CHAPTER 4

Group-Based Trajectory Modeling: An Overview

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INTRODUCTION

This chapter provides an overview of a group-based statistical methodology for analyzing developmental trajectories – the evolution of an outcome over age or time. A detailed account of the method's statistical underpinnings and a full range of applications are provided in Nagin (2005).

In this discussion, the term developmental trajectory is used to describe the progression of any phenomenon, whether behavioral, biological, or physical. Charting and understanding developmental trajectories is among the most fundamental and empirically important research topics in the social and behavioral sciences and medicine. A few prominent examples include: criminological analyses of the progression and causes of criminality over life stages or of time trends of reported crime across geographic locations, psychological studies of the course and antecedents of psychopathologies, sociological investigations into the interaction between human behavior and social context over time, and medical research on the impact of treatments on the progress of diseases.

Longitudinal data – data with a time-based dimension – provide the empirical foundation for the analysis of developmental trajectories. Most standard statistical approaches for analyzing developmental trajectories are designed to account for individual variability about a mean population trend. However, many of the most interesting and challenging problems in longitudinal analysis have a qualitative dimension that allows for the possibility that there are meaningful sub-groups within a population that follow distinctive developmental trajectories that are not identifiable *ex ante* based on some measured set of individual characteristics (e.g., gender or socioeconomic status). In psychology, for example, there is a long tradition of taxonomic theorizing about distinctive developmental progressions of these sub-categories. For research problems with a taxonomic dimension, the aim is to chart out the distinctive trajectories, to understand what factors account for their distinctiveness and to test whether individuals following the different trajectories also respond differently to a treatment such as a medical intervention or major life event such as the birth of a child. This chapter describes an approach, based upon a formal statistical model, for conducting group-based analysis with time- and age-based data.

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Across all application domains, this group-based statistical method lends itself to the presentation of findings in the form of easily understood graphical and tabular data summaries. In doing so, the method provides statistical researchers with a tool for figuratively painting a statistical portrait of the predictors and consequences of distinct trajectories of development. Data summaries of this form have the great advantage of being accessible to non-technical audiences and quickly comprehensible to audiences that are technically sophisticated.

AN ILLUSTRATION OF GROUP-BASED TRAJECTORY MODELING

Figure 4.1 reports a well-known application of group-based trajectory modeling that was first reported in Nagin and Tremblay (1999). It is based on the data assembled as part of a Montreal Longitudinal-Experimental Study of Boys that has tracked 1,037 males from school entry through young adulthood. Assessments were made on a wide range of factors. Among these were teacher reports of each boy's physical aggression at age 6 and again annually from age 10 to 15. The scale was based on items such as frequency of fighting and physically bullying.

The best model was found to involve four groups. A group called "lows" comprised individuals who display little or no physically aggressive behavior. This group is estimated to comprise about 15% of the sample population. A second group, comprising about 50% of the population, is best labeled "moderate declining." At age 6, boys in this group displayed a modest level of physical aggression, but by age 10 they had largely desisted. A third group, comprising about 30% of the population, is labeled "high declining." This group starts off scoring high on physical aggression at age 6 but scores far lower by age 15. Notwithstanding this marked decline, at age 15 they continue to display a modest level of physical aggression. Finally, there is a small group of "chronics," comprising less than 5% of the population, who display high levels of physical aggression throughout the observation period.

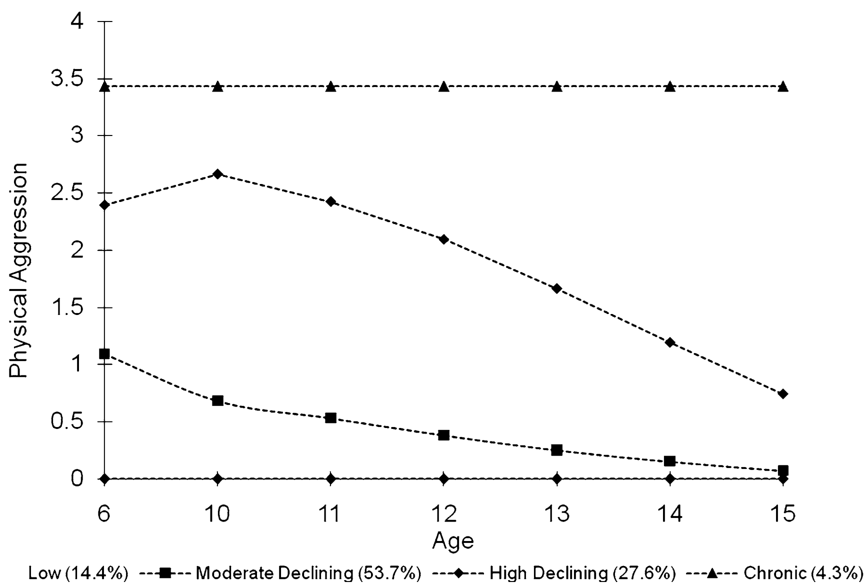

FIGURE 4.1. Trajectories of physical aggression.

