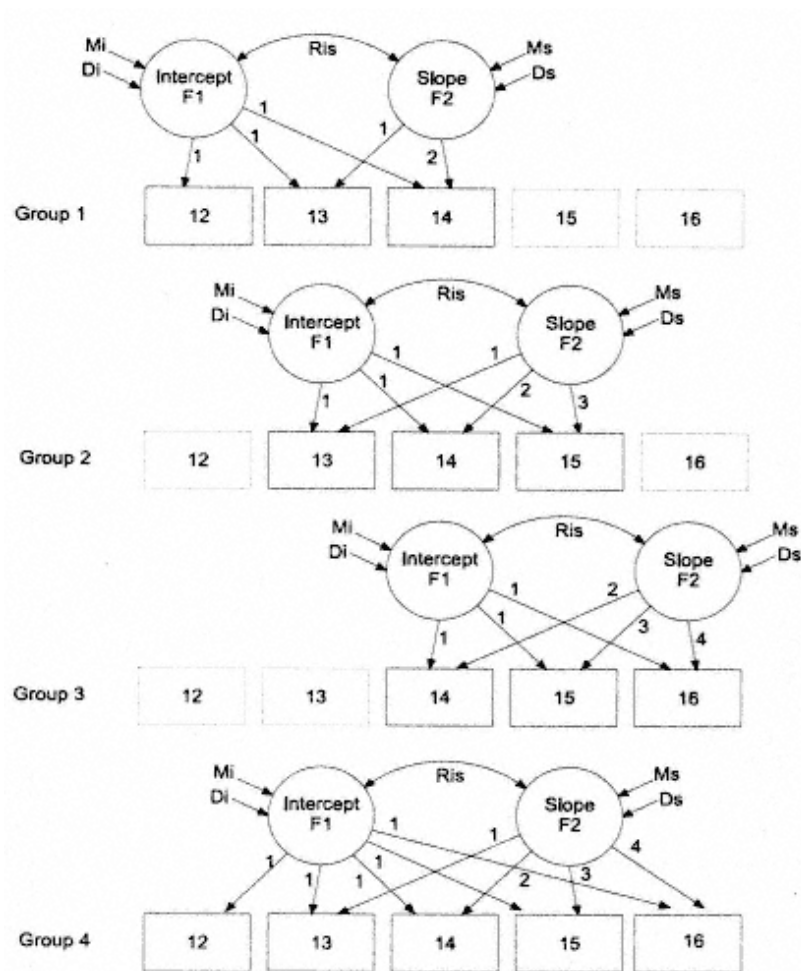


Fig. 6.1.  
Representation of the combined cohort-sequential-true longitudinal LGM.

model is assumed in each cohort, allowing for tests of hypotheses concerning convergence across separate groups and the feasibility of specifying a common growth trajectory over the 6 years represented by the design.

The cohort-sequential model serves as a proxy for the true longitudinal model, which uses data from yearly assessments of the 11-year-old cohort (Group 4) over a 5-year period beginning at 12 years of age. Descriptive statistics for the cohort-sequential (three cohorts; Groups 1 to 3) and true longitudinal (11-year-old cohort; Group 4) samples are presented in Table 6.1.

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TABLE 6.1  
Descriptive Statistics for the Cohort-Sequential and True Longitudinal Models

|                         | <i>Mean</i> | <i>SD</i> |
|-------------------------|-------------|-----------|
| Cohort-sequential model |             |           |
| Alcohol use age 12      | .33         | .69       |
| Alcohol use age 13      | .61         | .95       |
| Alcohol use age 14      | .93         | 1.07      |
| Alcohol use age 15      | 1.36        | 1.17      |
| Alcohol use age 16      | 1.87        | 1.27      |
| True longitudinal model |             |           |
| Alcohol use age 12      | .36         | .69       |
| Alcohol use age 13      | .54         | .79       |
| Alcohol use age 14      | 1.07        | 1.15      |
| Alcohol use age 15      | 1.44        | 1.21      |

Here, two basic growth models were analyzed: testing the hypothesized *linear* growth in alcohol use with fixed parameter restrictions, and testing an *unspecified* model with free estimation of the developmental trajectory, allowing possible nonlinearity and a test of the adequacy of the linear hypothesis. To identify these models, two slope loadings must be fixed to two different values. In the linear growth model, the loadings were fixed at 0, 1, 2, 3, and 4. In the unspecified model (see chap. 2), the first and second values were fixed at 0 and 1, respectively, with the third through fifth terms freely estimated. The intercept and slope factors were allowed to covary,  $R_{is}$ , which is represented by the double-headed arrow in Fig. 6.1.

Because of the overlap in ages in the cohort-sequential design, a quasi-longitudinal study spanning ages 12 to 16 was created. Moreover, because each age cohort, representing a different pattern of "missingness" due to design, contributed a different section to the overall developmental curve, the complete curve could be constructed using information from all cohorts simultaneously. In creating the full curve, it was assumed that one line could characterize the set of staggered age group curves, and that this line would accurately approximate the developmental trajectory developed from data generated from the 11-year-old cohort within the true longitudinal design.

#### Example 6.1 Cohort-Sequential LGM

Models were analyzed to determine whether similar trends were produced in the cohort-sequential and true longitudinal models under the assumption

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TABLE 6.2  
Parameter Estimates for the Linear LGM

|                    | <i>Cohort-sequential</i> |                | <i>True Longitudinal</i> |                | <i>Combined</i> |                |
|--------------------|--------------------------|----------------|--------------------------|----------------|-----------------|----------------|
|                    | <i>Effect</i>            | <i>t Value</i> | <i>Effect</i>            | <i>t Value</i> | <i>Effect</i>   | <i>t Value</i> |
| Intercept mean     | .310                     | 8.541          | .286                     | 6.329          | .304            | 11.020         |
| Intercept variance | .314                     | 5.216          | .280                     | 5.692          | .285            | 7.955          |
| Slope mean         | .384                     | 21.260         | .413                     | 19.978         | .394            | 29.396         |
| Slope variance     | .077                     | 4.385          | .044                     | 4.385          | .054            | 6.356          |
| Correlation        | -.140                    | -.712          | .129                     | .843           | .057            | .486           |

Note. *t* values of 1.96 (two-tailed) are significant at  $p < .05$ .

of linear growth. Model fitting procedures for the cohort-sequential model resulted in the following fit indices:  $\chi^2(17, N = 729) = 65.746, p < .001$ , NNFI = .948, and CFI = .902. Fit indices for the true longitudinal model were  $\chi^2(10, N = 215) = 60.172, p < .001$ , NNFI = .846, and CFI = .846. Intercept and slope means and variances, and correlations, are shown in Table 6.2. EQS program specifications are presented in Appendix 6.1. LISREL program specifications are presented in Appendix 6.2.

The significant slope means indicated that significant growth in alcohol use occurred over the 5 adolescent years approximated by the two models. In addition, the significant variances indicated that substantial variation existed in individual differences regarding initial status and trajectories of alcohol use.

Reproduced means are shown in Table 6.3. Examination of the means, variances, and reproduced means suggested considerable similarity in estimates across the cohort-sequential and true longitudinal models assuming linear growth in alcohol use.

A combined multiple-sample analysis was conducted with all four groups (three cohorts in the cohort-sequential model and the single cohort

TABLE 6.3  
Reproduced Means for the Linear LGM

|        | <i>Cohort-sequential</i> | <i>True Longitudinal</i> | <i>Combined</i> |
|--------|--------------------------|--------------------------|-----------------|
| Age 12 | .310                     | .286                     | .304            |
| Age 13 | .694                     | .700                     | .699            |
| Age 14 | 1.078                    | 1.113                    | 1.093           |
| Age 15 | 1.463                    | 1.527                    | 1.487           |
| Age 16 | 1.847                    | 1.940                    | 1.881           |

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assessed over 5 years in the true longitudinal model) to determine whether significant differences were apparent between the true longitudinal estimates and those from the cohort-sequential design. For this model, cross-group equality constraints across the cohorts were placed on latent means, latent variances, latent covariances, and residual errors. Model fitting procedures for the combined multiple-sample LGM specifying linear growth resulted in a chi-square test statistic value of  $\chi^2(37, N = 944) = 139.150, p < .001$ , and the following fit indices: NNFI = .936 and CFI = .876. The intercept and slope means and variances, and covariances for the combined model are shown in Table 6.2. Reproduced means for this model are shown in Table 6.3. EQS program specifications for the combined model are presented in Appendix 6.3.

LM tests were used to determine whether relaxing constraints between the true longitudinal design cohort and any of the other cohorts would significantly enhance model fit (see chap. 4 for more information regarding LM tests). Examination of the univariate and multivariate LM statistics between the cohort-sequential and the true longitudinal models revealed that no cross-group constraints would significantly enhance the model fit if released, a further indication of similarity in the accelerated and true longitudinal designs.

#### Example 6.2 Cohort-Sequential Unspecified Growth Models

Although the previous examples used specified linear growth functions, LGMs need not be so explicit. Neither the individual differences in growth curve parameters nor the form of the longitudinal curves has to be specified. Rather than using a model with fixed parameters, a two-factor unspecified model can be used, providing a developmental function that reflects an optimal pattern of growth in alcohol use. The freely estimated parameters represent the growth curve with maximal fit to the data (Meredith & Tisak, 1990). With enough time points to freely estimate factor loadings beyond the two required for identification of the model, the slope factor is interpreted as a general shape factor. If linear (i.e., straight line) growth models the data best, then the shape factor is called a slope factor. To test the adequacy of the hypothesized linear growth form and the possibility of nonlinear growth, alternative two-factor unspecified LGMs were performed.

Results of the model fitting procedures for the two-factor unspecified cohort-sequential and true longitudinal models,  $\chi^2(14, N = 729) = 36.967, p < .001$ , NNFI = .970, and CFI = .954, and  $\chi^2(7, N = 215) = 26.229, p < .001$ , NNFI = .916, and CFI = .941, respectively, indicated that the unspecified

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TABLE 6.4  
Parameter Estimates for the Unspecified Model

|                    | <i>Cohort-sequential</i> |                | <i>True Longitudinal</i> |               | <i>Combined</i> |                |
|--------------------|--------------------------|----------------|--------------------------|---------------|-----------------|----------------|
|                    | <i>Effect</i>            | <i>t Value</i> | <i>Effect</i>            | <i>Effect</i> | <i>Effect</i>   | <i>t Value</i> |
| Intercept mean     | .321                     | 7.785          | .357                     | 7.423         | .348            | 11.424         |
| Intercept variance | .265                     | 4.049          | .297                     | 6.770         | .285            | 8.904          |
| Slope mean         | .448                     | 9.650          | .191                     | 4.062         | .336            | 10.093         |
| Slope variance     | .059                     | 2.115          | .009                     | 1.881         | .030            | 3.826          |
| Correlation        | .201                     | .645           | .153                     | 1.187         | .195            | 1.693          |

*Note.* *t* values of 1.96 (two-tailed) and 1.65 (one-tailed) are significant at  $p < .05$ .

representation of growth was tenable. Intercept and slope means and variances, and correlations for these unspecified models are shown in Table 6.4.

Reproduced means for these unspecified models are shown in Table 6.5. For the cohort-sequential and true longitudinal models, basis terms (*Ls*) converged at values of .000, 1.000, 1.483, 2.562, 3.928, and .000, 1.000, 3.886, 5.837, and 9.446, respectively, suggesting some nonlinearity in the growth curve, especially for the true longitudinal data.

A combined multiple-sample analysis conducted with all four cohorts specifying cross-group equality constraints for latent means, latent variances, latent covariances, and residual errors resulted in an adequate model fit,  $\chi^2(34, N = 944) = 101.222, p < .001$ , NNFI = .954, and CFI = .919. For the combined multiple-sample model, the intercept and slope means and variances, and correlations, are shown in Table 6.4 and the reproduced means are shown in Table 6.5.

LM tests indicated that three constraints associated with the residual variance of alcohol use at ages 13 and 15, and the basis term of the third time point, would significantly improve the model fit if relaxed. When

TABLE 6.5  
Reproduced Means for the Unspecified Model

|        | <i>Cohort- sequential</i> | <i>True Longitudinal</i> | <i>Combined</i> |
|--------|---------------------------|--------------------------|-----------------|
| Age 12 | .321                      | .357                     | .348            |
| Age 13 | .769                      | .548                     | .683            |
| Age 14 | .985                      | 1.099                    | 1.130           |
| Age 15 | 1.469                     | 1.472                    | 1.478           |
| Age 16 | 2.082                     | 2.162                    | 2.136           |

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these constraints were relaxed, the model fit was  $\chi^2(31, N = 944) = 86.870, p < .001, NNFI = .959,$  and  $CFI = .932.$  Significantly more measurement error was associated with the cohort-sequential estimate of alcohol use at age 13 ( $E = .480$ ) than with the true longitudinal estimate of alcohol use at the same age ( $E = .340$ ). Significantly less error was associated with the cohort-sequential estimate of alcohol use at age 15 ( $E = .550$ ) compared to the true longitudinal estimate of alcohol use at the same age ( $E = .911$ ). Basis terms ( $L_s$ ) converged at values of .000, 1.000, 1.875, 3.368, 5.326, and .000, 1.000, 2.332, 3.368, and 5.326 for the cohort-sequential and true longitudinal models, respectively.

Despite the significantly smaller Time 3 basis term estimated for the cohort-sequential model ( $L = 1.875$ ) compared to the true longitudinal model ( $L = 2.332$ ), results suggested considerable similarity between the growth models in terms of model fit.

#### Summary

Although a true longitudinal design may be optimal, the benefits of a cohort-sequential design (Nesselrode & Baltes, 1979) are clear. This technique links segments consisting of limited longitudinal data on a specific age cohort with similar segments from other temporally related age cohorts to determine the existence of a common developmental trend, or growth curve. It has obvious benefits given the constraints of time and the cost of continual subject assessment in true longitudinal designs. However, concerns have been raised as to the viability of the accelerated longitudinal design (McArdle & Hamagami, 1991; Raudenbush & Chan, 1992, 1993; Tonry, Ohlin, & Farrington, 1991), foremost among them whether such a design can indeed approximate the true longitudinal curve.

Data presented here indicated similar developmental trends in alcohol use across the two designs for both the unspecified and linear growth models with virtually no estimates emerging as significantly different, thus lending support and validity to the use of an accelerated design. These analyses demonstrate the ability of the accelerated design to recover the true longitudinal curve, at least with self-reported adolescent alcohol use. Because the cohort-sequential approach has not been tested extensively, researchers using this technique have not yet determined the optimal number of time points per subject, the optimal number of points of overlap across adjacent cohorts, and the optimal number of subjects per cohort (Raudenbush & Chan, 1992). However, in order to reduce the likelihood of nonconvergence in fitting the cohort-sequential model, cohorts should overlap as much as possible, sample sizes within each cohort should be

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relatively large, and cohorts should be as comparable as possible (Tonry et al., 1991).

Despite the similarity in developmental trends found between the two designs in these data, it is important to acknowledge situations where growth in a behavior assessed within an accelerated longitudinal design versus a true longitudinal design might differ. Because the cross-sectional aspects of the accelerated design may not adequately reflect historical or other intervening processes, it is necessary to determine whether important information will be lost or if estimates of the underlying growth process will be biased in the absence of a true longitudinal design.

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#### Chapter 7 Testing Interaction Effects in LGMs

The present chapter discusses the strategy of modeling nonlinear interaction relations among latent factors with multiple indicators in the context of LGM. One recent methodological focus in the SEM literature is the modeling of interactions, and the extension and application of SEMs to situations with nonlinear relationships involving latent variables (Jaccard & Wan, 1996; Schumacker & Marcoulides, 1998). Several approaches have been proposed (see Schumacker & Marcoulides, 1998), each of which relies on the pioneering work of Kenny and Judd (1984). A recent article by Li, Harmer, T.E. Duncan, S.C. Duncan, Acock, and Boles (1998) provided a full explication and comparison of three such approaches to modeling interactions with static latent variables.

This chapter draws on the work of Kenny and Judd (1984), extending it to the analysis of more complex models with interactions among growth parameters. Of the approaches proposed for modeling interactions among latent variables, the procedure outlined by Jöreskog and Yang (1996) appears to be most relevant to LGMs having both first and second moments (i.e., means and variances).

In the following sections, the utility of Jöreskog and Yang's (1996) procedure is illustrated with LGMs testing hypotheses about how latent growth attributes interact over time to produce a joint effect on subsequent growth outcomes. Specifically, the LGMs presented in the previous chapters are extended to include an interaction effect between two latent growth, or shape, factors. Two models involving the interaction effect between growth factors are illustrated: a single-factor shape model (see chap. 2) and a two-factor level-shape model. The single-factor shape model represents an LGM in which individual differences in growth over time are modeled by a single dimension, a common factor approximating the observed growth curves. The two-factor level-shape model represents a growth model in which individual differences in initial status (level) and rate of change (shape) are approximated by curvilinear growth trajectories, explicitly modeled using an unspecified two-factor approach. Each model is specified with the parameterizations discussed by Jöreskog and Yang. Following the description of each model, an example using artificial data is provided.

Using the Kenny and Judd (1984) method, estimation of interaction effects involves specifying the indicators of a latent product term,  $XZ$  for example, by using all possible products of the indicators of the latent variables  $X$  and  $Z$ . Formulation of these product indicators requires software that accommodates nonlinear constraints, namely LISREL (Jöreskog & Sörbom, 1993), Mx (Neale, 1995), and SAS (SAS, 1990). EQS (Bentler & Wu, 1995), used throughout this book, has not implemented this feature (at least at the time this chapter was written), although some nonlinear restrictions can be handled by EQS through reparameterization (Wong & Long, 1987). Models illustrated in this chapter are parameterized within the LISREL SEM framework.

Example 7.1  
The Single-Factor Shape Model

The single-factor shape model represents a special case of a curve model (see chap. 2) and could be preferred over various multiple-factor (e.g., intercept-slope) models presented in previous chapters on the basis of parsimony because fewer factors are required. The model, however, operates on the assumption that the intercept is strictly proportional to the slope. The single-factor growth model is useful when the intercept factor can be eliminated (i.e., its mean and variance are zero) and only the interaction between the two latent slope parameters is of interest. A graphical representation of this single-factor model is presented in Fig. 7.1.

The model has two exogenous latent variables, symbolized by  $\xi_1$  and  $\xi_2$  in Fig. 7.1. These two factors, each measured by four repeated measures ( $X_1, X_2, X_3,$  and  $X_4$  for  $\xi_1$ , and  $X_5, X_6, X_7,$  and  $X_8$  for  $\xi_2$ , respectively), are nonproduct latent curve factors. The factor denoted by  $\xi_1\xi_2$  represents a latent product term of  $\xi_1$  and  $\xi_2$ , with its indicators formed by multiplying each indicator of  $\xi_1$  and  $\xi_2$ . Details on the formulation of these cross-product indicator terms are discussed in the following section. The model also includes a single-factor curve symbolized by  $\eta_1$ , which represents an endogenous latent growth variable, also measured by four repeated measures ( $Y_1, Y_2, Y_3,$  and  $Y_4$ ). The central focus here is the influence of the interaction between the two exogenous latent shape factors ( $\xi_1$  and  $\xi_2$ ) on the latent endogenous curve factor. The influence of factors  $\xi_1$  and  $\xi_2$  and their interaction  $\xi_1\xi_2$  on the endogenous latent growth factor,  $\eta_1$ , can be expressed by the nonlinear structural equation

$$\eta_1 = \alpha + \gamma_1\xi_1 + \gamma_2\xi_2 + \gamma_3\xi_1\xi_2 + \zeta, \tag{7.1}$$

where  $\alpha$  is the constant intercept term,  $\gamma_i$  is a regression coefficient, and  $\zeta$  is a disturbance term which is assumed to be independent of  $\xi_1$  and  $\xi_2$ .

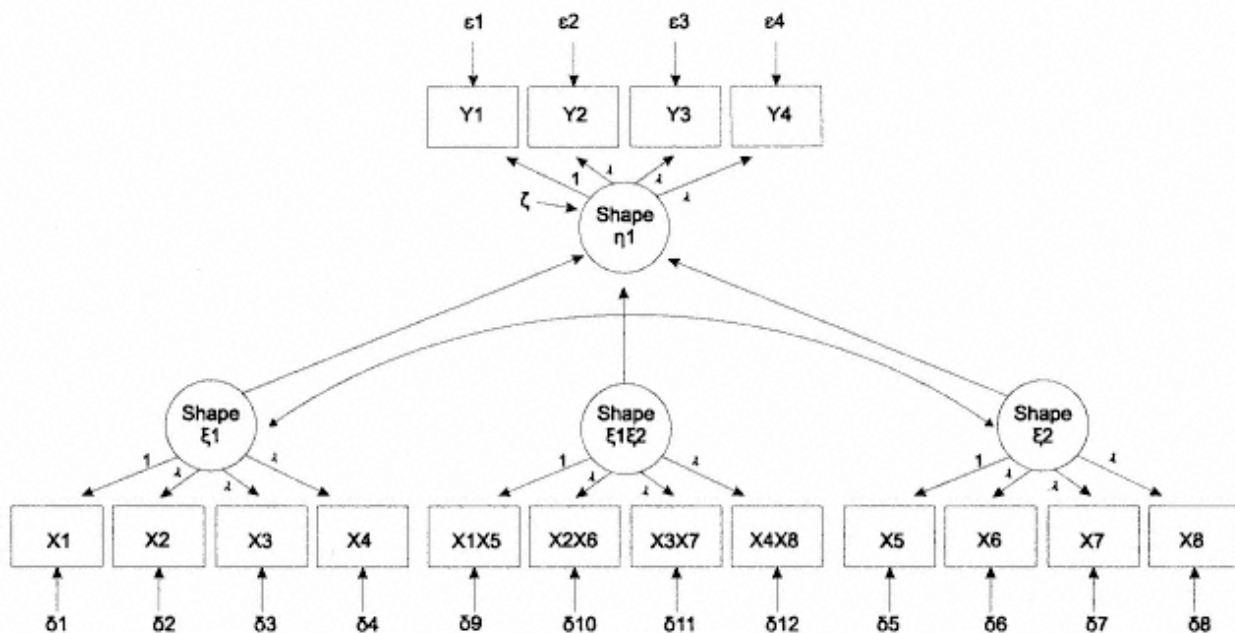


Fig. 7.1.  
Representation of the single-factor shape interaction LGM.

The following demonstrates how the cross-product indicators of the latent product variable  $\xi_1\xi_2$  are formulated. For ease of presentation, let  $a_i$  be  $X_1$ ,  $X_2$ ,  $X_3$ , and  $X_4$  for the latent factor  $\xi_1$ , and  $d_j$  be  $X_5$ ,  $X_6$ ,  $X_7$ , and  $X_8$  for the latent factor  $\xi_2$ . The measurement equation for the observed product indicators using the symbol  $a_i$  ( $i = 1, 2, 3$ , and 4) and  $d_j$  ( $j = 1, 2, 3$ , and 4) can be expressed as

$$\begin{aligned} a_i d_j &= (a_i)(d_j) = (\tau_i + \lambda_i \xi_1 + \delta_i) (\tau_j + \lambda_j \xi_2 + \delta_j) \\ &= \tau_i \tau_j + \tau_i \lambda_j \xi_2 + \tau_i \delta_j + \tau_j \lambda_i \xi_1 + \lambda_i \lambda_j \xi_1 \xi_2 \\ &\quad + \lambda_i \xi_1 \delta_j + \tau_j \delta_i + \lambda_j \xi_2 \delta_i + \delta_i \delta_j. \end{aligned} \quad 7.2$$

Applying the preceding equation to the four cross-product indicators ( $X_1X_5$ ,  $X_2X_6$ ,  $X_3X_7$ , and  $X_4X_8$ ) of  $\xi_1\xi_2$  in the model of Fig. 7.1, the following measurement equations are obtained (note that  $\lambda_1\xi_1 = \lambda_2\xi_2 = 1$  for scaling purposes):

$$\begin{aligned} X_1X_5 &= (\tau_1 + \xi_1 + \delta_1) (\tau_5 + \xi_2 + \delta_5) \\ &= \tau_1\tau_5 + \tau_1\xi_2 + \tau_5\xi_1 + \xi_1\xi_2 + \delta_9, \end{aligned} \quad 7.3$$

$$\text{where } \delta_9 = \tau_1\delta_5 + \tau_5\delta_1 + \xi_1\delta_5 + \xi_2\delta_1 + \delta_1\delta_5,$$

$$\begin{aligned} X_2X_6 &= (\tau_2 + \lambda_{21}\xi_1 + \delta_2) (\tau_6 + \lambda_{62}\xi_2 + \delta_6) \\ &= \tau_2\tau_6 + \tau_2\lambda_{62}\xi_2 + \tau_6\lambda_{21}\xi_1 + \lambda_{21}\lambda_{62}\xi_1\xi_2 + \delta_{10}, \end{aligned} \quad 7.4$$

$$\text{where } \delta_{10} = \tau_2\delta_6 + \tau_6\delta_2 + \lambda_{21}\xi_1\delta_6 + \lambda_{62}\xi_2\delta_2 + \delta_2\delta_6,$$

$$\begin{aligned} X_3X_7 &= (\tau_3 + \lambda_{31}\xi_1 + \delta_3) (\tau_7 + \lambda_{72}\xi_2 + \delta_7) \\ &= \tau_3\tau_7 + \tau_3\lambda_{72}\xi_2 + \tau_7\lambda_{31}\xi_1 + \lambda_{31}\lambda_{72}\xi_1\xi_2 + \delta_{11}, \end{aligned} \quad 7.5$$

$$\text{where } \delta_{11} = \tau_3\delta_7 + \tau_7\delta_3 + \lambda_{31}\xi_1\delta_7 + \lambda_{72}\xi_2\delta_3 + \delta_3\delta_7, \text{ and}$$

$$\begin{aligned} X_4X_8 &= (\tau_4 + \xi_1 + \delta_4) (\tau_8 + \xi_2 + \delta_8) \\ &= \tau_4\tau_8 + \tau_4\lambda_{82}\xi_2 + \tau_8\lambda_{41}\xi_1 + \lambda_{41}\lambda_{82}\xi_1\xi_2 + \delta_{12}, \end{aligned} \quad 7.6$$

$$\text{where } \delta_{12} = \tau_4\delta_8 + \tau_8\delta_4 + \lambda_{41}\xi_1\delta_8 + \lambda_{82}\xi_2\delta_4 + \delta_4\delta_8.$$

The terms of these measurement equations are then substituted into their corresponding LISREL  $\Lambda$  (factor loading) and  $\Theta$  (measurement error) matrices. The measurement model for exogenous dimensions of latent predictor variables is  $X = \tau x + \Lambda x \xi + \delta$ , or in matrix form

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$$\begin{pmatrix} X_1 \\ X_2 \\ X_3 \\ X_4 \\ X_5 \\ X_6 \\ X_7 \\ X_8 \\ X_1X_5 \\ X_2X_6 \\ X_3X_7 \\ X_4X_8 \end{pmatrix} = \begin{pmatrix} \tau_1 \\ \tau_2 \\ \tau_3 \\ \tau_4 \\ \tau_5 \\ \tau_6 \\ \tau_7 \\ \tau_8 \\ \tau_1\tau_5 \\ \tau_2\tau_6 \\ \tau_3\tau_7 \\ \tau_4\tau_8 \end{pmatrix} + \begin{pmatrix} 1 & 0 & 0 \\ \lambda_{21} & 0 & 0 \\ \lambda_{31} & 0 & 0 \\ \lambda_{41} & 0 & 0 \\ 0 & 1 & 0 \\ 0 & \lambda_{62} & 0 \\ 0 & \lambda_{72} & 0 \\ 0 & \lambda_{82} & 0 \\ \tau_5 & \tau_1 & 1 \\ \tau_6\lambda_{21} & \tau_2\lambda_{62} & \lambda_{21}\lambda_{62} \\ \tau_7\lambda_{31} & \tau_3\lambda_{72} & \lambda_{31}\lambda_{72} \\ \tau_8\lambda_{41} & \tau_4\lambda_{82} & \lambda_{41}\lambda_{82} \end{pmatrix} \begin{pmatrix} \xi_1 \\ \xi_2 \\ \xi_1\xi_2 \end{pmatrix} + \begin{pmatrix} \delta_1 \\ \delta_2 \\ \delta_3 \\ \delta_4 \\ \delta_5 \\ \delta_6 \\ \delta_7 \\ \delta_8 \\ \delta_9 \\ \delta_{10} \\ \delta_{11} \\ \delta_{12} \end{pmatrix}. \quad 7.7$$

The parameter vector of  $\kappa$  (exogenous latent variable means) and the parameter matrix of  $\Phi$  (covariances among exogenous latent variables) are



$$\theta_9 = \tau_1^2\theta_5 + \tau_5^2\theta_1 + \phi_{11\theta_5} + \phi_{22\theta_1} + \theta_{1\theta_5}, \quad 7.18$$

$$\theta_{10} = \tau_2^2\theta_6 + \tau_6^2\theta_2 + \lambda_{21}^2\phi_{11\theta_6} + \lambda_{62}^2\phi_{22\theta_2} + \theta_{2\theta_6}, \quad 7.19$$

$$\theta_{11} = \tau_3^2\theta_7 + \tau_7^2\theta_3 + \lambda_{31}^2\phi_{11\theta_7} + \lambda_{72}^2\phi_{22\theta_3} + \theta_{3\theta_7}, \text{ and} \quad 7.20$$

$$\theta_{12} = \tau_4^2\theta_8 + \tau_8^2\theta_4 + \lambda_{41}^2\phi_{11\theta_8} + \lambda_{82}^2\phi_{22\theta_4} + \theta_{4\theta_8}. \quad 7.21$$

Based on the assumption that data are multivariately normally distributed, the model can be estimated using maximum likelihood estimation. Refer to Jöreskog and Yang (1996) and Yang (1997) for alternative estimation methods (e.g., weighted least squares, weighted least squares based on the augmented moment matrix) when data are non-normally distributed.

