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Testing and Probing Interactions in Hierarchical Linear Growth Models

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Random effects growth models provide a powerful and flexible statistical tool to behavioral researchers for the study of individual differences in stability and change over time. Within the hierarchical linear modeling (HLM) framework, the functional form of the relationship between the repeated measures and time is specified in the level 1 model. Individual variability in initial levels and in rates of change may then be modeled as a function of one or more predictor variables specified in the level 2 model. In growth models, the inclusion of a main–effect predictor at level 2 represents an implicit "cross–level" interaction with the level 1 predictor, time. While this relation is clearly recognized within the HLM literature, cross–level interactions are not often more closely investigated using classical techniques such as testing of simple slopes and computing regions of significance. Here we demonstrate that methods for testing and probing interactions in the standard regression model can be generalized to a broad class of hierarchical linear models. Within the growth model, these techniques provide essential information for interpreting specifically how the relationships of predictors to the repeated measures change over time. This approach extends naturally to the examination of multiplicative interactions between level 2 variables, which then constitute three–way cross–level interactions with time. We present analytical developments and illustrate the use of these methods using an empirical example drawn from the Longitudinal Study of Optimal Aging.

4.1 Introduction

The basic premise behind growth modeling is that a set of repeated measures observed on a given individual can be used to estimate an unobserved trajectory that is believed to have given rise to the set of repeated measures. Once estimated, these trajectories then become the primary focus of analysis. Although easy to describe, growth models can be remarkably vexing to compute. Early examples of modeling individual trajectories include Gompertz (1825); Palmer, Kawakami, and Reed (1937); and Wishart (1938). Although both ingenious and well ahead of their time, these early attempts were limited by significant statistical and computational problems. Important recent developments in statistical theory and high-speed computing have allowed us to overcome many of these earlier limitations. Thanks to the work of Bryk and Raudenbush (1987); Goldstein (1986); McArdle (1988, 1989, 1991); Meredith and Tisak (1984, 1990), D. R. Rogosa and Willett (1985), and many others, there are now several statistical approaches that can be used to estimate a broad class of random effects trajectory models.

Within the social sciences, the two primary approaches to modeling longitudinal trajectories are based on the structural equation modeling (SEM) and the hierarchical linear modeling (HLM) framework. The SEM approach defines the repeated measures to be multiple indicators of one or more latent factors that are believed to represent the unobserved underlying random trajectories (e.g., Meredith & Tisak, 1984, 1990). In contrast, the HLM approach considers the repeated measures to be nonindependent observations nested within each individual and thus treats this as a hierarchically nested data problem (e.g., Bryk & Raudenbush, 1987). It has been shown that under some conditions, the SEM and HLM approaches to modeling trajectories are analytically equivalent, whereas in others they are not (MacCallum, Kim, Malarkey, & Kielcolt-Glaser, 1997; S. Raudenbush, 2001; Willett & Sayer, 1994).

Our topic of interest here is the testing and probing of higher-order interactions in the analysis of individual trajectories from the HLM perspective. It has long been known that a HLM with a single level 1 predictor and a single level 2 predictor results in a "cross-level" interaction in the reduced form model (e.g., Equation 2.21,

S. W. Raudenbush & Bryk, 2002). Such cross-level interactions are quite common in many HLM applications, especially models of individual trajectories. Despite the fact that cross-level interactions arise from the hierarchical nature of the model, this interaction is of the very same multiplicative form as occurs in the usual ordinary least squares (OLS) regression model (e.g., Aiken & West, 1991). In OLS regression, it has become standard to test and probe such higher-order interactions; however, there is limited evidence of widespread use of these same methods within HLM in general, and in the HLM approach to trajectory modeling in particular.

We are aware of a small number of examples in which probing of cross-level interactions has been used to aid in the interpretation of results from an HLM analysis (e.g., Bryk & Raudenbush, 1987, p. 154; Singer, 1998, p. 345; Willett, Singer, & Martin, 1998, p. 423). However, even in these important examples of probing cross-level interactions, the simple slopes of the probed relations were used more descriptively and were not formally tested as is typically done in OLS regression models. We believe that routinely incorporating such probing techniques in HLM would allow researchers to more fully capitalize on the information available from the models and would strengthen inferential tests of theoretically derived hypotheses.

