A Cross-Domain Model for Growth in Adolescent Alcohol Expectancies

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Methodologists have recently shown how the methods of individual growth modeling and covariance structure analysis can be integrated, bringing the flexibility of the latter to bear on the investigation of inter-individual differences in change. The individual growth-modeling framework uses a pair of hierarchical statistical models to represent: (a) individual status as a function of time, and (b) inter-individual differences in true change. Under the covariance structure approach, these level-1 and level-2 models can be reformatted as the "measurement" and "structural" components of the general LISREL model with mean structures. Consequently, a covariance structure analysis of longitudinal panel data can provide maximum-likelihood estimates for all level-2 parameters. In this article, using longitudinal data drawn from a school-based alcohol prevention trial, we demonstrate how the new approach can be used to investigate the inter-relationships among simultaneous individual changes in two domains — positive and negative alcohol expectancies — over the course of early to mid-adolescence, for both boys and girls. We represent individual change over time in positive expectancies with a piecewise growth model, and in negative expectancies with a straight-line growth model. Then, we use multi-sample covariance structure analysis to ask whether individual changes in positive and negative expectancies are related to each other and whether the pattern of inter-relationships differs by gender. Our approach can easily be generalized to more than two domains and has a variety of other advantages that we document in the discussion.

An important question in prevention research is whether substance use is simply a manifestation of an individual's underlying propensity to engage in antisocial and rebellious behavior of any type, or whether there is a singular attraction to one type of deviance. This question can be explored by examining correlations among behavior in several "domains", for example, multiple substance use, delinquency, early and promiscuous sexual behavior, and truancy. It is also profitable to ask whether change in one domain is

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related to change in another. An analytic strategy that Willett and Sayer 
(1996) refer to as “the cross-domain analysis of change” can be used to model 
the inter-relationships among the several types of changes. This strategy also 
permits us to ask whether any pattern of inter-relationships among changes in 
multiple domains is the same across groups as defined, for example, by 
gender, level of risk, or ethnicity. It is possible, for instance, that increasing 
alcohol consumption and increasing delinquency may be strongly inter-linked 
for high-risk adolescents but not for adolescents with moderate or low risk. 
The goal of this article is to describe the cross-domain approach and provide 
a worked example with empirical data on alcohol expectancies drawn from a 
school-based alcohol prevention trial.

Prevention researchers often enquire about systematic inter-individual 
differences in intra-individual change—that is, whether individual change in 
an attribute over time differs from person to person in systematic and 
interesting ways. Typically, such questions are concerned with the 
relationship between change in a single continuous outcome such as alcohol 
consumption and selected predictors of that change, such as family 
environment or peer influences. In recent years, investigators have used 
individual growth modeling in order to capitalize on the richness of 
multiwave data and have provided better methods for investigating 
systematic inter-individual difference in intra-individual change (Bryk, 1977; 
Bryk & Raudenbush, 1987; Rogosa, Brandt, & Zimowski, 1982; Rogosa & 
Willett, 1985; Willett, 1988, 1994). We provide a brief summary of the main 
tenets of this approach.

As a first step in the growth modeling approach, a suitable mathematical 
model must be chosen to represent individual change over time in each 
domain. These “level-1” models represent the outcomes of interest as a 
function of time and individual-specific “growth parameters.” If the 
investigator decides that individual change in alcohol consumption has a 
straight-line trajectory over time, then the level-1 growth model will contain 
two individual growth parameters: (a) an “intercept” parameter representing 
status, at a time defined by the investigator and (b) a “slope” parameter 
representing the rate of change. If, on the other hand, individual change in 
consumption is thought to follow a curvilinear trajectory that is quadratic with 
time, then the level-1 model for change will contain a third parameter 
representing curvature.

Within each domain, all population members are assumed to have growth 
trajectories of the same functional form, but different people may have 
different values of the level-1 individual growth parameters. For instance, 
when individual change is linear with time, inter-individual differences in 
progress may be due to heterogeneity in either intercept or slope (or both). If
individual change is a quadratic function of time, then inter-individual differences in curvature may also exist. When growth in one domain is related to growth in another, the individual growth parameters will covary across domains, perhaps with rate of change in one domain being related to curvature in the second. Such hypothesized links between individual growth parameters in the two domains can be described in a "between-person" or "level-2" statistical model.

Questions about simultaneous individual growth require panel data in each domain—that is, several longitudinal assessments on many individuals. To use the methods described here, several conditions must be met. First, three, or more, waves of data must be available on each individual in each domain. Second, the outcome variable must be measured on a continuous scale. Third, the variable must demonstrate both construct and metric invariance over time. Fourth, the data must be balanced in a particular way. In each domain, the occasions of measurement need not be separated by equal time intervals, but both the number and the spacing of assessments must be the same for all individuals. As we will demonstrate, the pattern of time-structuring may differ from domain to domain.

Various methods can be used to estimate the parameters of the level-1 and level-2 models in the analysis of change when growth is restricted to a single domain. These include exploratory ordinary and weighted least-squares regression-based methods (Rogosa, Brandt & Zimowski, 1982; Rogosa & Willett, 1985; Willett, 1988), hierarchical linear models (Bryk & Raudenbush 1987, 1992), and covariance and mean structure analysis (Meredith and Tisak, 1990; Muthén, 1991, 1992; Willett & Sayer, 1994). However, the multiple-domain case requires the flexibility provided by a general structural equation modeling program. In an earlier paper, Willett & Sayer (1996) provide a technical framework for representing simultaneous inter-individual differences in change in more than one domain and give examples of how model parameters can be estimated by maximum-likelihood methods. Several recent papers have provided empirical examples using that framework (Curran, Harford, & Muthén, 1997; MacCallum, Kim, Malarkey, & Kiecolt-Glaser, 1997). In each case, the analysis was based on the restricted case of equivalent growth models in each domain. In the current article, we extend our earlier presentation to include cross-domain analyses of change that permit the number of data waves and the functional form of the individual growth model to vary across domains.

This article has two sections and a concluding discussion. In the first section, we review the general cross-domain model. We specify level-1 growth models that represent individual change over time in two domains and we combine these into a composite "cross-domain" model for individual
change. Then, we formulate an “unconditional” level-2 model for inter-individual differences in change that describes average growth in each domain, as well as heterogeneity in change across multiple domains. In this latter model, the individual growth parameters of the level-1 individual growth models are permitted to covary across individuals. We illustrate how the level-1 and level-2 models of the individual growth modeling perspective map smoothly onto the general LISREL model with mean structures. Then, we demonstrate how the respective level-2 means, variances and covariances of the individual growth parameters that represent simultaneous change in several domains can be estimated straightforwardly by covariance and mean structure analysis. To close out the section, we describe the assumptions made at level-1 concerning the homoscedasticity and independence of the level-1 measurement error covariance structure within each domain. In the second section, we use a data-based example to frame our presentation throughout the article and we provide, in an appendix, illustrative LISREL programs for conducting the analyses on which our presentation is based. In conclusion, we discuss some advantages of this method for estimating cross-domain relationships.

The General Cross-Domain Model

Modeling Individual Change Over Time

Classical test theory describes the properties of scores on a single occasion, distinguishing observed from true scores (Lord & Novick, 1968). When individual growth is modeled, the model chosen must also contain a component describing a person’s true growth trajectory over time and a component representing the stochastic effect of measurement error.

Under the individual growth modeling framework, the “true” part of each person’s growth trajectory is represented by an algebraic function of time. In this section, we make some simplifying assumptions for illustrative purposes, each of which can be modified in any cross-domain analysis: (a) growth occurs in only two domains, referenced A and B, (b) three waves of data have been collected in each domain and (c) the same algebraic function of time adequately describes growth in each domain. The superscripts A and B are used to distinguish the domain-specific models.