Data were generated to illustrate the LGM model presented in Fig. 7.1, which contains one endogenous and two exogenous latent growth variables, each measured four times at equal intervals. The sample size was set at  $N = 250$ . Cross-product indicators defining the latent interaction variable ( $\xi_1\xi_2$ ) were formed using the indicators of  $\xi_1$  and  $\xi_2$ , as shown in Fig. 7.1.

The simulated data were estimated using the maximum likelihood estimation procedure. The model produced the following fit indices:  $\chi^2(110, N = 250) = 405.09$ ,  $p < .001$ , NNFI = .94, CFI = .95, and RMSEA = .10. The maximum likelihood estimates for the two direct effects of  $\xi_1$  and  $\xi_2$ , their interactive effect of  $\xi_1\xi_2$ , and  $t$  estimates for equation 7.1 are presented in Table 7.1.

Results indicated a significant ( $p < .05$ ) interaction effect for the estimate of  $\gamma_3$  in equation 7.1.

The population covariance matrix for the model of Fig. 7.1 and the LISREL program used for this example can be found in Appendix 7.1.

TABLE 7.1  
Estimates of Main and Interaction Effects

| Parameter    | Effect | SE  | t Value |
|--------------|--------|-----|---------|
| $\xi_1$      | -.10   | .08 | -1.29   |
| $\xi_2$      | .34    | .05 | -6.42   |
| $\xi_1\xi_2$ | .19    | .09 | 2.17    |

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### Example 7.2 The Two-Factor Level-Shape Model

This model shown in Fig. 7.2 is an extension of the model of Fig. 7.1 in that it contains a level as well as a shape factor. The product variable can be formed using the corresponding occasions of measurement of the two latent growth (shape) factors. In this illustration, repeated measures ( $X_1, X_2, X_3$ , and  $X_4$  for the shape factor of  $\xi_2$ , and  $X_5, X_6, X_7$ , and  $X_8$  for the shape factor of  $\xi_4$ ) are selected from the second time point measure and subsequent time points to form observed product indicators (i.e.,  $X_2X_6, X_3X_7$ , and  $X_4X_8$ ), as shown in Fig. 7.2. The LISREL specification for the  $\gamma$  measurement model is  $\gamma = \Lambda\eta + \epsilon$ , or in matrix form

$$\begin{pmatrix} Y_1 \\ Y_2 \\ Y_3 \\ Y_4 \end{pmatrix} = \begin{pmatrix} 1 & t_1 \\ 1 & t_2 \\ 1 & t_3 \\ 1 & t_4 \end{pmatrix} \begin{pmatrix} \eta_1 \\ \eta_2 \end{pmatrix} + \begin{pmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \\ \epsilon_4 \end{pmatrix}, \quad 7.22$$

where factor loadings for  $t_1$  and  $t_2$  are constrained to 0 and 1 for model identification purposes, and  $t_3$  and  $t_4$  are set to be freely estimated ( $\lambda_{32}$  and  $\lambda_{42}$  for  $\eta_2$ ) for the shape factor. This describes an unspecified linear spline model (Meredith & Tisak, 1990) where freely estimating factor loadings at  $t_3$  and  $t_4$  approximate curvilinear growth curves by a linear spline technique (a curve with distinct linear segments). The LISREL specification for the  $X$  measurement model has the form  $X = \tau x + \Lambda x \xi + \delta$ , or in matrix form

$$\begin{pmatrix} X1 \\ X2 \\ X3 \\ X4 \\ X5 \\ X6 \\ X7 \\ X8 \\ X2X6 \\ X3X7 \\ X4X8 \end{pmatrix} = \begin{pmatrix} \tau1 \\ \tau2 \\ \tau3 \\ \tau4 \\ \tau5 \\ \tau6 \\ \tau7 \\ \tau8 \\ \tau2\tau6 \\ \tau3\tau7 \\ \tau4\tau8 \end{pmatrix} + \begin{pmatrix} 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & \lambda32 & 0 & 0 & 0 \\ 1 & \lambda42 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 1 & \lambda74 & 0 \\ 0 & 0 & 1 & \lambda84 & 0 \\ 0 & \tau6 & 0 & \tau2 & 1 \\ 0 & \tau7\lambda32 & 0 & \tau3\lambda74 & \lambda32\lambda74 \\ 0 & \tau8\lambda42 & 0 & \tau4\lambda84 & \lambda42\lambda84 \end{pmatrix} \begin{pmatrix} \xi1 \\ \xi2 \\ \xi3 \\ \xi4 \\ \xi2\xi4 \end{pmatrix} + \begin{pmatrix} \delta1 \\ \delta2 \\ \delta3 \\ \delta4 \\ \delta5 \\ \delta6 \\ \delta7 \\ \delta8 \\ \delta9 \\ \delta10 \\ \delta11 \end{pmatrix} \quad 7.23$$

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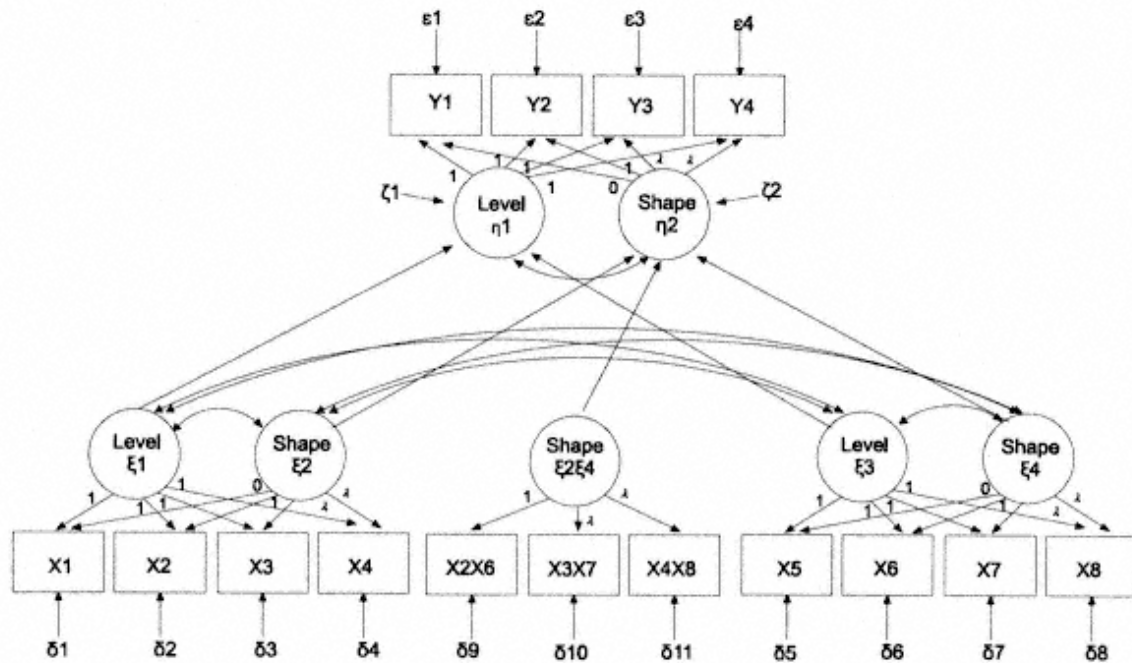


Fig. 7.2.  
Representation of the two-factor level-shape interaction LGM.

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The exogenous latent mean vector ( $\kappa$ ) and covariance matrix ( $\Phi$ ) of  $\xi$ s ( $\xi1, \xi2, \xi3, \xi4$ , and  $\xi2 \xi4$ ) are

$$\kappa = \begin{pmatrix} 0 \\ \kappa2 \\ 0 \\ \kappa4 \\ \phi42 \end{pmatrix}, \quad \Phi = \begin{pmatrix} \phi11 & & & & \\ \phi21 & \phi22 & & & \\ \phi31 & \phi32 & \phi33 & & \\ \phi41 & \phi42 & \phi43 & \phi44 & \\ 0 & 0 & 0 & 0 & \phi22\phi44 + \phi42^2 \end{pmatrix} \quad 7.24$$

The variance/covariance matrix of errors of measurement,  $\Theta\delta$ , is

$$\begin{pmatrix} \theta 1 \\ 0 & \theta 2 \\ 0 & 0 & \theta 3 \\ 0 & 0 & 0 & \theta 4 \\ 0 & 0 & 0 & 0 & \theta 5 \\ 0 & 0 & 0 & 0 & 0 & \theta 6 \\ 0 & 0 & 0 & 0 & 0 & 0 & \theta 7 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \theta 8 \\ 0 & \theta 9,2 & 0 & 0 & 0 & \theta 9,6 & 0 & 0 & \theta 9 \\ 0 & 0 & \theta 10,3 & 0 & 0 & 0 & 0 & \theta 10,7 & 0 & \theta 10 \\ 0 & 0 & 0 & \theta 11,4 & 0 & 0 & 0 & 0 & \theta 11,8 & 0 & \theta 11 \end{pmatrix} \cdot 7.25$$

where the error terms for the variances ( $\theta 1$  through  $\theta 11$ ) and the error terms for the covariances ( $\theta 9,2$ ,  $\theta 9,6$ ,  $\theta 10,3$ ,  $\theta 10,7$ ,  $\theta 11,4$ , and  $\theta 11,8$ ) are formulated as before.

The model of Fig. 7.2 was estimated using the same simulated data set as in the previous example. The first model tested consisted of all five exogenous latent variables, including the two intercept factors predicting the shape of the endogenous latent variable (see Fig. 7.2). However, the model failed to converge and, therefore, was rejected. The path from the two intercept factors to the endogenous slope factor was removed and the model re-estimated. The respecified model converged successfully without out-of-bounds parameter estimates (e.g., negative variances or correlations greater than 1). Results of the model fitting procedures,  $\chi^2(88, N = 250) = 358.63$ ,  $p < .001$ , NNFI = .93, CFI = .94, and RMSEA = .11, suggested a

TABLE 7.2  
Estimates of Main and Interaction Effects

| Parameter    | Effect | SE   | t Value |
|--------------|--------|------|---------|
| $\xi 1$      | -6.97  | 1.97 | -3.51   |
| $\xi 2$      | .15    | .07  | 2.10    |
| $\xi 3$      | -5.40  | 1.50 | -3.59   |
| $\xi 4$      | -.09   | .03  | -3.34   |
| $\xi 2\xi 4$ | .17    | .04  | 4.64    |

reasonable fit. The maximum likelihood estimates for the  $\xi$ s on both the level and shape factors ( $\eta 1$  and  $\eta 2$ ) shown in Fig. 7.2 are presented in Table 7.2.

Standard errors were high for the two intercept factors. This is likely due to the fact that the two factors are highly correlated,  $\phi_{31} = -.994$  ( $[\text{cov}(\xi 3, \xi 1) \div (\text{Var}(\xi 1) \times \text{Var}(\xi 3))^{1/2}] = [-.051 \div (.036 \times .073)^{1/2}]$ ). With this degree of collinearity, the standard errors of the estimates tend to become unstable. The interaction effect ( $\xi 2\xi 4$ ) was a statistically significant predictor, as indicated by the  $t$  value of 4.64. The LISREL program used for this example can be found in Appendix 7.2.

### Summary

This chapter presented examples of LGMs involving interaction effects. The method presented here is an extension of conventional nonlinear SEMs to LGMs where the primary focus is on modeling interactions between latent growth (shape) parameters. Using Jöreskog and Yang's (1996) method for modeling nonlinear interactions among latent variables, model specifications for testing interaction effects with LGMs were presented within the LISREL framework.

As shown in the preceding sections, interaction effects can be estimated by defining a measurement model for the latent product term. The cross-product indicators on the latent product variable are derived by multiplying together the measurement equations describing the relationships between the observed indicators and the latent nonproduct variables of  $X$  and  $Z$  (Jöreskog & Yang, 1996). Assuming multivariate normality of the data, models can be estimated through a maximum likelihood fitting function. In the presence of nonnormality, other functions may be used (see Jöreskog & Yang; Yang, 1997).

Two models, the single-factor shape model and the two-factor level-shape model, that included interactions between latent growth factors were illustrated with simulated data. The two-factor growth curve model is more



complex in terms of model specification, and its estimation involves latent intercepts of growth parameters that complicate model estimation. The restriction imposed on the nonproduct latent variable means was relaxed in the two-factor growth curve model to allow for model convergence. Standard SEMs that include interactions assume that all nonproduct latent variables have means of zero (Jöreskog & Yang, 1996; Kenny & Judd, 1984). However, in the context of LGMs where latent means are an important component of the growth parameters, forcing means to be zero may complicate parameter estimation.

In practice, the choice between the two-factor and single-factor curve models depends on substantive theory and empirical data. If parsimony is a consideration, given the reasonable assumption that the intercept factor can be eliminated or is strictly proportional to the slope, the predictive model with fewer parameters is preferred. On the other hand, the two-factor LGM allows for analyses that include interactions among growth parameters while taking initial status into account. The two-factor model, therefore, unlike the single-factor curve model, permits an unambiguous interpretation of the interaction effect on its outcome.

The use of interaction terms among latent variables directly parallels traditional multiple regression interaction procedures and shares the same limitations. The most fundamental limitation is that the technique requires careful model parameterization, as pointed out by a number of authors (e.g., Jaccard & Wan, 1996; Jöreskog & Yang, 1996). Mistakes can easily be made, the consequences of which may be worse than ignoring the interaction effect altogether. When possible, results should be compared with those from simpler alternatives.

Although there has been an increasing application of LGMs in the social sciences, LGMs with interactions representing different models of change have been conspicuously absent despite their promise for testing complex hypotheses in both cross-sectional and longitudinal studies. The method presented here can be a useful tool for detecting whether interactions between interindividual growth parameters improve prediction of static and time-varying behavioral outcomes.

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## Chapter 8 Missing Data Models

Despite the best intentions, few longitudinal studies are completed without the loss of subjects over time or the collection of incomplete data. Longitudinal data sets typically suffer from attrition and other forms of missing data. Attrition, omissions, and planned missingness have limited the ability of researchers to conduct the most appropriate analyses. Standard analyses of incomplete data assume that the data are missing completely at random (MCAR), although in many studies this assumption is highly questionable. Such analyses, generally involving the use of listwise deletion, take advantage of the balanced nature of the resulting data set to simplify computations. Although these procedures are practical, they are problematic in that they do not produce the best possible estimates, they discard a substantial amount of potentially useful data, and, when the assumption that the data are MCAR is not tenable, they display large sample bias (Muthén et al., 1987). Fortunately, a broad class of procedures now exists for virtually every missing data problem, and many of these solutions are finding their way into the mainstream of behavioral research. This chapter presents and compares the use of model-based procedures for analyses of incomplete longitudinal data (e.g., data missing through subject attrition in a true longitudinal design).

### A Taxonomy of Methods for Partial Missingness

The literature on the analysis of partially missing data is comparatively recent. Little and Rubin (1989) grouped these methods into the following not mutually exclusive categories: procedures for completely recorded units, weighting procedures, imputation-based procedures, and model-based approaches.

*Procedures for Completely Recorded Units.* Some methods of analysis are only intended for use with complete cases. When some variables are missing for some of the units, a simple expedient is to discard incompletely recorded units and analyze only units with complete data. Although this strategy is easy and may be satisfactory with small amounts of missing data, it can lead to serious biases and is inefficient.

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*Weighting Procedures.* Randomization inferences from sample survey data without nonresponse are commonly based on design weights that are inversely proportional to the probability of selection. Weighting is related to mean substitution. For example, weighting responding units by the proportion responding in each subclass, and substituting the subclass mean for missing units in each subclass, leads to the same estimates of population means, although not the same estimates of sampling variance unless adjustments are made to the data with imputed means.

*Imputation-Based Procedures.* Here, missing values are replaced with imputed values and the resultant complete data set is analyzed by standard methods. Commonly used imputation procedures include hot deck imputation, mean substitution, and regression imputation. To ensure valid inferences, standard analyses must be modified to account for the differing status of the real and imputed values.

*Model-Based Approaches.* These approaches define a model for the partially missing data, with parameters estimated by procedures such as maximum likelihood. Through the use of maximum likelihood estimation procedures, SEM programs can provide estimates of the missing data via multiple imputation; the imputations are repetitions of parameter estimates under a particular model of nonresponse (Rubin, 1987). Multiple imputation rectifies the disadvantages of single imputation techniques in that the resulting analyses support inferences that validly reflect sampling variability due to missing values.

### A Taxonomy of Missingness

Understanding the mechanisms that lead to missing values is key to choosing an appropriate analysis and interpreting the results. Data missing by *omissions* occur when a subject fails to complete an item within a survey, or fails to complete a survey. Generally, this type of missingness is little more than a nuisance. Another common occurrence in longitudinal studies is that some subjects drop out and are not remeasured. This kind of missingness, *attrition*, is a potential problem. When later waves of data are absent, it is possible that the scores on the missing variables are themselves the cause of missingness. A third kind of missingness is *planned missingness* (e.g., cohort-sequential design). Because this form of missingness is controllable, the data can be considered MCAR. Beyond some loss of statistical power, this type of missingness poses minimal threats to statistical conclusions.

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To illustrate the concept of missingness, consider a simple bivariate sample with variables  $X$  and  $Y$ , where only one variable,  $Y$ , is subject to missingness. Here, the missing-data mechanism is considered "ignorable" (Rubin, 1976) and the missing values are MCAR if the pattern of nonresponse on  $Y$  is independent of both  $X$  and  $Y$ . Therefore, the missing data are missing at random (MAR) and the observed data are observed at random (OAR). If the pattern of missingness is completely random, then the two subsamples can be regarded as distinct random samples from the same population. Therefore, all corresponding parameters should be equal and analyses based on complete data will be unbiased, despite the fact that they do not make full use of the available data (Little & Rubin, 1989).

If the data are not MCAR, it may be possible to proceed under a much less restrictive assumption that the missing data mechanism is ignorable (Rubin, 1976). When missingness depends on the values of a variable for which there is no missingness,  $X$  (rather than systematically related to the unobserved level of the missing variable,  $Y$ ), the missing data are called MAR, and the values of  $Y$  comprise a random sample of the sampled values defined by the values of  $X$ . If, however, the missingness depends on the value of the missing variable,  $Y$ , then the missing data mechanism is nonignorable, the data are neither MCAR nor MAR, and analyses based on any reduced sample (i.e., complete-case analyses) are subject to bias.

The model depicted in Fig. 8.1 represents an LGM with data collected over five yearly assessments. Data for the model examples were from the NYS (Elliott, 1976). The data set consisted of different patterns representing various stages of completeness. Compared with the combined sample of 240, the data in Group 1 ( $N = 215$ ; 108 males and 107 females) represented the complete data available for analysis. The data available for subsequent groups supplied various patterns of missingness, the result of attrition following the second (Group 2,  $N = 8$ ), third (Group 3,  $N = 6$ ), and fourth assessments (Group 4,  $N = 11$ ). Missing values constituted 10.4% of the data collected for the true longitudinal design.

#### Model-Based Approaches to Analyses with Partial Missingness

*Multiple-Group Analyses.* SEM methodology is often applied in situations where data are missing on specific variables. Although missing data theory provides viable alternatives to listwise deletion (see Anderson, 1957; Little & Rubin, 1987), they have not generally been applied in SEM practice. Muthén et al. (1987), however, have extended the use of latent

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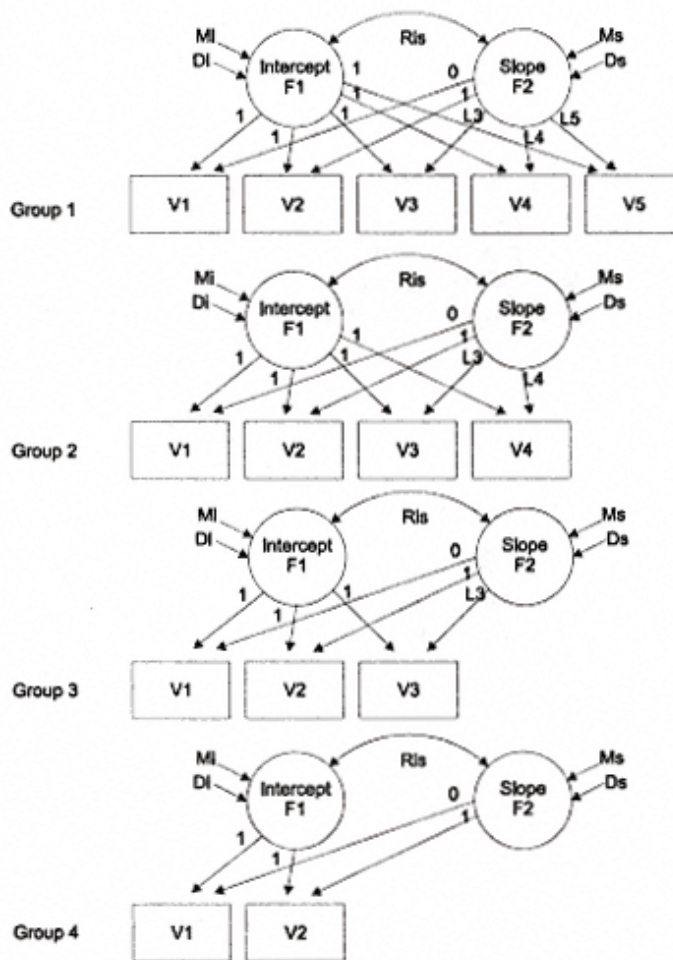


Fig. 8.1.  
Representation of the missing data LGM.

variable SEMs to include missingness. These researchers demonstrated that correct maximum likelihood (ML) estimation with missing data can be obtained under mildly restrictive assumptions concerning the missing data mechanism (Rubin, 1976). In many cases, model estimation with distinct missing data patterns can be carried out with existing SEM software which allows for the simultaneous analysis of multiple groups. Through the use of ML procedures, estimates of the missing data are provided under a particular model of nonresponse (Rubin, 1987).

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Briefly, the strategy for handling missing data consists of expanding the usual SEM to include means, or regression intercepts, and partitioning the sample into subgroups with distinct missing data patterns. Equality constraints across the various groups representing distinct patterns of missingness are used in a multiple-sample analysis to obtain unbiased and consistent estimates. These equality constraints are not of substantive interest, but, because the model is assumed to be invariant across groups, function solely to insure correct estimation of model parameters. To permit an appropriate large-sample chi-square test of model fit, one need only obtain the likelihood value for both restricted  $H0$  and unrestricted  $H1$  model hypotheses.

Under the unrestricted  $H1$  hypothesis, the parameters of interest are the variances, covariances, and means of the observed variables. The  $H1$  hypothesis involves the test of equality of the moment matrices reflecting the cross-group equality constraints for common parameters. The unrestricted, or saturated,  $H1$  model also tests whether the data are MCAR.

The restricted  $H0$  model (i.e., the hypothesized model of interest, which is assumed to be invariant across groups) imposes equality restrictions across the groups representing various missing data patterns for common parameters. Parameters are regression coefficients, variances, and covariances of the independent variables, and regression intercepts, or means, of the dependent variables.

Under the assumption of an ignorable response mechanism and MAR, the difference in chi-square values for the two analyses,  $H0$  versus  $H1$ , gives a correct test of the hypothesized model. The difference in degrees of freedom for the two analyses gives the correct degrees of freedom for testing  $H0$  against  $H1$ . The same degrees of freedom would be used in corresponding "complete-case" analyses which specify no missing data. If the test of  $H0$  against  $H1$  does not lead to rejection, and the missing data mechanism is ignorable (i.e., the data are MAR), correct ML estimates are obtained. However, even when MAR does not hold, the multiple-sample procedure is likely to reduce biases inherent in alternative (e.g., complete-case analyses using listwise deletion) estimation strategies (Muthén et al., 1987). Readers are referred to Allison and Hauser (1991), S.C. Duncan and T.E. Duncan (1994), Muthén et al., (1987) and Rubin (1976) for a more complete discussion and references on the issues surrounding the model-based approach to the analysis of missing data.

