

General Growth Mixture Analysis

with Antecedents and Consequences of Change^{*}

by

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In:

Piquero, A. & Weisburd, D.: Handbook of Quantitative Criminology

^{*}We like to thank Alex Piquero, David Weisburd, Nicholas Ialongo and Bengt Muthén for their helpful comments on a prior draft of this manuscript.

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Introduction

Describing and predicting the developmental course of individuals' involvement in criminal and antisocial behavior is a central theme in criminological inquiries. A large body of evidence is available documenting that individual differences in levels of criminal behavior across time can effectively be described qualitatively using a discrete number of criminal career patterns which vary by age of onset, career length, as well as type and frequency of the behavior. The majority of studies, using selective offender or population-based samples, have identified offending typologies made up of four to six distinct trajectory profiles. Most of these profiles are declining and are distinguished by the level of offending at their peak and the timing of the decline (Piquero, 2008). For example, Sampson & Laub (2003) identified several distinct offending trajectories patterns. One small group of individuals (3%) peaked in their offending behavior in the late 30s and declined to almost "0" at age 60 and were labeled "high-rate chronic". In addition, three desisting groups were identified, who declined after middle adolescence, late adolescence and early adulthood, respectively. Finally, a small group (8%) followed a low-rate chronic offending patterns between the ages of 19 and 39, and declined thereafter.

Childhood aggressive behavior is widely recognized as a precursor for antisocial and criminal behavior in adolescence and adulthood. Numerous prospective studies have demonstrated that conduct problems (as early as preschool) predict later delinquent behavior and drug use (Ensminger et al., 1983; Hawkins et al., 2000; Lynam, 1996; McCord and Ensminger, 1997; Yoshikawa, 1994). Motivated by developmental research (Loeber and Hay, 1997; Moffit, 1993; Patterson, DeBaryshe, & Ramsey, 1989), a large body of longitudinal research has

identified several developmental prototypes for individuals that vary in onset and course of aggressive behavior (Broidy et al, 2003; Dulmen, Goncy, Vest, & Flannery, 2008; Nagin & Tremblay, 1999; Schaeffer et al., 2006; Petras et al., 2004; Petras et al., 2008; Shaw, Gilliom, Ingoldsby, & Nagin, 2003). Despite differences in terminology and emphasis, each study identifies two to five distinct patterns of youth antisocial behavior over time with different behavior trajectories, risk factors, and prognoses for desistence from antisocial behavior as adults. Each proposed typology includes one to two chronic profiles with early and persistent aggression that is likely to be related to a biological or genetic vulnerability, exacerbated by poor parenting and early school failure. Each also identifies one or two less severe profiles with antisocial behavior that starts later, is less aggressive, is more sporadic, and stems from later socialization experiences such as deviant peer affiliations in early adolescence. Implicit in each typology is also the assumption that there is at least one other profile that characterizes youth who do not exhibit problems with antisocial behaviors. Additional evidence suggests that there is also a profile characterizing the substantial proportion of those children who display high levels of aggressive behavior in childhood but who do not manifest antisocial behavior in adolescence or adulthood (Maughan & Rutter, 1998).

In summary, many of the studies of youth, adolescents, and adults related to delinquent, antisocial, and criminal offending, have utilized a language of trajectory typologies to describe the individual differences in the behavioral course manifest in their longitudinal data. Although this language maps well onto some of the corresponding theories that provide the conceptual frameworks for these empirical investigations, the majority of these studies have not relied on subjective or heuristic taxonomies but instead relied on empirically-derived taxonomies based on statistical modeling techniques, analogous to clustering and, by doing so, have been able to

progressively evaluate the veracity of the underlying theories themselves. The two most common statistical methods currently in use are the semi-parametric group-based modeling, also known as latent class growth analysis (LCGA; Nagin & Land, 1993; Roeder, Lynch, & Nagin, 1999; Nagin, 2005), and general growth mixture analysis (GGMA; Muthén, 2001, 2002, 2004; Muthén & Asparouhov, 2008; Muthén & Muthén, 1998-2008; Muthén & Shedden, 1999).

Although there are differences in model specification and estimation (see the chapter in this handbook for more information on LCGA), both methods characterize some portion of the systematic population heterogeneity in the longitudinal process under study (i.e., between-individual variability not due to time-specific or measurement error) in terms of a finite number of trajectories groups (latent growth classes or mixture components) for which the mean or average growth within each group typifies one of the growth patterns or profiles manifest in the population. Together, the studies employing these methods have helped to shift the study of antisocial and criminal behavior away from what has been termed a “variable-centered” focus, describing broad predictors of behavior variance, toward a more “person-centered” focus, emphasizing discretely distinct individual differences in development (Magnusson, 1998).

In concert with the growing popularity of these data-driven, group-based methods for studying developmental and life-course behavior trajectories has come active and spirited ontological discussions about the nature of the emergent trajectory groups resulting from the analyses (Bauer & Curran, 2003, 2004; Nagin & Tremblay, 2005; Sampson, Laub, & Eggleston, 2004; Sampson & Laub, 2005), i.e., whether the resultant trajectory typology defined by the sub-groups derived from the data represent a “true” developmental taxonomy. Further debate involves whether it is reasonable to even apply these methods if there is not a true taxonomy underlying the data, under what conditions these methods should be applied, and how the results

should be interpreted if we consider the fact that, for any given data set, we cannot know the "truth" of the population distribution from which the observations were drawn. For example, we may not be able to make an empirical distinction between a sample of observations drawn from a population of values with a bimodal distribution and a sample of observations drawn from a mixture of two normally distributed subpopulations. Likewise, we may have a sample of observations for which a model that assumes a bimodal distribution is statistically indistinguishable from a model that assumes a finite mixture of two normal components. Thus, as is the case with any statistical modeling, the data can only empirically distinguish between models more or less consistent with the observations in the sample—they cannot identify the "truth" of the population between models with equivalent or nearly equivalent goodness-of-fit. Unfortunately, this issue of the *True* population distribution, i.e., the verity of the existence of latent subgroups in a given population, cannot be solved by means of replication since a new sample will give a similar distribution with similar ambiguities about the characteristics of the population distribution.

For the purposes of this chapter, we acknowledge that these debates are ongoing, but believe that the usefulness of these group-based models does not hinge on the ontological nature of the resultant trajectory groups. We presuppose that there are analytic, empirical, and substantive advantages inherent in using discrete components to (partially) describe population heterogeneity in longitudinal processes regardless of whether those discrete components are an approximation of a continuum of variability or if the components represent actual unobserved sub-populations within the larger population under study. In this chapter, we focus instead on the use of auxiliary information in terms of antecedents (predictors and covariates) and consequences (sequelae and distal static outcomes) of trajectory group membership in the

GGMA framework (Muthén, 2006). The use of auxiliary information, potentially derived from substantive theory, is highly relevant to determine the concurrent and prognostic validity of specific developmental trajectory profiles derived from a particular data set (Bushway, Brame, Paternoster, 1999; Heckman & Singer, 1984, Kreuter & Muthén, 2008). That is to say, the inclusion of auxiliary information in a growth mixture analysis is a necessary step in understanding as well as evaluating the fidelity and utility of the resultant trajectory profiles from a given study, regardless of one's beliefs about the veracity of the method itself. The remainder of the chapter is organized as follows: First, we briefly introduce the conventional latent growth curve model followed by a presentation of the unconditional growth mixture model, of which the latent growth curve model and latent class growth model are special cases. We then discuss the process for including antecedents and consequences of change in the general growth mixture analysis (GGMA) framework. We conclude this chapter with an empirical example using data from a large randomized trial in Baltimore.

The Unconditional Latent Growth Curve Model

Repeated measures on a sample of individuals results in a particular form of multilevel data, where time or measurement occasions at “Level 1” are nested within persons at “Level 2”. This data can be analyzed using a multilevel modeling framework where *intraindividual* change is described as a function of time and *interindividual* differences are described by random effects and coefficients (Multilevel Linear Models - MLM or Hierarchical Linear Models - HLM; Raudenbush & Bryk, 2002; Hox, 2000, 2002). Alternatively, a multivariate latent variable approach can be used where the parameters of the individual growth curves are modeled as latent variables (e.g., latent intercept and slope factors), with a covariance and mean structure (Latent Growth Curve Models - LGCM, Latent Growth Models - LGM, or Latent Variable Growth

Models - LVGM; Meredith & Tisak, 1990; Willet & Sayer, 1994; Muthén, 2004). A typical unconditional linear latent growth curve model with T time points and n individuals is specified below.