It is not clear why these techniques are not more widely used in HLM applications. One reason may be that, to our knowledge, it has not yet been clearly demonstrated that methods developed in OLS regression can be generalized to the HLM setting. Our first motivating goal is thus to demonstrate that the methods used for testing and probing interactions in standard OLS regression can indeed be generalized directly to HLM as well. Further, although the methods we describe here apply to a broad class of HLMs, our second goal is to focus explicitly on the analysis of individual trajectories. We argue that the testing and probing of interactions is not only of great use when interpreting complex model results, but such techniques should almost always be used when considering the effects of predictors of individual change over time. Finally, we will augment our analytical developments with the presentation of a fully worked empirical example in hopes that applied researchers might consider using these techniques in practice.

Although we focus here exclusively on the HLM approach to modeling individual trajectories, all of our developments and conclusions generalize directly to the SEM approach as well. We detail these extensions to SEM in Curran, Bauer, and Willoughby (2004). Because of the analytical overlap in the SEM and HLM approaches, there is logically much corresponding overlap between the work we discuss here and that which we presented in Curran et al. (2004). The core differences between the 2004 paper and this chapter is that here we focus exclusively on the HLM approach to modeling trajectories and, in the spirit of the topic of this book, we present a detailed worked example drawn from the empirical study of aging. Please see Curran et al. (2004) for a presentation of these ideas as manifested within the SEM approach, and for the detailed explication of an alternative empirical example.

We begin with a brief introduction to the empirical data set we will use to demonstrate our various modeling strategies. We then introduce the unconditional trajectory model followed by a conditional trajectory model with a single dichotomous predictor and a single continuous predictor. We show how these conditional models contain implicit cross–level interactions with time, and we propose methods for testing and probing these interactions as might be done in the OLS regression model. We then extend this conditional HLM to include higher–order interactions within level 2 and similarly demonstrate how to test and probe the cross–level interactions of the level 2 interaction terms with time. We conclude with a discussion of potential limitations and directions for future research.

4.1.1 Motivating Empirical Example

To demonstrate our proposed methods, we fit a series of models to data drawn from the Longitudinal Study of Optimal Aging (LSOA; see Bisconti & Bergeman, 1999, and Wallace & Bergeman, 1997, for further details). Briefly, the LSOA was designed to follow the health outcomes of older adults and consists of two subsamples of participants. At the first wave of assessment, the first subsample consisted of 250 participants over 65 years of age. Three follow–up assessments were conducted, spaced approximately 3 years apart. The second subsample consisted of 301 participants over age 55 who were followed for

a total of three waves of data collection, again spaced approximately 3 years apart. The maximum age at assessment between the two subsamples was 96 years of age. The high level of variability in age of assessment suggested that HLM would be an optimal data analysis approach. Our analyses include respondents who had complete data at their first wave of assessment, with possible missing data at later time periods ($N = 439$). Up to four repeated measures were obtained on a physical health scale scored as the sum of five items which ranged from 0 to 14 with higher values indicating worse health. Here we consider two predictors: the sex of the participant (where 0 denotes female and 1 denotes male) and perception of social support received from relatives scored as the sum of eight items which ranged from 8 to 34 with higher scores indicating greater support from relatives. Social support was grand mean centered for all analyses. The substantive questions of interest center on the trajectories of change over time in reported physical health problems and whether individual trajectories systematically vary as a function of (a) subject sex, (b) perceived social support from relatives, and (c) the interaction between sex and perceived social support.