The following section illustrates model-based procedures for analyses of incomplete longitudinal data on adolescent alcohol consumption.

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#### Example 8.1 Multiple-Group Analyses Incorporating Missing Data

Because the multiple-group SEM procedure requires each missing data pattern to have more subjects than variables to yield positive definite matrices, small subgroup samples are often problematic. Each group in the model depicted in Fig. 8.1 has more subjects than variables, but the small sample size in Group 2 produced a singular matrix for this subgroup. The singular matrix results from identical values for the Time 1 and Time 2 measures. To include this group in the analyses, the Time 1 measure was eliminated to resolve the singularity problem.

Under the unrestricted  $H1$  hypothesis, the model fit indices were  $\chi^2(23, N = 240) = 27.502, p < .235, NNFI = .990,$  and  $CFI = .986$ . Input statements for the  $H1$  model using EQS are presented in Appendix 8.1. Despite the relatively large sample size, MCAR can not be rejected for these four subsamples. Note that even if the data are found to be MCAR, a suitable measurement model may not exist.

For the test of the restricted  $H0$  model, model fitting procedures yielded the following fit indices:  $\chi^2(30, N = 240) = 52.153, p < .007, NNFI = .962,$  and  $CFI = .933$ . Parameter estimates and standard errors for the multiple-sample estimation for the model are presented in Table 8.1.

Input statements for the  $H0$  model using EQS are presented in Appendix 8.2.

TABLE 8.1  
Parameter Estimates for the Multiple-Group Analyses

| <i>Parameter</i> | <i>Effect</i> | <i>SE</i> |
|------------------|---------------|-----------|
| E1, E1           | .209          | .036      |
| E2, E2           | .348          | .041      |
| E3, E3           | .679          | .075      |
| E4, E4           | .654          | .080      |
| E5, E5           | .863          | .142      |
| D1, D1           | .290          | .043      |
| D2, D2           | .010          | .005      |
| D1, D2           | .008          | .007      |
| V3, F2           | 4.099         | .893      |
| V4, F2           | 5.511         | 1.205     |
| V5, F2           | 8.870         | 1.969     |

|                |      |      |
|----------------|------|------|
| Mean intercept | .346 | .046 |
| Mean slope     | .203 | .047 |

The difference in chi-square values and degrees of freedom for the two analyses gives a correct test of  $H_0$  against  $H_1$ ,  $\chi^2(7, N = 240) = 24.651, p < .001$ , and fit indices of NNFI = .977 and CFI = .932. Assuming that the model is correct, and that this test of  $H_0$  against  $H_1$  is not rejected (based on the NNFI and CFI), the ML estimates are not expected to exhibit large sample bias, as long as the nonresponse mechanism is ignorable.

Example 8.2  
Extensions of the Multiple-Group Approach

Two SEM programs, Mx (Neale, 1995) and Amos (Arbuckle, 1995), currently allow estimation with the ML function at the individual level. These SEM programs offer an approach to the analysis of partially missing data that is similar to the multiple-group method described earlier, but they calculate the log likelihood of the data for each observation (raw maximum likelihood estimation). These programs thus allow missing data estimation of parameters without resorting to multiple-group analyses.

The raw ML procedure, especially as implemented in Amos (Arbuckle, 1995), appears to be a viable approach to solving missing data problems with continuous data. Perhaps the most important advantage of the raw ML approach is that it provides reasonable estimates of standard errors with missing data.

In an analysis involving missing data, the raw ML approach does not produce a chi-square statistic for testing goodness of fit. Instead, it generates a "function of log likelihood." In general, the better a model fits the data, the smaller this statistic will be. Unfortunately, this statistic has no absolute standard by which to judge whether the fit of the model is acceptable. However, it is possible to make a comparison between the value of the function of log likelihood between the restricted  $H_0$  and unrestricted  $H_1$  model hypotheses. The difference between the  $H_0$  and  $H_1$  model log likelihood functions is an observation on a chi-square random variable with degrees of freedom equal to the difference between the number of parameters estimated in the  $H_0$  and  $H_1$  models.

Using incomplete longitudinal data on adolescent alcohol use, the model depicted in Fig. 8.1 was re-estimated using the raw ML method implemented in Amos that approximates the multiple-group analysis presented in the previous section. Under the unrestricted  $H_1$  hypothesis the function of log likelihood was 1008.973 with 20 distinct parameters estimated. Input statements for the  $H_1$  model using Amos are presented in Input 8.1.

INPUT 8.1  
Amos Specifications for the  $H_1$  Model

```
! MISSING DATA ANALYSES UNDER THE H1 HYPOTHESIS
$STRUCTURE
V1 = ( ) + (1) EPS1
V2 = ( ) + (1) EPS2
V3 = ( ) + (1) EPS3
V4 = ( ) + (1) EPS4
V5 = ( ) + (1) EPS5
EPS1 <-> EPS2
EPS1 <-> EPS3
EPS1 <-> EPS4
EPS1 <-> EPS5
EPS2 <-> EPS3
EPS2 <-> EPS4
EPS2 <-> EPS5
EPS3 <-> EPS4
EPS3 <-> EPS5
EPS4 <-> EPS5
$INPUT VARIABLES
V1
V2
V3
V4
V5
$SAMPLE SIZE =240
$MISSING=99
$RAW DATA
```

For the  $H_0$  hypothesis, the function of log likelihood was 1034.484 with 13 distinct parameters estimated. Input statements for the  $H_0$  model using Amos are presented in Input 8.2.

The difference in log likelihood functions and parameters estimated for the two analyses gives a correct test of  $H_0$  against  $H_1$ ,  $\chi^2(17, N = 240) = 25.511, p < .001$ .

INPUT 8.2  
Amos Specifications for the  $H_0$  Model

```

! MISSING DATA ANALYSES H0 HYPOTHESIS
$STRUCTURE
V1 = (1) F1 + (0) F2 + (1) EPS1
V2 = (1) F1 + (1) F2 + (1) EPS2
V3 = (1) F1 + (L3) F2 + (1) EPS3
V4 = (1) F1 + (L4) F2 + (1) EPS4
V5 = (1) F1 + (L5) F2 + (1) EPS5
F1 = (M1) + (1) ZETA1
F2 = (M2) + (1) ZETA2
ZETA1 <--> ZETA2
$INPUT VARIABLES
V1
V2
V3
V4
V5
$SAMPLE SIZE =240
$MISSING=99
$RAW DATA

```

INPUT 8.3  
Amos Specifications for the *H2* Model

```

! MISSING DATA ANALYSES UNDER THE H2 HYPOTHESIS
$STRUCTURE
V1 = ( ) + (1) EPS1
V2 = ( ) + (1) EPS2
V3 = ( ) + (1) EPS3
V4 = ( ) + (1) EPS4
V5 = ( ) + (1) EPS5
$INPUT VARIABLES
V1
V2
V3
V4
V5
$SAMPLE SIZE =240
$MISSING=99
$RAW DATA

```

One other raw ML model, an independence or null model, referred to as *H2*, was estimated to produce a function of log likelihood value which could be used to generate a chi-square random variable with degrees of freedom equal to the difference between the number of parameters estimated under the *H2* and *H1* models, reflecting the chi-square fit of the null or independence model. The parameters of the *H2* model are those of the variances of the independent variables and the regression intercepts, or means, of the dependent variables.

Under the *H2* hypothesis, the function of log likelihood was 1356.153 with 10 distinct parameters estimated. Input statements for the *H2* model using Amos are presented in Input 8.3. Parameter estimates and standard errors for the raw ML estimation are presented in Table 8.2.

TABLE 8.2  
Parameter Estimates for the Raw ML Approach to Missing Data

| <i>Parameter</i> | <i>Effect</i> | <i>SE</i> |
|------------------|---------------|-----------|
| EPS1             | .186          | .033      |
| EPS2             | .332          | .038      |
| EPS3             | .662          | .073      |
| EPS4             | .656          | .080      |
| EPS5             | .849          | .141      |
| V3 <-- F2 (L3)   | 4.166         | .893      |
| V4 <-- F2 (L4)   | 5.633         | 1.210     |
| V5 <-- F2 (L5)   | 9.078         | 1.974     |
| ZETA1            | .292          | .041      |
| ZETA2            | .010          | .005      |

|                     |      |      |
|---------------------|------|------|
| ZETA1 <--> ZETA2    | .006 | .007 |
| Mean intercept (M1) | .352 | .044 |
| Mean slope (M2)     | .198 | .045 |

The difference in log likelihood functions and parameters estimated for the *H1* and *H2* analyses gives a test of the null model,  $\chi^2(10, N = 240) = 347.18, p < .001$ . Given the chi-square and degrees of freedom for the null model, *H1* - *H2*, and those of the hypothesized model, *H1* - *H0*, alternative indices of fit can be calculated. The test of the hypothesized raw ML model resulted in fit indices of NNFI = .921 and CFI = .945.

### Summary

Nearly all longitudinal data sets suffer from various forms of missing data, stemming from attrition, omissions, and planned missingness in accelerated designs such as the cohort-sequential approach. Although numerous approaches to handling missing data are available, this chapter demonstrated and compared the utility of different model-based procedures for analyses of incomplete longitudinal data within an LGM framework. Parameters and standard errors were generated through the use of ML procedures, and compared across methods.

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 also would use a latent variable model to handle the missing data. Finally, the best procedures provide consistent and efficient parameter estimates.

Although the missing data procedures presented here are, in general, statistically sound, they weigh convenience and availability over statistical precision and efficiency. Both multiple-sample SEM and raw ML analyses incorporate all of the available data and produce consistent and efficient estimates. The multiple-sample SEM procedure is recommended when distinct missing data patterns are evident. However, the programming of cross-group constraints necessary for proper estimation becomes more tedious as the number of distinct patterns increases. The raw ML approach, in contrast, is simpler to program and provides more flexibility in handling various missing data patterns.

1 Beginning with version 4.0, Amos attempts to estimate saturated and independence models automatically with missing data. If successful, Amos computes fit chi-square statistics and all derived fit indices.

## Chapter 9 Multilevel Longitudinal Approaches

This chapter demonstrates the use of a general LGM that accounts for the dependence of data collected in a hierarchical fashion. Examples of hierarchically structured data include individuals nested within families, classes within schools, and neighborhoods within communities. Data containing measurements from different levels of the hierarchy require analytic techniques that are based on assumptions that are in agreement with the data structure. Researchers have long struggled with concepts such as hierarchically nested observations, intraclass correlation (ICC), the unit of analysis, and random rather than fixed effects. Not only are more traditional fixed effects analytical methods (e.g., ANOVA) limited in their handling of the technical difficulties posed by nested designs, but they are also limited in the questions they can address.

Multilevel models represent a useful extension of the traditional variance component models discussed by Winer, Brown, and Michels (1991) and Searle, Casella, and McCulloch (1992), and offer the possibility of making use of within-cluster differences in parameter estimates, treating these differences as a meaningful source of variance rather than as within-group error or as a nuisance parameter (Kreft, 1994). New analytic techniques that are more suited to the hierarchical data structure have recently emerged under the labels of hierarchical, or multilevel, models (see Aitkin & Longford, 1986; Burstein, 1980; de Leeuw & Kreft, 1986; T.E. Duncan, S.C. Duncan, Hops, & Stoolmiller, 1995; Goldstein, 1986; Longford, 1987; Mason, Wong, & Entwistle, 1984; Raudenbush & Bryk, 1988; Schmidt & Wisenbaker, 1986). Muthén and Satorra (1989) pointed out that such models account for the correlated observations and observations from heterogeneous populations having varying parameter values, gathered in hierarchical designs. Although appropriate techniques of this kind are now available for standard regression and ANOVA situations, Muthén and Satorra note the lack of techniques for covariance structure models, such as factor analysis, path analysis, and SEM.

Full ML methods are appropriate for hierarchical analyses with longitudinal data. Although higher order covariance and mean structure models are generally formulated as a means of modeling growth for multiple variables or scales over multiple occasions, this method is

easily extended to modeling growth for multiple informants over multiple occasions, as in longitudinal and hierarchically nested data. Using this parameterization, a multilevel model can be specified to examine whether a higher order factor adequately describes relationships among lower order developmental functions (e.g., intercept and rate of change).

If there are many groups of different size (e.g., unbalanced data), full ML estimation with hierarchical data can be accomplished using a multiple groups, or a model-based extension of the multiple groups, framework. However, if there are many groups and most groups are of different size, or if group sizes are large, ML estimation with hierarchical data is computationally heavy. Moreover, conventional software that requires positive definite input matrices (between-group covariance matrices will not be positive definite if the number of variables is greater than the number of observations) may not arrive at an acceptable solution.

Muthén (1991, 1994) proposed an ad hoc estimator, using limited information, that is simpler to compute than ML while still using the SEM framework. Muthén (1994) showed that this simpler estimator is identical to the ML estimator for balanced data, and gives results close to those of ML for data that is not badly unbalanced. This suggests that with many group sizes, little may be gained by the extra effort of ML computation. Taken together, these developments make possible the construction, estimation, and testing of a variety of complex growth models using hierarchically structured data.

This chapter demonstrates and compares the use of a full ML and a limited information (Muthén, 1991, 1994) approach to modeling *unbalanced* hierarchical and longitudinal data. Using these two multilevel LGM approaches, developmental changes in alcohol use for individuals and families were examined using adolescent and parent data from 369 families (888 individuals). Of the 369 families, 248, 92, and 29 consisted of two, three, and four family members, respectively. Data for the model examples were from the NYS (Elliott, 1976).

Example 9.1  
Full ML Estimation

The model depicted in Fig. 9.1 represents an unconditional (i.e., no predictor variables), three-level multivariate LGM for families comprised of four family members. Here, repeated measures within persons are viewed as the lowest level (Level 1; first-order observed variables,  $V_s$ ), representing within person change over time. The growth curves are then applied to each family member separately, representing between person change (Level 2; first-order latent factors,  $F_i$ s and  $F_s$ s) across the entire time series. The variation among families is captured at the highest level (Level 3; second-order latent factors,  $F_i$  and  $F_s$ ).

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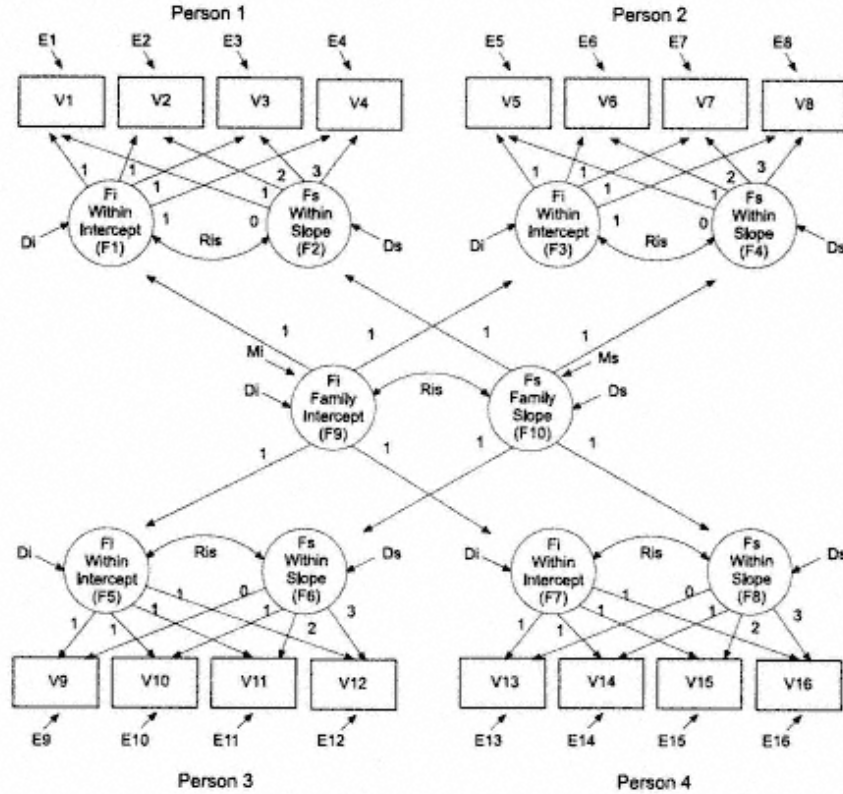


Fig. 9.1.  
Representation of the multilevel LGM.

For illustration purposes, equation 9.1 is presented in the form of a factor analytic model for  $V$  with first-order latent factors,  $F_i$  and  $F_s$ , and measurement errors,  $E$ , for a two-member family. Variables  $V_1$  through  $V_4$  represent observations for Person 1 and variables  $V_5$  through  $V_8$  represent observations for Person 2 from the same family or cluster.

The first term to the right of the equal sign corresponds to variation in the observed  $V$  variables due to the first-order within person growth process (temporal variation). The basis terms,  $0$ ,  $1$ ,  $L_2$ , and  $L_3$ , are the coefficients for the influence of the slope factors on the observed  $V$  variables. It is possible to fix these values to represent a specific form of growth (e.g., linear growth), or to accommodate nonlinear growth by estimating the third and fourth coefficients, holding the first two values fixed at 0 and 1, respectively, for identification purposes. In this example, the basis terms are fixed at values of 0, 1, 2, and 3 to represent linear

growth (see Fig. 9.1). The second term captures the error variation in the observed variables.

$$\begin{bmatrix} V1 \\ V2 \\ V3 \\ V4 \\ V5 \\ V6 \\ V7 \\ V8 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 \\ 1 & L2 & 0 & 0 \\ 1 & L3 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & L2 \\ 0 & 0 & 1 & L3 \end{bmatrix} \begin{bmatrix} Fi_{Person1} \\ Fs_{Person1} \\ Fi_{Person2} \\ Fs_{Person2} \end{bmatrix} + \begin{bmatrix} E1 \\ E2 \\ E3 \\ E4 \\ E5 \\ E6 \\ E7 \\ E8 \end{bmatrix} \quad 9.1$$

In Equation 9.1, the vector containing the terms  $Fi$  and  $Fs$  represents person-level latent growth rates involving a vector of means and variances. Because this three-level model specification results in the mean parameters being absorbed into the Level 3 vector  $M$  (described in equation 9.3), the means for the person-level factors are fixed to zero (a null vector), having only a vector of person-level latent factor scores (i.e.,  $F = Fi_{Person1}, Fs_{Person1}, Fi_{Person2}, Fs_{Person2}$ ). These Level 2 latent factor scores are further accounted for by a set of Level 3 latent growth factors, which have the following form:

$$\begin{bmatrix} Fi_{Person1} \\ Fs_{Person1} \\ Fi_{Person2} \\ Fs_{Person2} \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ 1 & 0 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} Fi_{Family} \\ Fs_{Family} \end{bmatrix} + \begin{bmatrix} Di_{Person1} & & & \\ Dis_{Person1} & Ds_{Person1} & & \\ 0 & 0 & Di_{Person2} & \\ 0 & 0 & Dis_{Person2} & Ds_{Person2} \end{bmatrix} \quad 9.2$$

The first component on the right side of the equal sign is a matrix of factor loadings, multiplied by a family-specific vector of unknown growth parameters with means and variances (standard deviations). This is added to a person-specific vector of unknown disturbance terms, where the intercept and slope for each individual are allowed to covary. The matrix defining the family level (Level 3) latent growth process can be expressed by the following matrix form:

$$\begin{bmatrix} Fi_{Family} \\ Fs_{Family} \end{bmatrix} = \begin{bmatrix} Mi_{Family} \\ Ms_{Family} \end{bmatrix} + \begin{bmatrix} Di_{Family} & & \\ Dis_{Family} & Ds_{Family} & \end{bmatrix} \quad 9.3$$

where the first term ( $Mi$  and  $Ms$ ) denotes overall family mean values in intercept and slope factors, and added to these is a vector of  $Ds$  containing the deviations of the family growth parameters from their respective means, allowing the intercept and slope to covary. As no predictor variables are specified in the model, the  $Ms$  and  $Ds$  at the third level represent variability among families. Equations 9.1 through 9.3 give the hierarchical LGM depicted in Fig. 9.1.

To compare the two methods, it is necessary in the multivariate LGM to restrict the covariances among the first-order latent growth curves to a value of zero, and to restrict factor loadings between the first- and second-order latent factors to be equal over time for each family member (as shown by the 1s in Fig. 9.1). This imposes a form of factorial invariance ensuring that the second-order factor scores are scaled to the same units.

More detailed rationales for these metric invariance assumptions are provided by Rozeboom (1978), Nesselroade (1983), and Meredith and Tisak (1982). The alternative possibility of varying the factor pattern over time is discussed by Harris (1963), Corballis and Traub (1970), Hakstian (1973), Nesselroade (1977), and Horn et al. (1983). In the current example, the metric scale restriction was imposed so that comparisons of the full ML and limited information approaches (introduced later) could be made.

For unbalanced data within the full ML approach, the raw ML approach to analyses with missingness as implemented in the Amos SEM program is followed. Details on this approach to missingness within the LGM framework are presented in chapter 8 (see also T.E. Duncan, S.C. Duncan, & Li, 1998). The  $H1$  model input statements using Amos are presented in Appendix 9.1. Input statements for the  $H0$  model are presented in Appendix 9.2.

Fitting the full ML second-order LGM resulted in a function of log likelihood of 7046.438 with 152 distinct parameters estimated under the  $H1$  hypothesis and 7362.173 with 12 distinct parameters estimated for  $H0$ . The difference in log likelihood functions and parameters estimated for the two analyses gives a correct test of  $H0$  against  $H1$ ,  $\chi^2(140) = 315.735$ ,  $p < .001$ .

Under the  $H2$  hypothesis, the function of log likelihood was 9271.812 with 32 distinct parameters estimated. The difference in log likelihood functions and parameters estimated for the  $H1$  and  $H2$  analyses gives a test of the null model,  $\chi^2(120) = 2225.374$ ,  $p < .001$ . The following indices of fit were calculated for the full ML second-order LGM: NNFI = .95 and CFI = 1.000. Parameter estimates indicated significant second-order mean levels in the intercept,  $Mi = 2.703$ ,  $SE = .075$ ,  $t = 36.229$ , and slope,  $Ms = .599$ ,  $SE = .026$ ,  $t = 22.763$ . Individual differences in each higher order growth factor were also significant with estimated variances of  $Di = .854$ ,  $SE = .166$ ,  $t =$



TABLE 9.1  
Parameter Estimates From the Hierarchical LGM

| Coefficient       | Second-Order |         | First-Order |         |
|-------------------|--------------|---------|-------------|---------|
|                   | Effect       | t Value | Effect      | t Value |
| Means             |              |         |             |         |
| Alcohol intercept | 2.703        | 36.229  |             |         |
| Alcohol slope     | .599         | 22.763  |             |         |
| Variances         |              |         |             |         |
| Alcohol intercept | .854         | 5.157   | 2.252       | 12.124  |
| Alcohol slope     | .093         | 4.447   | .195        | 6.552   |

5.157, and  $Ds = .093$ ,  $SE = .021$ ,  $t = 4.447$ . Parameter estimates are presented in Table 9.1.

The second- and first-order factor variances were estimated as .854 and 2.252, respectively, giving a second-order-to-total factor variance ratio of .275. For the slope, the second- and first-order factor variances were estimated as .093 and .195, respectively, giving a second-order-to-total factor variance ratio of .323. Considering the second-order-to-total factor variance ratio, approximately 27% of the total variation in alcohol intercept scores and approximately 32% of the total variation in alcohol slope scores could be accounted for by family membership.

#### Example 9.2 Multilevel LGM (MLGM)

The new methodology in Muthén (1997) involves two generalizations of previous SEM work: growth modeling as generalized to cluster data and SEM multilevel modeling as generalized to mean structures, wherein means appear in the between structure while within structure means are constrained at zero.

As pointed out in Muthén (1989), MLGM is a complex analysis that must follow a sound strategy. In this example, the total population covariance matrix,  $\Sigma T$ , is decomposed into two independent components, a between-families covariance matrix,  $\Sigma B$ , and a within-families covariance matrix,  $\Sigma W$ , or  $\Sigma T = \Sigma B + \Sigma W$ . Conventional covariance structure analysis that ignores grouping or clustering assumes that all observations are independent, implying that  $\Sigma B = 0$ . Thus, Muthén (1994) recommended that four important analytic steps precede the actual

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MLGM: conventional factor analysis of the total covariance matrix; estimation of between-level variation or ICC; estimation of within-level covariance structure; and estimation of between-level covariance structure. The analyses were performed using the EQS (Bentler & Wu, 1995) SEM program and a Fortran routine (SOURCEBW) developed by Nelson and Muthén (1991), which calculates the necessary within- and between-level covariance and mean structures, and provides ICC estimates and the ad hoc estimator needed for model estimation. The program code and instructions for the use of this program are given in Nelson and Muthén. The standard errors and chi-square tests of model fit are not exact but are reasonable approximations, which should be considered in statements about significance and model fit (Muthén, 1997).

*Step 1: Conventional Confirmatory Factor Analysis of the Total Covariance Structure.* Although multilevel covariance structure analyses (MCA) partition the total covariance structure into between- and within-level components, reflecting the hierarchical nature of the data, the test of the total sample covariance structure ( $ST$ ) is useful in generating and testing various models. Moreover, the test of fit using  $ST$  may be of practical use by giving a rough sense of fit for a proposed MCA model.

*Step 2: Estimation of Between-Level Variation or ICC.* The question is whether a multilevel analysis is warranted. This can be answered by computing the estimated ICC for each variable. The ICC is used to express the fact that observations in the same family or other cluster (e.g., class, school) are related, or tend on average to be more alike than observations from different families or clusters. The larger the ICC value, the more similar are observations in the same cluster relative to other clusters. These estimates may be obtained by random effects ANOVA (Winer et al., 1991). If all ICCs are near zero, an indication that the observations are truly independent of one another, multilevel analyses might not be worthwhile. A good overview of ICC estimation is given in Koch (1983).

*Step 3: Estimation of the Within-Level Covariance Structure.* The third step carries out the analysis of the sample pooled within covariance matrix,  $SPW$ . In our example, the analysis uses a sample size of  $N - G$  (888 - 369, or  $N = 519$ ) and either the normal theory generalized least squares or ML estimator. Because the  $SPW$  analysis is not distorted by the between-level covariation, it is expected to give a better model fit than the  $ST$  analysis (Keesling & Wiley, 1974; Muthén, 1989) and is, therefore, preferred for exploring individual-level variation.

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*Step 4: Estimation of the Between-Level Covariance Structure.* The fourth step investigates the between-level covariance structure. This analysis uses the same model as *SPW*, but models across-group (co)variation rather than focusing on the individual-level data. Here, the sample represents the number of family clusters ( $N = 369$ ). As in Cronbach (1976) and Hamqvist (1978), the same structure as that seen in the within level cannot be expected at the between level because the between components have a different meaning than the within components, and the between-group covariation may not follow a simple model. In practice, *SB* can be analyzed to reveal the between-level structure.