Level 1:

$$y_{ti} = \eta_{0i} + \eta_{si}a_{ti} + \varepsilon_{ti},$$

Level 2:

(1)

$$\eta_{0i} = \alpha_{00} + \zeta_{0i},$$

$$\eta_{si} = \alpha_{s0} + \zeta_{1i},$$

where

$$\boldsymbol{\varepsilon} \sim MVN(\mathbf{0}, \boldsymbol{\Theta}),$$

$$\boldsymbol{\zeta} \sim MVN(\mathbf{0}, \boldsymbol{\Psi}),$$

$$Cov(\boldsymbol{\varepsilon}_\cdot, \boldsymbol{\zeta}_\cdot) = 0.$$

Here, y_{ti} is the observed outcome y for individual i ($i = 1, \dots, n$) at time t ($t = 1, \dots, T$), a_{ti} is the time score for individual i at time t , η_{0i} is the random intercept factor (i.e., the "true score" value for individual i at time $a_{ti}=0$), and η_{si} is the random linear slope factor (i.e., the expected change in y_i for a one unit increase in time, on the scale of a_t). In latent variable modeling terms, the y_t 's are the *indicators* or *manifest variables* for the latent growth factors, η_0 and η_s . ε_{ti} represent measurement and time-specific error at time t and the ε_t 's are usually assumed to be

uncorrelated; however, that restriction can be relaxed. In the more traditional matrix notation of the latent variable framework, the equations in (1) can be written as

$$\begin{aligned}\mathbf{Y}_i &= \boldsymbol{\Lambda} \boldsymbol{\eta}_i + \boldsymbol{\varepsilon}_i, \\ \boldsymbol{\eta}_i &= \boldsymbol{\alpha} + \boldsymbol{\zeta}_i,\end{aligned}\tag{2}$$

where \mathbf{Y}_i is a $(Tx1)$ vector of observed scores for individual i , $\boldsymbol{\eta}_i$ is a $(px1)$ vector of growth factors, $\boldsymbol{\Lambda}$ is a (Txp) design matrix of factor loadings with each column corresponding to specific aspects of change, and $\boldsymbol{\alpha}$ is a $(px1)$ vector of growth factor means. In this specification, $a_{ti} = a_t, \forall i$, but it is possible to incorporate individual-varying times of measurement within this framework by treating time measures at each occasion as a time-varying covariate with a random effect. For a linear model, $p=2$, the loading matrix is given by

$$\begin{bmatrix} 1 & \lambda_{s1} \\ 1 & \lambda_{s2} \\ \vdots & \vdots \\ 1 & \lambda_{sT} \end{bmatrix}\tag{3}$$

where the loading values in the second column would be fixed to define the slope factor as the linear rate of change on the observed time metric; for example, $\boldsymbol{\lambda}_s = (0, 1, 2, \dots, T-1)'$. Typically, the first loading, λ_{s1} , is fixed at zero so that the intercept factor can be interpreted as the response at the first time of measurement ($t=1$). Although the above specification expresses the change in the outcome as a linear function of the time metric, it is possible (with an adequate number of repeated observations on each subject) to investigate interindividual differences in nonlinear trajectories of change. The most common approach is the use of polynomials where additional factors ($p>2$) represent quadratic or cubic functions of the observed time metric.

Nested models with increasing numbers of growth factors are assessed by chi-square difference testing as well as the use of SEM fit indices (Hu & Bentler, 1999). Alternative specifications of time can also be easily accommodated, including piece-wise linear growth models as well as exponential and sinusoidal models of change. Also, it is possible for the Level 1 equation in (1) and the residual variance/covariance structure of \mathbf{Y} to be specified as a generalized linear model to accommodate binary, multinomial, ordinal, and count measures for the change process in addition to continuous measures. The path diagram for the unconditional linear latent growth curve model is shown in Figure 1.

Although it is possible to specify analytically-equivalent unconditional models across the multilevel and latent variable modeling frameworks, utilizing the latent variable approach affords access to a variety of modeling extensions not as easily implemented in other frameworks, e.g., models that simultaneously include both antecedents and consequences of the changes process; higher order growth models with multiple indicators of the outcome at each assessment; multi-process and multilevel growth models; and models that employ both continuous and categorical latent variables for describing population heterogeneity in the change process (for more on growth modeling in a latent variable framework, see, for example, Bollen & Curran, 2006; Duncan, Duncan, & Strycker, 2006; Muthén, 2001, 2004). In the next section, we describe the last extension for which the latent growth curve model serves as a foundational and restricted case in the broader category of general growth mixture models.

The Unconditional General Growth Mixture Model

General growth mixture analysis (GGMA) stands at the intersection of latent growth curve modeling and finite mixture modeling. In finite mixture modeling, rather than making the

usual assumption that the observed responses in a data sample are *identically distributed*, i.e., are drawn from a singular homogeneous population, it is assumed that the data are drawn from a finite number of heterogeneous *subpopulations*. The finite mixture analysis divides the population into an unknown number of exhaustive and mutually exclusive subpopulations (or latent classes), each with its own response distribution. Figure 2 illustrates a mixture of two normally-distributed subpopulations. In the latent variable framework, the mixtures, or subpopulations, are represented by categories of a latent multinomial variable, usually termed a *latent class variable*. And the mixture components or subpopulations are referred to as *latent classes*. The distribution of an observed outcome, \mathbf{Y}_i is a mixture distribution defined as

$$f(\mathbf{Y}_i) = \sum_{k=1}^K [\Pr(C_i = k) \cdot f(\mathbf{Y}_i | C_i = k)], \quad (4)$$

where C_i represents the latent class membership for individual i , K is the total number of latent classes (subpopulations), $\Pr(C_i = k)$ is the mixing proportion for Class k , and $f(\mathbf{Y}_i | C_i = k)$ is the class-specific response distribution of \mathbf{Y}_i .

Latent class membership is unobserved and is determined by the class-specific model parameters. This brings us to a critical point, which we will emphasize repeatedly in this chapter. As with any latent variable, it is necessary to specify a measurement model for the latent class variable. Indicators for the latent class variable include *any* variables, observed or latent, that differ in values between individuals in the population due to latent class membership, as well as model parameters that are permitted to be class-specific, thereby designating those parameters as individually-varying or “random” effects in the given model. The latent classes are then characterized by the class-specific joint distribution of all those variables and random

effects and empirically based on the overall joint distribution in the sample. Thus, the estimation of the optimal number and size of the latent classes (class proportions), as well as the corresponding model parameter estimates (class-specific and overall) and interpretation of the resultant classes, will very much depend on: 1) which variables and random effects are included as latent class indicators and 2) the specification of the within-class joint distribution of those latent class indicators. This is analogous to selecting the attribute space and the resemblance coefficient in a cluster analysis. For example, if we specified a latent class model in which the classes differed only with respect to their mean structure and assumed conditional independence of all the class indicators, we may extract different classes (number, size, and class-specific parameters estimates) than a model in which the classes differed with respect to both their mean and variance-covariance structure.

In growth mixture modeling, rather than assuming the individual growth parameters (e.g., individual intercept and growth factors) are *identically distributed*, i.e., are drawn from a singular homogeneous population, as we do in latent growth curve modeling, it is assumed that the individual growth parameters are drawn from a finite number of heterogeneous subpopulations. The growth mixture analysis divides the population into an unknown number of exhaustive and mutually exclusive latent trajectory classes, each with a unique distribution of individual growth factors. In other words, the continuous latent growth factors serve as the indicators for the K -category latent class variable, C , in a growth mixture model, as expressed below.

$$\begin{aligned} \mathbf{Y}_i &= \boldsymbol{\Lambda} \boldsymbol{\eta}_i + \boldsymbol{\varepsilon}_i, \\ \boldsymbol{\eta}_i &= \boldsymbol{\alpha}_k + \boldsymbol{\zeta}_i, \end{aligned} \tag{5}$$

where

$$\boldsymbol{\varepsilon} \sim MVN(\mathbf{0}, \boldsymbol{\Theta}_k),$$

$$\boldsymbol{\zeta} \sim MVN(\mathbf{0}, \boldsymbol{\Psi}_k),$$

$$\Pr(C_i = k) = \frac{\exp(\pi_{0k})}{\sum_{h=1}^K (\exp(\pi_{0h}))}.$$

Here, C_i represents the latent trajectory class membership for individual i , where $C = 1, \dots, K$. The sizes of the latent classes in the mixture, i.e., the mixing proportions, are parameterized in the model using a multinomial logistic regression, where π_{0k} represents the log odds of membership in Class k relative to a reference class, usually Class K (and $\pi_{0K} = 0$ for identification). Notice that the residuals (on the growth factors and observed outcomes) are all assumed to be normally distributed *within* each latent class. Thus, the normality assumption is not imposed on the overall population but merely on the subpopulations, allowing for the possibility of highly non-normal distributions of responses at the overall population level. The path diagram for the general linear latent growth mixture model is shown in Figure 3. For a given value of K , these models can be fit using ML estimation via the EM algorithm (Muthén & Shedden, 1999). Based on the model-estimated response probabilities and observed data, each individual's estimated probability of class membership, \hat{p}_{ik} (termed the *posterior class probabilities*), can be calculated using the following:

$$\hat{p}_{ik} = \widehat{\Pr}(C_i = k | \mathbf{Y}_i) = \frac{\widehat{\Pr}(C_i = k) \widehat{\Pr}(\mathbf{Y}_i | C_i = k)}{\widehat{\Pr}(\mathbf{Y}_i)}. \quad (6)$$

The class-specific model parameters may include the growth factors means (\boldsymbol{a}_k), the growth factor variances and covariances ($\boldsymbol{\Psi}_k$), and the observed outcome residual variances and

covariances (Θ_k). However, as we mentioned before, one must give careful consideration to what is permitted to vary across the classes for it is those differences that define the classes themselves. Thus, if we wanted latent classes or mixtures that partitioned the population on the basis of differences in the systematic change process over time, i.e., mixture based exclusively on the joint distribution of latent growth factors, then we may not want to allow the outcome residual variances and covariances to be class-specific, i.e., we may want to constrain $\Theta_k = \Theta, \forall k$. As another example, if we changed the location of the intercept growth factor by centering the time scale at the end of the time range instead of the beginning, then the latent classes would be characterized by heterogeneity in the outcome level at the final time point and the outcome change over time rather than by heterogeneity in the outcome level at the first time point and outcome change over time. Only in models with Ψ_k unstructured and unconstrained across the latent classes will the maximum likelihood value be the same regardless of the time centering.