4.1.2 The Unconditional Random Trajectory Model

The random effects trajectory model can be thought of as a two–level model: The first level estimates a model within individual across time (i.e., intraindividual change), and the second level estimates a model across individuals (i.e., interindividual differences in intraindividual change). The population level 1 (or within person) equation for the standard linear growth model is

$$y_{it} = \alpha_i + \beta_i a_{it} + \varepsilon_{it}, \tag{4.1}$$

where y_{it} is the dependent measure assessed on individual $i = 1, 2, ...N$ at timepoint $t = 1, 2, ...T$, a_{it} is the measure of time that is allowed to vary over individual i and is typically coded $a_{it} = 0, 1, ..., T_i - 1$, and ε_{it} is the random residual error for individual i at timepoint t.[1,2]

[1] Although our notation differs substantially from the standard HLM notation used by S. W. Raudenbush and Bryk (2002), we retain our current notational scheme to correspond to similar models used in the SEM trajectory model.

[2] There are many different strategies available to code the passage of time, but we do not explore these in detail here. Throughout this discussion, we utilize a

Given this formulation, α_i and β_i represent the individual specific intercept and slope of the trajectory of y_t over time for person i. These individually varying intercepts and slopes are then treated as random variables and can be expressed as a population level 2 model such that

$$\begin{aligned} \alpha_i &= \mu_\alpha + \zeta_{\alpha_i} \\ \beta_i &= \mu_\beta + \zeta_{\beta_i}. \end{aligned} \tag{4.2}$$

The level 1 and level 2 distinction is for heuristic value only, and the level 2 equations can be substituted into level 1 to result in the "reduced form" equation

$$y_{it} = [\mu_\alpha + \mu_\beta a_{it}] + [\zeta_{\alpha_i} + a_{it}\zeta_{\beta_i} + \varepsilon_{it}]. \tag{4.3}$$

From this, the population mean of y at time t can be expressed as

$$\mu_{y_t} = \mu_\alpha + \mu_\beta a_t. \tag{4.4}$$

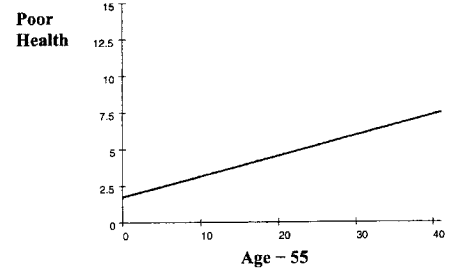
The expected values (or fixed effects) of the intercept and slope are $E(\alpha_i) = \mu_\alpha$ and $E(\beta_i) = \mu_\beta$, respectively, and these values represent the mean intercept and mean slope of the trajectory pooling over all individuals in the sample. The variances (or random effects) of the intercept and slope are $VAR(\alpha_i) = \psi_\alpha$ and $VAR(\beta_i) = \psi_\beta$, respectively, with covariance $COV(\alpha_i\beta_i) = \psi_{\alpha\beta}$, and these values represent the degree of individual variability around the mean intercept and slope values. Finally, the variance of the level 1 residual is $VAR(\varepsilon_{it}) = \sigma^2$, highlighting the standard (but not required) assumption of homoscedasticity of residuals over individual and time. This value represents the degree of error that exists in the estimation of the trajectory parameters. The analytical goal of the model is to estimate these parameters from our observed data.

To demonstrate the model in Equations 4.1 and 4.2, we fit an unconditional HLM to the four repeated measures of health perceptions from the LSOA. Time (i.e., a_{it}) was measured in years and centered

time coding scheme that begins with zero and allows for the intercept factor to be interpreted as the beginning of the trajectory. See Biesanz, Deeb-Sossa, Aubrecht, Bollen, and Curran (2004) and Metha and West (2000) for further discussion of these important issues.

at age 55 (i.e., $a_{it} = age_{it} - 55$) so that that intercept of the trajectory was defined as the model-implied value of health status at age 55 (the youngest observed age in the sample at the initial assessment). As expected, the mean of the individual intercepts ($\widehat{\mu}_\alpha = 1.74$) was significantly different from zero ($t(438) = 6.15$, $p < .0001$), indicating a significant level of health concerns even at age 55. The mean of the individual slopes ($\widehat{\mu}_\beta = .143$) was also significantly different from zero ($t(540) = 9.90$, $p < .0001$) indicating that, on average, reported health problems increased linearly[3] between age 55 and 96. The model-implied mean trajectory is presented in Fig. 4.1. Further, there was significant variability in both the intercept and slope trajectory components indicating the presence of meaningful individual differences around the mean trajectory. Thus, although the mean trajectory of health problems is increasing over time, there is substantial individual variability around this trajectory over time. We would next like to move toward predicting this individual variability as a function of sex and social support to better understand the developmental process of perceived health problems.