*Multilevel Covariance Structure Analyses (MCA).* The next set of steps uses the outcomes of the four initial steps to specify a sequence of MCAs. The MLGM makes use of *SPW* and *SB* simultaneously. The specification of this model for alcohol can be illustrated by a diagram such as that in Fig. 9.2. In line with structural modeling conventions, squares denote observed variables and circles denote latent variables. The part of the model below the squares refers to the within structure, while the part above refers to the between structure. As shown, the setup for the first group involves both between- and within-level structure, but the setup for the second group involves only within-level structure.

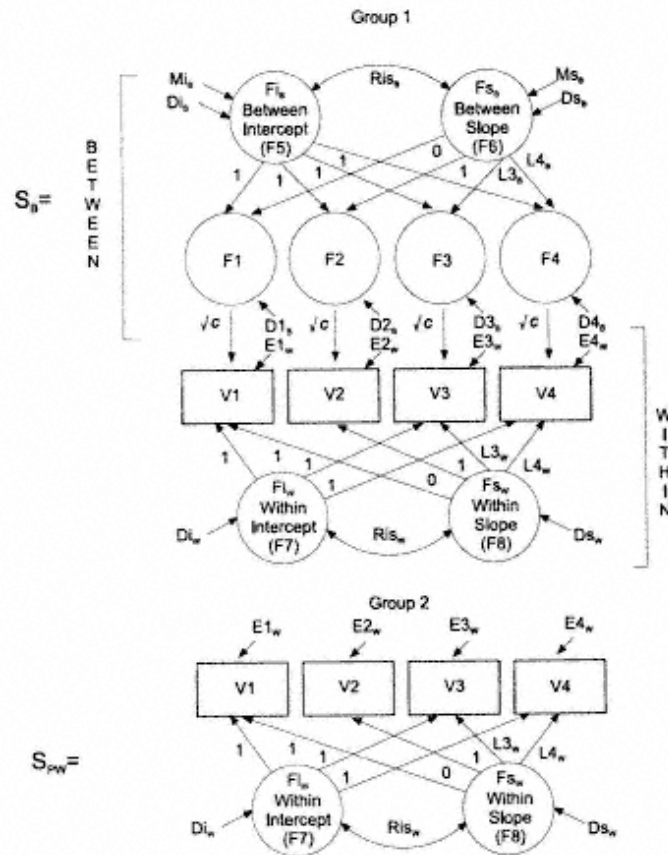
The MLGM model can be expressed by the following equation for the  $j$ th individual in the  $g$ th family:

$$V_{gj} = [1 \ L] \begin{bmatrix} Mi_B \\ Ms_B \end{bmatrix} + [1 \ L] \begin{bmatrix} Fi_{Bg} \\ Fs_{Bg} \end{bmatrix} + [D_{Bg}] + [1 \ L] \begin{bmatrix} Fi_{Wgj} \\ Fs_{Wgj} \end{bmatrix} + [E_{Wgj}], \quad 9.4$$

where  $[1 \ L]$  is a basis term matrix containing constant 1s in the first column and known  $t$  ( $t = 1, 2, \dots, T$ ) time coefficients in the second column. Equation 9.4 can be expanded to have the following matrix form:

$$\begin{bmatrix} V1_{gj} \\ V2_{gj} \\ V3_{gj} \\ V4_{gj} \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 1 & L3_B \\ 1 & L4_B \end{bmatrix} \begin{bmatrix} Mi_B \\ Ms_B \end{bmatrix} + \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 1 & L3_B \\ 1 & L4_B \end{bmatrix} \begin{bmatrix} Fi_{Bg} \\ Fs_{Bg} \end{bmatrix} + \begin{bmatrix} D1_{Bg} \\ D2_{Bg} \\ D3_{Bg} \\ D4_{Bg} \end{bmatrix} + \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 1 & L3_W \\ 1 & L4_W \end{bmatrix} \begin{bmatrix} Fi_{Wgj} \\ Fs_{Wgj} \end{bmatrix} + \begin{bmatrix} E1_{Wgj} \\ E2_{Wgj} \\ E3_{Wgj} \\ E4_{Wgj} \end{bmatrix}. \quad 9.5$$

The first term to the right of the equal sign captures the contribution of the means of the between-family slope and intercept factors to the means of the observed variables after multiplication by the between-family basis



coefficients. The second term corresponds to between-family variation in the observed  $V$  variables due to the between-families growth process. The third term represents the between-family disturbance. The fourth term corresponds to within-level variation in the observed  $V$  variables due to the within-level growth process. The fifth term reflects within-level error. Notice that factors  $Fi$  and  $Fs$  are specified at both the between-family level,  $FiB$  and  $FsB$ , and the within-family level,  $FiW$  and  $FsW$ . The basis terms,  $LW$  and  $LB$ , are the coefficients for the influence of the between- and within-slope factors on the observed  $V$  variables, and indicate that nonlinear growth can be accommodated for both between and within slopes separately by estimating the third and fourth coefficients, holding the first two values fixed at 0 and 1, respectively, for identification purposes. The

influence of the slope factors need not be the same on the between side as it is on the within side.

For actual estimation using conventional SEM software, the model is set up as a two-sample, multiple-group problem with  $SB$  used as input for the first group and  $SPW$  used as input for the second group. Modeling is done with  $SB$  rather than the ML estimate of  $\Sigma B$  for reasons outlined under the fourth preliminary step.

The three sample covariance matrices  $ST$ ,  $SPW$ , and  $SB$  are expressed as

$$S_T = (N-1)^{-1} \sum_{g=1}^G \sum_{j=1}^{N_g} (y_{gj} - \bar{y})(y_{gj} - \bar{y})', \quad 9.6$$

$$S_{PW} = (N-G)^{-1} \sum_{g=1}^G \sum_{j=1}^{N_g} (y_{gj} - \bar{y}_g)(y_{gj} - \bar{y}_g)', \text{ and} \quad 9.7$$

$$S_B = (G-1)^{-1} \sum_{g=1}^G N_g (\bar{y}_g - \bar{y})(\bar{y}_g - \bar{y})'. \quad 9.8$$

The matrix  $ST$  is used in conventional covariance structure analysis. In the multilevel case, it can be considered a consistent estimator of the total covariance matrix  $\Sigma W + \Sigma B$ . Muthén (1994) demonstrated that the pooled within matrix,  $SPW$ , is a consistent and unbiased estimator of  $\Sigma W$ , while the between matrix,  $SB$ , is a consistent and unbiased estimator of  $\Sigma W + C\Sigma B$ , where  $C$  reflects the family size, computed as:

$$C = \left[ N^2 - \sum_{g=1}^G N_g^2 \right] [N(G-1)]^{-1}. \quad 9.9$$

For unbalanced data,  $C$  is close to the mean of the family sizes. Note that the between-family matrix,  $SB$ , is the covariance matrix of family means weighted by the family size. Therefore, the ML estimate of  $\Sigma W$  is  $SPW$ , while the ML estimate of  $\Sigma B$  is

$$C^{-1}(S_B - S_{PW}). \quad 9.10$$

The fitting function that is minimized is

$$G(\ln|\Sigma_W + c\Sigma_B| + \text{trace}[(\Sigma_W + c\Sigma_B)^{-1}S_B] - \ln|S_B| - p) + \quad 9.11$$

$$(N - G)(\ln|\Sigma_W| + \text{trace}[\Sigma_W^{-1}S_{PW}] - \ln|S_{PW}| - p).$$

The top line of equation 9.11 corresponds to the first group in the multiple-group setup, which captures the between-level contribution to the total variation, weighted by  $G$ , the number of families. The bottom line of the equation corresponds to the second group, which captures the within-level contribution to the total variation, and is weighted by  $N - G$ , the total sample size minus the number of families. Note that for balanced data,  $C$  is the common family size and the two-group approach above is equivalent to full information ML estimation. The model setup in the first group, using  $SB$  as input, requires the creation of extra latent variables to capture the weighting by the constant,  $C$ . These extra latent variables are depicted as  $F1$  through  $F4$  in Fig. 9.2, and their contribution to the observed  $V$  variables is scaled by fixing the path (loading) to  $\checkmark C$ . The residual variances of  $F1$  through  $F4$  ( $D1$  through  $D4$ ) capture the between-level composite error variances. The mean structure for the MLGM arises from the four observed variable means for alcohol use, expressed as functions of the means of the  $FiB$  and  $FsB$  between-level factors. The means of the within-level growth factors are fixed at zero.

The second group in the multiple-group setup corresponds to the within-level variation. The covariance structure of  $\Sigma W$  is captured by using the same model structure as for the first group, following Fig. 9.2, but fixing all between-level coefficients and variance-covariance parameters to zero. Within-level composite error variance is captured by residual error variances,  $E1W$  through  $E4W$ , for the  $V$  variables. Because  $\Sigma W$  also appears in the covariance structure of the first group, equality restrictions across groups must be applied for the within parameters. For a complete exposition and computational details concerning the ad hoc estimation procedures, see Muthén (1991, 1994).

Following are the results of the initial analyses for the MLGM.

*Analysis of ST: Step 1.* This analysis is useful in generating and testing various model ideas. Recall that the chi-square test of model fit is usually inflated, particularly for data with large ICCs, large family sizes, and highly correlated variables, but fit indices may be of practical use by giving a rough sense of fit. The *ST* analysis yielded a reasonable fit,  $\chi^2(5, N = 888) = 96.470, p < .001, NNFI = .98,$  and  $CFI = .98.$  The power of the test was high due to the large sample size and thus rejection at the 5% level might reflect trivial deviations from the model. Results indicated an upward trend in the development of family alcohol use. Despite the adequate fit of the model to the data, however, this test is incorrect, in that it ignores the hierarchical nature of the data.

*Estimation of ICC: Step 2.* When considering all 369 families in the sample, there are three distinct cluster (family) sizes, ranging from two to four. Of interest is whether a multilevel analysis of these data is warranted.

This can be resolved by testing  $\Sigma B = 0,$  which can be accomplished by computing the estimated ICC for each variable. ICCs for the four repeated alcohol use measures were .22, .22, .30, and .27 (*V1, V2, V3, and V4*), making it reasonable to proceed to Step 3.

*Estimation of SPW: Step 3.* The third step analyzes the pooled within-level matrix, *SPW.* The pooled within-level matrix, *SPW,* was obtained from Muthén's SOURCEBW program. Conventional ML analysis provided an adequate fit for the two-factor *SPW* model,  $\chi^2(5, N = 519) = 92.521, p < .001, NNFI = .98,$  and  $CFI = .98.$

*Estimation of SB: Step 4.* The fourth step examines the between structure using *SB,* the sample between-families covariance matrix. In this example, the between-level variation concerns between-family variation in trajectories of alcohol use, which is conceptually similar to individual variation in alcohol use trajectories. Thus, a similar growth structure is expected for both within and between levels, although parameter estimates are allowed to differ across the two components. Some complications arise in exploring the structure of *SB.* First, as pointed out by Muthén (1994), *SB* actually estimates  $\Sigma W + C\Sigma B.$  For balanced data, *C* is the common family size. For unbalanced data and a large number of families, *C* is close to the mean of the family sizes. Thus, one can analyze *SB* to get a notion of the  $\Sigma B$  structure, but any simple structure expected to hold for  $\Sigma B$  does not necessarily hold for *SB.* Second, because  $C^{-1}(SB - SPW)$  is an ML estimate of  $\Sigma B,$  it might be tempting to analyze this matrix instead of *SB.* Unfortunately, the ML estimate of  $\Sigma B$  is frequently nonpositive definite and may even have negative variance estimates. Muthén noted that when it is possible to analyze both  $C^{-1}(SB - SPW)$  and *SB,* the results have been similar. Clearly, exploratory analyses of between-family structure is an area that needs more development. With these caveats in mind, the associative LGM analysis using the *SB* matrix generated from SOURCEBW and a two-factor unspecified model resulted in a model fit of  $\chi^2(5, N = 369) = 66.672, p < .001, NNFI = .98,$  and  $CFI = .98.$

The four initial analysis steps suggested an MLGM model with a two-factor unspecified structure for both within and between levels. Model fitting procedures resulted in the following indices of fit:  $\chi^2(15, N = 888) = 98.415, p < .001, NNFI = .978,$  and  $CFI = .981.$  Model parameters for the MLGM are presented in Table 9.2. Amos input specifications for the test of the MLGM model are presented in Appendix 9.3.

TABLE 9.2  
Parameter Estimates From the MLGM

| Coefficient       | Second-Order |         | First-Order |         |
|-------------------|--------------|---------|-------------|---------|
|                   | Effect       | t Value | Effect      | t Value |
| Means             |              |         |             |         |
| Alcohol intercept | 2.702        | 36.423  |             |         |
| Alcohol slope     | .596         | 22.782  |             |         |
| Variances         |              |         |             |         |
| Alcohol intercept | .799         | 4.741   | 2.311       | 12.224  |
| Alcohol slope     | .076         | 3.404   | .210        | 6.866   |

As can be seen from Table 9.2, fitting the two-factor LGM to the data resulted in the following mean intercepts and mean slopes for alcohol use:  $M_i = 2.702, SE = .074, t = 36.423, p < .001,$  and  $M_s = .596, SE = .026, t = 22.782, p < .01.$  The slope mean was significant, indicating substantial development in the use of alcohol over the specified time period.

The latent variances were also estimated. The variances for intercepts and slopes at the between level,  $D_i = .799, SE = .168, t = 4.741, p < .01,$  and  $D_s = .076, SE = .022, t = 3.404, p < .01,$  and at the within level,  $D_i = 2.311, SE = .189, t = 12.224, p < .01,$  and  $D_s = .210, SE = .031, t = 6.866, p < .01,$  suggested that significant variation existed in individual differences regarding initial status and developmental trajectories at both within and between levels.

For the intercept, the between- and within-factor variances were estimated as .799 and 2.311, respectively, giving a between-to-total ratio of .257. For the slope, the between- and within-factor variances were estimated as .076 and .210, respectively, giving a between-to-total ratio of .266. Considering the between-to-total factor variance ratio, approximately 26% of the total variation in alcohol intercept scores and approximately 27% of the total variation in alcohol slope scores could be accounted for by family membership.

### Summary

This chapter demonstrated how covariance structure models can be formulated for longitudinal data having nested structures, and how they can be analyzed using conventional SEM software. The basic LGM approach shown here integrates multiple informants and multiple occasions.

One extension of the basic LGM model describes individual differences within separate univariate series, and forms a common factor model to

describe individual differences among these basic growth curves. This full ML approach offers opportunities for evaluating the dynamic structure of both intra- and interindividual change at multiple levels of the hierarchy.

With many groups of different sizes, full maximum likelihood estimation with hierarchical data can be accomplished within a multiple-group or raw ML specification. Fitting the full ML second-order model to the family alcohol data indicated that the broadly similar univariate LGM characteristics could be adequately described by a common factor capturing family differences among these various growth curve parameters. The use of a common factor model within the SEM framework represents a logical progression in the paradigm of testing the adequacy of LGM representations of group dynamics, but these analyses can be computationally heavy and, if conventional software is used, the input specifications can be very tedious.

Muthén (1991, 1994) proposed an ad hoc estimator, using limited information, that is simpler to compute than ML while still using the SEM framework. Using this technique, a multilevel LGM of alcohol use was examined among individuals nested within families. The flexibility of the basic MLGM approach makes it an attractive tool for a variety of SEM analyses with data that are both longitudinal and multilevel. Although considered a quasi-likelihood estimator, the example in this chapter shows that this simpler estimator gives results close to those of ML with unbalanced data.<sup>1</sup>

<sup>1</sup> The multilevel LGM as presented can be considered a three-level random coefficients model with repeated observations nested within subjects, nested within families. Using notation from Bryk and Raudenbush (1992), a comparable model for estimating the growth of alcohol, without predictors at the between level, and only the basis term specified at the within level, can be denoted as:

Level 1

$Y_{tjk} = \pi_{0jk} + \pi_{1jk}at_{jk} + e_{tjk}$ , where  $Y_{tjk}$  = the observed score at time  $t$  for subject  $j$  in family  $k$ ,  $\pi_{0jk}$  = initial status for subject  $jk$ ,  $\pi_{1jk}$  = growth rate for subject  $jk$ ,  $at_{jk}$  = specified basis term, and  $e_{tjk}$  = random error;

Level 2

$\pi_{0jk} = \beta_{00k} + r_{0jk}$  and  $\pi_{1jk} = \beta_{10k} + r_{1jk}$ , where  $\beta_{00k}$  = mean initial status within family  $k$ ,  $\beta_{10k}$  = mean growth rate within family  $k$ , and  $r$  denotes the individual variability from families, with  $r_{0jk}$  = variation at initial status,  $r_{1jk}$  = variation at growth rate; and

Level 3

$\beta_{00k} = \gamma_{000} + u_{00k}$  and  $\beta_{10k} = \gamma_{100} + u_{10k}$ , where  $\gamma_{000}$  = overall mean initial status,  $\gamma_{100}$  = overall mean growth rate, and  $u$  denotes family variability, with  $u_{00k}$  = variation at initial status,  $u_{10k}$  = variation at growth rate.

Using limited information, the MLGM explicitly modeled the within-and between-level covariance matrices in familial alcohol use. The similarities in parameter estimates generated from the MLGM compared to the full ML estimation suggests that with many group sizes (e.g., unbalanced data) little may be gained by the extra effort of full maximum likelihood computation.

Just as ANOVA and multiple regression techniques can be considered special cases of the general SEM (Hoyle, 1995), so too can hierarchical linear models be viewed as special cases of the general multilevel covariance structure model. The multilevel covariance structure approach demonstrated here differs from more traditional hierarchical approaches in at least two important ways. First, and perhaps the most compelling, is the capacity of MCA to estimate and test relationships among latent variables. The isolation of concepts from uniqueness and unreliability of their indicators increases the probability of detecting relationships and obtaining sound estimates of parameters close to their population values. Second, MCA allows for a more comprehensive and flexible approach to research design and data analysis than any other single statistical model for hierarchical data in standard use by social and behavioral researchers.

The use of latent variable growth models that incorporate information from various levels of the hierarchy allows for potentially greater insight into the developmental nature, antecedents, and sequelae of a plethora of behavioral outcomes. Each of the extensions of the basic LGM to hierarchical data structures demonstrated here can be readily performed using conventional SEM software.

## Chapter 10 Latent Variable Framework for LGM Power Estimation

A question that arises from the various LGMs presented in the preceding chapters is that of statistical power for claiming and interpreting a tenable model. Although researchers have become increasingly sophisticated in applying tests for statistical significance, few are aware of the power of these tests. If a particular test is not statistically significant, it may be because there is truly no effect in the population or it may be because the study design made it unlikely that an effect, even if one did exist, would be detected. Power estimation can distinguish between these alternatives, and is a critical component of designing experiments and testing their results.

As a practical matter, the evaluation of statistical power requires the researcher to establish a level of significance, sample size, magnitude, and direction of the desired effects, and the within-class variance associated with the observations. This variation is related to the nature and reliability of the dependent outcome and the nature of the design. Therefore, the question of power is often couched in terms of the sample size necessary to detect deviation from the null hypothesis. Because these effects are defined as parameters and estimated from sample statistics, sample size determines the accuracy of parameter estimation.

For a majority of standard statistical methods, power can be calculated using tables or charts provided in many articles and texts (e.g., Cohen, 1988; Kraemer & Thiemann, 1987; Lipsey, 1990). These charts, however, often require some hand calculations before they can be used, including interpolation between tabled values. For example, Cohen presented an excellent discussion of the relations among  $\alpha$ ,  $n$ , effect size, and statistical power, and provided an extensive treatment of statistical power, supplying tables wherein power is estimated given values of the level of significance ( $\alpha$ ), measures of effect size ( $f$ ), the sample size ( $n$ ), and the degrees of freedom in the numerator of  $F$  ratios. Specifying the highest tolerable Type I error rate and the desired power, the researcher can use the charts to discover the sample size.

In the following sections, current power estimation methods using latent variable approaches are briefly reviewed. These methods involve the estimation of power for single and multiple parameters and overall model fit. This is followed by applications of these methods with simulated data. The applications presented include power estimation for a growth parameter in a single-sample LGM model and for treatment effects in a longitudinal experimental study.

#### Power Estimation within a Latent Variable Framework

The chi-square test statistic is conventionally used to evaluate latent variable models. Because of its sensitivity to sample size, however, this statistic presents problems in evaluating overall model fit. A model may be rejected due to either a large sample size or misspecification (i.e., specification errors). Large sample sizes are known to have greater power to detect a false hypothesis than do smaller samples for the same model. Although a variety of fit indices have been developed, these measures deal with misspecification of the covariance structure and not the relevant structural parameters (Saris & Satorra, 1993). The power of the significance test has drawn increasing attention; a number of authors have argued for the evaluation of latent variable models based on power considerations (e.g., Bollen, 1989; Kaplan, 1990, 1995; Saris & Satorra, 1993).

In the following section, methods for estimating the power of statistical tests are presented based on works of Satorra and Saris (1983, 1985) and MacCallum, Browne, and Sugawara (1996). The former compares a null model to an alternative model involving additional parameter values to be tested. The method allows sets of individual parameters to be evaluated in terms of power. Along the same line, a method introduced by Satorra (1989) calculates power based on the modification index. Alternatively, MacCallum et al.'s method uses a fit index (see also MacCallum & Hong, 1997) to evaluate the degree to which a model of close fit deviates from lack of fit in the population. This method is of particular use in testing hypotheses of overall model fit, that is, whether the model provides a reasonable approximation of the population covariance matrix. The methods presented in this chapter are not exhaustive. Other methods are available (see Kaplan, 1995; Saris & Satorra, 1993; Saris, Satorra, & Sörbom, 1987).

Estimation of power to detect misspecified latent variable models has been discussed in earlier work by Satorra and Saris (1983, 1985). These authors developed procedures to evaluate the power of the goodness-of-fit

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test against specific deviations from the hypothesized model. The procedure, requiring specification of an alternative model with given parameter values, can be used to determine power for the overall model test as well as for associated tests of individual parameters. When the hypothesized structural model is incorrect, but not highly misspecified, power can be approximated using a two-step procedure. This procedure involves two models, one that is assumed to be correctly specified, and the other, more restrictive, that is assumed to be misspecified. The two-step procedure outlined by Satorra and Saris (1985; see also Saris & Stronkhorst, 1984) is as follows:

1. Specify a complete model under the alternative hypothesis,  $H_a$ . The model contains parameters of a model under study and restrictions on sets of parameters to be tested. All parameters must be numerically specified. Next, a model covariance matrix for the model specified by  $H_a$  is computed using any input covariance matrix.
2. Estimate the model under a null hypothesis,  $H_0$ , using the implied model covariance matrix obtained in Step 1 with the same sample size. Specifications of  $H_0$  involve vectors of free and fixed sets of parameters. The chi-square test statistic from this analysis is the noncentrality parameter used in the power calculations.

The estimation of power employing this procedure is based on estimation of an "incorrect model" ( $H_0$ ) using the correct implied covariance matrix for the alternative model. Because the two models are nested, the discrepancy index between the correct and incorrectly specified models,  $H_a$  versus  $H_0$ , is reflected in the chi-square difference estimate (Likelihood Ratio test [LR]), except that the value corresponds to the noncentrality parameter in a statistical power analysis. Given the value of the noncentrality parameter obtained, the degrees of freedom and the probability level of the test chosen, the power of the test can be determined using the tables of the noncentral chi-square distribution (e.g., Haynam, Govindarajulu, & Leone, 1973).

Clearly, when there are many parameters to be evaluated, the method proposed by Satorra and Saris (1985) would be tedious to carry out in practice. An alternative to this power estimation procedure is the use of model modification strategies (Satorra, 1989). Instead of specifying an alternative value to be tested, the LM (Bentler, 1986) or the modification index (MI; Sörbom, 1989), test statistics can be used to approximate the noncentrality parameter for each restriction (1 degree of freedom) imposed in the model (Satorra). For a given fixed parameter or an equality constraint in a model, a modification index (LM in EQS, MI in LISREL) can be computed to predict the reduction in the model's chi-square that would accompany the freeing of a fixed parameter or the release of an equality constraint. Similarly, for a freely estimated parameter there is

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an associated test statistic, commonly referred to as a  $t$  value, which, when squared, is equivalent to the Wald (W) test (Lee, 1985). Unlike the LM test, the W test is concerned with eliminating a set of one or more unnecessary parameter estimates from a model.

Both LM and W statistics are asymptotically distributed as one degree-of-freedom noncentrality parameters that are used in relation to tabled values of noncentral chi-square distribution for power assessment. The relationships among the LM, W, and LR tests are asymptotically equivalent (Buse, 1982; Satorra, 1989), and the use of these test statistics for power approximation has been shown to be asymptotically similar to the Saris-Satorra (1985; also Saris & Stronkhorst, 1984) approach.

Adopting a different approach, MacCallum et al. (1996) propose a power estimation procedure that concerns overall model fit of the population covariance structure. Instead of testing exact fit for a given model versus a specific alternative, their approach involves the use of the RMSEA (Steiger & Lind, 1980). By hypothesizing and testing null,  $H_0$ , and alternative,  $H_a$ , models, the difference between RMSEA values is used to evaluate the degree to which a model is considered to be incorrect in the population. These values (i.e., RMSEA0 and RMSEAa) are used to determine values of noncentrality parameters for the noncentral chi-square distributions that are used in turn to determine power.

The procedure outlined by MacCallum et al. (1996) can be easily applied in practice. With this approach, the researcher specifies test hypotheses between a null and an alternative, along with sample size and model degrees of freedom required for achieving a predetermined power value (e.g., a conventional value of .80). For instance, if one takes a prespecified significance level  $\alpha = .05$  and (a) null hypothesis of close fit ( $RMSEA_0 \leq .05$ ) against an alternative of poorer fit ( $RMSEA_a = .08$ ) and (b) the null hypothesis of not-close fit ( $RMSEA_0 \leq .05$ ) against the alternative of close fit ( $RMSEA_a = .01$ ), power can be determined by consulting the table (Table 2, MacCallum et al., 1996, p. 142). Power estimates in this table show power as a monotonically increasing function of sample size and degrees of freedom. With small to moderate sample sizes (e.g.,  $N = 500$ ), models with fewer degrees of freedom (e.g.,  $df = 5$ ), such as a simple linear LGM, tend to have lower power estimates than models with higher degrees of freedom (e.g.,  $df = 20$ ).

In the following sections, power estimation procedures described previously are applied to LGMs in two situations. The first situation involves power estimation for growth rate variance in a simple LGM. The second example focuses on power estimation for mean growth rate in a multiple population context.