In both domains, the individual’s vector of responses $\mathbf{Y}$ are represented by a simple linear function of time. The following level-1 model represents individual change in Domain $A$ for the $t^{th}$ person on the $t^{th}$ occasion of measurement (where $t = 1, 2, 3$):
(1) \[ Y_{it}^{(A)} = \pi_{0i}^{(A)} + \pi_{1i}^{(A)}t_i + \epsilon_{it}^{(A)} \]

The \( \epsilon_{it}^{(A)} \) represent the level-1 measurement errors that distinguish true and observed scores in Domain A. We adopt a similar growth model for individual change in Domain B:

(2) \[ Y_{it}^{(B)} = \pi_{0i}^{(B)} + \pi_{1i}^{(B)}t_i + \epsilon_{it}^{(B)} \]

The shape of the hypothesized trajectory depends on the particular parameterization of time chosen and on the specific values of the individual growth parameters. The models in Equations 1 and 2 contain individual growth parameters representing the intercept and slope of each person’s trajectories over time. Thus, the slope parameter \( \pi_{1i}^{(A)} \) represents the true change in \( Y \) per unit time for the \( i^{th} \) person, whereas the intercept parameter \( \pi_{0i}^{(A)} \) represents the true status of person \( i \) when \( t_i \) is equal to zero. The \( \epsilon_{it}^{(A)} \) represent the errors of prediction. Provided that the growth model is correctly specified, these can be considered as measurement error. If the model is incorrect, model error and measurement error will be confounded.\(^1\)

A Matrix Representation For The Empirical Growth Records

Each person’s empirical growth record contained, in both domains, 3 measurements of observed status, \( Y_{1i}, Y_{2i}, \) and \( Y_{3i} \). Under the individual growth models in Equations 1 and 2, these records can be represented as:

(3) \[
\begin{bmatrix}
Y_{1i}^{(A)} \\
Y_{2i}^{(A)} \\
Y_{3i}^{(A)}
\end{bmatrix} =
\begin{bmatrix}
1 & t_1 \\
1 & t_2 \\
1 & t_3
\end{bmatrix}
\begin{bmatrix}
\pi_{0i}^{(A)} \\
\pi_{1i}^{(A)}
\end{bmatrix} +
\begin{bmatrix}
\epsilon_{1i}^{(A)} \\
\epsilon_{2i}^{(A)} \\
\epsilon_{3i}^{(A)}
\end{bmatrix}
\]

and:

(4) \[
\begin{bmatrix}
Y_{1i}^{(B)} \\
Y_{2i}^{(B)} \\
Y_{3i}^{(B)}
\end{bmatrix} =
\begin{bmatrix}
1 & t_1 \\
1 & t_2 \\
1 & t_3
\end{bmatrix}
\begin{bmatrix}
\pi_{0i}^{(B)} \\
\pi_{1i}^{(B)}
\end{bmatrix} +
\begin{bmatrix}
\epsilon_{1i}^{(B)} \\
\epsilon_{2i}^{(B)} \\
\epsilon_{3i}^{(B)}
\end{bmatrix}
\]

\(^1\) If multiple indicators of the response variable can be included in the analysis, it is possible to estimate the reliability of measurement and thus distinguish between measurement and model error.
A. Sayer and J. Willett

For reasons of parsimony, in Equations 3 and 4 and throughout the rest of the text, we have retained symbols \( t_i \) through \( t_j \) to represent the timing of the occasions of measurement. In any particular research project, each of these symbols will have known constant value. They represent the investigator’s a priori hypothesis about the shape of the growth trajectory. This is one distinguishing feature of our approach from latent growth curve modeling, in which the times of measurement are estimated from the data (cf. McArdle & Epstein, 1987).

For purposes of subsequent analysis, we combine the separate level-1 growth models of Equations 1 and 2 into a single composite “cross-domain” model that represents simultaneous individual change in domains \( A \) and \( B \), as follows:

\[
\begin{bmatrix}
Y^{(A)}_{1i} \\
Y^{(A)}_{2i} \\
Y^{(A)}_{3i} \\
Y^{(B)}_{1i} \\
Y^{(B)}_{2i} \\
Y^{(B)}_{3i}
\end{bmatrix} = \begin{bmatrix}
1 & t_1 & 0 & 0 \\
1 & t_2 & 0 & 0 \\
1 & t_3 & 0 & 0 \\
0 & 0 & 1 & t_1 \\
0 & 0 & 1 & t_2 \\
0 & 0 & 1 & t_3
\end{bmatrix} \begin{bmatrix}
p^{(A)}_{0i} \\
p^{(A)}_{1i} \\
p^{(A)}_{2i} \\
p^{(B)}_{0i} \\
p^{(B)}_{1i} \\
p^{(B)}_{2i}
\end{bmatrix} + \begin{bmatrix}
\epsilon^{(A)}_{1i} \\
\epsilon^{(A)}_{2i} \\
\epsilon^{(A)}_{3i} \\
\epsilon^{(B)}_{1i} \\
\epsilon^{(B)}_{2i} \\
\epsilon^{(B)}_{3i}
\end{bmatrix}
\]

(5)

Notice that, for person \( i \), the joint observed growth record in both domain \( A \) and \( B \) (on the left-hand side of Equation 5) can be regarded as a combination of three distinct components: (a) a matrix of known times (and constants) that is identical across all individuals, multiplied by (b) an individual-specific vector of unknown individual growth parameters (which we will refer to as the “latent growth vector”), added to (c) an individual-specific vector of unknown errors of measurement. The latent growth vector is the central focus of the subsequent cross-domain analysis of change.

Distribution of the Level-1 Measurement Errors

In Equations 1 and 2, we have stated that level-1 measurement error \( \epsilon_{1i} \) disturbs the true status of the \( i \)th person on the first occasion of measurement, \( \epsilon_{2i} \) on the second occasion, \( \epsilon_{3i} \) on the third, and so forth. However, we have made no claims about the shape of the distribution from which these errors are drawn. We usually begin by assuming that the measurement errors obey stringent “classical” assumptions within each domain — that is, we assume
initially that they are distributed independently and homoscedastically over time within domain. We assume that person \( i \) draws his or her measurement error vector from the following distribution:

\[
\begin{bmatrix}
\epsilon^{(A)}_{1i} \\
\epsilon^{(A)}_{2i} \\
\epsilon^{(A)}_{3i} \\
\epsilon^{(B)}_{1i} \\
\epsilon^{(B)}_{2i} \\
\epsilon^{(B)}_{3i}
\end{bmatrix}
\sim N
\begin{bmatrix}
0 \\
0 \\
0 \\
0 \\
0 \\
0
\end{bmatrix},

\begin{bmatrix}
\sigma^2_{\epsilon^{(A)}} & 0 & 0 & 0 & 0 & 0 \\
0 & \sigma^2_{\epsilon^{(A)}} & 0 & 0 & 0 & 0 \\
0 & 0 & \sigma^2_{\epsilon^{(A)}} & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma^2_{\epsilon^{(B)}} & 0 & 0 \\
0 & 0 & 0 & 0 & \sigma^2_{\epsilon^{(B)}} & 0 \\
0 & 0 & 0 & 0 & 0 & \sigma^2_{\epsilon^{(B)}}
\end{bmatrix}
\]

where the mean vector and covariance matrix on the right-hand side of Equation 6 are assumed identical across children. Notice that, although we are assuming initially that the level-1 measurement errors are homoscedastic \textit{within} domain, we are not assuming that they are homoscedastic \textit{across} domains, because there is no a-priori reason to believe that measurement error variance will be identical in both domains. If there were, then this constraint on the level-1 measurement error variance could easily be tested and imposed.

Unlike other methods for fitting individual growth models that assume within-individual error variance that is homoscedastic over time, the covariance structure approach that we will describe permits great flexibility in the modeling of the level-1 measurement error covariance structure. We can permit each person to draw their measurement error vector at random from a distribution with mean vector zero and an unknown covariance matrix whose shape can be specified as necessary. This flexibility permits us to test the fit of the classical error structure above against other, more liberal, hypotheses (such as the presence of within-person measurement error autocorrelation) because we can modify the level-1 error covariance structure as necessary. And regardless of the final structure adopted, we can, in theory, estimate all of the components of the hypothesized level-1 error covariance matrix. This facility is important in a study of individual change because knowledge of the magnitudes of the level-1 error variances and covariances underpins the estimation of measurement reliability.

In practice, it is difficult to estimate a completely unconstrained error covariance matrix due to the need for model identification. We suggest that the imposition of restrictions be guided by knowledge about the growth
process under consideration. For example, depending on the between-occasion intervals, it may be sensible to allow only temporally-adjacent errors to covary and constrain more distal pairs to zero covariance. If an autoregressive process is hypothesized, the error structure is modeled as block-diagonal and within-band covariances are set equal. To avoid problems of local identification we advocate the use of user-supplied start values for all models. Often, these can be obtained from executing a program that fails to converge but provides usable initial estimates of the parameters.

**Modeling Inter-Individual Differences in Change**

Even though all population members are assumed to share a common functional form for their changes in each domain, the true growth trajectories may still differ across people within-domain because of inter-individual variation in the values of the individual growth parameters. Furthermore, the individual changes may be linked across domains because of covariation among the individual growth parameters from domain to domain. Thus, when we conduct cross-domain analyses of change, we are interested in the population *between-person* distribution of the vector of individual growth parameters.