Much could be said about the implications of these trajectories for the development of physical aggression but for our purposes here two implications are emphasized. One implication follows from the observation that all the trajectories are either stable or declining from the initial assessment at age 6. This implies that to understand the developmental origins of physical aggression, it is important to begin studying physical aggression at an even earlier age. A second and related observation is that the onset of physical aggression is not in adolescence as many theories of delinquent behavior suggested. See Tremblay and Nagin (2005) for a full development of these two observations.

These two points are highlighted because they illustrate the value of conducting longitudinal analysis in terms of groups. The groups can be thought of as latent longitudinal strata in the data that are composed of individuals following approximately the same development course on the outcome of interest. These strata identify distinctive longitudinal features of the data. In this application, the fact that all the trajectories are stable or declining is a feature of the data that is of great substantive significance. Further the absence of a feature, namely a trajectory reflecting the adolescent onset of physical aggression also has important substantive significance.

The group-based methodology is intended to be responsive to calls for the development of "person-based" approaches to analyzing development (Bergman 1998; Magnusson 1998). Such appeals are motivated by a desire for methods that can provide a statistical snapshot of the distinguishing characteristics and behaviors of individuals following distinctive developmental pathways. The group-based method lends itself to creating such profiles. Table 4.1 reports profiles and the characteristics of individuals following the four physical aggression trajectories shown in Fig. 4.1. As developed in Chap. 5 of Nagin (2005), the model's parameter estimates can be used to calculate the probability of an individual belonging to each of the trajectory groups. To create the profiles reported in Table 4.1, individuals were assigned to the trajectory group to which they mostly likely belonged, based on their measured history of physical aggression. The summary statistics reported in the table are simply the product of a cross-tabulation of group membership with the various individual characteristics and outcomes reported in the table.

The profiles conform to longstanding findings on the predictors and consequences of problem behaviors such as physical aggression. Individuals in the chronic aggression group tend to have the least educated parents and most frequently, score in the lowest quartile of the sample's IQ distribution. By contrast, individuals in the low aggression group are least likely to suffer from these risk factors. Further, 90% of the chronic aggression group fail to reach the eighth grade on schedule and 13% have a juvenile record by age 18. By comparison, only 19% of the low aggression group had fallen behind grade level by the eighth grade and none have a juvenile record. In between are the moderate- and high- declining groups.

TABLE 4.1. Physical aggression group profiles

	Group			
Variable	Low	Moderate declining	High declining	Chronic
Years of school – Mother	11.1	10.8	9.8	8.4
Years of school – Father	11.5	10.7	9.8	9.1
Low IQ (%)	21.6	26.8	44.5	46.4
Completed 8th grade on time (%)	80.3	64.6	31.8	6.5
Juvenile record (%)	0.0	2.0	6.0	13.3
# of sexual partners at age 17 (past year)	1.2	1.7	2.2	3.5

Table 4.1 demonstrates that trajectory group membership varies systematically with the individual's psychosocial characteristics. An important generalization of the base model that is laid out in Chap. 6 of Nagin (2005) allows for joint estimation of both the shapes of the trajectory groups and the impact of psychosocial characteristics on the probability of trajectory group membership. For example, such an analysis shows that the probability of trajectory group membership is significantly predicted by low IQ, low paternal education, and being born to a mother who began child-bearing as a teenager (Nagin and Tremblay 2001).

As noted, trajectories are not immutable. Life events or interventions may alter trajectories for the better or worse. Nagin et al. (2003) explore the effect of grade retention from age 6 to 15 on the trajectories of physical aggression shown in Fig. 4.1. They find that grade retention seems to exacerbate physical aggression in the low declining and high declining trajectory groups but has no apparent effect on the physical aggression of the extreme groups – the lows and the chronics. The model extension allowing for this sort of analysis is developed in Chap. 7 of Nagin (2005). See also Haviland et al. (2007, 2008) for a discussion of the use of propensity score matching in combination with group-based trajectory modeling in making causal inferences about the effect of life events and interventions on developmental trajectories.