It is clear to see from the equations in (5) that the latent growth curve model describe in the previous section is simply a growth mixture model with $K=1$. Another special case is the latent class growth model developed by Nagin and colleagues (Nagin, 1999; Nagin & Land, 1993; Nagin, 2005; Roeder, Lynch, & Nagin, 1999; Jones, Nagin & Roeder, 2001) which is characterized by zero within-class growth factor variance and covariances, thus assuming homogeneity of individuals' systematic development within a particular class, i.e., $\Psi_k = \mathbf{0}, \forall k$. Not only does this stand as a special case of growth mixture modeling, it represents a very specific measurement model for the latent class variable portion such that the classes are differentiated by differences in the mean structure on the growth factors with *all* interindividual

variability on the growth factors and covariance between the growth factors explained by latent class membership. Certainly, the necessary number and nature of the latent classes extracted from a given data set under this model specification will deviate from those extracted using a different measurement model specification. To be more specific, a greater number of latent classes would be needed for a model in which *all* growth factor variance and covariance had to be captured by between-class differences compared to a model in which overall growth factor variance and covariance were partitioned into inter-class and intra-class variability. Models that assign all systematic variability in growth to class membership are usually less parsimonious but are more flexible and make fewer parametric assumptions. Interestingly, although the latent class growth model may be more parameter-laden, it may be easier to estimate, i.e., converge more readily, than a less constrained model with fewer classes but an equivalent number of free parameters, especially in cases for which the overall variability in one or more of the growth factors is small. In those cases, even with fewer classes, there may not be enough overall variance to parse out across the between- and within-class differences, leading to an empirical identification problem. Unfortunately, these are not problems that can be readily foreseen ahead of the actual data analysis and must be dealt with as it arises. Models with different within- and between-class differences can be compared in terms of relative goodness-of-fit using various information indices; however, nested models that differ in the number of latent classes cannot be compared using a standard chi-squared approximation for the likelihood ratio test (LRT), as is explained in the following section on model building (although alternatives are suggested).

Additionally, a K -class model with $\Psi_k = \mathbf{0}, \forall k$, cannot be directly compared to a K -class model with unconstrained Ψ_k using a standard chi-squared approximation for the LRT because the null

hypothesis lies on the boundary of the parameter space defined by the alternative (Stram & Lee, 1994).

Model Building in GGMA

Given the complexity of the model and the different measurement model specifications for the latent class variable, it is recommended that model building proceed in a systematic step-wise fashion. The first step in the process is specifying the functional form for individual change over time. Descriptive analyses at this first foray into the data can reveal commonalities across individuals and idiosyncrasies between individuals with respect to each person's pattern of growth over time. It is important to note that the shape of the mean change trajectory in the overall sample may not mirror the shape of individual trajectories within that sample. Thus, it is critical to examine smooth nonparametric as well as OLS trajectories across at least a random sample of subjects in the dataset to explore the shapes of individual change over time. In selecting a functional form, e.g. linear or curvilinear, one should consider adopting the most parsimonious choice that will adequately describe the individual trajectories, allowing for the fact that plots based on repeated measures of single subjects will reflect both systematic changes over time as well as random fluctuation due to measurement and time-specific error. (For more on this descriptive step, see, for example, Singer & Willett, 2003.)

The next step in the model building process is class enumeration. All of the mixture model specifications in the previous section were predicated on a known value for K . Although we may have very compelling substantive theories, as discussed in the introduction, regarding discrete typologies of change or growth, these theories are rarely specific enough to guide a purely confirmatory model fitting process, e.g., "we hypothesize three latent trajectory classes

with class-specific quadratic mean structures, class-specific growth factor variances, zero within-class growth factor covariances, and class-invariant outcome residual variances." Thus, the class enumeration process advances in more exploratory manner while giving due consideration to a prior substantive hypotheses regarding the number and nature of the subpopulations that may be represented in the data. (Recall that the use of mixtures may be as much for accommodating non-normality in the overall population as uncovering "true" subpopulations.)

This step begins by considering a set of models with an increasing number of latent classes under a given measurement model. It is advisable to begin with a somewhat restricted measurement model given some of the known pitfalls in mixture model estimation. Mixture models can have difficulty with convergence and a model specification that allows the growth factor (or outcome) residual variances to differ across class results in an unbounded likelihood function which can increase the chance of non-convergence because the candidate parameter space may include solutions with variances of zero and latent classes made up of single individuals (McLachlan & Peel, 2000). This, coupled with the previous discussed motivation, suggests beginning the class enumeration process with a measurement model for which $\Theta_k = \Theta, \forall k$. We may similarly consider constraining $\Psi_k = \Psi, \forall k$ in our initial model specification as well. However, rather than assuming that the covariances between the growth factors within each latent class are the same, it may be more reasonable to start with a model that, like traditional latent class and latent profile analysis, assumes conditional independence of the class indicators, i.e., fixes the covariances of the growth factors *within* class to zero such that the growth factors are independent conditional on latent class. In such a model, the latent class variable would be designed to account for (or explain) *all* of the covariance between the growth factors in the overall population while the overall variance of the growth factors would be

accounted for in part by the within-class continuous random variability on the growth factors and in part by the between-class differences in growth factor means. Thus, beginning ultimately with a measurement model where $\Psi_k = \text{Diag}(\psi_1, \dots, \psi_p)$ and $\Theta_k = \Theta, \forall k$, with α_k free to vary across the K latent classes. This particular specification represents a probabilistic variant of a *k-means* clustering algorithm applied to the “true” growth factor values for the individuals in the sample (Vermunt & Magidson, 2002). Once the class enumeration step is complete, one could theoretically use nested model tests and fit indices to investigate whether freeing the growth factor variances across the latent classes or relaxing the conditional independence assumption improves the fit of the model. However, by making such changes to the latent class measurement model specification, we should not be surprised if we see not only changes to the relative fit of the model, but also significant changes to the location, size, and substantive meaning of the latent classes. If this occurs, we may be given cause to reevaluate the final model selection from the latent class enumeration step or, more drastically, to reconsider the model specification used for the latent class enumeration process itself, and begin again.

Mixture models are also infamous for converging on local rather than global maxima when they do converge. The use of multiple starts from random locations in the parameter space can improve chance of convergence to global maxima (Hipp & Bauer, 2006). Ideally, replication of the maximum likelihood value across a large number of random sets of start values increases confidence that the solution obtained is a global maximum.

Once a set of models, differing only in the number of classes, has been estimated, the models are then compared to make a determination as to the smallest number of classes necessary to effectively describe the heterogeneity manifest through those classes. This first step in growth mixture modeling –deciding on the appropriate number of classes– can prove the most

taxing, particularly because there is no single method for comparing models with differing numbers of latent classes that is widely accepted as best (Muthén & Asparouhov, 2008; Nylund, Asparouhov, & Muthén, 2007); but by careful and systematic consideration of a set of plausible models, and utilizing a combination of statistical and substantive model checking (Muthén, 2003), researchers can improve their confidence in the tenability of their resultant model selection. Comparisons of model fit are based primarily on the log likelihood value. The standard chi-square difference test (likelihood ratio test; LRT) cannot be used in this setting, because regularity conditions of the test are violated when comparing a k -class model to a $(k-g)$ -class model (McLachlan & Peel, 2000). However, two alternatives, currently implemented in the Mplus V5.1 software (Muthén & Muthén, 1998-2008), are available: 1) The Vuong-Lo-Mendell-Rubin test (VLMR-LRT; Lo, Mendell, & Rubin, 2001) analytically approximates the LRT distribution when comparing a k -class to a $(k-g)$ -class finite mixture model for which the classes differ only in the mean structure, and 2) The parametric bootstrapped LRT (BLRT), recommended by McLachlan and Peel (2000), uses bootstrap samples (generated using parameter estimated from a $(k-g)$ -class model) to empirically derive the sampling distribution of the LRT statistic. Both of these tests and their performance across a range of finite mixture models is explored in detail in the simulation study by Nylund et al. (2007). As executed in Mplus, these tests compare a $(k-1)$ -class model (the null model) with a k -class model (the alternative, less restrictive model) and a statistically significant p -value suggests the k -class model fits the data better than a model with one fewer classes. In addition to these tests, likelihood-based information indices, such as the Bayesian Information Criterion (BIC; Schwarz, 1978) are used in model selection. This index and similar ones (e.g., sample-size adjusted BIC) are computed as a function of the log likelihood with a penalty for model complexity (e.g., the

number of parameters estimated relative to the sample size). In general, a lower value on an information criterion indicates a better model. Based on their simulation work, Nylund et al. (2007) recommend using the BIC and VLMR-LRT to trim the set of models under consideration and then including the BLRT for a smaller set of model comparisons (due to the computational demands of the BLRT).

Although the model likelihood will always improve with an increasing number of classes, sometimes none of the other fit indices reach a clear optimal value among the set of candidate model. For example, the BIC may never arrive at a single lowest value at some value for K and then begin to increase for all models with more than K classes, or the VLMR-LRT and BLRT may never return a significant p-value, favoring a $(k-1)$ -class model over a k -class model, before the number of classes is increased to the point at which the model no longer converges to a proper solution or fails to converge at all. However, in these cases, we can loosely explore the diminishing gains in model fit according to these indices with the use of “elbow” plots. For example, if we graph the maximum log likelihood values models with an increasing number of classes, the addition of the second and third class may add much more information, but as the number of classes increases, the marginal gain may drop, resulting in a (hopefully) pronounced angle in the plot. The number of classes at this point meets the “elbow criterion” for that index. We could make a similar plot for BIC values. Analogous to the scree plot for principal component analysis, we could also plot the percent of total growth factor variance explained by the latent classes for each class enumeration, i.e., the ratio of the between-class growth factor variance for the total variance (Thorndike, 1953). In addition to these elbow plots, graphic representations of each of the multivariate observations themselves could be used to guide in reducing the set of candidate models such as the tree plots suggested by Lubke and Spies (2008).