We specify that everyone in the population draws their latent growth vector independently from a multivariate normal distribution of the following form:

\[
\begin{bmatrix}
\pi_0^{(A)} \\
\pi_1^{(A)} \\
\pi_0^{(B)} \\
\pi_1^{(B)}
\end{bmatrix} \sim N
\begin{bmatrix}
\mu_{\pi_0}^{(A)} \\
\mu_{\pi_1}^{(A)} \\
\mu_{\pi_0}^{(B)} \\
\mu_{\pi_1}^{(B)}
\end{bmatrix},
\begin{bmatrix}
\sigma^{2(A)}_{\pi_0} & \sigma^{(A)(A)}_{\pi_0 \pi_1} & \sigma^{(A)(B)}_{\pi_0 \pi_1} & \sigma^{(A)(B)}_{\pi_0 \pi_1} \\
\sigma^{(A)(A)}_{\pi_0 \pi_1} & \sigma^{2(A)}_{\pi_1} & \sigma^{(A)(B)}_{\pi_1 \pi_1} & \sigma^{(A)(B)}_{\pi_1 \pi_1} \\
\sigma^{(A)(B)}_{\pi_0 \pi_1} & \sigma^{(A)(B)}_{\pi_1 \pi_1} & \sigma^{2(B)}_{\pi_0} & \sigma^{(B)(B)}_{\pi_0 \pi_1} \\
\sigma^{(A)(B)}_{\pi_0 \pi_1} & \sigma^{(A)(B)}_{\pi_1 \pi_1} & \sigma^{(B)(B)}_{\pi_0 \pi_1} & \sigma^{2(B)}_{\pi_1}
\end{bmatrix}
\]

(7)

This hypothesized distribution is a level-2 “between-person” model for inter-individual differences in true change. In Equation 7 there are a total of fourteen important between-person parameters: the four population means, four variances and six covariances of the latent growth vector. These parameters provide information on the average trajectory of true change within domain, the variation and covariation of true intercept and slope within domain, and the covariation of true intercept and slope between domains. All of these level-2 parameters can be estimated using the covariance structure approach that we describe on the following page.
Researchers are occasionally interested in estimating the individual (or level-1) growth parameters in Equations 1 and 2. Estimates are easily obtained when using weighted least-squares methods (Willett, 1988) or via empirical Bayes when using multilevel applications such as HLM (Bryk & Raudenbush, 1992). The LISREL program does not have an option to estimate individual parameters. It is possible to obtain these estimates indirectly by writing the matrix of factor scores regressions to a local file (adding the statement FS RM = FS to the OUtput line saves the equations to the file FS). This file can serve as input to a utility program that estimates the scores on the latent variable for each individual case. One suitable program for this purpose is the interactive FORTRAN program FSCORE (Molenaar, 1996). We note that these scores suffer from the usual problems of factor indeterminancy and cannot be computed exactly.

An Application of the Cross-Domain Model to Adolescent Alcohol Expectancies

Introducing the Data-Example

Alcohol expectancies are cognitive variables that describe an individual’s beliefs about the effects of alcohol on social behavior. Positive expectancies are beliefs that alcohol facilitates social interaction and enhances personal well-being, whereas negative expectancies are beliefs that alcohol impedes cognitive functioning and impairs physical and mental health. The importance of studying alcohol expectancies in childhood and adolescence is based on evidence that suggests that expectancies play a role in the initiation and maintenance of alcohol consumption (Critchlow, 1989). Several studies cited by Goldman (1994) suggest that expectancies predict up to 50% of the variance in alcohol consumption across individuals. Positive expectancies are particularly potent predictors in samples of middle-school adolescents. For example, Christiansen, Smith, Roehling & Goldman (1989) found that scores on the positive expectancies subscale of the Alcohol Expectancies Questionnaire were the strongest concurrent and prospective (one-year) predictor of quantity and frequency of alcohol consumption, problem drinking and transition to problem drinking in a sample of 871 eighth graders. In a similar vein, Killen, Hayward, Wilson, Haydel, Robinson, Taylor, Hammer, and Varady (1996) examined a set of individual-level variables including temperamental characteristics, depression, and self-esteem in a ninth-grade sample, and report that expectancy for enhanced social behavior was the only significant predictor of drinking onset. The potential predictive

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2 This program is available as freeware through the Mehtodology Center at Penn State University.
power of alcohol expectancies, along with the possibility of manipulating this
cognitive dimension by experimental intervention, has lead to the recognition
of its potential use in prevention research.

Do Expectancies Change Over Time?

Most researchers have relied on associating status (scores on an
expectancy questionnaire at a single point in time) with concurrent or future
alcohol consumption. There have been no multiwave longitudinal
investigations of patterns of change in alcohol expectancies over the course of
early adolescence. However, evidence from cross-sectional studies strongly
suggest that there are age-related differences in expectancy scores, with older
children having greater positive expectancies than younger (Christiansen,
Goldman, & Inn, 1982). Other evidence suggests that due to social-learning
influences, young children develop expectancies prior to pharmacological
experience with alcohol. These beliefs tend to consolidate into a form similar
to those held by adults by early adolescence (Miller, Smith & Goldman,
1990). In a short-term longitudinal study of grade-school children, Kraus,
Smith and Ratner (1994) found that expectancy scores increased from 2\textsuperscript{nd} to
4\textsuperscript{th} grade. In addition, researchers have found that attitudes toward other
types of deviance undergo rapid change during adolescence. For example,
Raudenbush and Chan (1993) found that the pattern of change in attitudes
toward general deviant behavior (e.g., truancy, petty shoplifting) follows a
cubic form. It is likely that other attitudinal variables such as alcohol
expectancies undergo similar changes, especially in light of the large cognitive
changes in perspective-taking during adolescence that permit adolescents to
consider the multiple consequences of their actions (Selman, 1980).

There is some empirical evidence to suggest that the form of this
attitudinal change may be discontinuous with time during early adolescence,
particularly over the transition from elementary to middle school. Eccles,
Lord, Roeser, Barber, and Hernandez Jozefowicz (1997) have reviewed the
empirical literature on school transitions and note the radical changes in the
school environment encountered by the young adolescent during the
transition from 6\textsuperscript{th} to 7\textsuperscript{th} grade. They argue that a lack of fit between the need
for experimentation and identity development and the more structured,
impersonal and bureaucratic organization of the school environment places
adolescents at risk for negative motivational outcomes. They present
evidence of a sharp disjuncture in the trajectories of achievement, school
engagement, and self-esteem, all of which decline rapidly after the shift to
junior high school (usually during the 7\textsuperscript{th} grade year).
One Domain or Two?

Although researchers agree that it is important to study both positive and negative beliefs about the effects of alcohol, there is little consensus about whether to regard alcohol expectancies as a bipolar trait or whether to treat positive and negative expectancies as independent constructs (Leigh & Stacy, 1991). They have been shown to be empirically independent; that is, they are differentially related to alcohol use. Positive expectancies predict onset, whereas negative expectancies tend not to be related to consumption. Results from investigations of the factor structure of expectancies vary by age. While several confirmatory factor analyses suggest the presence of distinct factors in adult populations, there is less evidence that adolescents are able to make the same discriminations (George, Frone, Cooper, Russell, Skinner, & Windle, 1995; Stacy, Widaman, & Marlatt, 1990). We will consider positive and negative expectancies as separate domains for the purposes of illustration.

Throughout this article, we illustrate the cross-domain analysis of change using panel data drawn from the Adolescent Alcohol Prevention Trial (AAPT), a longitudinal investigation of children enrolled in school-based prevention programs (Hansen & Graham, 1991). The AAPT study was designed to assess the relative impact of different school-based alcohol-prevention curricula designed for young adolescents. Data were collected on a large sample of children, from 5th through 11th grade, drawn from approximately 400 schools in Southern California. The dataset includes 4 panels of data, each one corresponding to a sample of children followed for several years. The subsample on which our analyses are based is drawn from Panel 1, which followed children from 5th through 10th grades. The children in Panel 1 were measured for the first time in 1986-87, and then assessed annually for a period of 6 years.

At grades 5, 6, 7, 9, and 10, children were administered a survey containing questions on alcohol beliefs. Both positive and negative expectancies were assessed using a series of questionnaire items. However, not all items were administered to all respondents at each occasion of measurement, as the AAPT study utilized a three-form design to minimize respondent burden and optimize the cost-to-benefit ratio. Positive expectancies were assessed on each occasion, whereas assessment of negative expectancies was restricted to the early years of the study. Thus, there are five waves of data on positive expectancies (grades 5, 6, 7, 9, and 10) and three waves of data on negative expectancies (grades 5, 6, and 7).

Each item presented an alcohol statement, for which the adolescents had to indicate extent of agreement using a 4 point Likert format. Positive alcohol expectancy was assessed using three items tapping the social consequences of drinking alcohol. They include: Does drinking alcohol make it easier to be
part of a group? Does drinking alcohol make parties more fun? Does drinking make it easier to have good time with friends? Negative alcohol expectancy was assessed using four items that tapped the problematic consequences of drinking alcohol. They include: If you drank alcohol regularly, would it give you liver disease? If you drank alcohol regularly, would you have bad breath? If you drank alcohol regularly, would you get into trouble at school? If you drank alcohol regularly, would you be worse at sports? Items were summed (within-domain) to create composite scale scores at each wave. A logarithmic transformation was used to correct the large positive skew we detected on inspection of the univariate distributions of these composites.

In Table 1 we provide five waves of observed (log) positive and three waves of observed (log) negative expectancy scores for 16 randomly-selected children. The table also contains a child identification code and a record of the child’s gender. Inspection of the table suggests that there is some heterogeneity at study entry in both (log) positive and (log) negative expectancy scores. There is also heterogeneity in progress over time, comparing domains within-child. For instance, Child 13 shows no change in (log) positive expectancy score during early adolescence (grades 5 through 7) but an upward trend is evident beyond 7th grade. The same child shows a decline in negative expectancies between 5th and 7th grade. In our article, we use these data to illustrate the cross-domain analysis of change by addressing three research questions: (a) Do expectancies change during the course of early adolescence? What is the pattern of change in each domain? (b) are individual changes in positive and negative expectancies and related? and, (c) Is the pattern of inter-relationship among these changes the same for boys and girls?