A trajectory charts the progression of an outcome over age or time. The examples discussed earlier all involve the developmental course of an individual-level behavior with age. It is important to emphasize that the outcome does not have to be a behavior. Mustillo et al. (2003), for example, analyze trajectories of body mass index and van Bokhoven et al. (2005) analyze trajectories of cortisol levels. Further the unit of analysis does not have to be an individual. Weisburd et al. (2004, 2008), for example, study trajectories of reported crimes at spatial units measured at the level of the street segment. Similarly, Griffith and Chavez (2004) analyze trajectories of homicides at the level of the census track. The Weisburd et al. and Griffith and Chavez studies also demonstrate that trajectory can be measured over time as well as age. In these studies, the time metric is the calendar year. Time can also be measured relative to some fixed point in time. Christ et al. (2002) for example, measure trajectories of internet usage from the date of gaining computer access to the internet and Krishnan (2008) examine trajectories of mobile phone ring tone downloads from the date of account activation. For a recent review of studies of crime using group-based trajectory modeling, see Piquero (2008).

LIKELIHOOD FUNCTION

Group-based trajectory models are a specialized application of finite mixture models. While the conceptual aim of the analysis is to identify clusters of individuals with similar trajectories, the model's estimated parameters are not the result of a cluster analysis. Rather they are the product of maximum likelihood estimation. As such, they share the many desirable characteristics of maximum likelihood parameter estimates – they are consistent and asymptotically normally distributed (Cramèr 1946; Greene 1990; Thiel 1971).

The specific form of the likelihood function to be maximized depends on the type of data being analyzed, but all are a special form of the following underlying likelihood function: let $Y_i = \{y_{i1}, y_{i2}, \ldots, y_{iT}\}$ denote a longitudinal sequence of measurements on individual i over T periods. For expositional convenience, y_{it} will generally be described as the behavior of an individual. However, the outcome of interest doesn't have to pertain to an individual or a behavior – y_{it} can reference an entity such as a community, block face, or an organization, or it can measure a quantity such as a poverty rate or a mean salary level.

Let $P(Y_i)$ denote the probability of Y_i. As developed in Chap. 2 of Nagin (2005), for count data $P(Y_i)$ is specified as the zero-inflated Poisson distribution, for censored data it is specified as the censored normal distribution, and for binary data, it is specified as the binary logit distribution. Whatever the probability distribution, the ultimate objective is to estimate a set of parameters, Ω, that maximizes the probability of Y_i. The particular form of this parameter set is distribution specific. However, across all distributions, these parameters perform the basic function of defining the shapes of the trajectories and the probability of group membership. As in standard grow curve modeling, the shapes of the trajectories are described by a polynomial function of age or time.

If the parameters of this polynomial function were constant across population members, the expected trajectory of all population members would be identical. Neither standard growth curve methods nor the group-based method assume such homogeneity. Indeed, the assumption of homogeneity is antithetical to the objective of either approach because both aim to analyze the reason for individual differences in development. Standard growth curve modeling assumes that the parameters defining the polynomial describe only a population mean and that the trajectories of individual population members vary continuously about this mean, usually according to the multivariate normal distribution. The group-based method assumes that individual differences in trajectories can be summarized by a finite set of different polynomial functions of age or time. Each such set corresponds to a trajectory group which is hereafter indexed by j. Let $P^j(Y_i)$ denote the probability of Y_i given membership in group j, and π_j denote the probability of a randomly chosen population member belonging to group j.

If it were possible to observe group membership, the sampled individuals could be sorted by group membership and their trajectory parameters estimated with readily available Poisson, censored normal (tobit), and logit regression software packages. However, group membership is not observed. Indeed, the proportion of the population comprising each group j, π_j, is an important parameter of interest in its own right. Thus, construction of the likelihood function requires the aggregation of the J conditional likelihood functions, $P^j(Y_i)$, to form the unconditional probability of the data, Y_i:

$$P(Y_i) = \sum_{j}^{J} \pi_j P^j(Y_i) \tag{4.1}$$

where $P(Y_i)$ is the unconditional probability of observing individual i's longitudinal sequence of behavioral measurements, Y_i. It equals the sum across the J groups of the probability of Y_i given i's membership in group j weighted by the probability of membership in group j. Equation 4.1 describes what is called a "finite mixture model" because it sums across a finite number of discrete groups that comprise the population. The term "mixture" is included in the label because the statistical model specifies that the population is composed of a mixture of unobserved groups.

For given j, conditional independence is assumed for the sequential realizations of the elements of Y_i, y_{it}, over the T periods of measurement. Thus,

$$P^j(Y_i) = \prod^{T} p^j(y_{it}), \tag{4.2}$$

where $p^j(y_{it})$ is the probability distribution function of y_{it} given membership in group j.