It can be noted that the set of the model comparisons discussed above are *relative* model comparisons, and evaluations of overall goodness-of-fit are conspicuously absent. For example, all of the relative comparisons may favor, say, a 3-class model over a 2-class model as a *better* fit to the data, but none of the fit indices or tests indicate whether either is a *good* fit to the data. However, depending on the measurement scale of the outcome variable and the presence of missing data, there are some model diagnostics available for overall goodness-of-fit. If the observed outcome variables are binary, ordinal, or count, it is possible to compute the overall univariate, bivariate, and multivariate model-estimated response pattern frequencies and relative frequencies for \mathbf{Y} , along with the corresponding standardized Pearson residuals. For continuous outcome variables, it is possible to compute the overall model-estimated means, variances, covariances, univariate skewness, and univariate kurtosis, along with the corresponding residuals. In each case, the overall model-estimated values are computed as a mixture across the latent classes. Additional residual graphical diagnostics designed to detect misspecification in growth mixture models regarding the number of latent trajectory classes, the functional form of the within-class growth trajectory (i.e., functional relationship between the observed outcome and time), and the within-class covariance structure are presented in a paper by Wang, Brown, and Bandeen-Roche (2005) but are not currently implemented directly in the software most commonly used by researchers in applied settings for growth mixture modeling.

In addition to the statistical criteria discussed above, it is also useful assess the value and utility of the resultant classes themselves. One measure which can be used for this purpose is entropy (Ramaswamy, Desarbo, Reibstein, & Robinson, 1993). Entropy summarizes the degree to which the latent classes are distinguishable and the precision with which individuals can be placed into classes. It is a function of the individual estimated posterior probabilities and ranges

from 0 to 1 with higher values indicating better class separation. Entropy is not a measure of fit, nor was it originally intended for model selection; however, if the intended purpose of the growth mixture model is to find homogeneous groupings of individuals with characteristically distinct growth trajectories, such that the between-class dispersion is much greater than the within-class dispersion, then low values of entropy may indicate that the model is not well serving its purpose (e.g., Nagin, 1999).

Beyond all these measures, it is also important to make some qualitative evaluations of the usefulness and face validity of the latent class extractions by examining and interpreting the estimates and corresponding plots of the model-implied mean class trajectories for different models. If the model permits class-specific growth factor variances and covariances, it would be informative to also examine scatterplots of the estimated individual growth factor scores according to either modal latent class assignment or by pseudo-class draw (explained in a later section) since classes would be distinguished by both the mean and variance-covariance structure. It may also be worthwhile noting class size and proportions since an over-extraction of classes might be revealed through particularly small and non-distinct classes emerging at higher enumerative values. Further validation of the primary candidate models can also be done. If there is an ample enough sample size, it is possible to carry out a split sample validation by conducting the exploration of latent structure on one random half of the sample and then evaluating the fit of the selected model on the second half of the sample. Additionally, auxiliary information, potentially derived from substantive theory, in the form of antecedent and consequent variables of the latent construct can be examined to evaluate the concurrent and prognostic validity of the latent structure as specified in a given model (Muthén, 2003). How this auxiliary information may be included is the topic of the next section.

Antecedents and Consequences in GGMA

Once an unconditional growth model has been fit to the repeated measures, and intraindividual change is appropriately modeled and marginal interindividual variability appropriately specified, the focus of the analysis usually shifts to investigating antecedents or predictors of individual differences in the change process as well as consequences or sequelae of change. For a single-class latent growth curve model, antecedents of change enter the model as predictors of the latent growth factors and sequelae of change enter the model as outcomes predicted by the latent growth factors as given in the equations below.

$$\begin{aligned} \mathbf{Y}_i &= \boldsymbol{\Lambda} \boldsymbol{\eta}_i + \boldsymbol{\varepsilon}_i, \\ \boldsymbol{\eta}_i &= \boldsymbol{\alpha} + \boldsymbol{\Gamma}^{(\eta)} \mathbf{X}_i + \boldsymbol{\zeta}_i, \\ \mathbf{Z}_i &= \boldsymbol{\omega} + \boldsymbol{\beta} \boldsymbol{\eta}_i + \boldsymbol{\xi}_i, \end{aligned} \tag{7}$$

where

$$\boldsymbol{\xi} \sim MVN(\mathbf{0}, \boldsymbol{\Omega}),$$

and where the first expression associating the observed repeated measures with the growth factors is the same as for the unconditional latent growth curve model. Here, \mathbf{X}_i is a $(qx1)$ vector of time-invariant covariate predictors of changes for individual i (although not shown here, time-varying covariates can be included in the first equation as part of the expression for \mathbf{Y}_i), $\boldsymbol{\Gamma}^{(\eta)}$ is a (pxq) matrix of regression coefficients representing the effect of \mathbf{X} on $\boldsymbol{\eta}$, $\boldsymbol{\alpha}$ is now a $(px1)$ vector of regression intercepts for $\boldsymbol{\eta}$, \mathbf{Z}_i is a $(dx1)$ vector of static outcomes of the change process, $\boldsymbol{\beta}$ is a $(d \times p)$ matrix of regression coefficients representing the effect of $\boldsymbol{\eta}$ on \mathbf{Z} , and $\boldsymbol{\omega}$

is a ($d \times 1$) vector of regression intercepts for \mathbf{Z} . It is possible for the third equation in (7) and the residual variance/covariance structure of \mathbf{Z} to be specified as a generalized linear model to accommodate not only continuous, but also binary, multinomial, ordinal, and count outcomes of changes. Notice that similar to the assumption of the unconditional single-class latent growth curve model that all individuals are drawn from a single population, the conditional model additionally assumes that predictors have the same influence on the growth factors for all individuals and that the growth factors have the same influence on subsequent outcomes for all individuals. Once we shift to a general growth mixture modeling approach, those assumptions are also relaxed by permitting predictors to influence latent class membership and then having latent class membership predict to subsequent outcomes. The standard assumptions of additive linear associations between predictors and growth factors and between growth factors and outcomes are also relaxed. The integration of antecedents and consequences of latent trajectory class membership also permit evaluation of the criterion-related validity for mapping the emergent classes onto theoretical developmental profiles and, ultimately, for evaluating the validity of the corresponding theory itself. For example, in Moffit's dual taxonomy, it is hypothesized that the life course persistent group consists of individuals with deficits in executive functioning (Moffit, 1993). If the probability of membership in the persistent trajectory class does not statistically differ in respect to theory driven covariates, such as executive functioning, then that particular model lacks crucial theoretical support. If there are repeated failures across various model specifications and samples to find such associations, we may begin to consider that the theory lacks critical empirical support.

Antecedents

In GGMA, covariates are related to latent trajectory class membership via multinomial logistic regression, as expressed below.

$$\Pr(C_i = k | X_i) = \frac{\exp(\pi_{0k} + \boldsymbol{\Gamma}_k^{(C)} \mathbf{X}_i)}{\sum_{h=1}^K \exp(\pi_{0h} + \boldsymbol{\Gamma}_h^{(C)} \mathbf{X}_i)}, \quad (8)$$

where Class K is the reference class and $\pi_{0K} = 0$ and $\boldsymbol{\Gamma}_K^{(C)} = \mathbf{0}$ for identification. Here, $\boldsymbol{\Gamma}_k^{(C)}$ is a $(1 \times q)$ vector of logistic regression coefficients representing the effect of \mathbf{X} on the log odds of membership in Class k relative to Class K , and π_{0k} is now the logistic regression intercept for Class k relative to Class K . These associations between \mathbf{X} and C are represented in the path diagram of Figure 3 by the arrow from \mathbf{X} to C .

The set of covariates may also be permitted to influence the within-class interindividual variability in the change process similar to the associations specified in the second equation of (7):

$$\boldsymbol{\eta}_i = \boldsymbol{\alpha}_k + \boldsymbol{\Gamma}^{(\eta)} \mathbf{X}_i + \boldsymbol{\zeta}_i, \quad (9)$$

where $\boldsymbol{\Gamma}^{(\eta)}$ is a (pxq) matrix of regression coefficients representing the effect of \mathbf{X} on $\boldsymbol{\eta}$, and $\boldsymbol{\alpha}_k$ is now a $(px1)$ vector of regression intercepts for $\boldsymbol{\eta}$ within Class k . These possible associations are represented in the path diagram of Figure 3 by a dashed arrow from \mathbf{X} pointing towards the growth factors. It is also possible to allow class-specific effects of \mathbf{X} on $\boldsymbol{\eta}$, that is,

$$\boldsymbol{\eta}_i = \boldsymbol{\alpha}_k + \boldsymbol{\Gamma}_k^{(\eta)} \mathbf{X}_i + \boldsymbol{\zeta}_i, \quad (10)$$

where $\boldsymbol{\Gamma}_k^{(\eta)}$ is a (pxq) matrix of regression coefficients representing the effect of \mathbf{X} on $\boldsymbol{\eta}$ within Class k , and \boldsymbol{a}_k is a $(px1)$ vector of regression intercepts for $\boldsymbol{\eta}$ within Class k .