Choosing an appropriate mathematical function to represent true individual change is an important first step in any project. If theory guides a rational choice of model, individual growth parameters will have powerful substantive interpretations. Often, however, the mechanisms governing change are poorly understood and a well-fitting polynomial is used to approximate the trajectory. One responsible preliminary strategy for choosing a valid model is to inspect each person’s empirical growth record by plotting their observed status against time. We believe that this type of individual-level data exploration is particularly important when covariance structure methods are being used to investigate change, as data are presented in an aggregate form.

Based on the work of Eccles and her colleagues (1997), we had some theoretical basis for expecting that the positive expectancy trajectories would be discontinuous with time. Initial exploratory plots and later confirmatory data analyses indicated that change in positive expectancies could be represented well by a “piecewise” growth model, which allowed a discontinuity in the trajectory at grade 7. Thus, the following level-1 model was selected to represent the positive
Table 1
Longitudinal data on a stratified random subsample of 15 adolescents with: (a) 5 waves of (log) positive expectancy scores at grades 5, 6, 7, 9, and 10 (b) 3 waves of (log) negative expectancy scores at grades 5, 6, and 7 (c) values of the indicator MALE (1 = male; 0 = female).

<table>
<thead>
<tr>
<th>ID</th>
<th>Positive Expectancies</th>
<th>Negative Expectancies</th>
<th>Male</th>
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<td></td>
<td>GR5</td>
<td>GR6</td>
<td>GR7</td>
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<td>1</td>
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<td>2.398</td>
<td>2.398</td>
<td>2.485</td>
</tr>
<tr>
<td>10</td>
<td>2.398</td>
<td>2.398</td>
<td>2.485</td>
</tr>
<tr>
<td>11</td>
<td>2.398</td>
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</tr>
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<td>12</td>
<td>2.457</td>
<td>2.398</td>
<td>2.398</td>
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<tr>
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<td>2.398</td>
<td>2.398</td>
<td>2.398</td>
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<tr>
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<td>2.428</td>
<td>2.398</td>
<td>2.398</td>
</tr>
<tr>
<td>15</td>
<td>2.428</td>
<td>2.512</td>
<td>2.485</td>
</tr>
</tbody>
</table>

alcohol expectancy $Y_{it}^{(p)}$ of the $i$th child on the $t$th occasion of measurement ($t = 5, 6, 7, 9, 10$) where the domain is denoted by the superscript $p$:

$$Y_{it}^{(p)} = \pi_{0i}^{(p)} + \pi_{1i}^{(p)}t_i + \pi_{2i}^{(p)}t_i^2 + \epsilon_{ni}^{(p)}$$

In this model, the metric of the time variable $t_i$ has been rescaled by the subtraction of a constant from each grade, so that $t_1$ through $t_5$ take on values -1, 0, 1, 3, 4 respectively. The shape of the hypothesized trajectory depends on the particular parameterization of time chosen and on the specific values of the individual growth parameters. Thus, the slope parameter $\pi_{1i}^{(p)}$ represents change in true (log) positive expectancies per unit time for the $i$th child. Adolescents whose expectancies increased the most rapidly between
grades 5 and 10 will have the largest values of this parameter. The intercept parameter \( \pi_{0i}^{(p)} \) represents the true expectancy score of child \( i \) when \( t_i \) is equal to zero, that is, at grade 6; children whose positive expectancies are higher in early adolescence will possess higher values of this parameter. The third parameter \( \pi_{2i}^{(p)} \) represents the increment to the growth rate beginning at grade 7. Here the variable \( a_i \) represents a second parameterization of time. Its presence in the model ensures that the slope of the trajectory is not constrained to be identical prior to and after grade 7. It measures linear time after grade 7 and is set equal to zero up to and including grade 7, so that \( t_i \) through \( t_5 \) take on values 0, 0, 0, 2, 3. Adolescents who experience a large positive increment to their growth rate after grade 7 will have high positive values of this parameter, whereas adolescents who experience a decrement in growth will have negative values.

Inspection of the empirical growth records suggested that change in negative expectancies was linear with time. We adopted a straight-line model for individual change in (log) negative expectancies:

\[
Y_{ni}^{(n)} = \pi_{0i}^{(n)} + \pi_{1i}^{(n)} t_i + \epsilon_{ni}^{(n)}
\]

In this model, the time metric has also been rescaled by the subtraction of a constant from each grade, so that \( t_i \) through \( t_5 \) take on values -1, 0, 1. This insures that the intercept parameter \( \pi_{0i}^{(n)} \) represents the true expectancy score of person \( i \) at grade 6 and will facilitate comparison between status scores in the two domains. The slope parameter \( \pi_{1i}^{(n)} \) represents the yearly growth rate of person \( i \) or the change in negative expectancies for a one-unit change in time.

As an evocative summary of our data exploration, we fitted the models of Equations 1 and 2 to the empirical growth records of each of the children in Table 1 using “within-child” OLS regression analysis. Figure 1 presents these OLS-fitted trajectories in both domains, displayed by gender. Notice that there is considerable evidence of heterogeneity in the positive expectancies trajectories for both boys and girls, whereas there is less evidence of variation in growth across children in negative expectancies. In fact, the trajectories appear relatively flat, indicating little change in negative expectancies from 5th to 7th grade. Comparison of the relative elevations of positive and negative expectancy trajectories suggests that children have higher expectations for the negative effects of alcohol than for positive effects between grades 5 through 7. It is these types of inference that the methods described in this article are intended to confirm.

In Table 2 (page 524), we present the sample mean vectors and covariance matrices for the variables that were introduced in Table 1, estimated using data on all boys \((n = 353)\) and girls \((n = 385)\) in the illustrative dataset. What kinds
**Girls**

![Graph showing discontinuous linear growth in (log) positive expectancies between grades 5 and 10 and linear growth in (log) negative expectancies between grades 5 and 7. These are displayed for the subsample of 15 randomly selected children whose empirical growth records are displayed in Table 1.]

**Boys**

![Graph showing discontinuous linear growth in (log) positive expectancies between grades 5 and 10 and linear growth in (log) negative expectancies between grades 5 and 7. These are displayed for the subsample of 15 randomly selected children whose empirical growth records are displayed in Table 1.]

**Figure 1**

OLS-fitted trajectories summarizing discontinuous linear growth in (log) positive expectancies between grades 5 and 10 and linear growth in (log) negative expectancies between grades 5 and 7. These are displayed for the subsample of 15 randomly selected children whose empirical growth records are displayed in Table 1.

of statements do these statistics readily support? Focus, first, on the statistics that describe the five waves of observed positive expectancies. Examining the wave-by-wave means (the first five entries in the left hand part of the sample mean vectors) we see that, on average, positive expectancy scores increase monotonically. The magnitudes of the variances in the leading diagonals of the covariance matrices [the (5 × 5) submatrices in the upper left hand corner of the sample covariance matrices] suggest that, for both groups, observed score variance increases over time. Inspection of the between-wave covariances
Table 2

Estimated Means and Covariances for the 5 waves of positive expectancy and the 3 waves of negative expectancy scores for girls (n = 385) and boys (n = 353).

<table>
<thead>
<tr>
<th></th>
<th>Positive Expectancies</th>
<th></th>
<th></th>
<th></th>
<th>Negative Expectancies</th>
<th></th>
<th></th>
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<tbody>
<tr>
<td></td>
<td>Grade5</td>
<td>Grade6</td>
<td>Grade7</td>
<td>Grade9</td>
<td>Grade10</td>
<td>Grade5</td>
<td>Grade6</td>
</tr>
<tr>
<td>Girls Covs</td>
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<td>.00209</td>
<td>.00222</td>
<td>.00393</td>
<td>.00356</td>
<td>.00226</td>
<td>.00137</td>
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<tr>
<td></td>
<td>.00001</td>
<td>.00015</td>
<td>.00013</td>
<td>.00003</td>
<td>.00005</td>
<td>.00015</td>
<td>.00032</td>
</tr>
<tr>
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<td>.00001</td>
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<td>.00003</td>
<td>.00017</td>
<td>.00017</td>
<td>.00003</td>
<td>.00001</td>
</tr>
<tr>
<td>Means</td>
<td>2.4166</td>
<td>2.4149</td>
<td>2.4209</td>
<td>2.4514</td>
<td>2.4568</td>
<td>2.5937</td>
<td>2.6036</td>
</tr>
<tr>
<td>Boys Covs</td>
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<td>.00275</td>
<td>.00241</td>
<td>.00447</td>
<td>.00516</td>
<td>.00178</td>
<td>.00194</td>
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<tr>
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<td>.00038</td>
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<td>.00258</td>
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<td>.00015</td>
<td>.00007</td>
<td>.00020</td>
<td>.00021</td>
<td>.00006</td>
<td>.00014</td>
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<tr>
<td>Means</td>
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<td>2.4209</td>
<td>2.4272</td>
<td>2.4512</td>
<td>2.4565</td>
<td>2.5983</td>
<td>2.6026</td>
</tr>
</tbody>
</table>

among the expectancy scores [again in the (5 x 5) covariance submatrices] suggests a generally small but positive association among observed scores over the five occasions of measurement. Similar statements can be made about the sample means, variances and covariances of the negative expectancy scores. Finally, inspection of the sub-matrices of covariances among the 5 waves of positive and the 3 waves of negative expectancy scores within each group [the (3 x 5) submatrices in the lower left corners of the sample covariance matrices], suggest that they are negatively associated on each of the occasions of measurement.