The rationale for the conditional independence assumption deserves elaboration. This assumption implies that for each individual within a given trajectory group j, the distribution of y_{it} for period t is independent of the realized level of the outcome in prior periods, $y_{it-1}, y_{it-2}, \ldots$. Thus, $p^j(y_{it})$ does not include prior values of y_{it} in its specification. This assumption greatly reduces the complexity of an already complex model. Due to this reduction in complexity, most applications of finite mixture modeling with longitudinal data assume conditional independence for the sake of tractability.

On its face, the conditional independence assumption may seem implausible because it would seem to imply that current behavioral outcomes are uncorrelated with past outcomes. At the level of the group, which are not observed, this is indeed the case. For individuals within a given group j, behavioral outcomes over time are assumed not to be serially correlated in the sense that individual-level deviations from the group trend are uncorrelated. However, even with the assumption of conditional independence at the level of the latent group, there will still be serial dependence over time at the level of the population. Specifically, past outcomes will be correlated with current outcomes (e.g., across individuals body mass index at period t will be correlated with its value in subsequent periods). Such serial dependence results from the group specific specification of $p^j(y_{it})$. Differences in this specification across groups allow for persistent differences of the outcome variable across population members.

The conditional independence assumption is also invoked in the standard random effect model that underlies conventional growth curve models. The random effect model assumes that the sequential realizations of y_{it} are independent, conditional upon the individual's random effect. Thus, in the group-based model the conditional independence assumption is made at the level of the group, whereas in the random effect model it is invoked at the level of the individual. In this sense, the conditional independence assumption is stronger in the group-based model than in the standard random effect model. Balanced against this disadvantage is the advantage that the group-based model does not make the very strong assumption that the random effect is independently and identically distributed according to the normal distribution.

The likelihood for the entire sample of N individuals is simply the product of the individual likelihood functions of the N individuals comprising the sample:

$$L = \prod^{N} P(Y_i).$$

Intuitively, the estimation procedure for all data types identifies distinctive trajectory groups as follows. Suppose a population is composed of two distinct groups: (1) youth offenders (comprising 50% of the population) who up to age 18 have an expected offending rate, λ, of 5 and who after age 18 have a λ of 1; and (2) adult offenders, (comprising the other 50% of the population) whose offending trajectory is the reverse of that of the youth offenders – through age 18 their $\lambda = 1$ and after age 18 their λ increases to 5. Longitudinal data on the recorded offenses of a sample of individuals from this population would reveal two distinct groups: a clustering of about 50% of the sample who have had many offenses prior to 18 and relatively few offenses after age 18, and another 50% clustering with the reverse pattern.

If these data were analyzed under the assumption that the relationship between age and λ was identical across all individuals, the estimated value of λ would be a "compromise" estimate of about 3 for all ages. From this, one might mistakenly conclude that the rate of offending is invariant with age in this population. If the data were instead analyzed using the group-based approach, which specifies the likelihood function as a mixing distribution, no such mathematical "compromise" would be necessary. The parameters of one component of the mixture would effectively be used to accommodate (i.e., match) the youth offending portion of the data whose offending declines with age and another component of the mixing distribution would be available to accommodate the adult offender data whose offending increases with age.

GROUP-BASED TRAJECTORY MODELING CONTRASTED WITH STANDARD GROWTH CURVE MODELING

Hierarchical modeling (Bryk and Raudenbush 1987, 1992; Goldstein 1995), and latent curve analysis (McArdle and Epstein 1987; Meredith and Tisak 1990; Muthén 1989; Willett and Sayer 1994) are two important alternative approaches to the group-based methodology for modeling developmental processes. Like the group-based approach that is the subject of this book, these two alternatives are designed to provide a statistical tool for measuring and explaining differences across population members in their developmental course. Because all three approaches share the common goal of modeling individual-level heterogeneity in developmental trajectories, each must make technical assumptions about the distribution of trajectories in the population. It is these assumptions that distinguish the three approaches.

While the assumptions underlying hierarchical modeling and latent curve analysis differ in important respects, they also have important commonalities (MacCallum, Kim, Malarkey, and Kiecolt-Glaser 1997; Willett and Sayer 1994; Raudenbush 2001). For the purposes of this book one commonality is crucial: both model the population distribution of trajectories based on *continuous* distribution functions. Unconditional models estimate two key features of the population distribution of trajectory parameters – their mean and covariance structure. The former defines average growth within the population and the latter calibrates the variances of growth throughout the population. The conditional models are designed to explain this variability by relating trajectory parameters to one or more explanatory variables.