Figure 4.1: Model-implied mean trajectory for entire group.



[3]We also tested for the presence of a nonlinear component by adding a quadratic term to our level 1 model, but the addition of this curvilinear effect did not result in a significant improvement in model fit. We thus focus on the linear model for the remainder of the analyses.

4.1.3 A Single Dichotomous Predictor of the Random Trajectories

We again consider the level 1 and level 2 model presented in Equations 4.1 and 4.2, but we now incorporate a single categorical predictor c within the level 2 equations where $c = 0$ denotes membership in group 1 (e.g., females) and $c = 1$ denotes membership in group 2 (e.g., males). The level 1 equation remains as before (e.g., Equation 4.1), but now we express the intercept and slope as a function of the categorical predictor c such that

$$\begin{aligned} \alpha_i &= \mu_\alpha + \gamma_1 c_i + \zeta_{\alpha_i} \\ \beta_i &= \mu_\beta + \gamma_2 c_i + \zeta_{\beta_i}. \end{aligned} \tag{4.5}$$

Here, c represents a direct effect in the prediction of the intercept and slope components. We can again create a reduced form expression of the model, and with simple rearrangement of terms, the relation between c and y can be expressed as an additive function of γ_1 and the product of $\gamma_2 a_{it}$.

$$y_{it} = [\mu_\alpha + a_{it}\mu_\beta] + [\gamma_1 + \gamma_2 a_{it}]c_i + [\zeta_{\alpha_i} + a_{it}\zeta_{\beta_i} + \varepsilon_{it}] \tag{4.6}$$

We can factor our measure of time out of the equation to highlight that the model–implied mean of y at time t now includes information about group membership c such that

$$\mu_{y_t} = [\mu_\alpha + \gamma_1 c] + [\mu_\beta + \gamma_2 c]a_t. \tag{4.7}$$

Here, c interacts with time in the prediction of the repeated measures. The influence of group membership c is seen both as an increment to the intercept of the trajectory (via γ_1) and an increment to the slope of the trajectory (via γ_2). To stress, although c is a *main effect* predictor of the intercept and the slope components (i.e., Equation 4.5), c *multiplicatively interacts* with time in the prediction of the repeated measures (i.e., Equation 4.7). Thus, the single dichotomous predictor c must be treated as a two–way interaction with time.

This is more clearly expressed by considering the model–implied mean of y at time t within each of two levels of c such that

$$\begin{aligned} \mu_{y_t}|_{c=0} &= [\mu_\alpha] + [\mu_\beta]a_t \\ \mu_{y_t}|_{c=1} &= [\mu_\alpha + \gamma_1] + [\mu_\beta + \gamma_2]a_t. \end{aligned} \tag{4.8}$$

Equation 4.8 highlights several important aspects of the conditional HLM. First, in the conditional HLM, μ_α and μ_β represent the mean intercept and mean slope of the trajectory when the predictor equals zero (i.e., the mean intercept and slope for group $c = 0$). Further, γ_1 reflects the difference between the mean intercept for group $c = 1$ compared to group $c = 0$, and γ_2 reflects the difference between the mean slope for group $c = 1$ compared to group $c = 0$. Although we have a formal test of the difference in mean slopes *between* the two groups, we do not yet have an estimate of the trajectory *within* group $c = 1$.

To highlight this, we regressed the intercept and slope parameters of the health trajectories onto the single dichotomous predictor, sex, where a value of 0 denotes female and a value of 1 denotes male. Of key interest is the finding that sex significantly predicted both the intercept parameter ($\hat{\gamma}_1 = -2.17$; $t(437) = -3.22$, $p = .0014$) and the slope parameter ($\hat{\gamma}_2 = .074$; $t(539) = 2.18$, $p = .0296$), indicating that women reported higher levels of health problems at age 55 and smaller slopes over the following 40 years when compared to men. Thus, the test of $\hat{\gamma}_2$ indicates that the magnitude of the rate of change of y over time varies as a function of participant sex. However, this test does not inform us about the characteristics of the trajectories *within* each of these two groups. For this, we turn to the estimation and testing of simple slopes.