As is evident from this description of the contents of Table 2, between-wave statistics do not provide a “view” that supports easy inference about differences in individual change. Rather than summarizing data as between-wave variances and covariances, one must use individual growth trajectories. For instance, in the positive expectancy domain, it is easier to see from Figure 1 that observed change can be either positive or negative, that individuals are
diverging over time, and that there is heterogeneity in status, rate of change, and increments to rate across people.

Starting with the sample mean vector and covariance matrix in Table 2 as "input", we can claim that our hypothesized growth models fit when, having estimated the parameters of Equations 6 and 7, we can accurately predict the between-wave covariance structure of the observed data. As Meredith, Tisak, McArdle and Muthén have pointed out, the growth formulation that we have posited — the level-1 models of Equations 1 through 6 and the level-2 model of Equation 7 — falls naturally into the framework offered by the LISREL model with mean structures (Jöreskog & Sörbom, 1996). Thus, maximum-likelihood estimates of the important parameters in Equations 6 and 7 can be obtained by covariance structure analysis, as we will now demonstrate.

Rewriting the Composite Cross-Domain Individual Growth Model as the LISREL Measurement Model for $Y$

When covariance structure analysis is used to conduct cross-domain analyses of change over time, the hypothesized composite cross-domain individual growth model in Equation 5 plays the role of the LISREL measurement model for the vector of endogenous variables $Y$. For instance, in our illustrative example, the combined empirical growth record of the $i^{th}$ child in both positive and negative expectancies can be written as:

\[
\begin{bmatrix}
Y_{1p}^{(p)} \\
Y_{2p}^{(p)} \\
Y_{3p}^{(p)} \\
Y_{4p}^{(p)} \\
Y_{5p}^{(p)} \\
Y_{1n}^{(n)} \\
Y_{2n}^{(n)} \\
Y_{3n}^{(n)} \\
\end{bmatrix}
= 
\begin{bmatrix}
1 & t_1 & a_1 & 0 & 0 \\
1 & t_2 & a_2 & 0 & 0 \\
1 & t_3 & a_3 & 0 & 0 \\
1 & t_4 & a_4 & 0 & 0 \\
1 & t_5 & a_5 & 0 & 0 \\
0 & 0 & 0 & 1 & t_1 \\
0 & 0 & 0 & 1 & t_2 \\
0 & 0 & 0 & 1 & t_3 \\
\end{bmatrix}
\begin{bmatrix}
\pi_{0p}^{(p)} \\
\pi_{1p}^{(p)} \\
\pi_{2p}^{(p)} \\
\pi_{0n}^{(n)} \\
\pi_{1n}^{(n)} \\
\pi_{2n}^{(n)} \\
\pi_{3n}^{(n)} \\
\end{bmatrix}
+ 
\begin{bmatrix}
\epsilon_{1p}^{(p)} \\
\epsilon_{2p}^{(p)} \\
\epsilon_{3p}^{(p)} \\
\epsilon_{4p}^{(p)} \\
\epsilon_{5p}^{(p)} \\
\epsilon_{1n}^{(n)} \\
\epsilon_{2n}^{(n)} \\
\epsilon_{3n}^{(n)} \\
\end{bmatrix}
\]

which has the format of the LISREL measurement model for endogenous variables $Y$: 525
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(11) \[ Y = \tau_y + \Lambda_y \eta + \epsilon \]

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

\[
\begin{bmatrix}
Y_{1p}^{(p)} \\
Y_{2p}^{(p)} \\
Y_{3p}^{(p)} \\
Y_{4p}^{(p)} \\
Y_{5p}^{(p)} \\
Y_{1p}^{(n)} \\
Y_{2p}^{(n)} \\
Y_{3p}^{(n)}
\end{bmatrix},
\begin{bmatrix}
\tau_{0p}^{(p)} \\
\tau_{1p}^{(p)} \\
\tau_{0p}^{(n)} \\
\tau_{1p}^{(n)}
\end{bmatrix},
\begin{bmatrix}
\epsilon_{1p}^{(p)} \\
\epsilon_{2p}^{(p)} \\
\epsilon_{3p}^{(p)} \\
\epsilon_{4p}^{(p)} \\
\epsilon_{5p}^{(p)} \\
\epsilon_{1p}^{(n)} \\
\epsilon_{2p}^{(n)} \\
\epsilon_{3p}^{(n)}
\end{bmatrix}
\]

(12) \[ Y = Y_{1p}^{(p)}, \quad \eta = \begin{bmatrix} \tau_{0p}^{(p)} \\ \tau_{1p}^{(p)} \\ \tau_{0p}^{(n)} \\ \tau_{1p}^{(n)} \end{bmatrix}, \quad \epsilon = \begin{bmatrix} \epsilon_{1p}^{(p)} \\ \epsilon_{2p}^{(p)} \\ \epsilon_{3p}^{(p)} \\ \epsilon_{4p}^{(p)} \\ \epsilon_{5p}^{(p)} \\ \epsilon_{1p}^{(n)} \\ \epsilon_{2p}^{(n)} \\ \epsilon_{3p}^{(n)} \end{bmatrix} \]

and, unlike the usual practice of covariance structure analysis, the elements of the LISREL \( \tau_y \) and \( \Lambda_y \) parameter matrices are entirely constrained to contain only known values and constants:

(13) \[ \tau_y = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \quad \Lambda_y = \begin{bmatrix} 1 & t_1 & a_1 & 0 & 0 \\ 1 & t_2 & a_2 & 0 & 0 \\ 1 & t_3 & a_3 & 0 & 0 \\ 1 & t_4 & a_4 & 0 & 0 \\ 1 & t_5 & a_5 & 0 & 0 \\ 0 & 0 & 0 & 1 & t_1 \\ 0 & 0 & 0 & 1 & t_2 \\ 0 & 0 & 0 & 1 & t_3 \end{bmatrix} \]
and the error vector $\epsilon$ is distributed with zero mean vector and covariance matrix $\Theta_\epsilon$, which, under the classical assumptions of Equation 6, is given by:

$$
\Theta_\epsilon = \text{Cov}(\epsilon) = 
\begin{bmatrix}
\sigma_{\epsilon(p)}^2 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \sigma_{\epsilon(p)}^2 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \sigma_{\epsilon(p)}^2 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma_{\epsilon(p)}^2 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \sigma_{\epsilon(n)}^2 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \sigma_{\epsilon(n)}^2 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \sigma_{\epsilon(n)}^2
\end{bmatrix}
$$

(14) $\Theta_\epsilon = \text{Cov}(\epsilon)$

Re-Writing the Model for Inter-Individual Differences in Change as the LISREL Structural Model

Notice that, unlike more familiar standard covariance structure analyses, we have chosen to specify the entire LISREL $\Lambda_y$ parameter matrix in Equation 11 as a matrix of known times and constants rather than as collection of unknown parameters to be estimated. This specification acts to "pass" the critical level-1 individual growth parameters ($\pi_{01}^{(p)}$, $\pi_{11}^{(p)}$, $\pi_{21}^{(p)}$, $\pi_{01}^{(n)}$, and $\pi_{11}^{(n)}$) from the composite cross-domain level-1 growth model into the LISREL endogenous construct vector $\eta$, which we have then referred to as the latent growth vector. In other words, our fully-constrained specification of $\Lambda_y$ has forced the $\eta$-vector to contain the very individual-level parameters whose level-2 distribution must become the focus of our subsequent between-person analyses.