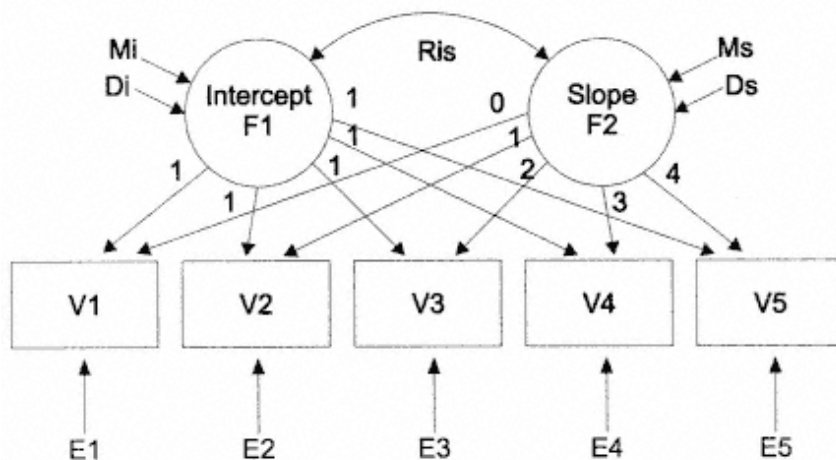


Fig. 10.1.  
Representation of the linear growth model.

Example 10.1  
Power Estimation in LGM

The model to be used in illustrating power testing is depicted in Fig. 10.1 and represents a linear growth curve model with five measures for a sample of 500 cases.

The parameter values for the model of Fig. 10.1 are:  $M_i = 1.379$ ,  $M_s = .019$ ,  $D_i = .152$ ,  $E_1 = .051$ ,  $E_2 = .074$ ,  $E_3 = .118$ ,  $E_4 = .138$ , and  $E_5 = .267$ , where  $E$  represents measurement errors. For simplicity, the covariance,  $R_{is}$ , is assumed to be zero. These values can be specified in a model in which no specific growth rate is hypothesized. This is the  $H_0$  model.

Suppose that the interest of the test is to determine the variance of the growth rate. Based on prior research, assume that the variance of the growth rate,  $D_s$ , is 3% of the variance of its initial status factor,  $D_i$ , that is,  $D_s = .005$ . This value of  $D_s$ , along with values specified in  $H_0$ , constitutes  $H_a$ .

Following Satorra and Saris' (1985) steps previously outlined, an implied covariance matrix with aforementioned sets of parameter values is generated using the EQS program shown in Input 10.1. Parameter values include the hypothesized  $D_s$  value, which is labeled  $D_2$  in Input 10.1.

INPUT 10.1  
EQS Specifications for the Original Model

```

/TITLE
STEP 1: THE ORIGINAL MODEL SPECIFICATIONS
/SPECIFICATIONS
CAS=500; VAR=5; ME=ML; MA=COV; ANAL=MOMENT;
/LABELS
V1=VAR_T1; V2=VAR_T2; V3=VAR_T3; V4=VAR_T4; V5=VAR_T5;
F1=VAR_INT; F2=VAR_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
V4=F1+3F2+E4;
V5=F1+4F2+E5;
F1=1.379*V999+D1;
F2= .019V999+D2;
/VARIANCES
E1=.051; E2=.074; E3=.118; E4=.138; E5=.267; D1=.152; D2=.005;
/MATRIX
1

```

```

0 1
0 0 1
0 0 0 1
0 0 0 0 1
/STANDARD DEVIATIONS
1 1 1 1 1
/MEANS
0 0 0 0 0
/PRINT
CORRELATION=YES;
/TECH
ITER=0;
/END

```

Note that all parameters in the input program are fixed at the values listed above so that no iteration is needed (as shown in lines /TECH ITER = 0;). The covariance matrix among the five variables generated from this run and their reproduced mean values are displayed in Table 10.1.

TABLE 10.1  
Variance/Covariance Matrix and Means From Simulated Data

| Variable | Var 1 | Var 2 | Var 3 | Var 4 | Var 5 |
|----------|-------|-------|-------|-------|-------|
| Var 1    | .203  |       |       |       |       |
| Var 2    | .152  | .231  |       |       |       |
| Var 3    | .152  | .162  | .290  |       |       |
| Var 4    | .152  | .167  | .182  | .335  |       |
| Var 5    | .152  | .172  | .192  | .212  | .499  |
| Mean     | 1.379 | 1.398 | 1.417 | 1.436 | 1.455 |

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INPUT 10.2  
EQS Specifications for  $H_0$  Model

```

/TITLE
STEP 2: TESTING H0 FROM STEP 1 MATRIX
/SPECIFICATIONS
CAS=500; VAR=5; ME=ML; MA=COV; ANAL=MOMENT;
/LABELS
V1=VAR_T1; V2=VAR_T2; V3=VAR_T3; V4=VAR_T4; V5=VAR_T5;
F1=VAR_INT; F2=VAR_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
V4=F1+3F2+E4;
V5=F1+4F2+E5;
F1=1.379*V999+D1;
F2= .019*V999+D2;
/VARIANCES
E1=.051*; E2=.074*; E3=.118*; E4=.138*; E5=.267*;
D1=.152*; D2=0;
/MATRIX
.203
.152 .231
.152 .162 .290
.152 .167 .182 .335
.152 .172 .192 .212 .499
/MEANS
1.379 1.398 1.417 1.436 1.455
/LMTEST
/END

```

Next, the implied covariance matrix from Table 10.1 is analyzed under  $H_0$ , assuming  $D_s = 0$ , while keeping the sample size the same ( $N = 500$ ). The input necessary for this EQS run is presented in Input 10.2.



The analysis yielded a test statistic value of 26.682,  $p < .009$ , with 12 degrees of freedom. Given this estimate of the noncentrality parameter, the power of the test could be determined from a power table. Based on power estimates at the .05 level,  $df = 12$ ,  $N = 500$ , and noncentrality parameter of 26.682, the power was .95, suggesting a .95 probability of detecting a false  $H_0$  when the alternative parameter value ( $D_s$ ) is true. This indicates that the test specified in this example is highly sensitive regarding the growth rate variance omitted in the  $H_0$  model. The LM-based estimate, obtained from the same EQS run under  $H_0$ , for  $D_s$  was 29.301, the estimate of the noncentrality parameter. Consulting the power table at an  $\alpha$  level of .05 and 1  $df$  noncentrality parameter showed large power (.97) for this individual parameter test.

To evaluate the full growth curve model using MacCallum et al.'s (1996) method, two hypotheses are tested: a test of close fit and a test of not-close fit. For the test of close fit,  $RMSEA_0 = .05$  and  $RMSEA_a = .08$  were specified. For the test of not-close fit,  $RMSEA_0 = .05$  and  $RMSEA_a = .01$

were specified. Using the program written in SAS (SAS, 1990; MacCallum et al., 1996, p. 148) the power of the test for the overall model, with  $N = 500$ ,  $\alpha$  level of .05, and  $df$  of 11, was .65 for the close fit test and .59 for the not-close fit test. Thus, overall statistical power for this model, based on MacCallum et al.'s method, was moderately high.

**Example 10.2**  
Power Estimation in a Multiple Population Context

Traditionally, the effectiveness of an intervention is assessed in terms of group level mean and variance of the targeted behavior. True random assignment to condition attempts to equate the treatment and control groups prior to the intervention, and the treatment effect is typically measured as the difference between the mean values of the two groups on the outcome behavior after the intervention. The hypothesis tested, the null hypothesis, assumes that the means of the treatment populations are equal. The alternative hypothesis is a mutually exclusive statement asserting that some population treatment means are not equal, that is, treatment effects are present.

Many interventions aim not to alter a targeted behavior at a particular time, but to change the normative growth trajectory for the targeted behavior over time. Recasting treatment evaluation in terms of growth, the effectiveness of an intervention is the extent to which it is capable of altering the normative growth trajectory that exists without the treatment. Although typical analytic approaches can be useful in evaluating treatment effects under rather restrictive assumptions, key limitations arise when these techniques are used to study systematic change. These include reduced statistical power, an inability to model individual differences in change, and unnecessary restriction of inferences that can be obtained from the observed data (Rogosa, 1988; Rogosa & Willett, 1985). These limitations are particularly salient when attempting to assess an intervention's influence on the rate of change over time.

Muthén and Curran (1997) provide a framework for analysis of treatment effects in intervention studies. Their strategy is based on the two-group formulation described by a path diagram such as the one shown in Fig. 10.2. In this figure, the top group represents the control condition and the bottom group represents the treatment group. The two groups may be regarded as two different populations (Jöreskog & Sörbom, 1979) in that the control group represents normative growth, which would have been observed in the intervention group absent treatment. The intervention

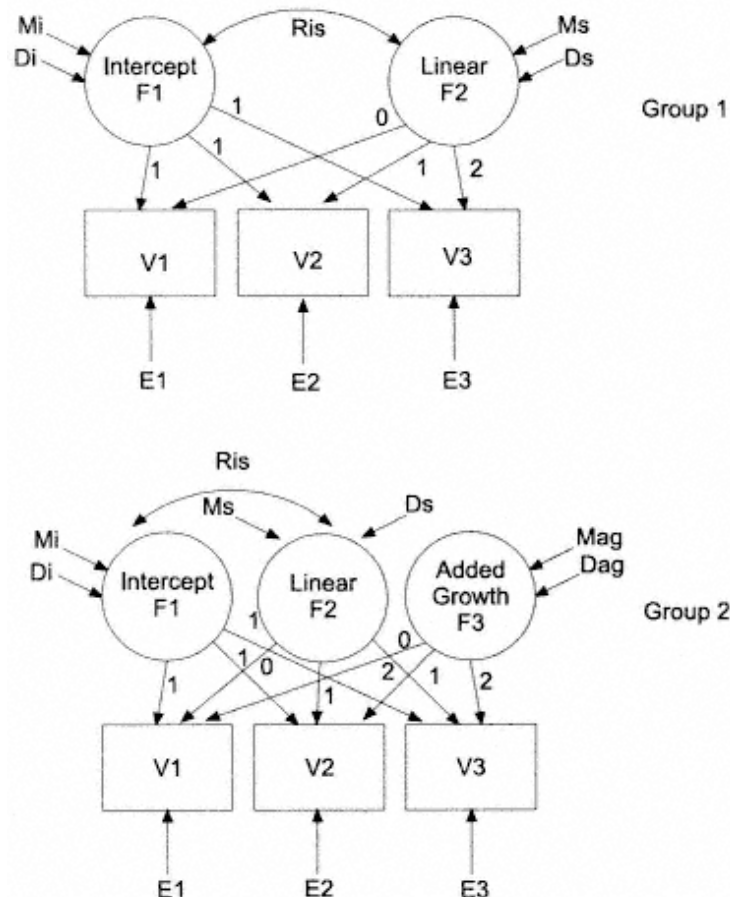


Fig. 10.2.  
Representation of the multiple-sample LGM.

effect is assessed by comparing the set of growth trajectories in the treatment population with those in the control population.

Although treatment effects can be tested by imposing equality constraints across the two groups with a two-factor growth model hypothesized for each condition, Muthén and Curran (1997) propose an alternative method of adding a growth factor ( $F_3$  in Fig. 10.2) to the treatment group. Whereas the first two factors (i.e., intercept and slope) are constrained to be equal in both groups, the third growth factor in the

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TABLE 10.2  
Parameter Estimates for the Intervention Growth Model

| <i>Parameter</i> | <i>Group 1 Effect</i> | <i>Group 2 Effect</i> |
|------------------|-----------------------|-----------------------|
| <b>Means</b>     |                       |                       |
| Intercept        | 1.510                 | 1.510                 |
| Slope            | .174                  | .174                  |
| Added growth     |                       | .254                  |
| <b>Variances</b> |                       |                       |
| Intercept        | 1.032                 | 1.032                 |
| Slope            | .343                  | .343                  |
| Added growth     |                       | .178                  |
| Covariance       | -.075                 | -.075                 |

treatment group reflects the degree of incremental/decremental growth that is attributable to the treatment condition.

An artificial longitudinal treatment data set was generated to demonstrate the analysis of treatment effects and power estimation using Muthén and Curran's (1997) method. The developmental model was based on a sample of 300 cases, equally distributed over the two conditions (150 treatment and 150 control). Specific parameters in this model include intercepts, slopes, and added growth means and variances, and the covariance between the intercept and slope factors, which are shown in Table 10.2.

Suppose that the interest here is to detect the treatment effect,  $M_{ag}$ . As a first step, a model representing  $H_a$  is estimated. The EQS input specifications for this model are presented in Appendix 10.1.

The implied covariance matrix and the reproduced means generated for the separate treatment and control groups using the parameter estimates from Table 10.2 are presented in Table 10.3.

TABLE 10.3  
Covariance Matrix and Reproduced Means for the Hypothesized Model

|           | <i>V1</i> | <i>V2</i> | <i>V3</i> |
|-----------|-----------|-----------|-----------|
| Treatment | 1.854     |           |           |
|           | .957      | 2.200     |           |
|           | .882      | 1.493     | 2.685     |
|           | 1.510     | 1.684     | 1.858     |
| Control   | 1.854     |           |           |
|           | .957      | 2.378     |           |
|           | .882      | 1.849     | 3.397     |
|           | 1.510     | 1.938     | 2.366     |

*Note.* Covariances are in the triangle; means are presented in the bottom rows of each matrix.

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For an evaluation of treatment effects in terms of its power, the model of Fig. 10.2 is fit to population moments shown in Table 10.3 under  $H_0$  in which the added growth factor mean is constrained to zero. EQS input for this model is presented in Appendix 10.2.

The model procedures for this test resulted in a test statistic of  $\chi^2(9, N = 300) = 7.264, p = .60$ . Given the chi-square value of 7.238 with 1 degree of freedom and  $\alpha = .05$ , power was estimated at approximately .77.

For the LM-based estimate, constraining the added growth factor mean to zero resulted in an LM value of 7.196. Similarly, the squared  $t$  value for the freely estimated factor mean was 7.355. The noncentrality parameters for all three procedures were very close (7.264 for LR, 7.196 for LM, and 7.355 for W). With  $df = 1, \alpha = .05, N = 300$ , and a noncentrality parameter of approximately 7, the power of the test of the null hypothesis for the added growth factor mean was .77. These conditions produced a .77 probability of detecting a false null hypothesis when the alternative parameterization (i.e., the restriction imposed on the added growth factor mean) is true.

The next question related to power estimation is how well the model hypothesized in Fig. 10.2 approximates the population covariance matrix in terms of the RMSEA index. Again, similar tests of both close fit and not-close fit hypotheses demonstrated previously were conducted. With 9 degrees of freedom and a moderate sample size of 300, the overall model fit of Fig. 10.2, according to MacCallum et al.'s (1996) method, showed a low power value of .39 for the close fit test and .28 for the not-close fit test. Assuming the model is correct (i.e., no specification errors), a sample size of about 900 cases would be required to achieve a power of .80 for this model, which is characterized by low degrees of freedom ( $df = 9$ ).

Power for a comparable factorial repeated measures ANOVA model was estimated at about .61 for the same group by linear trend interaction (e.g., differences in mean level growth between treatment and control groups). In this case, resorting to the more traditional ANOVA approach to power analysis reduced the power of the test. To achieve a power of .77, as was obtained from the LGM analysis, with the ANOVA method, the sample size ( $N = 300$ ) would have to be increased to 436. This can be shown by taking the noncentrality parameter value of 7.264 generated by the LGM procedure and substituting the value into the following formula (Saris & Stronkhorst, 1984, p. 212):

$$(NCP_r / NCP_o) N_s = N_r \quad 10.1$$

where  $NCP_r$  is the required value of the noncentrality parameter,  $NCP_o$  is the obtained value of the noncentrality parameter,  $N_s$  is the sample size used, and  $N_r$  is the required sample size.

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Substituting the appropriate values into the equation resulted in the value of 436 (i.e.,  $(7.264 / 5.00) \times 300$ ), indicating that a sample of at least 436 subjects would be required for a power of .77 to detect a misspecification in the added growth factor mean, assuming a .05 level of significance. Findings suggest that the LGM model had substantially greater power to detect the very same effect compared to the repeated measures ANOVA model, and required 30% fewer subjects for the same effect size and power as the ANOVA model. These findings are similar to those reported by Curran and Muthén (in press), who found that to detect a small effect size at a power of .80, the LGM model they tested required 28% fewer subjects than that required for the same effect size and power in a comparable analysis of covariance (ANCOVA) model.

## Summary

In this chapter, methods and applications related to power estimation were presented within a latent variable growth curve framework. Specifically, based on the work of Satorra and Saris (1983, 1985; Satorra, 1989) and MacCallum et al. (1996), methods for evaluating power of a single parameter and overall model fit were described in the context of LGMs. Subsequent applications of power estimation in growth analysis, involving studies of natural growth processes (e.g., growth rate) and treatment effects in experimental designs, were illustrated.

In fitting latent variable models, inferences are made from observed data to the model which is believed to be generating those observations (Tanaka, 1987). These inferences depend, in part, on the degree to which the information in the sample is representative of the complete population, which, in turn, depends on the adequacy of the obtained sample size. Because large samples contain more information, they are likely to yield models more accurately representing those processes that exist within the population (Tanaka, 1987).

Statistical theory in latent variable modeling is asymptotic in nature, based on the premise that confidence can be expressed in the distribution of the obtained test statistics and standard errors as long as the sample is large. However, studies attempting to provide some sample size guidelines have been largely inconclusive (i.e., Gerbing & Anderson, 1985; Tanaka, 1987), making it difficult to establish rules for determining adequate sample sizes. Despite conflicting results, however, the general consensus is that sample size appropriateness ultimately depends on the ratio of the number of subjects in the sample to the number of parameters estimated in the model (Tanaka).

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Another approach to the sample size problem has been to rely more heavily on alternative goodness-of-fit indices (e.g., NNFI, CFI, and RMSEA). These indices are generalizable to any latent variable model; however, they are particularly useful in smaller samples for detecting possible model misspecifications. In these situations, alternative fit indices may be more valid than relying on the chi-square statistic, which, in small samples, may not be distributed as a chi-square variable (Tanaka, 1987).

Ideally, power analysis should be integrated within the same statistical framework used in regular analyses. From a statistical point of view, the best procedures for power estimation should:

1. Employ the same statistical model for power and sample size estimation as that used to perform the desired analysis.
2. Cover the situations most commonly encountered by researchers.
3. Be flexible enough to deal with new or unusual situations.
4. Allow easy exploration of multiple values of input parameters.

5. Allow estimation of sampling variance from pilot data and sampling variability statistics reported in the literature.

Given the generality of the latent variable approach to modeling growth and developmental processes, power estimation and sample size determination are readily available through standard latent variable techniques. Power estimation within the latent variable modeling framework is directly related to the parameter values of a specified model. The relations among values of the level of significance, measures of effect size, the sample size, and the degrees of freedom are identical to those presented in earlier sections. Within the latent variable framework, a number of competing models and relationships can easily be assessed, providing important guidance for design considerations.

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## Chapter 11 Summary

Longitudinal models have a number of important advantages over cross-sectional models. One advantage is that alternative assumptions can be made concerning the parameters of the model. Usually, this allows for a less ambiguous determination of the direction and relative magnitude of causality between variables measured at two points in time (Gollob & Reichardt, 1987).

Perhaps the most important advantage of longitudinal models is their correspondence with commonly stated conditions for inferring a causal connection between two variables. Among SEM methodologists, there is clear consensus that three conditions must be satisfied to infer causality: the presumed cause and effect are related, the presumed cause precedes the effect in time, and other competing explanations for the observed effect can be ruled out (Bollen, 1989; Kessler & Greenberg, 1981). With cross-sectional data, the second condition can never be met.

A standard approach to studying change has been the autoregressive or residual change model, although some researchers have disputed the central role of autoregressive effects (residual change scores) and have instead focused on the simple difference score or on the analysis of growth curves when data are collected on more than two points in time (Rogosa et al., 1982). Even though researchers have pointed out some of the shortcomings of autoregressive models, some developmentalists feel that the most serious problems with autoregressive models have not been highlighted strongly enough (Rogosa & Willett, 1985).

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 hazards involved in using linear panel models when nonlinear growth processes are operative. Linear panel models are not optimal for studying linear growth processes, either. The best that can be done even in multiwave data is to focus on simple change scores between any two points in time.

If one believes that change is systematically related to the passage of time (i.e., growth processes are at work) then growth models have a number of advantages for the study of change and should be employed.

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## Advantages of LGM

LGM methodology provides a number of advantages to researchers studying 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 shape 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. Within the two-factor LGM specification it is possible to test the adequacy of the hypothesized growth form as linear, using a specified growth function, or as nonlinear, using freely estimated parameters that describe the growth form with maximal fit to the data. 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). Simpler, one-factor models may be adequate and preferable on the basis of parsimony, in cases where growth is highly structured. However, the decision to move to a simpler model should be supported by the data in hand. The premature adoption of single-factor models can confound initial status with change and lead to incorrect conclusions about the role of predictor variables.

Another advantage of LGM methodology is its ability to incorporate 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. In addition, with the use of multivariate LGMs, it is possible to determine whether development in one behavior covaries with other behaviors when assessed repeatedly. The associative model represents a means by which to model multiple behaviors simultaneously over time, and to determine the extent of covariation in the development of pairs of behaviors. Higher order LGMs extend the test of dynamic associations of behaviors over time by examining the degree to which relations among the growth factors can be described by common higher order constructs. For example, the curve-of-

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factors model merges a psychometric common factor model for the multiple measures within a specific occasion and testing of a growth curve model of the common factor scores over time. A different higher order multivariate model, the factor-of-curves model, describes individual differences within separate univariate series and forms a common factor model to describe these differences among the basic growth curves. In practical terms, these three multivariate LGMs offer differing opportunities for evaluating the dynamic structure of both intra- and interindividual change, and represent a logical progression in the paradigm of testing the adequacy of latent growth curve representations of behavioral dynamics.

Similar to other SEMs, LGMs also allow for the testing of multiple samples in the same model. When data are gathered from different individuals who can be identified as belonging to certain groups, such as males and females, age cohorts, ethnicities, and treatment versus control conditions, it is often of interest to explore whether there are multiple populations rather than a single population, as well as multiple developmental pathways rather than a single underlying trajectory for all individuals. Through the use of multiple-sample analyses, developmental hypotheses on multiple populations can be evaluated simultaneously when data exist on the same variables over the same developmental period. First, growth can be studied by a separate analysis of each group. Next, a multiple-group analysis can be performed to fit growth factors found in the single-sample analyses to all populations simultaneously. The similarity and invariance of key parameters across populations can be tested (Alwin & Jackson, 1981; Bentler & Wu, 1995; Jöreskog, 1971), providing useful information about growth and covariates of growth across varying populations.

A specific example of the multiple-sample approach, and of a study where data are missing by design, is the cohort-sequential LGM. This accelerated design provides a means by which adjacent segments consisting of limited longitudinal data on a specific age cohort can be linked with similar segments from other temporally related age cohorts to determine the existence of a common developmental trend, or growth curve. This technique allows the researcher to approximate a long-term longitudinal study by conducting several short-term longitudinal studies of different age cohorts simultaneously. A cohort-sequential design can reduce problems of cumulative testing effects and attrition, and produce results more quickly than in a single-cohort design over the same developmental period. Another advantage of the cohort-sequential design is that following several cohorts, rather than one, allows the researcher to test for cohort effects, to determine whether those trends observed in the repeated observations are corroborated within short time periods for each age cohort.

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Hierarchical or multilevel models are also possible within the LGM approach. Hierarchical models represent a useful extension of traditional variance component models and offer the possibility of making use of within-cluster differences in parameter estimates (Kreft, 1994). Within the SEM framework, it is now possible to test hierarchical LGMs using full ML or limited information approaches, such as Muthén's (1991, 1994) MCA approach. These developments permit the construction, estimation, and testing of a variety of complex models using hierarchically structured data, and allow for potentially greater insight into the developmental nature, antecedents, and sequelae of a number of behavioral outcomes. The flexibility of the multilevel covariance structure model makes it a particularly attractive analytic tool for LGM, and for investigations of growth and development among variables of interest with clustered and multilevel data.

Although researchers analyzing regression models have routinely incorporated interaction effects, testing nonlinear and interactive effects of latent variables using SEM methodology has been rare, partly due to the difficulty of incorporating nonlinear functions of latent variables in the models. With methodological advances, however, techniques are increasingly available for including interaction effects in SEM analyses, including LGMs. The ability to include interactive effects, of not only static variables but also growth processes, affords the opportunity to test hypotheses that will likely contribute to the understanding of behavioral processes in a variety of domains.

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. Within LGM, model-based procedures can be used to analyze incomplete data using either multiple-sample SEM or raw 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.

#### Limitations of LGM

Despite numerous attractions, LGM is not always the appropriate analytical choice. The technique has limitations, including the necessity for relatively large samples. In fitting latent variable models, inferences are made from observed data to the model thought to be generating those observations (Tanaka, 1987). In part, these inferences depend on the degree

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to which the information in the sample is representative of the same information in the complete population, which in turn depends on the adequacy of the sample size. More confidence can be expressed in a model based on a large sample that represents accurately those processes that exist within the population (Tanaka, 1987). The statistical theory in LGM is asymptotic in nature, based on the premise that confidence can be expressed in the distribution of the obtained test statistics and standard errors as long as the total sample size is large.

Another limitation of the LGM approach involves the restrictive requirement of equal number and spacing of assessments for all individuals. Ware (1985) refers to this kind of data as "balanced-on-time." If the number of time points or the spacing between time points varies across individuals, other, more appropriate growth curve techniques are available (e.g., Bryk & Raudenbush, 1987; Hui & Berger, 1983; Kleinbaum, 1973).

Clearly, a fundamental assumption of growth curve methodology is that change for each individual is systematically related to the passage of time, at least over the 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. In this case, a repeated measures regression approach, such as Generalized Estimating Equations (Liang & Zeger, 1986), would likely be a better choice (see T.E. Duncan, S. C. Duncan, Hops, & Stoolmiller, 1995 for an application of GEE to substance use data).

#### Concluding Remarks

Although acknowledging some limitations of the LGM approach, this book has demonstrated many advantages of LGM, including its flexibility, practicality, and value for modeling developmental processes within the SEM framework. Naturally, there is no single preferred statistical procedure for the analysis of longitudinal data, as different research questions will dictate different data structures and, consequently, different statistical models and methods. However, growth curve methodology, in any form, provides a powerful tool to assist researchers in their efforts to model development at both the inter- and intraindividual levels, and to identify important predictors and outcomes of change.