Aiken and West (1991) defined a simple slope within the OLS regression model to be the conditional relation between a predictor x and a criterion y at a given value of a second predictor z. This same definition applies to the use of a single dichotomous predictor in HLM. However, we will refer to these conditional relations between the repeated dependent measures of y and time at a given value of the predictor as *simple trajectories*, given our interest in the model–implied trajectory within each group.

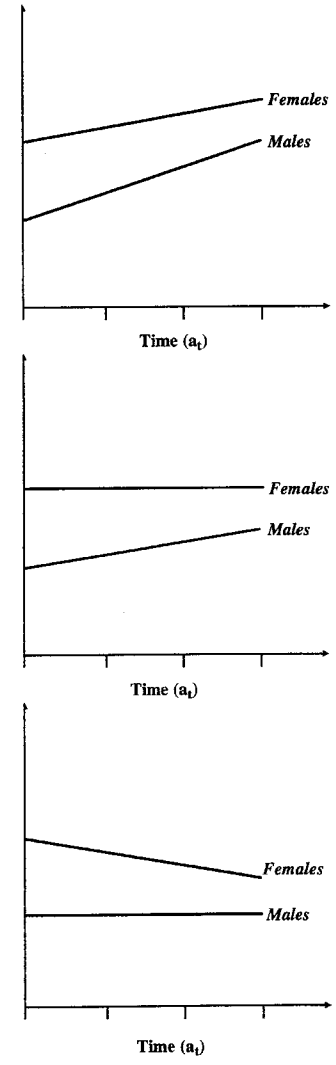
Why is consideration of the simple trajectories so important? Without considering simple trajectories within each group, we could easily find ourselves in a situation in which the simple trajectories between the two groups differ significantly from one another (i.e., the $\hat{\gamma}_1$ or $\hat{\gamma}_2$ is significantly different from zero), but one or even both simple trajectories within each group might itself not differ from zero. Figure 4.2 depicts three hypothetical situations in which there is precisely

the same difference between model–implied intercepts and slopes for males versus females, but the simple trajectories reflect fundamentally different relations within each group. The top panel reflects that the two simple trajectories are both increasing over time; the middle panel reflects that the female simple trajectory is not changing, but the male simple trajectory is increasing over time; finally, the bottom panel reflects that the female simple trajectory is decreasing over time, whereas the male simple trajectory is not changing at all. It is important to stress that for all three of these conditions, precisely the same parameter estimates hold for the regression parameters relating subject sex to the random trajectories in the conditional HLM. That is, all three have the same difference between intercepts and the same difference between slopes, yet the simple trajectories within each group are fundamentally different. It is critically important that we probe these simple trajectories further in order to gain a full understanding of the relation between time and change in y as a function of group membership.

4.1.4 Probing Simple Trajectories with a Single Dichotomous Predictor

The conditional HLM with a single dichotomous predictor provides a formal test of the magnitude of the difference between mean intercept and mean slope for group $c = 1$ compared to group $c = 0$. Our goal here is to compute the point estimates and corresponding standard errors for the simple trajectory within group $c = 0$ and the simple trajectory within group $c = 1$. There are two ways in which we can accomplish this. First, we can derive the standard errors for the simple trajectories within each group as a quadratic weighted function of the standard errors of the regression parameters predicting the random trajectories (i.e., the standard errors of $\hat{\gamma}_1$ and $\hat{\gamma}_2$). Alternatively, we can estimate two models using any standard HLM software package, and by simply recoding group membership for the two analyses, we can obtain precisely the same point estimates and standard errors for the simple trajectories as would be derived analytically.