These required level-2 analyses are conducted in the "structural" part of the general LISREL model — it is this part of the LISREL model that permits the distribution of the $\eta$-vector to be modeled explicitly in terms of selected population means, variances and covariances. And, of course, the particular population means, variances and covariances that we select as parameters of the structural model are those that we have hypothesized are the important parameters in the joint distribution of the latent growth vector in Equation 7. All that is required is to rewrite the latent growth vector as follows:
\[
\begin{bmatrix}
\pi_{0p}^{(p)} \\
\pi_{1p}^{(p)} \\
\pi_{2p}^{(p)} \\
\pi_{0p}^{(n)} \\
\pi_{1p}^{(n)}
\end{bmatrix}
= \begin{bmatrix}
\mu_{\pi_0}^{(p)} \\
\mu_{\pi_1}^{(p)} \\
\mu_{\pi_2}^{(p)} \\
\mu_{\pi_0}^{(n)} \\
\mu_{\pi_1}^{(n)}
\end{bmatrix}
+ \begin{bmatrix}
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0
\end{bmatrix}
+ \begin{bmatrix}
\pi_{0p}^{(p)} \\
\pi_{1p}^{(p)} \\
\pi_{2p}^{(p)} \\
\pi_{0p}^{(n)} \\
\pi_{1p}^{(n)}
\end{bmatrix}
- \begin{bmatrix}
\mu_{\pi_0}^{(p)} \\
\mu_{\pi_1}^{(p)} \\
\mu_{\pi_2}^{(p)} \\
\mu_{\pi_0}^{(n)} \\
\mu_{\pi_1}^{(n)}
\end{bmatrix}
\]

which has the form of the reduced LISREL structural model:

\[
\eta = \alpha + B\eta + \zeta
\]

with a latent residual vector \(\zeta\) that contains the deviations of the individual growth parameters from their respective population means:

\[
\zeta = \begin{bmatrix}
\pi_{0p}^{(p)} - \mu_{\pi_0}^{(p)} \\
\pi_{1p}^{(p)} - \mu_{\pi_1}^{(p)} \\
\pi_{2p}^{(p)} - \mu_{\pi_2}^{(p)} \\
\pi_{0p}^{(n)} - \mu_{\pi_0}^{(n)} \\
\pi_{1p}^{(n)} - \mu_{\pi_1}^{(n)}
\end{bmatrix}
\]

and parameter matrices:

\[
\alpha = \begin{bmatrix}
\mu_{\pi_0}^{(p)} \\
\mu_{\pi_1}^{(p)} \\
\mu_{\pi_2}^{(p)} \\
\mu_{\pi_0}^{(n)} \\
\mu_{\pi_1}^{(n)}
\end{bmatrix}
, \quad B = \begin{bmatrix}
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0
\end{bmatrix}
\]
Notice that we have removed the population averages of the individual growth parameters — a true intercept and slope, in both domains — into the LISREL $\alpha$ vector. This permits these important mean parameters to be estimated explicitly. The elements of the LISREL latent residual vector, $\xi$, in Equations 14 and 15 contain deviations of $\pi_{0i}^{(p)}$, $\pi_{1i}^{(p)}$, $\pi_{0i}^{(n)}$, $\pi_{1i}^{(n)}$ and $\pi_{1i}^{(n)}$ from their respective population means. The $\xi$ vector of latent residuals is of special interest in the cross-domain analysis of change because it is distributed with zero mean vector and covariance matrix $\Psi$ — the latter matrix containing the very variance and covariance parameters in which we are most interested in an investigation of inter-individual differences in change. Note that in Equation 18 the $B$ matrix containing the regression coefficients is constrained to zero, thus permitting the relations among the growth parameters to be expressed exclusively as covariances in the $\Psi$ matrix. If the researcher is interested in directional effects or prediction (rather than association) it would be possible to estimate those relationships by freeing the appropriate elements in $B$.

$$\Psi = Cov(\xi) =$$

$$\begin{bmatrix}
\begin{array}{cccc}
\sigma_{\pi_0^{(p)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(p)}} & \sigma_{\pi_0^{(n)}} \\
\sigma_{\pi_0^{(n)}} & \sigma_{\pi_1^{(p)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(n)}} \\
\sigma_{\pi_0^{(p)}} & \sigma_{\pi_1^{(n)}} & \sigma_{\pi_1^{(p)}} & \sigma_{\pi_1^{(n)}} \\
\sigma_{\pi_0^{(p)}} & \sigma_{\pi_1^{(n)}} & \sigma_{\pi_1^{(p)}} & \sigma_{\pi_1^{(n)}} \\
\sigma_{\pi_0^{(p)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(n)}} \\
\sigma_{\pi_0^{(n)}} & \sigma_{\pi_1^{(n)}} & \sigma_{\pi_1^{(p)}} & \sigma_{\pi_1^{(n)}} \\
\sigma_{\pi_0^{(p)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(n)}} \\
\sigma_{\pi_0^{(n)}} & \sigma_{\pi_1^{(n)}} & \sigma_{\pi_1^{(p)}} & \sigma_{\pi_1^{(n)}} \\
\sigma_{\pi_0^{(p)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(n)}} & \sigma_{\pi_0^{(n)}} \\
\sigma_{\pi_0^{(n)}} & \sigma_{\pi_1^{(n)}} & \sigma_{\pi_1^{(p)}} & \sigma_{\pi_1^{(n)}} \\
\end{array}
\end{bmatrix}$$

To summarize, in Equations 1 through 7, the individual growth modeling framework provides baseline level-1 (within-person) and level-2 (between-person) models that represent our initial hypotheses about the growth structure underlying the three waves of panel data in positive and negative expectancies in our data-example. Then, in Equations 8 through 17 we have shown that these important models can be rewritten, without loss of generality, using the format and notation of the LISREL model with mean structures. By carefully choosing our specification of the various standard LISREL parameter matrices, we have forced the LISREL Y-measurement model to become our original level-1 composite cross-domain individual growth model (including all existing assumptions on the distribution of the measurement errors), and we have forced a reduced form of the LISREL structural model to become our level-2 model for inter-individual differences in true change in both domains.
Fitting the Models to Data: Are Changes in Positive and Negative Alcohol Expectancies Related?

Because of the direct and explicit mapping of the individual growth modeling perspective onto that of covariance structure analysis, we can easily test whether our hypothesized growth formulation underpins the matrix of observed between-wave variances and covariances in Table 2 using the LISREL program. If the implied covariance structure fits the data then we obtain, and can interpret, LISREL-provided maximum likelihood estimates of the unknown parameters in our growth models that now reside in the \( \alpha \) vector, the \( \Theta_e \)-matrix and the \( \Psi \)-matrix.

We did not simply investigate the hypothesized inter-relationships among simultaneous growth in positive and negative expectancies as specified in the second research question. We had also to ascertain whether any pattern of inter-relationship among the elements of the latent growth vector differed by adolescent gender (the third research question). For this reason, we carried out all estimation and model fitting using multisample analysis. We fitted a taxonomy of such models so that comparisons among the goodness-of-fit statistics of nested models could be used to test hypotheses linked to the third research question.\(^3\)

Conceptually, all adolescents were assumed to be experiencing potentially-interrelated growth in both positive and negative expectancies. However, males and females could differ in their average growth trajectories (for example, males could have higher positive expectancies at grade 7 and experience a more rapid escalation in growth than females) and in the magnitude and direction of the pattern of inter-relationships among the individual growth parameters, both within and across domains. To test whether there were gender differences in growth, we began by fitting the most "constrained" model. In this model, the \( \tau \), \( \Lambda \), \( \Theta_e \), \( \alpha \), \( B \), and \( \Psi \) parameter matrices for all adolescents were patterned as described in Equations 11, 12, 16 and 17, but the unknown matrix elements in the \( \Theta_e \), \( \alpha \), and \( \Psi \) matrices were constrained to take on identical values for males and females. That is, the average growth trajectories (the parameters in \( \alpha \)), the reliability of growth (the parameters in \( \Theta_e \)), and the cross-domain links (the parameters in \( \Psi \)) were not permitted to vary by gender. We summarize the goodness-of-fit of this model in Table 3 (as "Model I"). Model I fits poorly — the \( \chi^2 \) statistic is large relative to its degrees of freedom, and the values of the various incremental fit indices are less than .9 (see Bollen, 1989, for a discussion of the use of summary statistics in model evaluation).

\(^3\) In the Appendix, we provide annotated LISREL VII programs for our analyses.
<table>
<thead>
<tr>
<th>ID</th>
<th>Model Description</th>
<th>Goodness-of-Fit Statistics</th>
<th>( \chi^2 )</th>
<th>df</th>
<th>GFI</th>
<th>NNFI</th>
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<th>RMSEA</th>
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<tr>
<td></td>
<td>( \Psi ) equal across gender</td>
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<td>298.14</td>
<td>66</td>
<td>.904</td>
<td>.762</td>
<td>.719</td>
<td>.098</td>
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<tr>
<td>I</td>
<td>( \Theta_e ) equal across gender</td>
<td>( \alpha_y ) equal across gender</td>
<td>Independent, homoscedastic errors</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>( \Theta_e ) equal across gender</td>
<td>( \alpha_y ) equal across gender</td>
<td>Independent, homoscedastic errors</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
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<td>( \Psi ) unequal across gender</td>
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<td>51</td>
<td>.907</td>
<td>.771</td>
<td>.791</td>
<td>.096</td>
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<td>( \Theta_e ) equal across gender</td>
<td>( \alpha_y ) unequal across gender</td>
<td>Independent, homoscedastic errors</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>IV</td>
<td>( \Psi ) unequal across gender</td>
<td>( \Theta_e ) equal across gender</td>
<td>( \alpha_y ) unequal across gender</td>
<td>Independent, homoscedastic errors</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>V</td>
<td>( \Psi ) unequal across gender</td>
<td>( \Theta_e ) unequal across gender</td>
<td>( \alpha_y ) unequal across gender</td>
<td>Independent, homoscedastic errors</td>
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<tr>
<td>VI</td>
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<td>( \Theta_e ) unequal across gender</td>
<td>( \alpha_y ) unequal across gender</td>
<td>Independent, heteroscedastic errors</td>
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</tr>
</tbody>
</table>