Modeling individual-level differences requires that assumptions be made about the distribution of trajectory parameters in the population. Both hierarchical modeling and latent curve analysis assume that the parameters are continuously distributed throughout the population according to the multivariate normal distribution. Group-based trajectory modeling takes a qualitatively different approach to modeling individual differences. Rather than assuming that the population distribution of trajectories varies continuously across individuals and in a fashion that can ultimately be explained by a multivariate normal distribution of population parameters, it assumes that there may be clusters or groupings of distinctive developmental trajectories that themselves may reflect distinctive etiologies. In some applications, the groups may be literal entities. For example, the efficacy of some drugs depends on the users' genetic make-up. However, in many other application domains, the groups should not be thought of as literally distinct entities. Rather they serve as a statistical approximation to a more complex underlying reality.

One use of finite mixture models is to approximate a continuous distribution function (Everitt and Hand 1981; Heckman and Singer 1984; McLachlan and Peel 2000; Titterington et al. 1985). Heckman and Singer (1984) built upon the approximating capability of finite mixture models to construct a nonparametric maximum likelihood estimator for the distribution of unobservables in duration models. The motivation for this seminal innovation was their observation that social science theory rarely provides theoretical guidance on the population of distribution of unobserved individual differences yet statistical models of duration data were often sensitive to the assumed form of the distribution of such differences. Their proposed estimator finessed the problem of having to specify a distribution of unobserved individual difference by approximating the distribution with a finite mixture model.

The idea of using a finite number of groups to approximate a continuous distribution is easily illustrated with an example. Suppose that Panel A in Fig. 4.2 depicts the population distribution of some behavior z. In Panel B, this same distribution is replicated and overlaid with a histogram that approximates its shape. Panel B illustrates that any continuous distribution with finite end-points can be approximated by a discrete distribution (i.e., a histogram) or alternatively by a finite number of "points of support" (i.e., the dark shaded "pillars"). A higher number of support points yields a discrete distribution that more closely approximates the true continuous distribution.

Why use groups to approximate a continuous population distribution of developmental trajectories? This brings us back to the key distinction between standard growth curve modeling and group-based trajectory modeling. Both approaches model individual trajectories with a polynomial relationship that links age to behavior. The approaches differ in their modeling strategy for incorporating population heterogeneity in the growth curve parameters (e.g., β_0, β_1, β_2, and β_3 in a cubic function of age or time). In conventional growth curve modeling, the parameters describing individual-level trajectories are assumed to be

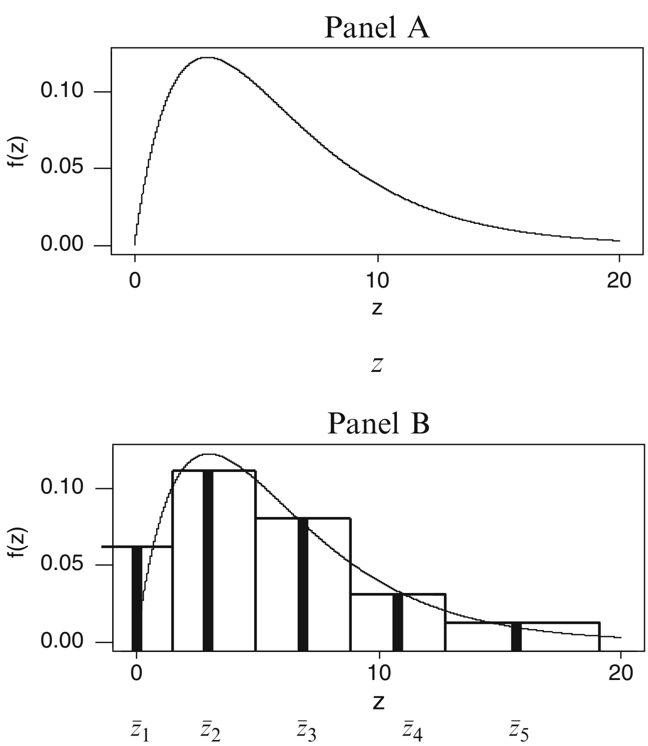

FIGURE 4.2. Using groups to approximate an unknown distribution.

distributed according to a specific function, usually the multivariate normal distribution. In the group-based trajectory model, the distribution is approximated by a finite number of trajectory groups, aka points of support.

By identifying latent strata of individuals with similar developmental trajectories, differences that may explain or at least predict individual-level heterogeneity can be expressed in terms of group differences. By contrast, a modeling strategy that assumes a continuous distribution of trajectories must explain individual level heterogeneity in terms of that distribution function. This difference has fundamental implications for the framing of the statistical analysis.