There are several critical points to which to pay attention when incorporating covariates or predictors of change into a growth mixture model. First and foremost, selection and order of covariate inclusion should follow the same process as with any regular regression model, with respect to risk factors or predictors of interest, control of potential confounders, etc. Secondly, although covariates can certainly assist in understanding, interpreting, and assigning meaning to the resultant classes, i.e., to *inform* the classes, one should exercise caution if the mixture model identification is dependent upon the inclusion of covariates or if the formation of the latent classes is sensitive to the particular subset of covariates included as predictors of class membership. Based on the simulation work of Nylund and Masyn (2008), misspecification of covariate effects in a latent class analysis can lead to over-extraction of latent classes more often than when the latent class enumeration is conducted without covariates. Once the enumeration process is complete, covariates should first be added to the model only as predictors of the latent class variable. If the covariates are permitted to influence the change process exclusively through their effects on class membership in the model and the classes themselves changes substantively in size or meaning (i.e., the class proportion or class-specific growth parameter estimates), this can signal a misspecification of the covariate associations with the latent class indicators. If that occurs, then direct effects, initially class-invariant, from the covariates to the growth factors themselves should be explored, as given in Equation (9). The covariates should be centered so that there is not a radical shift in how the centroids of the latent classes are located, facilitating comparisons in class formation between the unconditional and conditional models. In the conditional model, the centroids of the latent classes, defined by class-specific

growth factor mean vectors, α_k , become the center of growth factor values for the classes at $\mathbf{X} = \mathbf{0}$. Assuming correct specification of the indirect (via the latent class variable) and direct effects of the covariates on the growth factors, the resultant classes should align more closely to the classes obtained from the unconditional growth mixture model. If effects directly from the covariates to the growth factors are specified in the model, careful consideration should be given before allowing those effects to be class-varying as well, as in Equation (10). Recall that any parameter that is permitted to vary across the latent classes becomes an *indicator* of that latent class variable. Thus, including class-varying covariate effects on the growth factors results in latent classes which are defined not only by heterogeneity in growth trajectories but also heterogeneity in the effect of those covariates on the growth trajectories. This is not an incorrect model specification, but it does represent what could be a significant departure from the measurement model originally intended for the latent class variable in the unconditional model. If the classes continue to change in significant ways relative to the unconditional growth mixture model with changing subsets of covariates, then careful attention should be paid to the stability of the model estimation under the original specification and to the solution sensitivity to covariate inclusion and the entire modeling approach should be reevaluated for data sample at hand.

Consequences

In addition to including covariates and predictors of change, it is often of interest to relate the growth trajectories to distal outcomes or sequelae of change (depicted by the arrow from C to Z and the dashed arrow pointing from η towards Z in Figure 3). This facilitates the assessment of the predictive power of class membership. While the inclusion of distal outcomes is fairly

straightforward for the single class latent growth curve model, as given in the third equation of (7), evaluating the associations between growth mixtures and sequelae of change can pose an analytic dilemma.

There are two primary ways to frame a distal outcome of the change process when a latent class variable is involved and each way is conceptually and analytically different—the choice between them is not one that can be made by the data but must be made by the researcher with understanding of the implications for each alternative. The first way is to treat the distal outcome(s) as an additional *indicator* of the latent class variable. The second way is to treat the latent class variable and distal outcome(s) as a cause-effect pairing such that the distal outcome(s) is a true consequence of latent class membership.

For the first approach, the indicators for the measurement model of the latent class variable are made up of the latent growth factors *and* the distal outcomes (for more, see Muthén & Shedden, 1999). The latent class variable is characterized by heterogeneity in *both* the change process *and* a later outcome. In other words, the latent class variable captures variability in the growth factors, variability in the distal outcomes, *and* the association *between* the growth factors and the distal outcomes. In addition to the equations in (5), we add the following to the measurement model for the latent class variable:

$$\mathbf{Z}_i = \boldsymbol{\omega}_k + \boldsymbol{\xi}_i, \quad (11)$$

where

$$\boldsymbol{\xi} \sim MVN(\mathbf{0}, \boldsymbol{\Omega}_k).$$

Here, again, \mathbf{Z}_i is a $(dx1)$ vector of static outcomes of the change process. $\boldsymbol{\omega}_k$ is a $(dx1)$ vector of class-specific means for \mathbf{Z} given membership in Class k . It is possible for Equation (11) and the residual variance/covariance structure of \mathbf{Z} to be specified as a generalized linear model to accommodate not only continuous, but also binary, multinomial, ordinal, and count outcomes of changes. If $\boldsymbol{\eta}$ and \mathbf{Z} are both being used as indicators of the latent class variable, then it may be desirable to include \mathbf{Z} in the class enumeration process since \mathbf{Z} would be part of the measurement model for C . In this case, the residual variance/covariance matrix for \mathbf{Z} could be constrained in a similar way to the one for $\boldsymbol{\eta}$, i.e., $\boldsymbol{\Omega}_k = \text{Diag}(\Omega_1, \dots, \Omega_d)$, and \mathbf{Z} and $\boldsymbol{\eta}$, as indicators for the latent class variable, could be assumed to be conditionally independent given class membership, i.e., $\text{Cov}(\boldsymbol{\Psi}_k, \boldsymbol{\Omega}_k) = \mathbf{0}$. Although it would be possible to specify and estimate a regression association within class from $\boldsymbol{\eta}$ to \mathbf{Z} similar to the third equation of (7),

$$\mathbf{Z}_i = \boldsymbol{\omega}_k + \boldsymbol{\beta}_k \boldsymbol{\eta}_i + \boldsymbol{\xi}_i, \quad (12)$$

this would fundamentally change the measurement model for C , where instead of just including \mathbf{Z} as an indicator of C , individual heterogeneity in the association between $\boldsymbol{\eta}$ and \mathbf{Z} along with the marginal distribution of $\boldsymbol{\eta}$ would characterize C . Constraining the effect of $\boldsymbol{\eta}$ on \mathbf{Z} to be class-invariant would reduce the impact of this path on formation of the classes but be the equivalent of relaxing the conditional independence assumption between $\boldsymbol{\eta}$ and \mathbf{Z} within class. In either case, with class-varying or class-invariant effects of $\boldsymbol{\eta}$ on \mathbf{Z} , the centroids of the latent classes on to the scale of \mathbf{Z} will be the class-specific means of \mathbf{Z} when $\boldsymbol{\eta} = \mathbf{0}$.

The second way to frame \mathbf{Z} is as actual an *outcome*, *effect*, or *consequence* of latent class membership, rather than as an indicator of the latent class variable, C , such that C is a predictor of \mathbf{Z} as given below.

$$\mathbf{Z}_i = \boldsymbol{\omega} + \sum_{h=1}^K (\boldsymbol{\beta}_h^{(C)} \cdot \mathbf{I}(C_i = h)) + \boldsymbol{\xi}_i, \quad (13)$$

where

$$\boldsymbol{\xi} \sim MVN(\mathbf{0}, \boldsymbol{\Omega}).$$

Here, $\boldsymbol{\beta}_k^{(C)}$ is a $(dx1)$ vector of regression coefficients for the indicator variable, $\mathbf{I}(C_i = k)$, which is equal to unity when $C_i = k$ and zero otherwise. If we fix $\boldsymbol{\beta}_K^{(C)}$ at zero, then $\boldsymbol{\omega}$ represents the mean vector for \mathbf{Z} among those in Class K . Then the vector of regression coefficients, $\boldsymbol{\beta}_k^{(C)}$, represents the vector of mean differences on \mathbf{Z} between Class k and Class K . Alternatively, we could set $\boldsymbol{\omega}$ to zero so that all the $\boldsymbol{\beta}_k^{(C)}$'s are freely estimated and each represent the mean vector for \mathbf{Z} given membership in Class k . In order to utilize this second approach to distal outcomes, \mathbf{Z} cannot be included in the model which estimates the growth mixtures and related covariate effects. If it is included, it will automatically be treated as an indicator of the latent class variable. Instead, the growth mixture model with covariates must first be estimated without \mathbf{Z} . Then, the $\boldsymbol{\beta}_k^{(C)}$ parameters are estimated using what is referred to as the *pseudo-class draw* technique (see Bandeen-Roche, Miglioretti, Zeger, & Rathouz, 1997; Muthén & Asparouhov, 2007; Wang et al., 2005). Based on the estimated growth mixture model with covariates, the posterior latent class probability distribution, $\hat{\Pr}(C_i) = (\hat{p}_{i1}, \hat{p}_{i2}, \dots, \hat{p}_{iK})$, for each individual in the sample is computed using the estimated model and the observed data for that individual, where

$$\hat{p}_{ik} = \widehat{\Pr}(C_i = k | \mathbf{Y}_i, \mathbf{X}_i) = \frac{\widehat{\Pr}(C_i = k) \widehat{\Pr}(\mathbf{Y}_i | C_i = k, \mathbf{X}_i)}{\widehat{\Pr}(\mathbf{Y}_i | \mathbf{X}_i)}. \quad (14)$$