Note: \( \Psi \) = Population covariance matrix of the individual growth parameters, \( \Theta_e \) = Population error covariance structure, \( \alpha_y \) = Population mean vector of the individual growth parameters, GFI = Goodness of Fit Index, CFI = Comparative Fit Index, NNFI = Non-normed Fit Index, RMSEA = Root Mean Square Error of Approximation.
In the second model fitted in the taxonomy, we constrained the average growth trajectories and the level-1 measurement errors to be identical across gender, but permitted the covariance structure of the latent growth vector to differ from group to group (see Model II in Table 3). In comparison to Model I, this was a better fit to the data ($\Delta \chi^2$ of 75.45 relative to a change of 15 df). The incremental fit indices did not improve, however, indicating that alternative models should be tested. These models are listed as Models III, IV, and V in Table 3. A series of decrement-to-chi-square tests indicated that Model IV, which constrained the level-1 measurement errors to be identical across gender but permitted both the average growth trajectories and the covariance structure of the latent growth vector to vary for boys and girls, was the best-fitting model.

The imposition of the classical assumptions of independence and homoscedasticity on the level-1 measurement errors in both domains is common but, with measurements being obtained repeatedly on the same child over time, these assumptions may not be tenable. The precision with which an attribute can be measured may not be identical at all ages, and so the measurement errors may be heteroscedastic. Therefore, in a final model in the sequence (Model VI), we retained the equality constraints on the $\Theta_e$ and continued to permit the $\alpha$ vector and $\Psi$ matrix to differ by gender, but specified that the level-1 measurement errors were heteroscedastic. The $\Theta_e$ matrix was hypothesized to be:

$$
\Theta_e = \begin{bmatrix}
\sigma^2_{e_1} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \sigma^2_{e_2} & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \sigma^2_{e_3} & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma^2_{e_4} & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \sigma^2_{e_5} & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \sigma^2_{e_6} & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \sigma^2_{e_7} & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma^2_{e_8}
\end{bmatrix}
$$

with error variances freely estimated within each domain. Model VI fits considerably better than any of the earlier models in the taxonomy.
(CFI = .951, NNFI = .980, RMSEA = .052) and the change in the $\chi^2$ goodness-of-fit statistic between Models IV and VI suggests that classical assumptions on the error structure are untenable ($\Delta \chi^2 = 129.59$ between Models IV and VI, for a loss of 11 df). We therefore report interpretations of Model VI in the rest of this article.\(^4\)

**Average Trajectories of Change in Positive and Negative Expectancies**

In Table 4, we provide maximum likelihood estimates of the population means of the true growth parameters in both positive and negative expectancies, along with approximate p-values.\(^5\) Notice that distinct values of each are provided within each gender, as a consequence of the freeing of the $\alpha$ vector in Models IV and VI and the determination that average growth in both domains differed by gender. In both domains, boys and girls had identical intercept values (grade 6 scores). Gender differences appear in the rates of change. On average, the positive expectancies trajectory for boys is increasing over time, whereas the trajectory for girls is flat (the slope parameter, or base rate, is not significantly different from zero). However, both experience an upward shift in trajectory after grade 7, indicating that the

<table>
<thead>
<tr>
<th>Gender</th>
<th>Positive Expectancies</th>
<th>Negative Expectancies</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>True Status at Grade 6</td>
<td>Base Rate of True Change</td>
</tr>
<tr>
<td>Male</td>
<td>2.42**</td>
<td>.004*</td>
</tr>
<tr>
<td>Female</td>
<td>2.42**</td>
<td>.003</td>
</tr>
</tbody>
</table>

\(^*p < .01. \quad **p < .001.\)

\(^4\) Interestingly, despite the change in the parameterization of the level-1 error covariance structure between Models IV and VI, the parameter estimates describing the mean-vector and covariance matrix of the latent growth remained robust. Output is available on request.

\(^5\) The approximate p-value tests the null hypothesis that the value of a parameter is zero in the population, using a test statistic that is the ratio of the parameter estimate to its asymptotic standard error (see Bollen, 1989, p. 286).
developmental pattern is similar in both groups. The average true growth trajectories of boys and girls are very similar to each other in the domain of negative expectancies; there appears to be little change over time.

**Heterogeneity in True Change in Positive and Negative Expectancies**

Based on maximum-likelihood estimates of the $\Psi$ matrix, Table 5 summarizes inter-individual differences in true change that were detected in both domains. As a consequence of the comparison described earlier between Models I and II of Table 3, we know that the magnitudes and directions of these inter-individual differences differ by gender. In rows #1, #2, #3, #7 and #8 of Table 5, there is evidence of considerable inter-individual heterogeneity in true change in both domains; tests associated with

<table>
<thead>
<tr>
<th>Table 5</th>
<th>Estimated Variances and Covariances of Within-Domain Growth Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Population Parameter</strong></td>
<td><strong>Verbal Description</strong></td>
</tr>
<tr>
<td><strong>Domain 1: Positive Expectancies</strong></td>
<td></td>
</tr>
<tr>
<td>$\sigma^2_{\pi_{0}(p)}$</td>
<td>Variance of true status (at grade 6)</td>
</tr>
<tr>
<td>$\sigma^2_{z_{1}(p)}$</td>
<td>Variance of base rate of true change</td>
</tr>
<tr>
<td>$\sigma^2_{z_{2}(p)}$</td>
<td>Variance of increment to base rate</td>
</tr>
<tr>
<td>$\rho_{\pi_{0}(p)z_{1}}$</td>
<td>Correlation of true status (at grade 6) and base rate</td>
</tr>
<tr>
<td>$\rho_{\pi_{0}(p)z_{2}}$</td>
<td>Correlation of true status (at grade 6) and increment</td>
</tr>
<tr>
<td>$\rho_{z_{1}(p)z_{2}}$</td>
<td>Correlation of base rate and increment to base rate</td>
</tr>
<tr>
<td><strong>Domain 2: Negative Expectancies</strong></td>
<td></td>
</tr>
<tr>
<td>$\sigma^2_{\pi_{0}(n)}$</td>
<td>Variance of true status (at grade 6)</td>
</tr>
<tr>
<td>$\sigma^2_{z_{1}(n)}$</td>
<td>Variance of base rate of true change</td>
</tr>
<tr>
<td>$\rho_{\pi_{0}(n)z_{1}}$</td>
<td>Correlation of true status (at grade 6) and rate of change</td>
</tr>
</tbody>
</table>

*p < .10.  "p < .01.  ***p < .001.
the population variances of the five individual growth parameters indicate that adolescents differ widely in their growth trajectories in both positive and negative expectancies. This is an important finding, for it permits us to consider potential correlates of change in future studies. Gender differences in heterogeneity appear in terms of true status (boys are more variable in both domains) and rates of change (girls are more variable in positive expectancies, but less so in negative expectancies). In rows #4, #5, #6, and #9, we also present the within-domain correlations among the growth parameters. In both domains, we find that true intercept and true rate of change are positively correlated, suggesting that adolescents with higher expectancies in grade 6 tend to grow more rapidly over time.

In Table 6, we present the core findings of the cross-domain analysis of change. The table contains maximum-likelihood estimates of the pair-wise

<table>
<thead>
<tr>
<th>Population Parameter</th>
<th>Verbal Description</th>
<th>Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>( p_{\pi_0}^{(p)} )</td>
<td>Correlation of true status (at grade 6) in positive and negative expectancies</td>
<td>-.169*</td>
</tr>
<tr>
<td>( p_{\pi_1}^{(p)} )</td>
<td>Correlation of rate of true change in positive and negative expectancies</td>
<td>-.37***</td>
</tr>
<tr>
<td>( p_{\pi_2}^{(p)} )</td>
<td>Correlation of rate increment in positive and true status (at grade 6) in negative expectancies</td>
<td>.202*</td>
</tr>
<tr>
<td>( p_{\pi_2}^{(p)} )</td>
<td>Correlation of rate increment in positive and rate of true change in negative expectancies</td>
<td>.298**</td>
</tr>
<tr>
<td>( p_{\pi_0}^{(p)} )</td>
<td>Correlation of true status (at grade 6) in positive and rate of true change in negative expectancies</td>
<td>-.143</td>
</tr>
<tr>
<td>( p_{\pi_1}^{(p)} )</td>
<td>Correlation of rate of true change in positive and true status (at grade 6) in negative expectancies</td>
<td>-.26**</td>
</tr>
</tbody>
</table>

* \( p < .05 \)  ** \( p < .01 \)  *** \( p < .001 \)
correlations between individual growth parameters representing change in positive expectancies and those representing change in negative expectancies. Notice that there are negative correlations between the true status parameters for both groups, suggesting that strong positive expectancies are associated with weak negative expectancies, and this relationship is more pronounced for girls. The most interesting finding contained in Table 6 are the gender differences in the correlations among the growth parameters representing the relationship of change in one domain with change in the other. These parameters are moderately (and negatively) correlated for boys, indicating that increases in positive expectancies are associated with decreases in negative expectancies. For girls, the correlations among the rates are not significantly different from zero. This suggests that the expectancy processes are linked for boys, but not for girls. It is possible that negative expectancies are more salient for boys, or that they make finer distinctions in terms of expectancy beliefs.