The application depicted in Fig. 4.3 may serve to illustrate the difference in approach between group-based trajectory modeling and conventional growth curve modeling. The data used in this application were also from the Montreal-based study used to estimate the trajectories of physical aggression. In this case, the trajectories are based on annual self-reports from age 11 to 17 about involvement with a delinquent gang in the past year. Application of the group-based method to this gang involvement data identified the three highly distinct groups shown in the figure (Lacourse et al. 2003). The trajectory for each group is described by the probability of gang membership at each age. One trajectory, called the never group, is estimated to comprise 74.4% of the population. This group's probability of gang membership was very small over all ages. The second group, called the childhood onset group, began at age 11 with a high probability of gang membership that modestly rises till age 14 and declines thereafter. The third group, called the adolescent onset group, had a near-zero probability of gang membership at age 11, but thereafter, the probability rose to a rate that actually exceeded that of the childhood onset group. The latter two groups are each estimated to constitute 12.8% of the sampled population.

Had standard growth curve modeling methods been applied to these data, the product of the analysis would have been entirely different. The counterpart to the results in Fig. 4.2 would have been the unconditional model which would have described the average probability trajectory of gang involvement at each age from 11 to 17 and an associated set of variance parameters measuring the population variability about this mean trajectory. Thus, the points

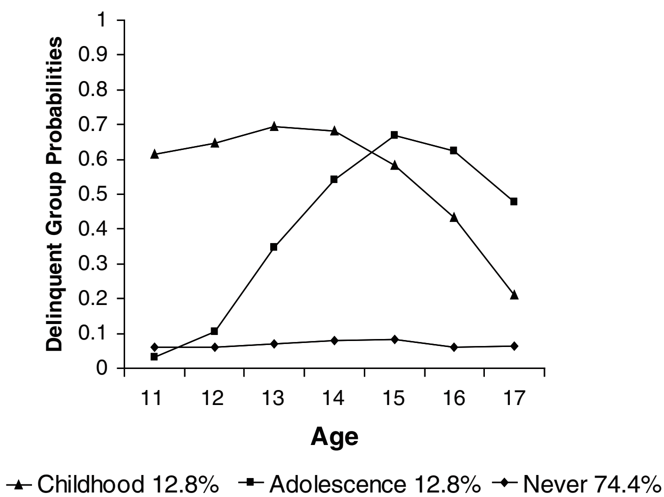

FIGURE 4.3. Trajectories of gang membership following would be the footnotes.

of departure of the two modeling approaches for drawing inferences about data are fundamentally different. The growth curve approach aims to identify the factors that account for individual variability about the population's mean trajectory of development. By contrast, the group-based approach frames questions of statistical inferences in terms of the trajectory group: what factors distinguish group membership and how do groups differ, if at all, in their response to events that might alter a trajectory?

For what types of problems is the group-based approach more appropriate than standard growth curve modeling and conversely, for what types of problems is the standard approach a better fit? This is a question without a clear answer. Still some guidelines are possible. One guideline relates to the adjective "growth" that modifies "curve modeling." The prototypical application of standard growth curve modeling involves a process in which populations members follow a common developmental pattern of either increase or decline. Raudenbush (2001) offers language acquisition as a quintessential example of such a process. Another good example is time spent with peers from childhood through adolescence (Warr 2002). Standard growth curve methods are well suited for analyzing such developmental phenomena because it is reasonable to assume that most individuals experience a common process of growth or decline, albeit at different rates. However, there are large classes of developmental phenomena for which the conception of a common growth process does not naturally fit. Raudenbush describes the population differences for this class of problems as "multinomial" and for such problems, he recommends a group-based approach as particularly appropriate. Raudenbush (2001:59) uses depression as an example. He observes: "It makes no sense to assume that everyone is increasing (or decreasing) in depression… many persons will never be high in depression, others will always be high, while others will become increasingly depressed."

The basis for Raudenbush's making a distinction between the developmental processes underlying language acquisition and depression is fundamental and cannot be overstressed. The former are appropriately analyzed by conventional analysis of variation; the latter are not. Because the vocabularies of all young children from normal populations increase with age, it is sensible to ask questions such as: What is the average growth curve of children's vocabulary over a specified age range? How large is the variation across children in their individual-level language acquisition growth curves? How do such "between person" variations relate to factors such as the child's cognitive functioning and parental education? How are "within person" changes in acquisition related to changes in interactions with primary caregivers due, for example, to parental conflict?