A specified number of random draws, M , are made from the discrete posterior probability distributions for all individuals in the sample ($M=20$ is recommended in general, see Wang et al., 2005). For example, suppose there was an individual with a posterior latent class probability distribution from a $K=3$ class growth mixture model computed as $\widehat{\Pr}(C_i) = (\hat{p}_{i1} = .80, \hat{p}_{i2} = .15, \hat{p}_{i3} = .05)$. Pseudo-class membership for individual i from 20 random draws might look like the following:

$$\begin{aligned} C_i^1 &= 1, C_i^2 = 1, C_i^3 = 1, C_i^4 = 2, C_i^5 = 1, C_i^6 = 1, C_i^7 = 1, C_i^8 = 1, C_i^9 = 1, C_i^{10} = 1, \\ C_i^{11} &= 1, C_i^{12} = 3, C_i^{13} = 1, C_i^{14} = 1, C_i^{15} = 3, C_i^{16} = 1, C_i^{17} = 3, C_i^{18} = 1, C_i^{19} = 1, C_i^{20} = 1, \end{aligned}$$

where C_i^m is the pseudo-class membership for individual i based on random draw m from the posterior distribution, $\widehat{\Pr}(C_i)$. For each pseudo-class draw, the association between \mathbf{Z} and C is estimated using the pseudo-class membership and observed \mathbf{Z}_i for each individual in the sample; thus, for Equation (13), we would obtain $\widehat{\beta}_k^{(C^m)}$ and $\widehat{\Omega}^m$: the estimates for $\beta_k^{(C)}$ and Ω , respectively, based on the m^{th} pseudo-class draw. Consistent estimates for $\beta_k^{(C)}$ are then obtained by averaging the $\widehat{\beta}_k^{(C^m)}$ estimates across the M pseudo-class draws (for proof, see Bandeen-Roche et al., 1997):

$$\widehat{\beta}_k^{(C)} = \frac{1}{M} \sum_m \widehat{\beta}_k^{(C^m)}. \quad (15)$$

The asymptotic variance of the estimate can be obtained using a similar method to multiple imputations (described by Rubin, 1987 and Schafer, 1997). Take the simple case with a single distal outcome of interest, such that $d=1$ and $\beta_k^{(C)}$ is a scalar quantity. Suppose that $\widehat{\mathbf{U}}_k^m$ is the

square of the standard error associated with $\hat{\beta}_k^{(C^m)}$. Then the overall square of the standard error for $\hat{\beta}_k^{(C)}$ is given by

$$\hat{V} = \hat{V}_w + \left(1 + \frac{1}{M}\right) \hat{V}_b, \quad (16)$$

where \hat{V}_w is the within-imputation (pseudo-class draw) variance of $\hat{\beta}_k^{(C)}$ given by

$$\hat{V}_w = \frac{1}{M} \sum_m \hat{U}_k^m,$$

and \hat{V}_b is the between-imputation (pseudo-class draw) variance of $\hat{\beta}_k^{(C)}$ given by

$$\hat{V}_b = \frac{1}{M-1} \sum_m \left(\hat{\beta}_k^{(C^m)} - \hat{\beta}_k^{(C)} \right)^2.$$

A significance test of the null hypothesis $\beta_k = 0$ can be performed by comparing the ratio

$$\frac{\hat{\beta}_k^{(C)}}{\sqrt{\hat{V}}}$$

to a Student's t-distribution with degrees of freedom

$$df = (M-1) \left(1 + \frac{M\hat{V}_w}{(M+1)\hat{V}_b} \right)^2.$$

In the modeling software, Mplus V5.1 (Muthén & Muthén, 1998-2008), the pseudo-class draw technique is implemented to perform Wald tests of mean differences on distal outcomes across the latent classes. A Wald test is performed separately for each outcome variable (for details, see Muthén & Asparouhov, 2007). However, this pseudo-class draw technique could be

expanded to include multivariate distal outcomes with other observed predictors of the distal outcomes as well as including the growth factors themselves as predictors in addition to the latent trajectory class variable, for a more complex model for sequelae of change, as given below.

$$\mathbf{Z}_i = \boldsymbol{\omega} + \sum_{h=1}^K (\boldsymbol{\beta}_h^{(C)} \cdot \mathbf{I}(C_i = h)) + \boldsymbol{\beta}^{(\eta)} \mathbf{n}_i + \boldsymbol{\beta}^{(X)} \mathbf{X}_i + \boldsymbol{\xi}_i. \quad (17)$$

We now illustrate the general growth mixture modeling process from class enumeration to the inclusion of antecedents and distal outcomes of the change process using longitudinal data from a large population-based randomized trial. All analyses were conducted using the statistical modeling software, Mplus¹, V5.1 (Muthén & Muthén, 1998-2008).

Data Illustration: Development of Aggressive Behavior with Correlates and Consequences

Sample

The data come from a large randomized intervention trial consisting of two cohorts totaling 2311 students within the 19 participating Baltimore City Public Schools in first grade (Kellam et al., 2008). Of the population, 1151 (49.8%) were male of which 476 (41.4%) were assigned to intervention conditions not pertinent to this paper (i.e., Mastery Learning, Good Behavior Game). Of the remaining 675 control males, 53 (7.9%) had missing values on all aggression ratings and an additional 7 (1%) had missing values on the covariates. The remaining sample consisted of 615 male students who did not receive an intervention and who have at least one valid teacher rating of aggression and no missing values on the covariates. Over 60% of this sample was African-American (61.6%) and the average age in fall of first grade was 6.3 (SD=0.47).

Longitudinal Outcome

In fall of first grade, teacher reports of child aggressive-disruptive behavior were gathered twice during first grade and then once per year during second through seventh grade. The analyses in this chapter focus on the five teacher ratings conducted in spring of first grade to spring of fifth grade.

Teacher ratings of aggressive-disruptive behavior were obtained using the Teacher Observation of Classroom Adaptation-Revised (TOCA-R; Werthamer-Larsson et al., 1991). The TOCA-R is a structured interview with the teacher administered by a trained assessor. The level of adaptation is rated by teachers on a six-point frequency scale (1=almost never through 6=almost always). The analysis herein used the authority-acceptance subscale which includes the following items: (1) breaks rules, (2) harms others and property, (3) breaks things, (4) takes others property, (5) fights, (6) lies, (7) trouble accepting authority, (8) yells at others, (9) stubborn, and (10) teases classmates. For this chapter, the item-averaged summation scores are used.

Covariates

For this illustration, two covariates measured in fall of first grade were included in the analysis: 1) student ethnicity (Black = 1, non-Black = 0) and 2) standardized reading test scores. The California Achievement Test (CAT, Forms E & F). The CAT represents one of the most frequently used standardized achievement batteries (Wardrop, 1989). Subtests in CAT-E and F cover both verbal (reading, spelling, and language) and quantitative topics (computation, concepts, and applications). Internal consistency coefficients for virtually all of the subscales exceed .90. Alternate form reliability coefficients are generally in the .80 range (CAT, Forms E

& F). The CAT represents one of the most frequently used standardized achievement batteries (Wardrop, 1989). Subtests in CAT-E and F cover both verbal (reading, spelling, and language) and quantitative topics (computation, concepts, and applications). Internal consistency coefficients for virtually all of the subscales exceed .90. Alternate form reliability coefficients are generally in the .80 range.

Consequent Outcomes

Records of violent and criminal behavior were obtained at the time of the young adult follow-up interview and repeated yearly searches were conducted thereafter. The latest search was conducted in 2007, thus covering adult arrest records up to age 25. Records of incarceration for an offense classified as a felony in the Uniform Crime Reports system (i.e., armed/unarmed robbery, assault, kidnapping, weapons, domestic offense, rape/sex offense, attempted murder, homicide) was used as an indicator of violent and criminal behavior offenses. Drug and property related offenses (i.e., drug conspiring, distribution, possession, auto theft, burglary, larceny, and motor vehicle) were coded as non-violent offenses. Violent and nonviolent offenses were then aggregated over offenses and years such that one or more records of an arrest during that age range would result in a value of “1” on the nonviolent or the nonviolent crime indicator. These data were obtained from the Maryland Department of Correction and are considered public record.

Results

Model Building: Functional Form. Visual inspection of a plot of the sample mean trajectory shows that, on average, in spring of first grade, males start at a level of 2.2 in aggressive-disruptive behavior and tend to increase gradually towards an average level of 2.5 in

spring of fifth grade (see Figure 4). Further inspection of individual trajectories makes clear that there is a tremendous variation around that mean pattern, as is evident by the random subset of observed individual trajectories plotted in Figure 4. Initial descriptive analysis, as recommended in the earlier section on model building, suggested that a linear growth model was adequate to describe intra-individual change across time allowing for fluctuations due to measurement and time-specific error. Furthermore, a random intercept and a random linear slope had a reasonable fit to the first and second moments of the current data on the boys' developmental course of aggressive-disruptive behavior: $\chi^2=20.586$, df=10, p=0.0242; CFI=0.981; TLI=0.981; RMSEA=0.041. (The remaining details of this first step of data screening and descriptive analyses are omitted in the interest of space.)

Model Building: Class Enumeration

The next step in the model building process is the latent class enumeration. As explained in detail throughout the first part of this chapter, model specification at this juncture in the analysis must be purposeful in terms of how the latent classes are to be characterized. In these analyses, we follow the recommendations given earlier and begin with a set of candidate models that allow the growth factor means to vary across the latent classes, constrain the growth factor variances and error variances to be class-invariant, and fix the growth factor covariances and error covariances to zero within-class. We also need to consider at this point the role of the distal outcomes in our analysis.

Previously, two alternative latent class measurement model specifications upon which the class enumeration can performed were described. The first way is to treat the distal outcomes as additional indicators of the latent class variable and to therefore include the distal outcomes in

the class enumeration process. The second approach treats the distal outcomes as true effects or consequences of the latent class variable and to therefore exclude them from this step in the analysis. The results of these two alternative specifications are now described in more detail.