Discussion

In recent years, pioneering authors (McArdle & Epstein, 1987; Meredith & Tisak, 1990; Muthén, 1991) have demonstrated how notions of individual growth modeling can be accommodated within the general framework offered by covariance structure analysis. In this article, we have extended our earlier work (Willett & Sayer, 1994) to explore and review the links between these two formerly-distinct conceptual arenas, carefully laying out in detail the mapping of the one onto the other, and showing how the ensuing new methods provide a convenient technique for addressing research questions about the relationship between individual true growth in multiple domains.

Specifically, we have reviewed and illustrated how the level-1 ("within-person") and level-2 ("between-person") models of the individual growth modeling framework can be reformatted to correspond, respectively, to the "measurement" and "structural" components of the general LISREL model with mean structures. The direct correspondence between these two pairs of models permits the population covariance matrix of the errors of measurement and the relationships among the individual growth parameters in both domains to be modeled explicitly within a covariance structure framework. Consequently, critical parameters in the investigation of inter-individual differences in change can readily be estimated. This innovative application of covariance structure analysis offers several important features to the data-analyst.

1. Cross-domain analyses of change can simultaneously examine individual growth in many domains. The cross-domain analysis of inter-
individual differences in change need not be limited to two domains, as in our example. Within the normal constraints imposed by the requirements of statistical power and the tenets of common sense, analyses can be conducted in many domains; the model specifications that we have provided extend straightforwardly to these more complex situations.

2. The method can accommodate any number of waves of longitudinal data, with differing numbers of waves in each domain. Willett (1988, 1989) showed that the collection of more waves of data leads to higher precision for the estimation of individual growth trajectories and greater reliability for the measurement of change. In the covariance structure analyses of change, extra waves of data extend the length of the empirical growth record and expand the sample between-wave covariance matrix (thereby increasing degrees of freedom for model-fitting), but do not change the fundamental parameterization of the level-1 and level-2 models. We demonstrated a cross-domain model with discrepant waves.

3. Occasions of measurement need not be equally-spaced, and can be spaced differently in each domain. In our example, the expectancy measures were separated by yearly intervals, with the exception of the interval between 7th and 9th grade. However, equal-spacing of the occasions of measurement is not required. Change data may be collected at irregular intervals either for convenience or because the investigator wishes to estimate certain features of the trajectory more precisely (by clustering data-collection points more closely at times of greater research interest). Such irregularly spaced data is easily accommodated by the method, provided everyone in the sample is measured on the same set of irregularly-spaced occasions within each domain.

4. Individual change can be represented by either a straight-line or a curvilinear trajectory, and different individual growth models can be adopted in each domain. In our article, we have used piecewise or discontinuous growth models to represent individual change over time in one domain, and a linear (or straight-line) model in the other. Different growth models can be used in a cross-domain analysis, and the investigator is not restricted to linear models. This approach can accommodate any type of curvilinear growth in which status is linear in the individual growth parameters. That is, the outcome must be represented as a weighted linear combination of the model growth parameters.

5. The covariance structure of the occasion-by-occasion "Level-1" measurement errors can be modeled explicitly, and different error covariance structures can be hypothesized in each domain. Unlike other popular methods for longitudinal data analysis, the approach we have described does not restrict the population measurement error covariance matrix to a
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particular shape or pattern. The investigator need not accept unchecked the classical level-1 independence and homoscedasticity assumptions. The effectiveness of a variety of reasonable error structures can be systematically compared and the structure that is most appropriate for the particular problem adopted.

6. By comparing the goodness-of-fit of explicitly-specified and nested models, the investigator can test complex hypotheses about the nature of inter-individual differences in true change. One benefit of fitting an explicitly parameterized covariance structure to data using a flexible software package like LISREL is that selected model parameters can be individually or jointly constrained during analysis to particular values. This allows the investigator to conduct a variety of nested tests on the variability of the individual growth parameters across people.

7. The flexibility of the LISREL model permits cross-domain analysis of change to be extended in substantively interesting ways. There are several extensions of the covariance structure approach that are facilitated by the flexibility of the LISREL model. First, not only can we examine the inter-relationships among several types of simultaneous change, we can also predict change in one or more domains by simultaneous changes in other domains (Sayer, 1995). Second, we can introduce additional exogenous variables as predictors of any, or all, of these changes. Finally, the method enables the modeling of intervening effects, whereby a predictor may not act directly on change, but indirectly via the influence of intervening factors, each of which may be either time-invariant or a measure of change itself.

References


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and Clinical Psychology, 61, 941-951.

APPENDIX: Example LISREL8 Programs

We present LISREL8 programs used in the multisample analyses for Models I through IV, cited in text. We present the program for Model I in its entirety and, for remaining models, only the distinguishing lines. Note that in Models I through V, the level-1 errors of measurement are independent and homoscedastic within-domain.

Model I

In this model, the $\Psi$, $\Theta$, and $\alpha$ matrices are invariant across gender.

Line #1 provides a title for the entire analysis. Lines #2 though #23 contain specifications for the first group (Boys). After a sub-group title (line #2), the data definition (DA) line specifies a two-group multisample analysis (NG = 2), eight input variables (NI = 8) and first group sample size (NO = 353). Line #4 identifies the raw data source. We label the input variables (LA) in lines #5 and #6. The model definition (MO) line (#7) describes the hypothesized LISREL
variable and parameter matrices. Y and η score vectors are dimensioned (NY, NE) and the shape and initial contents of the \( \tau_y, \alpha, \) and \( \Psi \) parameter matrices are specified (TY, AL, PS). In lines #8 and #9, the elements of the latent growth record are labeled (LE). Then, we specify the fixed and free parameters of the measurement and structural models, as defined in the text. Lines #11 through #18 completely fix the contents of the \( \Lambda_y \) matrix (following the "MA LY" line). In lines #19 through #21, we free appropriate elements of the \( \Theta_e \) vector (FR TE) and set them equal to each other (EQ TE) within domain. In line #22 we specify starting values for all parameters. In the "output" line #23 (OU), we require that estimates be printed to 6 decimal places (ND = 6), limit the maximum number of iterations (IT = 1000), and disable the check on solution admissibility (AD = OFF).

The remaining lines of the program contain additional instructions required for the multi-sample analysis of the remaining group. For the second group (GIRLS), lines #25 and #26 identify new data sources and lines #27 and #28 repeat variable labeling information. Line #29 specifies the covariance structure model to be fitted. Notice that, consistent with the hypotheses underlying Model 1, the \( \alpha \) vector and the \( \Psi \) and \( \Theta_e \) matrices are declared to have values identical to those in the first group (AL = IN, PSI = IN, TE = IN). Labeling and output details in lines #30 through #32 are identical to the first group.

The complete LISREL program follows, with line numbers inserted on the left to facilitate description.6

**Model I**

1. Unconditional Cross-Domain Model for (log) Positive and (log) Negative Expectancies
2. Boys
3. DA NG = 2 NI = 8 NO = 353
4. RA FI = A:\BOYS.DAT
5. LA
7. MO NY = 8 TY = ZE NE = 5 TE = SY, FI AL = FR PS = SY, FR
8. LE
9. PosLevel PosRate PosInc NegLevel NegRate
10. MA LY
11. 1 -1 0 0 0

---

6 These line numbers should not be included in the LISREL program itself.
In Models II through V, line #29 (the model line for the second group) is modified to free restrictions on the $\Psi$ and $\Theta_e$ matrices and the $\alpha$ vector, as follows:

**Model II**: MO NY=8 TY=ZE LY=IN NE=5 TE=IN AL=IN PS=SY,FR

**Model III**: MO NY=8 TY=ZE LY=IN NE=5 TE=IN AL=FR PS=IN

**Model IV**: MO NY=8 TY=ZE LY=IN NE=5 TE=IN AL=FR PS=SY,FR

**Model V**: MO NY=8 TY=ZE LY=IN NE=5 TE=FR AL=FR PS=SY,FR

*Model VI*
In this model, the level-1 errors of measurement are heteroscedastic within domain (they are freed to be estimated in line #19, and lines #20 & 21, which constrain the errors to be equal within-domain, are omitted). As in Model IV, the $\Theta_e$ matrix is invariant across gender (IN) and the $\alpha$ vector (AL = FR) and the $\Psi$ matrix (PS = SY,FR) are freely estimated in both groups.

19. FR TE(1,1) TE(2,2) TE(3,3) TE(4,4) TE(5,5) TE(6,6) TE(7,7) TE(8,8)