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## References

- Aber, M.S., & McArdle, J.J. (1991). Latent growth curve approaches to modeling the development of competence. In M. Chandler & M. Chapman (Eds.), *Criteria for competence: Controversies in the conceptualization and assessment of children's abilities* (pp. 231-258). Mahwah, NJ: Lawrence Erlbaum Associates.
- Aitchison, J., & Silvey, D.C. (1958). Maximum likelihood estimation of parameters subject to restraints. *Annals of Mathematical Statistics*, 29, 813-828.
- Aitkin, M., & Longford, N. (1986). Statistical modeling issues in school effectiveness studies. *Journal of the Royal Statistical Society, Series A*, 149, 1-43.
- Akaike, H. (1974). A new look at the statistical model identification. *IEEE Transactions in Automatic Control*, 19, 716-723.
- Allison, P.D., & Hauser, R.M. (1991). Reducing bias in estimates of linear models by remeasurement of a random subsample. *Sociological Methods and Research*, 19, 466-492.
- Alwin, D.F., & Jackson, D.J. (1981). Applications of simultaneous factor analysis to issues of factorial invariance. In D. Jackson & E. Borgatta (Eds.), *Factor analysis and measurement in sociological research: A multi-dimensional perspective* (pp. 249-279). Beverly Hills, CA: Sage.
- Anderson, E.R. (1993). Analyzing change in short-term longitudinal research using cohort-sequential designs. *Journal of Consulting and Clinical Psychology*, 61, 929-940.
- Anderson, E.R. (1995). Accelerating and maximizing information from short-term longitudinal research. In J.M. Gottman (Ed.), *The analysis of change* (pp. 139-163). Mahwah, NJ: Lawrence Erlbaum Associates.
- Anderson, T.W. (1957). ML estimates for a multivariate normal distribution when some observations are missing. *Journal of the American Statistical Association*, 52, 200-203.
- Arbuckle, J.L. (1995). *Amos for Windows. Analysis of moment structures. Version 3.5*. Chicago, IL: SmallWaters.
- Arbuckle, J.L. (1996). Full information estimation in the presence of incomplete data. In G.A. Marcoulides & R.E. Schumacker (Eds.), *Advanced structural equation modeling: Issues and techniques* (pp. 243-277). Mahwah, NJ: Lawrence Erlbaum Associates.
- Bell, R.Q. (1953). Convergence: An accelerated longitudinal approach. *Child Development*, 24, 145-152.
- Bentler, P.M. (1986). *Lagrange Multiplier and Wald tests for EQS and EQS/PC*. Los Angeles, CA: BMDP Statistical Software.
- Bentler, P.M., & Chou, C.P. (1986, April). *Statistics for parameter expansion and contraction in structural models*. Paper presented at the American Educational Research Association Meeting, San Francisco, CA.
- Bentler, P.M., & Dijkstra, T. (1985). Efficient estimation via linearization in structural models. In P.R. Krishnaiah (Ed.), *Multivariate analysis VI* (pp. 9-42). Amsterdam: North-Holland.
- Bentler, P.M., & Wu, E. (1995). *EQS structural equations program manual*. Encino, CA: Multivariate Software.
- Biglan, A., Duncan, T.E., Ary, D., & Smolkowski, K. (1995). Peer and parental influences on adolescent tobacco use. *Journal of Behavioral Medicine*, 18, 315-330.
- Bollen, K.A. (1989). *Structural equations with latent variables*. New York: Wiley.
- Bozdogan, H. (1987). Model selection and Akaike's information criteria (AIC): The general theory and its analytical extensions. *Psychometrika*, 52, 345-370.

- Browne, M., & Cudeck, R. (1993). Alternative ways of assessing model fit. In K.A. Bollen & J.S. Long (Eds.), *Testing structural equation models* (pp. 136-162). Newbury Park, CA: Sage.
- Bryk, A.S., & Raudenbush, S.W. (1987). Application of hierarchical linear models to assessing change. *Psychological Bulletin*, 101, 147-158.
- Bryk, A., & Raudenbush, S. (1992). *Hierarchical linear models in social and behavioral research: Applications and data analysis methods*. Newbury Park, CA: Sage.
- Burchinal, M., & Appelbaum, M.I. (1991). Estimating individual developmental functions: Methods and their assumptions. *Child Development*, 62, 23-43.
- Burstein, L. (1980). The analysis of multilevel data in educational research and evaluation. *Review of Research in Education*, 8, 158-233.
- Buse, A. (1982). The likelihood ratio, Wald, and Lagrange multiplier tests: An expository note. *The American Statistician*, 36, 153-157.
- Chassin, L., Curran, P.J., Hussong, A.M., & Colder, C.R. (1996). The relation of parent alcoholism to adolescent substance use: A longitudinal follow-up study. *Journal of Abnormal Psychology*, 105, 70-80.
- Cohen, J. (1988). *Statistical power analysis for the behavioral sciences* (2nd ed.). Mahwah, NJ: Lawrence Erlbaum Associates.
- Corballis, M.C., & Traub, R.E. (1970). Longitudinal factor analysis. *Psychometrika*, 35, 79-99.

Cronbach, L.J. (1976). *Research on classrooms and schools: Formulation of questions, design, and analysis*. Unpublished manuscript, Palo Alto, CA: Stanford University, Stanford Evaluation Consortium, School of Education.

Curran, P.J., & Muthén, B.O. (in press). The application of latent curve analysis to testing developmental theories in intervention research. *American Journal of Community Psychology*.

Curran, P.J., Stice, E., & Chassin, L. (1997). The relation between adolescent alcohol use and peer alcohol use: A longitudinal random coefficients model. *Journal of Consulting and Clinical Psychology, 65*, 130-140.

de Leeuw, J., & Kreft, I. (1986). Random coefficient models for multilevel analysis. *Journal of Educational Statistics, 11*, 57-85.

Duncan, S.C., Alpert, A., Duncan, T.E., & Hops, H. (1997). Adolescent alcohol use development and young adult outcomes. *Drug and Alcohol Dependence, 49*, 39-48.

Duncan, S.C., & Duncan, T.E. (1994). Modeling incomplete longitudinal substance use data using latent variable growth curve methodology. *Multivariate Behavioral Research, 29*, 313-338.

Duncan, S.C., & Duncan, T.E. (1996). A multivariate latent growth curve analysis of adolescent substance use. *Structural Equation Modeling, 3*, 323-347.

Duncan, S.C., & Duncan, T.E., & Hops, H. (1996). Analysis of longitudinal data within accelerated longitudinal designs. *Psychological Methods, 1*, 236-248.

Duncan, T.E., & Duncan, S.C. (1995). Modeling the processes of development via latent variable growth curve methodology. *Structural Equation Modeling, 2*, 187-213.

Duncan, T.E., & Duncan, S.C., Alpert, A., Hops, H., Stoolmiller, M., & Muthén, B. (1997). Latent variable modeling of longitudinal and multilevel substance use data. *Multivariate Behavioral Research, 32*, 275-318.

Duncan, T.E., Duncan, S.C., & Hops, H. (1994). The effect of family cohesiveness and peer encouragement on the development of adolescent alcohol use: A cohort-sequential approach to the analysis of longitudinal data. *Journal of Studies on Alcohol, 55*, 588-599.

Duncan, T.E., Duncan, S.C., & Hops, H. (1996). The role of parents and older siblings in predicting adolescent substance use: Modeling development via structural equation latent growth methodology. *Journal of Family Psychology, 10*, 158-172.

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Duncan, T.E., Duncan, S.C., Hops, H., & Stoolmiller, M. (1995). An analysis of the relationship between parent and adolescent marijuana use via generalized estimating equation methodology. *Multivariate Behavioral Research, 30*, 317-339.

Duncan, T.E., Duncan, S.C., & Li, F. (1998). A comparison of model- and multiple imputation-based approaches to analyses with partial missingness. *Structural Equation Modeling, 5*, 1-21.

Duncan, T.E., Duncan, S.C., & Stoolmiller, M. (1994). Modeling developmental processes using latent growth structural equation methodology. *Applied Psychological Measurement, 18*, 343-354.

Duncan, T.E., & McAuley, E. (1993). Social support and efficacy cognitions in exercise adherence: A latent growth curve analysis. *Journal of Behavioral Medicine, 16*, 199-218.

Duncan, T.E., Tildesley, E.A., Duncan, S.C., & Hops, H. (1995). The consistency of family and peer influences on the development of substance use in adolescence. *Addiction, 90*, 1647-1660.

Elliott, D.S. National Youth Survey [United States]: Wave I, 1976 [Computer file]. ICPSR version. Boulder, CO: University of Colorado, Behavioral Research Institute [producer], 1977. Ann Arbor, MI: Inter-university Consortium for Political and Social Research [distributor], 1994.

Ge, X., Lorenz, F.O., Conger, R.D., & Elder, G.H. (1994). Trajectories of stressful life events and depressive symptoms during adolescence. *Developmental Psychology, 30*, 467-483.

Gerbing, D.W., & Anderson, J.C. (1985). The effects of sampling error and model characteristics on parameter estimation for maximum likelihood confirmatory factor analysis. *Multivariate Behavioral Research, 30*, 255-271.

Goldstein, H.I. (1986). Multilevel mixed linear model analysis using iterative general least squares. *Biometrika, 73*, 43-56.

Gollob, H.F., & Reichardt, C.S. (1987). Taking account of time lags in causal models. *Child Development, 58*, 80-92.

Hakstian, A.R. (1973). Procedures for factor analytic treatment of measures obtained on different occasions. *British Journal of Mathematical and Statistical Psychology, 26*, 219-239.

Harnqvist, K. (1978). Primary mental abilities of collective and individual levels. *Journal of Educational Psychology, 70*, 706-716.

Harris, C.W. (1963). *Problems in measuring change*. Madison: University of Wisconsin Press.

Hayduck, L. (1987). *Structural equation modeling with LISREL*. Baltimore, MD: Johns Hopkins University Press.

Haynam, G.E., Govindarajulu, Z., & Leone, F.C. (1973). Tables of the cumulative noncentral chi-square distribution. In H.L. Harter and D.B. Owen (Eds.), *Selected tables in mathematical statistics* (Vol. 1, pp. 1-78). Providence, RI: Mathematical Statistical Society.

Horn, J.L., McArdle, J.J., & Mason, R. (1983). When is invariance not invariant: A practical scientist's look at the ethereal concept of factor invariance. *The Southern Psychologist, 1*, 179-188.

Hoyle, R. (1995). The structural equation modeling approach: Basic concepts and fundamental issues. In R.H. Hoyle (Ed.), *Structural equation modeling: Issues and applications* (pp. 1-15). Thousand Oaks, CA: Sage.

Hu, L., & Bentler, P.M. (1995). Evaluating model fit. In R.H. Hoyle (Ed.), *Structural equation modeling: Issues and applications* (pp. 76-99). Thousand Oaks, CA: Sage.

Hui, S.L., & Berger, J.O. (1983). Empirical Bayes estimation of rates in longitudinal studies. *Journal of the American Statistical Association*, 78, 753-760.

Jaccard, J., & Wan, C.K. (1996). *LISREL approaches to interaction effects in multiple regression*. Thousand Oaks, CA: Sage.

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---

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Jöreskog, K.G. (1971). Simultaneous factor analysis in several populations. *Psychometrika*, 57, 409-426.

Jöreskog, K.G., & Sörbom, D. (1979). *Advances in factor analysis and structural equation models*. Cambridge, MA: Abt Books.

Jöreskog, K.G., & Sörbom, D. (1993). *LISREL 8: Structural equation modeling with the SIMPLIS command language*. Chicago: Scientific Software International.

Jöreskog, K.G., & Yang, F. (1996). Non-linear structural equation models: The Kenny-Judd model with interaction effects. In G.A. Marcoulides & R.E. Schumacker (Eds.), *Advanced structural equation modeling: Issues and techniques* (pp. 57-88). Mahwah, NJ: Lawrence Erlbaum Associates.

Kaplan, D. (1990). Evaluating and modifying covariance structure models: A review and recommendation. *Multivariate Behavioral Research*, 25, 137-155.

Kaplan, D. (1995). Statistical power in structural equation modeling. In R.H. Hoyle (Ed.), *Structural equation modeling: Concepts, issues, and applications* (pp. 100-137). Thousand Oaks, CA: Sage.

Keesling, J.W., & Wiley, D.E. (1974, March). *Regression models of hierarchical data*. Paper presented at the Annual Meeting of the Psychometric Society, Palo Alto, CA.

Kenny, D., & Judd, C.M. (1984). Estimating the nonlinear and interaction effects of latent variables. *Psychological Bulletin*, 96, 201-210.

Kessler, R.C., & Greenberg, D.F. (1981). *Linear panel analysis: Models of quantitative change*. New York: Academic Press.

Kirk, R.E. (1982). *Experimental design: Procedures for the behavioral sciences* (2nd ed.) Monterey, CA: Brooks/Cole.

Kleinbaum, D.C. (1973). A generalization of the growth curve model which allows missing data. *Journal of Multivariate Analysis*, 3, 117-124.

Koch, G.G. (1983). Intraclass correlation coefficient. *Encyclopedia of Statistical Sciences*, 4, 212-217.

Kraemer, H.C., & Thiemann, S. (1987). *How many subjects?* Thousand Oaks, CA: Sage.

Kreft, I.G. (1994). Multilevel models for hierarchically nested data: Potential applications in substance abuse prevention research. In L. Collins & L. Seitz, (Eds.), *Advances in data analysis for prevention intervention research* (NIDA Research Monograph No. 142; pp. 140-183). Washington, DC: Government Printing Office.

Lee, S.Y. (1985). On testing functional constraints in structural equation models. *Biometrika*, 57, 239-251.

Lee, S.Y., & Bentler, P.M. (1980). Some asymptotic properties of constrained generalized least squares estimation in covariance structure models. *South African Statistical Journal*, 14, 1221-1236.

Li, F., Harmer, P., Duncan, T.E., Duncan, S.C., Acock, A., & Boles, S. (1998). Approaches to testing interaction effects using structural equation modeling methodology. *Multivariate Behavioral Research*, 33, 1-39.

Liang, K.Y., & Zeger, S.L. (1986). Longitudinal data analysis using generalized linear models. *Biometrika*, 73, 13-22.

Lipsey, M.W. (1990). *Design sensitivity: Statistical power for experimental research*. Newbury Park, CA: Sage.

Little, R.J.A., & Rubin, D.B. (1987). *Statistical analysis with missing data*. New York: Wiley.

Little, R.J.A., & Rubin, D.B. (1989). The analysis of social science data with missing data. *Sociological Methods and Research*, 18, 292-326.

Longford, N.T. (1987). A fast scoring algorithm for maximum likelihood estimation in unbalanced mixed models with nested effects. *Biometrika*, 74, 817-827.

page\_146

---



- MacCallum, R.C., Browne, M.W., & Sugawara, H.M. (1996). Power analysis and determination of sample size for covariance structure modeling. *Psychological Methods, 1*, 130-149.
- MacCallum, R.C., & Hong, S. (1997). Power analysis in covariance structure modeling using GFI and AGFI. *Multivariate Behavioral Research, 32*, 193-210.
- Marsh, H. (1985). The structure of masculinity/femininity: An application of confirmatory factor analysis to higher-order factor structures and factorial invariance. *Multivariate Behavioral Research, 20*, 427-449.
- Mason, W.M., Wong, G., & Entwistle, B. (1984). Contextual analysis through the multilevel linear model. In S. Leinhardt (Ed.), *Sociological Methodology* (pp. 72-103). San Francisco: Jossey-Bass.
- McArdle, J.J. (1988). Dynamic but structural equation modeling of repeated measures data. In R.B. Cattell & J. Nesselroade (Eds.), *Handbook of multivariate experimental psychology* (2nd ed., pp. 561-614). New York: Plenum Press.
- McArdle, J.J., & Anderson, E.R. (1989). Latent growth models for research on aging. In L.E. Biren & K.W. Schaie (Eds.), *The handbook of the psychology of aging* (3rd ed., pp. 21-44). San Diego, CA: Academic Press.
- McArdle, J.J., Anderson, E., & Aber, M.S. (1987). Convergence hypotheses modeled and tested with linear structural equations. Data for an aging population. *Proceedings of the 1987 Public Health Conference on Records and Statistics* (DHHS Pub. No. (PHS) 88-1214), Hyattsville, MD.
- McArdle, J.J., & Epstein, D. (1987). Latent growth curves within developmental structural equation models. *Child Development, 58*, 110-133.
- McArdle, J.J., & Hamagami, F. (1991). Modeling incomplete longitudinal and cross-sectional data using latent growth structural models. In L.M. Collins & J.C. Horn (Eds.), *Best methods for the analysis of change* (pp. 276-304). Washington, DC: American Psychological Association.
- McArdle, J.J., & Hamagami, F. (1992). Modeling incomplete longitudinal and cross-sectional data using latent growth structural models. Special Issue: Quantitative topics in research on aging. *Experimental Aging Research, 18*, 145-166.
- McArdle, J.J., Hamagami, F., Elias, M.F., & Robbins, M.A. (1991). Structural modeling of mixed longitudinal and cross-sectional data. *Experimental Aging Research, 17*, 29-52.
- McArdle, J.J., & Nesselroade, J.R. (1994). Using multivariate data to structure developmental change. In H.C. Stanley & R. Hayne Waring (Eds.), *Life-span developmental psychology: Methodological contributions* (pp. 223-267). Mahwah, NJ: Lawrence Erlbaum Associates.
- Meredith, W., & Tisak, J. (1982). Canonical analysis of longitudinal and repeated measures data with stationary weights. *Psychometrika, 47*, 47-67.
- Meredith, W., & Tisak, J. (1990). Latent curve analysis. *Psychometrika, 55*, 107-122.
- Muthén, B. (1987). *LISCOMP: Analysis of linear structural equations with a comprehensive measurement model. Theoretical integration and user's guide*. Mooresville, IN: Scientific Software.
- Muthén, B. (1989). Latent variable modeling in heterogeneous populations. *Psychometrika, 54*, 557-585.
- Muthén, B. (1991). Multilevel factor analysis of class and student achievement components. *Journal of Educational Measurement, 28*, 338-354.
- Muthén, B. (1994). Multilevel covariance structure analysis. *Sociological Methods & Research, 22*, 376-398.
- Muthén, B. (1997). Latent variable modeling of longitudinal and multilevel data. In A. Raftery (Ed.), *Sociological methodology* (pp. 453-480). Boston: Blackwell.

- Muthén, B., & Curran, P. (1997). General growth modeling of individual differences in experimental designs: A latent variable framework for analysis and power estimation. *Psychological Methods, 2*, 371-402.
- Muthén, B., Kaplan, D., & Hollis, M. (1987). On structural equation modeling with data that are not missing completely at random. *Psychometrika, 52*, 431-462.
- Muthén, B., & Satorra, A. (1989). Multilevel aspects of varying parameters in structural models. In R.D. Bock (Ed.), *Multilevel analysis of educational data* (pp. 87-99). San Diego, CA: Academic Press.
- Neale, M.C. (1995). *Mx: Statistical modeling*. Richmond, VA: Department of Human Genetics, Medical College of Virginia.
- Nelson, G., & Muthén, B. (1991). *Analysis preparation steps for multilevel analysis using LISCOMP* (Tech. Rep.). Los Angeles: University of California.
- Nesselroade, J.R. (1977). Issues in studying developmental change in adults from a multivariate perspective. In J.E. Birren & K.W. Schaie (Eds.), *Handbook on the psychology of aging* (pp. 59-69). New York: Van Nostrand-Reinhold.
- Nesselroade, J.R. (1983). Temporal selection and factor invariance in the study of development and change. *Life-Span Development and Behavior, 5*, 59-87.
- Nesselroade, J.R., & Baltes, P.B. (1979). *Longitudinal research in the study of behavior and development*. New York: Academic Press.
- Patterson, G.R. (1993). Orderly change in a stable world: The antisocial trait as a chimera. *Journal of Consulting and Clinical Psychology, 61*, 911-919.
- Rao, C.R. (1958). Some statistical methods for comparison of growth curves. *Biometrics, 14*, 1-17.
- Raudenbush, S., & Bryk, A. (1988). Methodological advances in studying effects of schools and classrooms on student learning. In E.Z. Roth (Ed.), *Review of research in education* (pp. 423-475). Washington, DC: American Educational Research Association.

- Raudenbush, S.W., & Chan, W. (1992). Growth curve analysis in accelerated longitudinal designs. *Journal of Research in Crime and Delinquency*, 29, 387-411.
- Raudenbush, S.W., & Chan, W. (1993). Application of a hierarchical linear model to the study of adolescent deviance in an overlapping cohort design. *Journal of Consulting and Clinical Psychology*, 61, 941-951.
- Raykov, T. (1991). Measurement of change in longitudinal data: A classical test theory approach within the structural equation modeling methodology. *Studia Psychologica*, 33, 44-49.
- Raykov, T. (1992a). On structural models for analyzing change. *Scandinavian Journal of Psychology*, 33, 247-265.
- Raykov, T. (1992b). Structural models for studying correlates and predictors of change. *Australian Journal of Psychology*, 44, 101-112.
- Raykov, T. (1994). Studying correlates and predictors of longitudinal change using structural equation modeling. *Applied Psychological Measurement*, 18, 63-77.
- Rindskopf, D. (1984). Using phantom and imaginary latent variables to parameterize constraints in linear structural models. *Psychometrika*, 49, 37-47.
- Rogosa, D. (1988). Myths about longitudinal research. In K.W. Schaie, R.T. Campbell, W. Meredith, & S.C. Rawlings (Eds.), *Methodological issues in aging research* (pp. 171-209). New York: Springer.
- Rogosa, D.R., Brandt, D., & Zimowski, M. (1982). A growth curve approach to the measure of change. *Psychological Bulletin*, 92, 726-748.
- Rogosa, D., & Willett, J.B. (1985). Understanding correlates of change by modeling individual differences in growth. *Psychometrika*, 50, 203-228.
- Rozeboom, W.W. (1978). *General linear dynamic analyses*. Unpublished manuscript, University of Alberta, Edmonton, Canada.

- Rubin, D.B. (1976). Inference and missing data. *Biometrika*, 61, 581-592.
- Rubin, D.B. (1987). *Multiple imputation for nonresponse in surveys*. New York: Wiley.
- Saris, W.E., & Satorra, A. (1993). Power evaluations in structural equation models. In K. A. Bollen & J.S. Long (Eds.), *Testing structural equation models* (pp. 181-204). Newbury Park, CA: Sage.
- Saris, W.E., Satorra, A., & Sörbom, D. (1987). The detection and correction of specification errors in structural equation models. In C.C. Clogg (Ed.), *Sociological methodology* (pp. 105-129). San Francisco: Jossey-Bass.
- Saris, W.E., & Stronkhorst, H. (1984). *Causal modeling in nonexperimental research: An introduction to the LISREL approach*. Amsterdam: Sociometric Research Foundation.
- SAS Institute, Inc. (1990). *SAS/STAT users guide*. Cary, NC: Author.
- Satorra, A. (1989). Alternative test criteria in covariance structure analysis: A unified approach. *Psychometrika*, 54, 131-151.
- Satorra, A., & Saris, W.E. (1983). The accuracy of a procedure for calculating the power of the likelihood ratio test as used within the LISREL framework. In C.O. Middendorp (Ed.), *Sociometric research 1982* (pp. 129-190). Amsterdam: Sociometric Research Foundation.
- Satorra, A., & Saris, W.E. (1985). The power of the likelihood ratio test in covariance structure analysis. *Psychometrika*, 50, 83-90.
- Schmidt, W., & Wisenbaker, J. (1986). *Hierarchical data analysis: An approach based on structural equations* (Tech. Rep. No. 4.). East Lansing: Michigan State University, Department of Counseling Educational Psychology and Special Education.
- Schumacker, R.E., & Marcoulides, G. (1998). *Interaction and nonlinear effects in structural equation modeling*. Mahwah, NJ: Lawrence Erlbaum Associates.
- Searle, S.R., Casella, G., & McCulloch, C.E. (1992). *Variance components*. New York: Wiley.
- Sobel, M.E. (1982). Asymptotic confidence intervals for indirect effects in structural equation models. In S. Leinhardt (Ed.), *Sociological methodology* (pp. 290-312). San Francisco: Jossey-Bass.
- Sobel, M.E. (1986). Some new results on indirect effects and their standard errors in covariance structure models. In N.B. Tuma (Ed.), *Sociological methodology* (pp. 159-186). Washington, DC: American Psychological Association.
- Sobel, M.E. (1987). Direct and indirect effects in linear structural equation models. *Sociological Methods & Research*, 16, 155-176.
- Sörbom, D. (1989). Model modification. *Psychometrika*, 54, 371-384.
- SPSS 7.0 [Computer Software]. (1996). Chicago: SPSS.
- Steiger, J.H., & Lind, J.C. (1980, May). *Statistically-based tests for the number of common factors*. Paper presented at the Annual Meeting of the Psychometric Society, Iowa City, IA.
- Stoolmiller, M. (1994). Antisocial behavior, delinquent peer association, and unsupervised wandering for boys: Growth and change from childhood to early adolescence. *Multivariate Behavioral Research*, 29, 263-288.
- Stoolmiller, M. (1995). Using latent growth curve models to study developmental processes. In J.M. Gottman (Ed.), *The analysis of change* (pp. 103-138). Mahwah, NJ: Lawrence Erlbaum Associates.

Stoolmiller, M., & Bank, L. (1995). Autoregressive effects in structural equation models: We see some problems. In J.M. Gottman (Ed.), *The analysis of change* (pp. 261-276). Mahwah, NJ: Lawrence Erlbaum Associates.

Stoolmiller, M., Duncan, T., Bank, L., & Patterson, G.R. (1993). Some problems and solutions in the study of change: Significant patterns in client resistance. *Journal of Consulting and Clinical Psychology, 61*, 920-928.

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Tanaka, J.S. (1987). "How big is big enough?": Sample size and goodness of fit in structural equation models with latent variables. *Child Development, 58*, 134-146.

Tisak, J., & Meredith, W. (1990). Descriptive and associative developmental models. In A. von Eye (Ed.), *Statistical methods in developmental research* (Vol. 2, pp. 387-406). San Diego, CA: Academic Press.

Tisak, J., & Tisak, M.S. (1996). Longitudinal models of reliability and validity: A latent curve approach. *Applied Psychological Measurement, 20*, 275-288.

Tonry, M., Ohlin, L., & Farrington, D.P. (1991). *Human development and criminal behavior: New ways of advancing knowledge*. New York: Springer-Verlag.

Tucker, L.R. (1958). Determination of parameters of a functional relation by factor analysis. *Psychometrika, 23*, 19-23.

Tucker, L.R. (1966). Learning theory and multivariate experiment: Illustration by determination of parameters of generalized learning curves. In R.B. Catell (Ed.), *Handbook of multivariate experimental psychology* (pp. 476-501). Chicago: Rand McNally.

Walker, A.J., Acock, A.C., Bowman, S.R., & Li, F. (1996). Amount of care given and caregiving satisfaction: A latent growth curve analysis. *Journals of Gerontology Series B Psychological Sciences and Social Sciences, 51B*, 130-142.