Figure 4.2: Three possible simple trajectories all corresponding to precisely the same $\hat{\gamma}_1$ and $\hat{\gamma}_2$ regression parameters predicting intercepts and slopes.



Computation of point estimates and standard errors for simple trajectories

To maintain notation consistent with that of more complicated models to be presented later, we will consider the simple trajectory between y and time at different conditional values of c, denoting the conditional values as cv_c. A value of $cv_c = 0$ denotes the simple trajectory conditioned on membership in group 1 and $cv_c = 1$ denotes the simple trajectory conditioned on membership in group 2. Thus, the intercept and slope of the simple trajectory for conditional value cv_c is

$$\begin{aligned} \hat{\alpha}|_{cv_c} &= \hat{\mu}_\alpha + \hat{\gamma}_1 cv_c \\ \hat{\beta}|_{cv_c} &= \hat{\mu}_\beta + \hat{\gamma}_2 cv_c, \end{aligned} \tag{4.9}$$

where $\hat{\alpha}|_{cv_c}$ and $\hat{\beta}|_{cv_c}$ represent the sample estimates of the population intercept and slope values of the simple trajectory at $c = cv_c$. The standard errors of these sample estimates are

$$\begin{aligned} SE(\hat{\alpha}|_{cv_c}) &= [VAR(\hat{\mu}_\alpha) + 2cv_c COV(\hat{\mu}_\alpha, \hat{\gamma}_1) + \\ &\quad cv_c^2 VAR(\hat{\gamma}_1)]^{1/2} \\ SE(\hat{\beta}|_{cv_c}) &= [VAR(\hat{\mu}_\beta) + 2cv_c COV(\hat{\mu}_\beta, \hat{\gamma}_2) + \\ &\quad cv_c^2 VAR(\hat{\gamma}_2)]^{1/2}, \end{aligned} \tag{4.10}$$

where VAR and COV represent the appropriate variance and covariance elements from the asymptotic covariance matrix of parameter estimates (see Bauer & Curran, in press, and Curran et al., 2004, for further technical details).[4] The ratio of the sample estimate to the standard error follows a t distribution and allows for usual tests of significance. Note that for $cv_c = 0$, Equation 4.10 simplifies to

$$\begin{aligned} SE(\hat{\alpha}|_{cv_c}) &= \sqrt{VAR(\hat{\mu}_\alpha)} \\ SE(\hat{\beta}|_{cv_c}) &= \sqrt{VAR(\hat{\mu}_\beta)}, \end{aligned} \tag{4.11}$$

which are simply the standard errors for the intercept terms of the intercept and slope trajectory equations when regressed on the dichotomous predictor.[5] When $cv_c = 1$, the additional variance and covariance terms in Equation 4.10 are needed to compute the appropriate standard errors for the simple trajectories within group 2.

An equivalent method can be used to compute these same values using any standard HLM software package. Because Equation 4.10 simplifies to Equation 4.11 for $cv_c = 0$, the estimated intercept terms and associated standard errors of the intercept and slope trajectory equations from the conditional HLM represent the simple trajectory for group 1. The model can be re–estimated with group 2 coded as $cv_c = 0$ and group 1 coded as $cv_c = 1$, and the intercept terms of the intercept and slope equations now represent the simple trajectory for group 2. These point estimates and standard errors will be identical to those computed using equations 4.9 and 4.10.[6]

To demonstrate the estimation and testing of the simple trajectories, we probed the simple trajectories of health over time as a function of sex. The resulting simple trajectory for the women was $\hat{\mu}_{y_t} = 2.23 + .128a_t$ and for the men, $\hat{\mu}_{y_t} = .06 + .202a_t$. These model–implied trajectories are presented in Fig. 4.3. Importantly, only the intercept of the simple trajectory for women significantly differed from zero ($t(437) = 7.13$, $p < .0001$). The intercept for the male trajectory was nonsignificant ($t(437) = .10$, $p = .92$), implying that at age 55, men reported, on average, good overall health. The slopes from the female and male trajectories were both increasing at a significant rate ($p < .0001$). It is critical to note that only through the probing of the simple trajectories can we make these conclusions.