Models with distals-as-class-indicators. In Table 1, the aforementioned fit statistics are shown for models with an increasing number of classes. There are three 1-class models listed in the table. The first 1-class model is the independence model for which associations between all the class indicators, growth factors and distal outcomes are fixed at zero. The second 1-class model allows the growth factors to co-vary but fixes associations between the distal outcomes and the distal outcomes with the growth factors to zero. The third 1-class model allows the growth factors to co-vary, allows the growth factors to associate with the distal outcomes, but fixes the residual covariance between the distal outcomes to zero. This third and final 1-class model is the most reasonable single-class baseline model for this class enumeration sequence since it is the model we would specify if we were working within a conventional latent growth curve framework and not considering the addition of a latent class variable. Starting with this 1-class model, the BIC decreased (indicating better fit) towards a 4-class model. However, the change in the BIC from three to four classes is much smaller than from one to two or from two to three as is evident by the “elbow” in the top BIC plot of Figure 5. (A proper solution could not be obtained for a 5-class model without additional constraints, indicating problems with model identification.) The VLMR-LRT test indicates that a 2-class model can be rejected in favor of a 3-class model ($p < .01$), while a 3-class model was not rejected in favor of a 4-class model. The BLRT indicates that a 4-class solution fits superior as compared to a 3-class model. Further inspection of the estimated mean trajectories reveals that the 4-class solution does not yield a fourth trajectory class substantively distinct from three trajectory classes derived from the 3-class

solution. Given the small change in BIC, the non-significant VLMR-LRT, and the non-distinct fourth class, the 3-class solution was selected as the final model to carry forward to the next step of the analysis.

In the 3-class model (see top plot of Figure 6), the largest class (72%) follows a low-stable development of aggression, starting at a level of “1.8” in spring of first grade. The two smaller classes are reasonable comparable in size. One of these classes (16%) starts at a similar intercept as the low-stable class, but escalates in aggression towards fifth grade. The last class (12%) starts at a high level of aggressive behavior in spring of first grade followed by a decline towards fifth grade, which falls below the level of aggressive-disruptive behavior seen for the low-escalating class.

Models with distals-as-class-consequences. In Table 2, the class enumeration results are shown for the models without the distal outcomes as additional class indicators. There are two 1-class models listed in the table. The first 1-class model is the independence model for which the association between the growth factors is fixed at zero. The second 1-class model allows the growth factors to co-vary. This second 1-class model is the most reasonable single-class baseline model for this class enumeration sequence since it is the model we would specify if we were working within a conventional latent growth curve framework and not considering the addition of a latent class variable. Starting with this 1-class model the BIC decreased with additional classes added and reached its lowest value for a 4-class solution. However, the change in the BIC from three to four classes is somewhat smaller than from one to two or from two to three as is evident by the “elbow” in the bottom BIC plot of Figure 5. (A proper solution could not be obtained for a 5-class model without additional constraints, indicating problems with model identification.) The VLMR-LRT indicates that a 2-class solution can be rejected in favor

of a 3-class solution. The BLRT indicates that a 4-class solution fits superior as compared to a 3-class model. Further inspection of the estimated mean trajectories reveals that the 4-class solution does not yield a fourth latent class substantively distinct from three latent classes derived from the 3-class solution. Given the small change in BIC, the non-significant VLMR-LRT, and the non-distinct fourth class, the 3-class solution was selected as the final model to carry forward to the next step of the analysis. As in the first measurement model specification, the 3-class solution (see bottom plot of Figure 6) yields a low-stable class (72%), a low-escalating class (15%), and a high-declining class (13%).

When comparing the results of the class enumeration process using the two alternative measurement model specification, strong similarities regarding the extracted trajectories in terms of shape and prevalence are found. Additionally, there is very little difference in estimated within-class growth factor variances: Intercept factor est. SD = 0.45, 0.47; Slope factor est. SD = 0.05, 0.08. We would expect some similarity given the overlap in information on which latent class formation is based. However, by simply comparing the estimated mean trajectories, we might incorrectly infer that the latent classes based on the two model specifications are the *same* in that the distal outcomes do not contribute to the class characterizations and that class membership at the individual level is identical across models. Although we do not directly observe latent class membership, we can explore differences in class membership by comparing modal class assignment based on the individual posterior class probabilities for each model, as shown in Table 3. While 94% of individuals assigned to the low-stable trajectory class in at least one of the models were assigned to that class in both models, only 86% of individuals were assigned to the high-declining class in both models, and only 54% of individuals for the low-escalating class. The root of these class formation differences despite the near identical mean

growth trajectories become evident in later section in which we present the class differences with respect to the distal outcomes.

Predictors of Aggressive-Disruptive Behavior Development

Antecedents of class membership are important to further understand the profile of individuals in each class as well as to evaluate the criterion-related validity of the latent classes relative to substantive theory. For this chapter, two covariates measured in fall of first grade were included. In addition to the students' ethnicity, the results of a standardized reading test were used. As suggested by Nylund and Masyn (2008), we first compared the results of the final unconditional growth mixture model from the class enumeration step to the same model with the mean-centered covariates included as predictors of class membership, looking for any evidence of changes in the size and meaning of the classes. While the model results did not change for either of the three class solutions, the size and meaning of the extracted classes changed for the four class solutions. This level of instability indicates not only potential model misspecification of the covariate effects, but also that the three class solution is the preferred model for this sample. Given the high level of correspondence in class membership for all but the smallest trajectory class for the two alternative model specifications and the similarity in mean growth trajectories, it was not surprising to find that the covariate associations to latent class membership were similar (see Tables 4 and 5). In both cases, Black individuals were more likely to be in the high-declining and low-escalating classes relative to the low-stable class compared to non-Black individuals, and individuals with higher reading scores were less likely to be in the high-declining or low-escalating classes relative to the low-stable class. Neither covariate distinguished between the high-declining and low-escalating classes in either model. The most noticeable differences across the models are in the estimated size and significance of

effects of race/ethnicity and reading on membership in the low-escalating class relative to the low-stable class, with the stronger effects present in the model with distals-as-class-indicators.

Distal Outcomes of Aggressive-Disruptive Behavior Development

A Department of Correction record for a violent or nonviolent crime as an adult is used as distal outcomes for aggressive-disruptive behavior trajectories in childhood. When including the distal outcomes in the class enumeration process (see Table 6), the high-declining and low-escalating classes were both characterized by significantly higher rates of nonviolent and violent arrests than the low-stable class. Furthermore, the low-escalating class was characterized by significantly higher rates of nonviolent and violent arrests than the low-escalating class. These class distinctions are similar (both for pair-wise comparisons and overall comparisons) for each arrest type.

By comparison, when treating the distal outcomes as consequences of trajectory class memberships (see Table 7), membership in the high-declining and low-escalating classes is predictive of higher rates of both nonviolent and violent arrests in adulthood relative to the low-stable class; however, membership in the low-escalating class is not distinct from membership in the high-declining class relative to predicted arrest rates. However, similar to the other model, pair-wise differences due to class membership are similar across arrest type although the overall effect was stronger for nonviolent than violent arrests.

These disparities between the two model specification help explain why there were differences in class membership despite the similarity in mean class trajectories. In the model using the distal outcomes as latent class indicators, individuals placed in the low-escalating trajectory class were individuals who had *both* an aggressive-disruptive behavior trajectory

resembling the low-escalating mean trajectory *and* a high probability of non-violent and violent arrests. These individuals could very well be those who persist in their higher levels of aggressive-disruptive behavior into adolescence. For the model in which trajectory classes are based exclusively on aggressive-disruptive behavior in first through fifth grade, there is not a high level of predictive validity for adult arrest outcomes beyond that given by any deviation from the low-stable trajectory pattern, suggesting that information from later childhood and adolescence may be needed to distinguish arrest risk among those who display non-normative behavior patterns in middle childhood.

It is important to note here that if we had used the distals-as-class-indicators specification but then *interpreted* the model results treating the distal outcomes as effects or consequences of the trajectory classes, we would have incorrectly infer that individuals in the low-escalating class were at significantly higher risk for arrest than individuals in the high-declining class. Results from the distals-as-class-consequences model showed this not to be the case.

Discussion

This chapter has examined the process of including antecedents and consequences of a developmental process in a growth mixture modeling framework. We have shown that in addition to the flexibility growth mixture models offer over conventional latent growth curve models in terms of the way in which population heterogeneity in the growth process itself is characterized, there is also flexibility gained in terms of how the associations of predictors and distal outcomes with the growth process are parameterized. We have discussed the unconditional growth mixture model building process and then demonstrated the addition of covariates as predictors of the growth process and as possible means for evaluating the

concurrent validity of resultant trajectory classes. We have also presented two different approaches for including distal outcomes of the growth process. In one approach, the distal outcomes are included as additional indicators of the latent class variable and, thus, resultant classes are characterized by individual response patterns on *both* growth outcomes *and* distal outcomes. We noted that if using this approach, one must be careful not to interpret the class-specific rates of the distal outcome as representing class-predicted patterns but, rather, class-defining outcome patterns. In the other approach, the distal outcomes are treated as true effects or consequences of the growth process. The approach offers the possibility of evaluating the prognostic validity of the resultant trajectory classes. Some recent work has been done to quantify the predictive validity of trajectory class membership as a screening mechanism for identifying individuals at-risk for maladaptive distal outcomes using the distal-as-class-indicator approach (Feldman, Masyn, & Conger, 2008) and this work could be extended to the distal-as-class-consequence approach. Other work has been done to examine the prediction power of trajectory class membership in one developmental period for trajectory class membership in a subsequent development period (see, for example, Boscardin et al., 2008; and for a preventive intervention settings, see, Petras, Masyn, & Ialongo, 2008) and this work could be extended to the models presented in this chapter where the earlier latent class variable is treated as an antecedent or the later latent class variable is treated as a consequence.