Ware, J.H. (1985). Linear models for the analysis of longitudinal studies. *American Statistician, 39*, 95-101.

Wickrama, K.A.S., Lorenz, F.O., & Conger, R.D. (1997). Parental support and adolescent physical health status: A latent growth-curve analysis. *Journal of Health and Social Behavior, 38*, 149-163.

Willett, J.B., Ayoub, C.C., & Robinson, D. (1991). Using growth modeling to examine systematic differences in growth: An example of change in the function of families at risk of maladaptive parenting, child abuse, or neglect. *Journal of Consulting and Clinical Psychology, 59*, 38-47.

Willett, J.B., & Sayer, A.G. (1994). Using covariance structure analysis to detect correlates and predictors of individual change over time. *Psychological Bulletin, 116*, 363-381.

Winer, B.J., Brown, D.R., & Michels, K.M. (1991). *Statistical principles in experimental design*. New York: McGraw-Hill.

Wong, S.K., & Long, J.S. (1987). *Parameterizing nonlinear constraints in models with latent variables* (Tech. Rep.). Pullman, WA: Washington State University.

Yang, F. (1997). *Non-linear structural equation models: Simulation studies of the Kenny-Judd model*. Unpublished doctoral dissertation, Uppsala University, Sweden.

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## Appendix 2.1 LISREL Program Specifications for the Model Depicted in Fig. 2.3

This appendix provides the input statements necessary to estimate the model depicted in Fig. 2.3 using the LISREL structural equation modeling program.

```
LATENT GROWTH MODEL USING LISREL8
DA NI=3 NO=343 MA=CM
MODEL NY=3 NE=2 AL=FR PS=SY, FR LY=FU, FR TE=DI
LA
  ALCT1 ALCT2 ALCT3
LE
  LEVEL SLOPE
KM
  1.0000
  .4859 1.0000
  .3988 .5332 1.0000
ME
  8.31 10.00 10.81
SD
  7.39 7.99 8.08
FI LY (1,1) LY (2,1) LY (3,1)
VA 1 LY (1,1) LY (2,1) LY (3,1)
FI LY (1,2) LY (2,2)
VA 0 LY (1,2)
VA 1 LY (2,2)
EQ TE (1,1) TE (2,2) TE (3,3)
OU XM ND=3
```

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Appendix 4.1  
EQS Program Specifications for the Multiple-Sample Model Depicted in Fig. 4.1

The following program specifications and input data correspond to those necessary to test the multiple-sample model using the EQS structural equations program.

```

/TITLE
LGM MULTISAMPLE GROUP 1
/SPECIFICATIONS
CAS=196; VAR=3; ME=ML; MA=COV; ANAL=MOMENT; GROUPS=2;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
F1=*V999+D1;
F2=*V999+D2;
/VARIANCES
E1 TO E3=*; D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/LABELS
/MATRIX
1.764
.933 2.291
.856 1.645 2.355
/MEANS
1.4435 1.7231 1.8312
/PRINT
/END
/TITLE
LGM MULTISAMPLE GROUP 2
/SPECIFICATIONS
CAS=95; VAR=3; ME=ML; MA=COV; ANAL=MOMENT;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
F1=*V999+D1;
F2=*V999+D2;
/VARIANCES
E1 TO E3=*; D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/LABELS

```

*Continued*

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```

/MATRIX
1.941
.978 2.223
.901 1.645 2.729
/MEANS
1.5545 1.8648 2.2804
/CONSTRAINTS
(1,F1,V999)=(2,F1,V999);
(1,F2,V999)=(2,F2,V999);
(1,D1,D1)=(2,D1,D1);
(1,D2,D2)=(2,D2,D2);
(1,D1,D2)=(2,D1,D2);
(1,E1,E1)=(2,E1,E1);
(1,E2,E2)=(2,E2,E2);
(1,E3,E3)=(2,E3,E3);
/LMTEST
/PRINT
/END

```

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Appendix 4.2  
EQS Program Specifications for the Multiple-Sample Added Growth Model Depicted in Fig. 4.2

The following program specifications and input data correspond to those necessary to test the added growth model using the EQS structural equations program.

```

/TITLE
LGM MULTISAMPLE GROUP 1
/SPECIFICATIONS
CAS=196; VAR=3; ME=ML; MA=COV; ANAL=MOMENT; GROUPS=2;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
F1=*V999+D1;
F2=*V999+D2;
/VARIANCES
E1 TO E3=*; D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/LABELS
/MATRIX
1.764
.933 2.291
.856 1.645 2.355
/MEANS
1.4435 1.7231 1.8312
/PRINT
/END
/TITLE
LGM MULTISAMPLE GROUP 2
/SPECIFICATIONS
CAS=95; VAR=3; ME=ML; MA=COV; ANAL=MOMENT;
/EQUATIONS
V1=F1+0F2+0F3+E1;
V2=F1+1F2+1F3+E2;
V3=F1+2F2+2F3+E3;
F1=*V999+D1;
F2=*V999+D2;
F3=*V999+D3;
/VARIANCES
E1 TO E3=*; D1 TO D3=*;
/COVARIANCES
D1 TO D2=*;
/LABELS

```

*Continued*

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```

/MATRIX
1.941
.978 2.223
.901 1.645 2.729
/MEANS
1.5545 1.8648 2.2804
/CONSTRAINTS
(1,F1,V999)=(2,F1,V999);
(1,F2,V999)=(2,F2,V999);
(1,D1,D1)=(2,D1,D1);
(1,D2,D2)=(2,D2,D2);
(1,D1,D2)=(2,D1,D2);
(1,E1,E1)=(2,E1,E1);
(1,E2,E2)=(2,E2,E2);
(1,E3,E3)=(2,E3,E3);
/LMTEST
/PRINT
/END

```

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Appendix 5.1  
EQS Program Specifications for the Associative Model Depicted in Fig. 5.1

The following program specifications and input data correspond to those necessary to test the associative LGM for alcohol, tobacco, and marijuana use, using the EQS structural equations program.

```

/TITLE
ASSOCIATIVE MODEL FOR ALCOHOL, TOBACCO, & MARIJUANA
/SPECIFICATIONS
CAS=357; VAR=12; ME=ML; MA=COR; FI=5; ANAL=MOM;
/LABELS
V1=TALC1YR2; V2=TALC1YR3; V3=TALC1YR4; V4=TALC1YR5; V5=TTOB1YR2;
V6=TTOB1YR3; V7=TTOB1YR4; V8=TTOB1YR5; V9=TPOT1YR2; V10=TPOT1YR3;
V11=TPOT1YR4; V12=TPOT1YR4; F1=ALC_INT; F2=ALC_SLP; F3=TOB_INT;
F4=TOB_SLP; F5=POT_INT; F6=POT_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
V4=F1+3F2+E4;
V5=F3+0F4+E5;
V6=F3+1F4+E6;
V7=F3+2F4+E7;
V8=F3+3F4+E8;
V9=F5+0F6+E9;
V10=F5+1F6+E10;
V11=F5+2F6+E11;
V12=F5+3F6+E12;
F1=*V999+D1;
F2=*V999+D2;
F3=*V999+D3;
F4=*V999+D4;
F5=*V999+D5;
F6=*V999+D6;
/VARIANCES
E1 TO E12=*;
D1 TO D6=*;
/COVARIANCES
D1 TO D6=*;
/CONSTRAINTS
/MATRIX
1.000
.725 1.000
.595 .705 1.000
.566 .624 .706 1.000
.419 .281 .303 .283 1.000
.344 .362 .350 .367 .671
.224 .281 .353 .360 .548

```

*Continued*

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```

.183 .234 .300 .384 .458
.579 .482 .410 .303 .455
.532 .571 .501 .440 .347
.439 .507 .648 .496 .378
.431 .469 .527 .571 .345
1.000
.783 1.000
.696 .823 1.000
.333 .244 .179 1.000
.444 .352 .272 .663 1.000
.419 .430 .345 .551 .709
.424 .427 .412 .499 .682
1.000
.736 1.000
/MEANS
1.3389 1.5910 2.0196 2.3641 .8627
1.2185 1.4454 1.7563 .5546 .8908
1.0336 1.1232
/STANDARD DEVIATIONS
1.2609 1.3348 1.4406 1.3766 1.7094
1.9480 2.1175 2.2659 1.1995 1.4327
1.4968 1.5033

```

```
/PRINT
EFFECTS=YES;
/END
```

Appendix 5.2
EQS Program Specifications for the Factor-of-Curves Model Depicted in Fig. 5.2

The following program specifications and input data correspond to those necessary to test the factor-of-curves LGM for alcohol, tobacco, and marijuana use, using the EQS structural equations program.

```
/TITLE
FACTOR-OF-CURVES MODEL FOR ALCOHOL, TOBACCO, & MARIJUANA
/SPECIFICATIONS
CAS=357; VAR=12; ME=ML; MA=COR; FI=5; ANAL=MOM;
/LABELS
V1=TALC1YR2; V2=TALC1YR3; V3=TALC1YR4; V4=TALC1YR5; V5=TTOB1YR2;
V6=TTOB1YR3; V7=TTOB1YR4; V8=TTOB1YR5; V9=TPOT1YR2; V10=TPOT1YR3;
V11=TPOT1YR4; V12=TPOT1YR4; F1=ALC_INT; F2=ALC_SLP; F3=TOB_INT;
F4=TOB_SLP; F5=POT_INT; F6=POT_SLP;
/EQUATIONS
V1=1F1+0F2+E1;
V2=1F1+1F2+E2;
V3=1F1+2F2+E3;
V4=1F1+3F2+E4;
V5=1F3+0F4+E5;
V6=1F3+1F4+E6;
V7=1F3+2F4+E7;
V8=1F3+3F4+E8;
V9=1F5+0F6+E9;
V10=1F5+1F6+E10;
V11=1F5+2F6+E11;
V12=1F5+3F6+E12;
F1=0*V999+*F7+D1;
F2=0*V999+*F8+D2;
F3=0V999+F7+D3;
F4=0V999+F8+D4;
F5=0*V999+*F7+D5;
F6=0*V999+*F8+D6;
F7=0*V999+D7;
F8=0*V999+D8;
/VARIANCES
E1 TO E12=*;
D1 TO D6=*;
D7=*;D8=*;
/COVARIANCES
D1 TO D6=0;
D7 TO D8=*;
/CONSTRAINTS;
(F1,F7)=(F2,F8);
(F5,F7)=(F6,F8);
```

Continued

```
/MATRIX
1.000
.725 1.000
.595 .705 1.000
.566 .624 .706 1.000
.419 .281 .303 .283 1.000
.344 .362 .350 .367 .671
.224 .281 .353 .360 .548
.183 .234 .300 .384 .458
.579 .482 .410 .303 .455
.532 .571 .501 .440 .347
.439 .507 .648 .496 .378
.431 .469 .527 .571 .345
1.000
.783 1.000
.696 .823 1.000
.333 .244 .179 1.000
```

```

.444 .352 .272 .663 1.000
.419 .430 .345 .551 .709
.424 .427 .412 .499 .682
1.000
.736 1.000
/MEANS
1.3389 1.5910 2.0196 2.3641 .8627
1.2185 1.4454 1.7563 .5546 .8908
1.0336 1.1232
/STANDARD DEVIATIONS
1.2609 1.3348 1.4406 1.3766 1.7094
1.9480 2.1175 2.2659 1.1995 1.4327
1.4968 1.5033
/PRINT
EFFECTS=YES;
/END

```

### Appendix 5.3 EQS Program Specifications for the Curve-of-Factors Model Depicted in Fig. 5.3

The following program specifications and input data correspond to those necessary to test the curve-of-factors LGM for alcohol, tobacco, and marijuana use, using the EQS structural equations program.

```

/TITLE
CURVE-OF-FACTORS MODEL FOR ALCOHOL, TOBACCO, & MARIJUANA
/SPECIFICATIONS
CAS=357; VAR=12; ME=ML; MA=COR; FI=5; ANAL=MOM;
/LABELS
V1=TALC1YR2; V2=TALC1YR3; V3=TALC1YR4; V4=TALC1YR5; V5=TTOB1YR2;
V6=TTOB1YR3; V7=TTOB1YR4; V8=TTOB1YR5; V9=TPOT1YR2; V10=TPOT1YR3;
V11=TPOT1YR4; V12=TPOT1YR5;
F1=T1; F2=T2; F3=T3; F4=T4; F5=INT; F6=HOSLP;
/EQUATIONS
V1=*V999+*F1+E1;
V2=*V999+*F2+E2;
V3=*V999+*F3+E3;
V4=*V999+*F4+E4;
V5=0V999+F1+E5;
V6=0V999+F2+E6;
V7=0V999+F3+E7;
V8=0V999+F4+E8;
V9=*V999+*F1+E9;
V10=*V999+*F2+E10;
V11=*V999+*F3+E11;
V12=*V999+*F4+E12;
F1=F5+0F6+D1;
F2=F5+1F6+D2;
F3=F5+2F6+D3;
F4=F5+3F6+D4;
F5=0*V999+D5;
F6=0*V999+D6;
/VARIANCES
E1 TO E12=*;
D1 TO D4=0*;
D5 TO D6=*;
/COVARIANCES
E1 TO E12=0;
E1 TO E4=*;
E5 TO E8=*;
E9 TO E12=*;
D1 TO D4=0;
D5 TO D6=*;

```

*Continued*



```

/CONSTRAINTS
(V1,F1)=(V2,F2)=(V3,F3)=(V4,F4);
(V9,F1)=(V10,F2)=(V11,F3)=(V12,F4);
/MATRIX
1.000
.725 1.000
.595 .705 1.000
.566 .624 .706 1.000
.419 .281 .303 .283 1.000
.344 .362 .350 .367 .671
.224 .281 .353 .360 .548
.183 .234 .300 .384 .458
.579 .482 .410 .303 .455
.532 .571 .501 .440 .347
.439 .507 .648 .496 .378
.431 .469 .527 .571 .345
1.000
.783 1.000
.696 .823 1.000
.333 .244 .179 1.000
.444 .352 .272 .663 1.000
.419 .430 .345 .551 .709
.424 .427 .412 .499 .682
1.000
.736 1.000
/MEANS
1.3389 1.5910 2.0196 2.3641 .8627
1.2185 1.4454 1.7563 .5546 .8908
1.0336 1.1232
/STANDARD DEVIATIONS
1.2609 1.3348 1.4406 1.3766 1.7094
1.9480 2.1175 2.2659 1.1995 1.4327
1.4968 1.5033
/PRINT
EFFECTS=YES;
/END

```

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## Appendix 6.1 EQS Program Specifications for the Linear Cohort-Sequential Model

The following program specifications and input data correspond to those necessary to test the linear cohort-sequential model using the EQS structural equations program.

```

/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 1
/SPECIFICATIONS
CAS=248; VAR=5; ME=ML; MA=COV; ANAL=MOMENT; GROUPS=3;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E1 TO E3=*;
D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/MATRIX
.483
.303 .899
.271 .488 1.258
.000 .000 .000 .000
.000 .000 .000 .000 .000
/MEANS
.335 .774 .964 1.000 1.000
/PRINT
EFFECTS=YES;
/END
/TITLE

```

```

MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 2
/SPECIFICATIONS
CAS=250; VAR=5; ME=ML; MA=COV; ANAL=MOMENT;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V2=F1+1F2+E2;
V3=F1+2F2+E3;
V4=F1+3F2+E4;
F1=0*V999+D1;
F2=0*V999+D2;

```

Continued

```

/VARIANCES
E2 TO E4=*;
D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/MATRIX
.000
.000 .759
.000 .400 .988
.000 .412 .683 1.315
.000 .000 .000 .000 .000
/MEANS
1.000 .764 .992 1.384 1.000
/PRINT
EFFECTS=YES;
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 3
/SPECIFICATIONS
CAS=231; VAR=5; ME=ML; MA=COV; ANAL=MOMENT;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V3=F1+2F2+E3;
V4=F1+3F2+E4;
V5=F1+4F2+E5;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E3 TO E5=*;
D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/MATRIX
.000
.000 .000
.000 .000 1.170
.000 .000 .711 1.371
.000 .000 .662 .936 1.709
/MEANS
1.000 1.000 .939 1.541 2.170
/PRINT
EFFECTS=YES;
/CONSTRAINTS
(1,D1,D2)=(2,D1,D2)=(3,D1,D2);
(1,D1,D1)=(2,D1,D1)=(3,D1,D1);
(1,D2,D2)=(2,D2,D2)=(3,D2,D2);
(1,F1,V999)=(2,F1,V999)=(3,F1,V999);
(1,F2,V999)=(2,F2,V999)=(3,F2,V999);
(1,E2,E2)=(2,E2,E2);
(1,E3,E3)=(2,E3,E3)=(3,E3,E3);
(2,E4,E4)=(3,E4,E4);
/LMTEST
/TECH
ITER=100;
/END

```

Note. For Group 1, V1, V2, and V3 represent adolescent alcohol use at 12, 13, and 14 years of age respectively. For Group 2, V2, V3, and V4 represent adolescent alcohol use at 13, 14, and 15 years of age respectively, and so on for the remaining group.

Appendix 6.2  
LISREL Program Specifications for the Linear Cohort-Sequential Model

The following program specifications and input data correspond to those necessary to test the hypothesized linearcohort-sequential model using the LISREL structural equations program.

```
ACCELERATED LATENT GROWTH MODEL USING LISREL8
GROUP 1
DA NI=3 NO=248 MA=CM NG=3
MODEL NY=3 NE=7 AL=FI PS=SY,FI LY=FU,FI TE=FI,DI
LE
  ALCT1 ALCT2 ALCT3 ALCT4 ALCT5 LEVEL SLOPE
CM
.483
.303 .899
.271 .488 1.258
ME
.335 .774 .964
MA LY
1 0 0 0 0 1 0
0 1 0 0 0 1 1
0 0 1 0 0 1 2
MA PS
1
0 1
0 0 1
0 0 0 0
0 0 0 0 0
0 0 0 0 0 1
0 0 0 0 0 .1 1
FR PS 6 6 PS 7 7 PS 7 6
FR PS 1 1 PS 2 2 PS 3 3
FR AL 1 6 AL 1 7
ST .310 AL 1 6
ST .384 AL 1 7
ST .314 PS 6 6
ST .077 PS 7 7
ST -.022 PS 7 6
ST .5 PS 2 2 PS 3 3
ST .178 PS 1 1
OU NS RS SE TV PT PC FD ND=3 ADD=OFF SS WP
GROUP 2
DA NI=3 NO=250 MA=CM
LE
  ALCT1 ALCT2 ALCT3 ALCT4 ALCT5 LEVEL SLOPE
CM
.759
.400 .988
.412 .683 1.315
```

*Continued*

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```
ME
.764 .992 1.384
MODEL NY=3 NE=7 AL=FI PS=SY,FI LY=FU,FI TE=FI,DI
MA LY
0 1 0 0 0 1 1
0 0 1 0 0 1 2
0 0 0 1 0 1 3
MA PS
0
0 1
0 0 1
0 0 0 1
0 0 0 0 0
0 0 0 0 0 1
0 0 0 0 0 .1 1
FR AL 1 6 AL 1 7
FR PS 6 6 PS 7 7 PS 7 6
FR PS 2 2 PS 3 3 PS 4 4
ST 30 PS 4 4
EQ PS 1 6 6 PS 2 6 6
EQ PS 1 7 7 PS 2 7 7
```

```

EQ PS 1 7 6 PS 2 7 6
EQ PS 1 2 2 PS 2 2 2
EQ PS 1 3 3 PS 2 3 3
EQ AL 1 6 AL 2 6
EQ AL 1 7 AL 2 7
OU NS RS SE TV PT PC FD ND=3 ADD=OFF SS WP
GROUP 3
DA NI=3 NO=231 MA=CM
LE
  ALCT1 ALCT2 ALCT3 ALCT4 ALCT5 LEVEL SLOPE
CM
  1.170
  .711 1.371
  .662 .936 1.709
ME
  .939 1.541 2.170
MODEL NY=3 NE=7 AL=FI PS=SY,FI LY=FU,FI TE=FI,DI
MA LY
0 0 1 0 0 1 2
0 0 0 1 0 1 3
0 0 0 0 1 1 4
MA PS
0
0 0
0 0 1
0 0 0 1
0 0 0 0 1
0 0 0 0 0 1
0 0 0 0 0 .1 1
FR AL 1 6 AL 1 7
FR PS 6 6 PS 7 7 PS 7 6
FR PS 3 3 PS 4 4 PS 5 5
EQ PS 1 6 6 PS 3 6 6
EQ PS 1 7 7 PS 3 7 7
EQ PS 1 7 6 PS 3 7 6
EQ PS 2 3 3 PS 3 3 3
EQ PS 2 4 4 PS 3 4 4
ST 30 PS 5 5
EQ AL 1 6 AL 3 6
EQ AL 1 7 AL 3 7OU NS RS SE TV PT PC FD ND=3 ADD=OFF SS WP

```

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### Appendix 6.3 EQS Program Specifications for the Combined Model Depicted in Fig. 6.1

The following program specifications and input data correspond to those necessary to test the linear combined cohort-sequential and true-longitudinal model using the EQS structural equations program.

```

/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 1
/SPECIFICATIONS
CAS=248; VAR=5; ME=ML; MA=COV; ANAL=MOMENT; GROUPS=4;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E1 TO E3=*;
D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/MATRIX
.483
.303 .899
.271 .488 1.258
.000 .000 .000 .000
.000 .000 .000 .000 .000
/MEANS
.335 .774 .964 1.000 1.000
/PRINT
EFFECTS=YES;
/END

```

```
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 2
/SPECIFICATIONS
CAS=250; VAR=5; ME=ML; MA=COV; ANAL=MOMENT;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
```

Continued

```
/EQUATIONS
V2=F1+1F2+E2;
V3=F1+2F2+E3;
V4=F1+3F2+E4;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E2 TO E4=*;
D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/MATRIX
.000
.000 .759
.000 .400 .988
.000 .412 .683 1.315
.000 .000 .000 .000 .000
/MEANS
1.000 .764 .992 1.384 1.000
/PRINT
EFFECTS=YES;
```

```
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 3
/SPECIFICATIONS
CAS=231; VAR=5; ME=ML; MA=COV; ANAL=MOMENT;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
```

```
/EQUATIONS
V3=F1+2F2+E3;
V4=F1+3F2+E4;
V5=F1+4F2+E5;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E3 TO E5=*;
D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/MATRIX
.000
.000 .000
.000 .000 1.170
.000 .000 .711 1.371
.000 .000 .662 .936 1.709
/MEANS
1.000 1.000 .939 1.541 2.170
/PRINT
EFFECTS=YES;
```

```
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 4
/SPECIFICATIONS
CAS=215; VAR=5; ME=ML; MA=COV; ANAL=MOMENT;
```

Continued

```

/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
V4=F1+3F2+E4;
V5=F1+4F2+E5;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E1 TO E5=*;
D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/CONSTRAINTS
/MATRIX
.477
.285 .632
.362 .429 1.330
.342 .431 .872 1.472
.277 .419 .648 .860 1.806
/MEANS
.367 .544 1.072 1.442 2.200
/PRINT
EFFECTS=YES;
/CONSTRAINTS
(1,D1,D2)=(2,D1,D2)=(3,D1,D2)=(4,D1,D2);
(1,D1,D1)=(2,D1,D1)=(3,D1,D1)=(4,D1,D1);
(1,D2,D2)=(2,D2,D2)=(3,D2,D2)=(4,D2,D2);
(1,F1,V999)=(2,F1,V999)=(3,F1,V999)=(4,F1,V999);
(1,F2,V999)=(2,F2,V999)=(3,F2,V999)=(4,F2,V999);
(1,E1,E1)=(4,E1,E1);
(1,E2,E2)=(2,E2,E2)=(4,E2,E2);
(1,E3,E3)=(2,E3,E3)=(3,E3,E3)=(4,E3,E3);
(2,E4,E4)=(3,E4,E4)=(4,E4,E4);
(3,E5,E5)=(4,E5,E5);
/LMTEST
/TECH
ITER=100;
/END

```

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### Appendix 7.1 LISREL Program Specifications for Estimating the Interaction Model Depicted in Fig. 7.1

```

TESTING INTERACTION: A SINGLE-FACTOR SHAPE MODEL
DA NI=16 NO=250 MA=CM
LA
Y1 Y2 Y3 Y4 X1 X2 X3 X4 Z1 Z2 Z3 Z4 INT1 INT2 INT3 INT4
CM
.177
.142 .225
.123 .147 .237
.108 .147 .162 .241
-.043 -.060 -.077 -.078 .283
.002 -.042 -.039 -.076 .103 .290
-.016 -.071 -.097 -.093 .126 .147 .316
-.049 -.088 -.102 -.112 .106 .155 .182 .311
-.151 -.164 -.164 -.148 .138 .057 .069 .093 .605
-.150 -.192 -.159 -.205 .087 .115 .096 .170 .235 .832
-.098 -.151 -.187 -.221 .133 .161 .139 .142 .332 .389 .680
-.105 -.192 -.172 -.230 .154 .175 .202 .218 .326 .353 .489
.797
-.606 -.744 -.809 -.755 1.582 .649 .793 .751 2.471 1.143 1.566
1.588 14.591
-.505 -.812 -.688 -.975 .736 1.571 .931 1.212 .994 3.290 1.905
1.875 6.516 17.805
-.386 -.805 -.997 -1.067 .961 1.144 1.769 1.233 1.357 1.641 2.824
2.438 8.423 10.053 16.903
-.541 -.992 -.959 -1.180 .936 1.220 1.426 1.998 1.426 1.879 2.177
3.493 8.227 11.320 13.149 19.849
MEAN

```

1.390 1.388 1.375 1.378 3.431 3.412 3.409 3.344 4.359  
 4.215 4.212 4.229 15.093 14.496 14.494 14.359  
 MO NY=4 NX=12 NE=1 NK=3 LX=FU LY=FU TD=SY TE=SY PS=SY,FR PH=SY  
 GA=FU KA=FU TX=FU C TY=ZE AL=FU,FR BE=FU,FI  
 LK  
 KSI1 KSI2 INT  
 LE  
 SHAPE  
 FI LY(1,1)  
 VA 1 LY(1,1)  
 FR LY(2,1) LY(3,1) LY(4,1)  
 FI LX(1,1)  
 VA 1 LX(1,1)  
 FR LX(2,1) LX(3,1) LX(4,1)  
 FI LX(5,2)  
 VA 1 LX(5,2)  
 FR LX(6,2) LX(7,2) LX(8,2)  
 FI LX(9,3)  
 VA 1 LX(9,3)