These questions are framed in the language of analysis of variance as reflected in the use of terms such as "within person change" and "between person change." This is only natural because standard growth curve analysis has its roots in analysis of variance. Like analysis of variance, growth curve analysis is designed to sort out factors accounting for variation about a population mean.

To meaningfully frame an analysis in the conceptual apparatus of analysis of variance requires that it be sensible to characterize population differences in terms of variation about the population mean. For processes such as language acquisition the mean trend is, in fact, a sensible statistical anchor for describing individual variability. However, for many processes evolving over time or age, it is not. For example, it makes no sense to frame a statistical analysis of population differences in the developmental progression of attention deficit disorder (ADD) in terms of variation about the mean trajectory of ADD, because ADD is the exception, not the norm, within the general population. Other examples of evolving behavioral phenomena that are not properly described in terms of variation about a population mean are most forms of psychopathology and abuse of both licit and illicit drugs. More generally, a group-based approach to analyzing longitudinal data is usefully applied to phenomena in which there may be qualitatively different trajectories of change over age or time across subpopulations that are not identifiable *ex ante* based on measured characteristics such as gender or race.

The assumption that all individuals follow a process that increases or decreases regularly within the population may also be violated because there may not be a single explanation for the differences in the developmental trajectories of subpopulation. For example, Nagin and Tremblay (2001) found that a host of predictors involving the individual's psychological make-up and family circumstances distinguished individuals following low versus high trajectories of physical aggression in childhood. However, a comparison of two distinct subpopulations of high childhood trajectories – those following a trajectory of chronic aggression versus those who started childhood with high aggression but later declined – revealed that only two maternal characteristics distinguished these groups. Using standard growth curve modeling methods, it would have been very difficult to identify this important difference in variables that distinguished among trajectories of childhood physical aggression. Identification of such differences is far easier with a methodology that clusters individuals with similar developmental trajectories.

A second guideline concerns the motivation for the analysis. One common aim of analyses of longitudinal data is to uncover distinctive developmental trends in the outcome variable of interest. For example, do sizable numbers of youths follow a trajectory of adolescent onset conduct disorder? The group-based approach is ideally suited for testing whether such distinctive patterns are present in the data. By contrast, another common aim of developmental studies is to test whether some identifiable characteristic or set of characteristics are associated with individual differences in trajectories of development. An example is whether trajectories of conduct disorder differ across sexes. For this type of problem, standard growth curve modeling provides a natural starting point for framing the statistical analysis – a comparison of the mean trajectories for boys and girls. Thus according to this second guideline, the group-based approach lends itself to analyzing questions that are framed in terms of the shape of the developmental course of the outcome of interest, whereas standard growth curve modeling lends itself to analyzing questions framed in terms of predictors of the outcome's developmental course.

A third guideline concerns the possibility of path dependencies in the response to turning point events, such as marriage, or to treatments, such as hospitalization for a psychiatric disorder. Path dependencies occur when the response to a turning point event or treatment is contingent upon the individual's developmental history. For example, Nagin et al. (2003) find that the seeming impact of grade retention on physical aggression depended upon the child's trajectory of physical aggression. The subsequent physical aggression of children who had been following trajectories of little physical aggression or of chronic physical aggression appeared to be unaffected by the event of being held back in school. By contrast, the physical aggression of individuals who had been following trajectories of declining physical aggression seemed to be exacerbated. Such path dependencies are commonplace in the literature on human development (Elder 1985). Indeed the possibility of path dependencies is a key rationale for longitudinal studies. The group-based trajectory model is well suited for identifying and testing whether the response to a turning point event or treatment is contingent upon the individual's developmental trajectory.

Laying out guidelines for the use of alternative statistical methods is a precarious exercise. Users naturally desire bright line distinctions. Yet bright line distinctions are generally not possible. The first guideline implies that developmental processes can be cleanly divided between those involving regular growth or decline and those that do not. The reality is that for many developmental processes, it is not possible to confidently make this distinction. The second guideline implies that the objective of an analysis can be classified as either identifying distinctive developmental trajectories or testing predictors of developmental trajectories. The reality is that most analyses have both objectives. Still, a further complication is that standard growth curve modeling can be used to identify distinctive developmental trajectories for *predefined* groups (e.g., races or genders) and the group-based modeling can be used to test theories about the underlying predictors and causes of population differences in developmental trajectories. The third guidelines might be interpreted as implying that it is not possible to identify path dependencies with conventional growth curve models. This is not the case. Stated differently, both methods are designed to analyze change over time. The group-based method focuses on the identification of different trajectory shapes and on examining how the prevalence of the shape and shape itself relates to predictors. By contrast, standard growth curve modeling focuses on the population mean trajectory and how individual variation about that mean relates to predictors. Thus, the alternative approaches are best thought of as complementary, not competing.