There are several interesting areas of investigation for future work. One area involves extending the distal-as-consequence model to permit more complex models for the distal outcomes. As specified in this chapter, the distal outcome is assumed to be an observed univariate or multivariate outcome. However, the distal outcome could itself be a latent variable with its own measurement model. Another area involved further exploration into the implication

for model specification if the latent trajectory class membership is conceptualized as a time-invariant attribute at the individual level that merely manifests over time but it is, itself, independent of time; or if membership is conceptualized as malleable and time-dependent. A further, and much more complex, matter not dealt with in this chapter, is the collection of the antecedents, growth process, and consequences as a variable system. In both model approaches for the distal outcomes, we did not explicitly consider what the implication would be if part of the shared variance between the growth process and the distal outcomes was due to the antecedent variables. Confounding of the associations between the growth process and distal outcomes by the antecedents would have differing impact depending on how the association was modeled, i.e., distals-as-class-indicators or distals-as-class-consequences. The same is true if the growth process acted as a mediator of the antecedent effect on the distal outcome or if the antecedents acted as moderators of the associations between the growth process and the distal outcomes.

Clearly, these models hold great potential for aiding empirical investigations of developmental theories of normative and non-normative behaviors and maladaptive outcomes across the lifespan. In no way is this more evident than in the marked increase in their use among applied researchers in criminology and other behavioral sciences. We maintain, as expounded at the beginning of this chapter, that the value and future potential of these models for examining population heterogeneity in developmental processes and correlates thereof, holds regardless of whether the resultant latent trajectory classes represent "true" subpopulations or simply reflect non-normality in the population distribution of the growth factors. However, there is still much opportunity in the realm of methods development to capitalize on the potential of these models and extensions to better accommodate the complexities of our developmental

theories. And, as with any statistical tool, the research question along with previous theoretical and empirical work, should guide these models' application in a particular study, with thoughtful and purposeful choices for model specification, selection, and interpretation.

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Footnotes

¹ Although we chose to use the Mplus modeling software, there are other software packages that can be used to estimate some (or all) of the models presented herein. Among the most prominent are: HLM (Raudenbush, Bryk, Cheong, & Congdon, 2000); SAS Proc TRAJ (Jones, Nagin, & Roeder, 2001); GLAMM (Rabe-Hesketh, Skrondal, & Pickles, 2004); MLwiN (Rasbash, Steele, Browne, & Prosser, 2004); Latent Gold (Vermunt & Magidson, 2005); SuperMix (Hedeker & Gibbons, 2008); and LISREL (Jöreskog & Sörbom, 1996).

Table 1

Fit Indices for Models with Distals-as-class-indicators

Model	LL	# free parameters	BIC	VLMR-LRT	BLRT	Entropy	Smallest class r.f. (f)
1-class [*]	-3435.87	11	6942.38	n/a	n/a	n/a	n/a
1-class ⁺	-3434.65	12	6948.36	n/a	n/a	n/a	n/a
1-class [†]	-3368.77	16	6840.29	n/a	n/a	n/a	n/a
2-class [*]	-3349.88	16	6802.50	p<.0001	p<.0001	.73	.21 (129)
3-class [*]	-3309.19	21	6753.22	p=.002	p<.0001	.76	.12 (77)
4-class [*]	-3292.89	26	6752.73	p=.15	p<.0001	.74	.06 (37)

^{*}Cov(ζ)=0, Cov(ζ , ξ)=0, Cov(ξ)=0; ⁺ Cov(ζ , ξ)=0, Cov(ξ)=0; [†]Cov(ξ)=0

Table 2

Fit Indices for Models with Distals-as-class-consequences

Model	LL	# free parameters	BIC	VLMR-LRT	BLRT	Entropy	Smallest class r.f. (f)
1-class *	-3019.49	9	6096.77	n/a	n/a	n/a	n/a
1-class	-3019.27	10	6102.75	n/a	n/a	n/a	n/a
2-class *	-2971.97	12	6021.00	p<.0001	p<.0001	.80	.15 (94)
3-class *	-2940.06	15	5976.45	p=.0001	p<.0001	.74	.13 (78)
4-class *	-2927.12	18	5969.82	p=.20	p<.0001	.73	.06 (34)

* Cov(ζ)=0

Table 3

Cross-tabulation of Modal Latent Class Assignment based on Model with Distals-as-class-indicators versus Distals-as-class-consequences

		Distals-as-class-consequences			Total
		Low-Stable	High-Declining	Low-Escalating	
Distals-as-class-indicators	Low-Stable	442	6	20	468
	High-Declining	1	66	2	69
	Low-Escalating	22	2	54	78
	Total	465	74	76	615

Table 4

Latent Class Multinomial Regression Results for 3-Class Model with Distals-as-class-indicators

Covariate	Target Class	Reference Class	Est.	S.E.	p-value	Est. OR*
Race/Ethnicity	High-Declining	Low-Stable	0.90	0.36	.01	2.46 ⁺
	Low-Escalating		1.27	0.43	.004	3.56 ⁺
	High-Declining	Low-Escalating	-0.37	0.55	.51	0.69 ⁺
Reading	High-Declining	Low-Stable	-0.01	0.004	<.001	0.67 [†]
	Low-Escalating		-0.01	0.004	.001	0.67 [†]
	High-Declining	Low-Escalating	0.001	0.01	.89	1.04 [‡]

*Odds (membership in target class) : Odds (membership in reference class) among individuals in either target or reference class

⁺Calculated for Ethnicity = Black vs. Ethnicity = Non-Black[†]Calculated for a 1 SD increase in reading score

Table 5

Latent Class Multinomial Regression Results for 3-Class Model with Distals-as-class-consequences

Covariate	Target Class	Reference Class	Est.	S.E.	p-value	Est. OR*
Race/Ethnicity	High-Declining	Low-Stable	0.84	0.35	.02	2.32 ⁺
	Low-Escalating		0.92	0.44	.04	2.51 ⁺
Reading	High-Declining	Low-Escalating	-0.08	0.54	.88	0.92 ⁺
	High-Declining	Low-Stable	-0.01	0.003	<.001	0.67 [†]
	Low-Escalating		-0.01	0.005	.03	0.67 [†]
	High-Declining	Low-Escalating	-0.001	0.005	.78	0.96 [†]

*Odds (membership in target class) : Odds (membership in reference class) among individuals in either target or reference class

⁺Calculated for Ethnicity = Black vs. Ethnicity = Non-Black[†]Calculated for a 1 SD increase in reading score

Table 6

Class-specific Model Estimated Probabilities of Nonviolent and Violent Arrests and Pair-wise Comparisons Based on 3-Class Model with Distals-as-class-indicators

Arrest Type (Overall*)	Target Class	Reference Class	Est. ⁺	Est. OR [†]	p-value
Nonviolent $(\chi^2=18.69,$ $df=2, p<.001)$	Low-Stable		.03	1.00	-
	High-Declining	Low-Stable	.24	10.21	.001
	Low-Escalating		.50	32.33	<.001
Violent $(\chi^2=18.10,$ $df=2, p<.001)$	Low Escalating	High-Declining		3.17	.04
	Low-Stable		.02	1.00	-
	High-Declining	Low-Stable	.13	7.32	.01
	Low-Escalating		.38	30.03	<.001
	Low Escalating	High-Declining		4.10	.02

*Overall test of class differences in arrest rates

[†]Pr(arrest | membership in target class)

[‡]Odds (arrest | membership in target class) : Odds (arrest | membership in reference class)

Table 7

Class-specific Model Estimated Probabilities of Nonviolent and Violent Arrests and Pair-wise Comparisons Based on 3-Class Model with Distals-as-class-consequences

Arrest Type (Overall*)	Target Class	Reference Class	Est. ⁺	Est. OR [†]	p-value
Nonviolent $(\chi^2=11.40,$ $df=2, p=.003)$	Low-Stable		.08	1.00	-
	High-Declining	Low-Stable	.21	3.06	.01
	Low-Escalating		.29	4.70	<.001
Low Escalating		High-Declining		1.54	.29
Violent $(\chi^2=5.66,$ $df=2, p=.06)$	Low-Stable		.06	1.00	-
	High-Declining	Low-Stable	.14	2.55	.06
	Low-Escalating		.19	3.67	.01
Low Escalating		High-Declining		1.44	.37

*Overall test of class differences in arrest rates

⁺Pr(arrest | membership in target class)

[†]Odds(arrest | membership in target class) : Odds(arrest | membership in reference class)

Figure Captions

Figure 1. Path diagram for an unconditional linear latent growth curve model. Model is shown with fixed times of measurement, but individually-varying times of measurement may be specified.

Figure 2. Illustration of a finite mixture of two normally-distributed subpopulations (dashed lines) and the resultant *mixed* population distribution (solid line).

Figure 3. Path diagram for a general (linear) growth mixture model with observed static antecedents (X) and consequences (Z) of change.

Figure 4. Sample average trajectory (bolded) and observed individual trajectories (random subset, n=25)

Figure 5. BIC “elbow” plots for models with distals-as-class-indicators (top) and with distals-as-class-consequences (bottom).

Figure 6. Model-estimated class-specific mean growth trajectory plots based on 3-class model with distals-as-class-indicators (top) and 3-class model with distals-as-class-consequences (bottom).