Continued

CO LX(9,1)=TX(5)  
 CO LX(10,1)=TX(6)\*LX(2,1)  
 CO LX(11,1)=TX(7)\*LX(3,1)  
 CO LX(12,1)=TX(8)\*LX(4,1)  
 CO LX(9,2)=TX(1)  
 CO LX(10,2)=TX(2)\*LX(6,2)  
 CO LX(11,2)=TX(3)\*LX(7,2)  
 CO LX(12,2)=TX(4)\*LX(8,2)  
 CO LX(10,3)=LX(2,1)\*LX(6,2)  
 CO LX(11,3)=LX(3,1)\*LX(7,2)  
 CO LX(12,3)=LX(4,1)\*LX(8,2)  
 PA TE  
 1  
 0 1  
 0 0 1  
 0 0 0 1  
 PA PH  
 1  
 1 1  
 0 0 1  
 PA GA  
 1 1 1  
 PA KA  
 1 1 1  
 PA AL  
 0  
 PA TY  
 1 1 1 1  
 PA TX  
 1 1 1 1 1 1 1 1 1 1  
 CO TX(9)=TX(1)\*TX(5)  
 CO TX(10)=TX(2)\*TX(6)  
 CO TX(11)=TX(3)\*TX(7)  
 CO TX(12)=TX(4)\*TX(8)  
 CO KA(3)=PH(2,1)  
 CO PH(3,3)=PH(1,1)\*PH(2,2)+PH(2,1)\*\*2  
 CO TD(9,9)=TX(1)\*\*2\*TD(5,5)+TX(5)\*\*2\*TD(1,1)+PH(1,1)\*TD(5,5) + C  
 PH(2,2)\*TD(1,1)+TD(1,1)\*TD(5,5)  
 CO  
 TD(10,10)=TX(2)\*\*2\*TD(6,6)+TX(6)\*\*2\*TD(2,2)+LX(2,1)\*\*2\*PH(1,1)\*TD(6,6) + C  
 LX(6,2)\*\*2\*PH(2,2)\*TD(2,2)+TD(2,2)\*TD(6,6)  
 CO  
 TD(11,11)=TX(3)\*\*2\*TD(7,7)+TX(7)\*\*2\*TD(3,3)+LX(3,1)\*\*2\*PH(1,1)\*TD(7,7) + C  
 LX(7,2)\*\*2\*PH(2,2)\*TD(3,3)+TD(3,3)\*TD(7,7)  
 CO TD(12,12)=TX(4)\*\*2\*TD(8,8)+TX(8)\*\*2\*TD(4,4) + C  
 LX(4,1)\*\*2\*PH(1,1)\*TD(8,8)+  
 LX(8,2)\*\*2\*PH(2,2)\*TD(4,4)+TD(4,4)\*TD(8,8)  
 CO TD(9,1)=TX(5)\*TD(1,1)  
 CO TD(9,5)=TX(1)\*TD(5,5)  
 CO TD(10,2)=TX(6)\*TD(2,2)  
 CO TD(10,6)=TX(2)\*TD(6,6)  
 CO TD(11,3)=TX(7)\*TD(3,3)  
 CO TD(11,7)=TX(3)\*TD(7,7)  
 CO TD(12,4)=TX(8)\*TD(4,4)  
 CO TD(12,8)=TX(4)\*TD(8,8)

Appendix 7.2  
LISREL Program Specifications for Estimating the Interaction Model Depicted in Fig. 7.2

TESTING INTERACTION: A LEVEL-SHAPE MODEL  
DA NI=15 NO=250  
LA  
Y1 Y2 Y3 Y4 X1 X2 X3 X4 Z1 Z2 Z3 Z4 INT2 INT3 INT4  
CM  
.177  
.142 .225  
.123 .147 .237  
.108 .147 .162 .241  
-.043 -.060 -.077 -.078 .283  
.002 -.042 -.039 -.076 .103 .290  
-.016 -.071 -.097 -.093 .126 .147 .316  
-.049 -.088 -.102 -.112 .106 .155 .182 .311  
-.151 -.164 -.164 -.148 .138 .057 .069 .093 .605  
-.150 -.192 -.159 -.205 .087 .115 .096 .170 .235 .832  
-.098 -.151 -.187 -.221 .133 .161 .139 .142 .332 .389 .680  
-.105 -.192 -.172 -.230 .154 .175 .202 .218 .326 .353 .489  
.797  
-.505 -.812 -.688 -.975 .736 1.571 .931 1.212 .994 3.290 1.905  
.875 17.805  
-.386 -.805 -.997 -1.067 .961 1.144 1.769 1.233 1.357 1.641 2.824  
.437 10.053 16.903  
-.541 -.992 -.959 -1.180 .936 1.220 1.426 1.998 1.426 1.879 2.177  
3.493 11.320 13.149 19.849  
MEAN  
1.390 1.388 1.375 1.378 3.431 3.412 3.409 3.344 4.359  
4.215 4.212 4.229 14.496 14.494 14.359  
MO NY=4 NX=11 NE=2 NK=5 TD=SY TE=DI PS=SY GA=FU KA=FR TX=FU TY=FU  
LK  
KSI1 KSI2 KSI3 KSI4 INT  
LE  
INT SLP  
FI LY(1,1) LY(2,1) LY(3,1) LY(4,1)  
VA 1 LY(1,1) LY(2,1) LY(3,1) LY(4,1)  
FI LY(1,2) LY(2,2) LY(3,2) LY(4,2)  
VA 0 LY(1,2)  
VA 1 LY(2,2)  
VA 3 LY(3,2)  
VA 8 LY(4,2)

Continued

FI LX(1,1) LX(2,1) LX(3,1) LX(4,1)  
VA 1 LX(1,1) LX(2,1) LX(3,1) LX(4,1)  
FI LX(1,2) LX(2,2) LX(3,2) LX(4,2)  
VA 0 LX(1,2)  
VA 1 LX(2,2)  
FR LX(3,2)  
FR LX(4,2)  
ST 1 LX(3,2) LX(4,2)  
FI LX(5,3) LX(6,3) LX(7,3) LX(8,3)  
VA 1 LX(5,3) LX(6,3) LX(7,3) LX(8,3)  
FI LX(5,4) LX(6,4) LX(7,4) LX(8,4)  
VA 0 LX(5,4)  
VA 1 LX(6,4)  
FR LX(7,4)  
FR LX(8,4)  
ST 1 LX(7,4) LX(8,4)  
PA PH  
1  
1 1  
1 1 1  
1 1 1 1  
0 0 0 0 1



```

PA GA
1 0 1 0 0
0 1 0 1 1
FI LX(9,5)
VA 1 LX(9,5)
CO LX(10,5)=LX(3,2)*LX(7,4)
CO LX(11,5)=LX(4,2)*LX(8,4)
CO LX(9,2)=TX(6)
CO LX(9,4)=TX(2)
CO LX(10,2)=TX(7)*LX(3,2)
CO LX(10,4)=TX(3)*LX(7,4)
CO LX(11,2)=TX(8)*LX(4,2)
CO LX(11,4)=TX(4)*LX(8,4)
PA TY
1 1 1 1
PA TX
1 1 1 1 1 1 1 1 1 1
CO TX(9)=TX(2)*TX(6)
CO TX(10)=TX(3)*TX(7)
CO TX(11)=TX(4)*TX(7)
CO PH(5,5)=PH(2,2)*PH(4,4)+PH(4,2)**2
CO TD(9,9)=TX(2)**2*TD(6,6)+TX(6)**2*TD(2,2)+PH(2,2)*TD(6,5) + C
PH(4,4)*TD(2,2)+TD(2,2)*TD(6,6)
CO
TD(10,10)=TX(3)**2*TD(7,7)+TX(7)**2*TD(3,3)+LX(3,2)**2*PH(2,2)*TD(7,7)+ C LX(7,4)**2*PH(4,4)*TD(3,3)+TD(3,3)*TD(7,7)
CO
TD(11,11)=TX(4)**2*TD(8,8)+TX(8)**2*TD(4,4)+LX(4,2)**2*PH(2,2)*TD(8,8) + C
LX(8,4)**2*PH(4,4)*TD(4,4)+TD(4,4)*TD(8,8)

```

*Continued*

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```

CO TD(9,2)=TX(6)*TD(2,2)
CO TD(9,6)=TX(2)*TD(6,6)
CO TD(10,3)=TX(7)*TD(3,3)
CO TD(10,7)=TX(3)*TD(7,7)
CO TD(11,4)=TX(8)*TD(4,4)
CO TD(11,8)=TX(4)*TD(8,8)
PA KA
0 1 0 1 1
CO PH(5,5)=PH(2,2)*PH(4,4)+ PH(4,2)**2
CO KA(5)=PH(4,2)
ST .5 TD(1,1) - TD(8,8)
ST .5 TE(1,1) - TE(4,4)
ST 1 TY 1 - TY 4
ST 3 TX 1 - TX 4
ST 4 TX 5 - TX 8
ST .1 GA 1 1
ST 1 KA 2 KA 4 KA 5
OU SC IT=900 AD=OFF ND=3 NS EP=.01

```

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## Appendix 8.1 EQS Program Specifications for The *HI* Model

In the test of the *HI* hypothesis, the parameters of interest are the variances (*E*), covariances, and means (*V999*) of the observed variables. The *HI* hypothesis involves the test of equality of the moment matrices reflecting the cross-group equality constraints for common parameters. The unrestricted *HI* model provides a test of whether the data are MCAR.

```

/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 1
/SPECIFICATIONS
CAS=215; VAR=5; ME=ML; MA=COR; ANAL=MOMENT; GROUPS=4;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=*V999+E1;
V2=*V999+E2;
V3=*V999+E3;
V4=*V999+E4;
V5=*V999+E5;
/VARIANCES
E1 TO E5=*;
/COVARIANCES
E1 TO E5=*;
/CONSTRAINTS
/MATRIX
1.000
.519 1.000
.454 .468 1.000
.408 .447 .623 1.000
.298 .392 .418 .527 1.000
/MEAN
.3674 .5442 1.1721 1.4419 2.2000
/STANDARD DEVIATION
.6903 .7952 1.1533 1.2133 1.3437
/PRINT
EFFECTS=YES;
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 2

```

*Continued*

```

/SPECIFICATIONS
CAS=8; VAR=5; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
!V1=*V999+E1;
V2=*V999+E2;
V3=*V999+E3;
V4=*V999+E4;
/VARIANCES
E2 TO E4=*;
/COVARIANCES
E2 TO E4=*;
/MATRIX
1.000
1.000 1.000
.612 .612 1.000
-.309 -.309 .168 1.000
.000 .000 .000 .000 1.000
/MEAN
.5000 .5000 1.0000 1.3750 .000
/STANDARD DEVIATION
.7559 .7559 .9258 .9161 .000
/PRINT
EFFECTS=YES;
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 3
/SPECIFICATIONS
CAS=6; VAR=5; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=*V999+E1;
V2=*V999+E2;
V3=*V999+E3;
/VARIANCES
E1 TO E3=*;
/COVARIANCES
E1 TO E3=*;
/CONSTRAINTS

```

```

/MATRIX
1.000
.316 1.000
-.171 .434 1.000
.000 .000 .000 1.000
.000 .000 .000 .000 1.000
/MEAN
.3333 .6667 1.1667 .000 .000
.5164 .8165 .7528 .000 .000

```

Continued

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```

/PRINT
EFFECTS=YES;
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 4
/SPECIFICATIONS
CAS=11; VAR=5; ME=ML; MA=COR; ANAL=MOMENT;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=*V999+E1;
V2=*V999+E2;
/VARIANCES
E1 TO E2=*;
/COVARIANCES
E1 TO E2=*;
/CONSTRAINTS
/MATRIX
1.000
.630 1.000
.000 .000 1.000
.000 .000 .000 1.000
.000 .000 .000 .000 1.000
/MEAN
.1818 .4545 .000 .000 .000
/STANDARD DEVIATION
.4045 1.2136 .000 .000 .000
/PRINT
EFFECTS=YES;
/CONSTRAINTS
(1,V1,V999)=(3,V1,V999)=(4,V1,V999);
(1,V2,V999)=(2,V2,V999)=(3,V2,V999)=(4,V2,V999);
(1,V3,V999)=(2,V3,V999)=(3,V3,V999);
(1,V4,V999)=(2,V4,V999);
(1,E1,E1)=(3,E1,E1)=(4,E1,E1);
(1,E2,E2)=(2,E2,E2)=(3,E2,E2)=(4,E2,E2);
(1,E3,E3)=(2,E3,E3)=(3,E3,E3);
(1,E4,E4)=(2,E4,E4);
(1,E1,E2)=(3,E1,E2)=(4,E1,E2);
(1,E1,E3)=(3,E1,E3);
(1,E2,E3)=(2,E2,E3)=(3,E2,E3);
(1,E2,E4)=(2,E2,E4);
(1,E3,E4)=(2,E3,E4);
/LMTEST
/TECH
ITER=100;
/END

```

Note. In Group 2 the first variable (V1) is not included in the model (!V1 = \*V999 + E1;) because of a linear dependency that exists between V1 and V2 for that group.

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Appendix 8.2  
EQS Program Specifications for the *H0* Model Depicted in Fig. 8.1

The restricted *H0* model imposes equality restrictions across the groups for common parameters. Parameters of interest are the regression coefficients, variances, and covariances of the independent variables, and regression intercepts, or means, of the dependent variables.

```

/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 1
/SPECIFICATIONS
CAS=215; VAR=5; ME=ML; MA=COR; ANAL=MOM; GROUPS=4;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2*F2+E3;
V4=F1+3*F2+E4;
V5=F1+4*F2+E5;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E1 TO E5=*; D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/MATRIX
1.000
.519 1.000
.454 .468 1.000
.408 .447 .623 1.000
.298 .392 .418 .527 1.000
/MEAN
.3674 .5442 1.1721 1.4419 2.2000
/STANDARD DEVIATION
.6903 .7952 1.1533 1.2133 1.3437
/CONSTRAINTS
/PRINT
EFFECTS=YES;
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 2

```

*Continued*

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```

/SPECIFICATIONS
CAS=8; VAR=5; ME=ML; MA=COR; ANAL=MOM;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
!V1=*V999+E1;
V2=F1+1F2+E2;
V3=F1+2*F2+E3;
V4=F1+3*F2+E4;
F1=0*V999+D2;
F2=0*V999+D2;
/VARIANCES
E2 TO E4=*; D1=*; D2=*;
/COVARIANCES
D1,D2=*;
/MATRIX
1.000
1.000 1.000
.612 .612 1.000
-.309 -.309 .168 1.000
.000 .000 .000 .000 1.000
/MEAN
.5000 .5000 1.0000 1.3750 .000
/STANDARD DEVIATION
.7559 .7559 .9258 .9161 .000
/PRINT
EFFECTS=YES;
/END

```

```

/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 3
/SPECIFICATIONS
CAS=6; VAR=5; ME=ML; MA=COR; ANAL=MOM;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2*F2+E3;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E1 TO E3=*; D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/CONSTRAINTS
/MATRIX
1.000
.316 1.000
-.171 .434 1.000
.000 .000 .000 1.000
.000 .000 .000 .000 1.000

```

Continued

```

/MEAN
.3333 .6667 1.1667 .000 .000
.5164 .8165 .7528 .000 .000
/PRINT
EFFECTS=YES;
/END
/TITLE
MULTISAMPLE LONGITUDINAL ANALYSIS GROUP 4
/SPECIFICATIONS
CAS=11; VAR=5; ME=ML; MA=COR; ANAL=MOM;
/LABELS
V1=ALC_T1; V2=ALC_T2; V3=ALC_T3; V4=ALC_T4; V5=ALC_T5;
F1=ALC_INT; F2=ALC_SLP;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
F1=0*V999+D1;
F2=0*V999+D2;
/VARIANCES
E1 TO E2=*; D1 TO D2=*;
/COVARIANCES
D1 TO D2=*;
/CONSTRAINTS
/MATRIX
1.000
.630 1.000
.000 .000 1.000
.000 .000 .000 1.000
.000 .000 .000 .000 1.000
/MEAN
.1818 .4545 .000 .000 .000
/STANDARD DEVIATION
.4045 1.2136 .000 .000 .000
/PRINT
EFFECTS=YES;
/CONSTRAINTS
(1,D1,D2)=(2,D1,D2)=(3,D1,D2)=(4,D1,D2);
(1,D1,D1)=(2,D1,D1)=(3,D1,D1)=(4,D1,D1);
(1,D2,D2)=(2,D2,D2)=(3,D2,D2)=(4,D2,D2);
(1,F1,V999)=(2,F1,V999)=(3,F1,V999)=(4,F1,V999);
(1,F2,V999)=(2,F2,V999)=(3,F2,V999)=(4,F2,V999);
(1,E1,E1)=(3,E1,E1)=(4,E1,E1);
(1,E2,E2)=(2,E2,E2)=(3,E2,E2)=(4,E2,E2);
(1,E3,E3)=(2,E3,E3)=(3,E3,E3);
(1,E4,E4)=(2,E4,E4);
(1,V3,F2)=(2,V3,F2)=(3,V3,F2);
(1,V4,F2)=(2,V4,F2);
/LMTEST
/TECH
ITER=100;
/END

```

Appendix 9.1  
Amos Program Specifications for the Hierarchical H1 LGM Model Depicted in Fig. 9.1 Using the Raw Maximum Likelihood Approach

```
! USING RAW ML APPROACH H1 MODEL
$MSTRUCTURE
V16
V15
V14
V13
V12
V11
V10
V9
V8
V7
V6
V5
V4
V3
V2
V1
$FITTEDMOM
$SAMPLEMOM
$INPUT VARIABLES
V1
V2
V3
V4
V5
V6
V7
V8
V9
V10
V11
V12
V13
V14
V15
V16
$SAMPLE SIZE = 369
$MISSING=99
$RAW DATA
```

Appendix 9.2  
Amos Program Specifications for the Hierarchical H0 LGM Model Depicted in Fig. 9.1 Using the Raw Maximum Likelihood Approach

```
! USING RAW ML APPROACH H0 MODEL
$STRUCTURE
V1= (1)F1 + (0)F2 + (1)EPS1
V2= (1)F1 + (1)F2 + (1)EPS2
V3= (1)F1 + (2)F2 + (1)EPS3
V4= (1)F1 + (3)F2 + (1)EPS4
V5= (1)F3 + (0)F4 + (1)EPS5
V6= (1)F3 + (1)F4 + (1)EPS6
V7= (1)F3 + (2)F4 + (1)EPS7
V8= (1)F3 + (3)F4 + (1)EPS8
V9= (1)F5 + (0)F6 + (1)EPS9
V10=(1)F5 + (1)F6 + (1)EPS10
V11=(1)F5 + (2)F6 + (1)EPS11
V12=(1)F5 + (3)F6 + (1)EPS12
V13=(1)F7 + (0)F8 + (1)EPS13
V14=(1)F7 + (1)F8 + (1)EPS14
V15=(1)F7 + (2)F8 + (1)EPS15
V16=(1)F7 + (3)F8 + (1)EPS16
```

F1= (1)F9 + (1)ZETA1  
F2= (1)F10 + (1)ZETA2  
F3= (1)F9 + (1)ZETA3  
F4= (1)F10 + (1)ZETA4  
F5= (1)F9 + (1)ZETA5  
F6= (1)F10 + (1)ZETA6  
F7= (1)F9 + (1)ZETA7  
F8= (1)F10 + (1)ZETA8  
F9= ( ) + (1)ZETA9  
F10=( ) + (1)ZETA10

ZETA9<->ZETA10  
ZETA1<->ZETA2(R1)  
ZETA3<->ZETA4(R1)  
ZETA5<->ZETA6(R1)  
ZETA7<->ZETA8(R1)

EPS1(E1)  
EPS5(E1)  
EPS9(E1)  
EPS13(E1)  
EPS2(E2)  
EPS6(E2)  
EPS10(E2)  
EPS14(E2)  
EPS3(E3)

*Continued*

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EPS7(E3)  
EPS11(E3)  
EPS15(E3)  
EPS4(E4)  
EPS8(E4)  
EPS12(E4)  
EPS16(E4)  
ZETA1(Z1)  
ZETA3(Z1)  
ZETA5(Z1)  
ZETA7(Z1)  
ZETA2(Z2)  
ZETA4(Z2)  
ZETA6(Z2)  
ZETA8(Z2)

\$INPUT VARIABLES

V1  
V2  
V3  
V4  
V5  
V6  
V7  
V8  
V9  
V10  
V11  
V12  
V13  
V14  
V15  
V16

\$SAMPLE SIZE = 369

\$RAW DATA

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Appendix 9.3  
Amos Program Specifications for the Test of the MLGM Model Depicted in Fig. 9.2

```

! MLGM USING BETWEEN AND WITHIN MATRICES
! USING RAW ML APPROACH
$STRUCTURE
V1=(1.551)F1 + (1)F7 + (0)F8 + (1)EPS1
V2=(1.551)F2 + (1)F7 + (1)F8 + (1)EPS2
V3=(1.551)F3 + (1)F7 + (2)F8 + (1)EPS3
V4=(1.551)F4 + (1)F7 + (3)F8 + (1)EPS4
F1=          (1)F5 + (0)F6 + (1)ZETA1
F2=          (1)F5 + (1)F6 + (1)ZETA2
F3=          (1)F5 + (2)F6 + (1)ZETA3
F4=          (1)F5 + (3)F6 + (1)ZETA4
F5=( )              + (1)ZETA5
F6=( )              + (1)ZETA6
F7=(0)              + (1)ZETA7
F8=(0)              + (1)ZETA8
ZETA5<->ZETA6(R1)
ZETA7<->ZETA8(R2)
EPS1(E1)
EPS2(E2)
EPS3(E3)
EPS4(E4)
ZETA1(Z1)
ZETA2(Z1)
ZETA3(Z1)
ZETA4(Z1)
ZETA7(Z7)
ZETA8(Z8)
$INPUT VARIABLES
V1
V2
V3
V4
$SAMPLE SIZE =    369
$STANDARDIZED
$MEANS
4.21150  4.92070  6.42293  6.85264
$COVARIANCES
4.82428
4.09989  5.82624
3.70615  4.99469  7.51219
3.24240  4.33173  5.61828  7.01698
$NEXTGROUP

```

*Continued*

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```

$STRUCTURE
V1=(1)F7 + (0)F8 + (1)EPS1
V2=(1)F7 + (1)F8 + (1)EPS2
V3=(1)F7 + (2)F8 + (1)EPS3
V4=(1)F7 + (3)F8 + (1)EPS4
F7=(0)          + (1)ZETA7
F8=(0)          + (1)ZETA8
ZETA7<->ZETA8(R2)
EPS1(E1)
EPS2(E2)
EPS3(E3)
EPS4(E4)
ZETA7(Z7)
ZETA8(Z8)
$INPUT VARIABLES
V1
V2
V3
V4
$SAMPLE SIZE =    519
$STANDARDIZED
$MEANS
.000      .000      .000      .000
$COVARIANCES
2.86625

```



2.14419 3.45777  
1.62187 2.22238 3.75128  
1.55395 1.86127 2.31647 3.70665

Appendix 10.1  
EQS Program Specifications for the *Ha* Model Depicted in Fig. 10.2

```
/TITLE
MULTIPLE POPULATION POWER ESTIMATION GROUP 1
/SPECIFICATIONS
CAS=150; VAR=3; ME=ML; MA=COV; ANAL=MOMENT; GROUPS=2;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
F1=1.510*V999+D1;
F2=.174*V999+D2;
/VARIANCES
E1=.822*; E2=.975*; E3=.581*; D1=1.032*; D2=.343*;
/COVARIANCES
D1 TO D2=-.075*;
/MATRIX
1.000
.000 1.000
.000 .000 1.000
/MEANS
1.000 1.000 1.000
/PRINT
CORR=YES;
/END
/TITLE
MULTIPLE POPULATION POWER ESTIMATION GROUP 2
/SPECIFICATIONS
CAS=150; VAR=3; ME=ML; MA=COV; ANAL=MOMENT;
/EQUATIONS
V1=F1+0F2+0F3+E1;
V2=F1+1F2+1F3+E2;
V3=F1+2F2+2F3+E3;
F1=1.510*V999+D1;
F2=.174*V999+D2;
F3=.254*V999+D3;
/VARIANCES
E1=.822*; E2=.975*; E3=.581*; D1=1.032*; D2=.343*; D3=.178*;
/COVARIANCES
D1 TO D2=-.075*;
/LABELS
/MATRIX
1.000
.000 1.000
.000 .000 1.000
/MEANS
1.000 1.000 1.000
/CONSTRAINTS
(1,F1,V999)=(2,F1,V999);
(1,F2,V999)=(2,F2,V999);
```

*Continued*

```
(1,D1,D1)=(2,D1,D1);
(1,D2,D2)=(2,D2,D2);
(1,D1,D2)=(2,D1,D2);
(1,E1,E1)=(2,E1,E1);
(1,E2,E2)=(2,E2,E2);
(1,E3,E3)=(2,E3,E3);
/LMTEST
/TECH
ITER=0;
/PRINT
CORR=YES;
/END
```

Appendix 10.2  
EQS Program Specifications for the  $H_0$  Model Depicted in Fig. 10.2

```

/TITLE
MULTIPLE POPULATION POWER ESTIMATION GROUP 1
/SPECIFICATIONS
CAS=150; VAR=3; ME=ML; MA=COV; ANAL=MOMENT; GROUPS=2;
/EQUATIONS
V1=F1+0F2+E1;
V2=F1+1F2+E2;
V3=F1+2F2+E3;
F1=1.510*V999+D1;
F2=.174*V999+D2;
/VARIANCES
E1=.822*; E2=.975*; E3=.581*; D1=1.032*; D2=.343*;
/COVARIANCES
D1 TO D2=-.075*;
/MATRIX
1.000
.000 1.000
.000 .000 1.000
/MEANS
1.000 1.000 1.000
/PRINT
CORR=YES;
/END
/TITLE
MULTIPLE POPULATION POWER ESTIMATION GROUP 2
/SPECIFICATIONS
CAS=150; VAR=3; ME=ML; MA=COV; ANAL=MOMENT;
/EQUATIONS
V1=F1+0F2+0F3+E1;
V2=F1+1F2+1F3+E2;
V3=F1+2F2+2F3+E3;
F1=1.510*V999+D1;
F2=.174*V999+D2;
F3=0V999+D3;
/VARIANCES
E1=.822*; E2=.975*; E3=.581*; D1=1.032*; D2=.343*; D3=.178*;
/COVARIANCES
D1 TO D2=-.075*;
/LABELS
/MATRIX
1.000
.000 1.000
.000 .000 1.000
/MEANS
1.000 1.000 1.000
/CONSTRAINTS
(1,F1,V999)=(2,F1,V999);
(1,F2,V999)=(2,F2,V999);

```

*Continued*

```

(1,D1,D1)=(2,D1,D1);
(1,D2,D2)=(2,D2,D2);
(1,D1,D2)=(2,D1,D2);
(1,E1,E1)=(2,E1,E1);
(1,E2,E2)=(2,E2,E2);
(1,E3,E3)=(2,E3,E3);
/LMTEST
/TECH
ITER=0;
/PRINT
CORR=YES;
/END

```

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