AN ALTERNATIVE CONCEPTION OF A GROUP FROM THE STRUCTURAL EQUATION MODELING TRADITION

In group-based trajectory modeling, the parameters of the polynomial function defining the mean trajectory of group j are denoted by a vector β^j. Muthén and Shedden (1999) develop an elegant and technically demanding extension of the uncensored normal model which adds random effects to the parameters, β^j, that defines a group's mean trajectory.

This extension allows the trajectories of individual-level group members to vary about the group's mean trajectory. The model for each group can be interpreted in a manner that is equivalent to that for the conventional normal-based growth curve model. The estimate of β^j defines the mean trajectory for the group and the estimate of the covariance matrix of the random effects characterizes the variation of group members' trajectories about this mean. The fundamental difference between the Muthen and Shedden model and the conventional growth curve model is that the former is comprised of multiple latent groups whereas the latter is defined by a single group.

Muthén (2001) uses the term generalized growth mixture modeling (GGMM) to label this modeling extension. The principal advantage of GGMM is that the addition of random effects may improve model fit. Balanced against this important benefit are a number of disadvantages. One is that the addition of random effects to a group-based model can result in the use of fewer trajectory groups because their addition allows for more within group heterogeneity. In group-based trajectory modeling, a group is conceptually thought of as a collection of individuals who follow approximately the same developmental trajectory. The groups correspond to the points of support in Fig. 4.2. They describe the distinctive features of the population distribution of trajectories. Population variability is captured by differences across groups in the shape and level of their trajectories. Because the trajectory groups are intended to define clusters of individuals following approximately the same developmental course, increasing within group heterogeneity can be counterproductive to this objective.

In the GGMM schema, a latent group is a population of individuals with *heterogeneous* developmental trajectories that can nonetheless be described by a single probability distribution. The population-at-large is only comprised of multiple latent groups when more than one probability distribution is required to model individual differences within the population. Stated differently, the GGMM describes population heterogeneity with multiple layers of heterogeneity. This layering of heterogeneity may serve to improve model fit but it can also result in a fundamental indeterminancy in the conception of a group because it implies that an individual belonging to group A might actually have a trajectory that more closely corresponds to the mean trajectory of group B.

The layering of heterogeneity also raises difficult issues of model identification. The challenge of identification is reflected in the work of Bauer and Curran (2003, 2004). Their analyses show that under the GGMM definition of a group, relatively modest errors in the specification of the group's probability distribution can result in mistaken inferences about the number of groups comprising the population. Specifically, one might conclude that multiple groups are required to model the population when, in fact, the population can be described by a single correctly specified probability distribution. Thus, Bauer and Curran conclude that GGMM is vulnerable to creating the illusion of groups when, in fact, there are none.

Bauer and Curran's analysis is technically sound. However, their caution about illusory groups has little relevance to the actual application of group-based trajectory modeling as developed in this chapter. In all applications of group-based modeling known to the author, the researchers are attempting to identify whether there are distinctive clusters of trajectories and, if so, whether individuals following such trajectories are distinctive in some respects. In this context, a group bears no relationship to the definition of a group analyzed by Bauer and Curran. Specifically, it is not a sub-population of *heterogeneous* individuals that can be described by a single probability distribution. Instead, it is a cluster of approximately *homogenous* individuals, in the sense that they are following about the same developmental course, who may have distinctive characteristics from other clusters of individuals following different developmental courses.

CONCLUDING REMARKS

A hallmark of modern longitudinal studies is the variety and richness of measurements that are made about the study's subjects and their circumstances. Less often acknowledged is that this abundance of information is accompanied by a difficult companion – complexity. Commonly, researchers are confronted with the dilemma of how best to explore and communicate the rich set of measurements at their disposal without becoming so bogged down in complexity that the lessons to be learned from the data are lost on them and their audience.

An important motivation for my commitment to developing and promoting the group-based trajectory method is the belief that alternative methods for analyzing development in longitudinal data sets too often leave the researcher with a Hobson's choice of balancing comprehensibility against an adequate exploration of complexity. Group-based trajectory modeling does not solve the problem of balancing comprehensibility and complexity. However, it does provide researchers with a valuable tool for identifying, summarizing, and communicating complex patterns in longitudinal data.

Summarizing data necessarily requires reduction. Reduction requires approximation. In the case of group-based models, the approximation involves the grouping of individuals who are not entirely homogenous. Balanced against this reduction error is a greatly expanded capability for creating dense, yet comprehensible, descriptions of groups of people through time.

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