Regions of significance for simple slopes

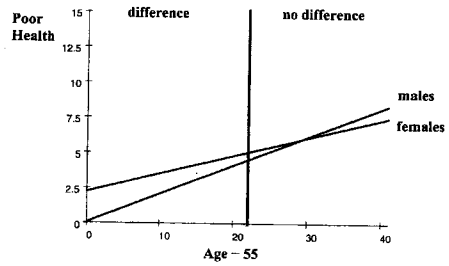
Although we can explicitly test the simple trajectories within each of the two groups (i.e., $\hat{\alpha}|_{cv_c}$ and $\hat{\beta}|_{cv_c}$), this can be extended one step

[4] All of the point estimates, standard errors, and regions of significance can be computed using online calculators at www.unc.edu/~curran.

[5] It is important to distinguish between the *intercept* of the random trajectory and the *intercept terms* of the equations that regress the random intercepts and slopes on the explanatory variable. When probing the simple trajectories across specific levels of the predictors, we are always referring to the intercept terms of the regression equations.

[6] There are other ways of testing these within software packages, including the use of two dummy vectors without an intercept term and the calculation of specific contrasts (e.g., the "estimate" command in MIXED). Here we only describe the method of multiple programs for maximal simplicity.

Figure 4.3: Model–implied simple trajectory of poor health as a function of gender.



further to derive the precise point in time when the difference between the two simple trajectories is nonsignificant. To accomplish this, we used methods originally developed by Johnson and Neyman (1936) and extended by Pothoff (1964) and D. Rogosa (1980). The middle term of Equation 4.6 highlights that the difference in μ_{y_t} (denoted Δ_y) as a function of c at any time point a_t is given as

$$\Delta_y = \gamma_1 + \gamma_2 a_t. \tag{4.12}$$

We can test the magnitude of the sample estimate of this difference by calculating the ratio of the estimate to the corresponding standard error such that

$$t_{\hat{\Delta}_y} = \frac{\hat{\Delta}_y}{\sqrt{VAR(\hat{\gamma}_1) + 2a_t COV(\hat{\gamma}_1, \hat{\gamma}_2) + a_t^2 VAR(\hat{\gamma}_2)}}, \tag{4.13}$$

in which this ratio follows a t distribution. As with t tests, an obtained value exceeding an absolute value of about 1.96 would imply a significant difference on the repeated measure y at time a_t as a function of group c (for large df). However, we can set the left side of Equation 4.13 to any desired critical t value (e.g., $t = 1.96$ to define $\alpha = .05$) and then solve for a_t. This will identify the specific points in time at which μ_{y_t} does and does not significantly differ as a function of group membership c. This is called a *region of significance.*[7]

[7]Pothoff (1964)) distinguishes between *simultaneous* and *nonsimultaneous* regions of significance. For ease of presentation, we only focus on nonsimultaneous regions here, although the computation of simultaneous regions are easily obtained (see Pothoff, 1964, Equation 3.1).

Equation 4.13 is a quadratic expression, the solution of which involves two roots (see Curran et al., 2004, for further details). The lesser and greater roots reflect the lower and upper time points at which μ_{y_t} significantly differs as a function of c, respectively. (See D. Rogosa, 1981, for a clear discussion of these calculations and interpretations within the standard regression model.) Applying Equation 4.13 to our empirical data showed that the mean of y_t significantly varied ($p < .05$) as a function of membership c when $a_t < 21.88$ and $a_t > 129.84$. Because our coding of time ranges from 0 to 41 (corresponding to the age range of 55 to 96), these results imply that women report significantly worse health than men only between ages 55 and 76.88 and that there are no statistically significant sex differences thereafter.

4.1.5 A Single Continuous Predictor of the Random Trajectories

In the conditional trajectory model presented in Equation 4.7, the random intercepts and slopes are regressed onto a single dichotomous measure c in which values were equal to either 0 or 1. There are many situations, however, in which we would like to examine the relation between a continuously distributed predictor and the random trajectories. To accomplish this, we make a simple change to Equations 4.5, 4.6, and 4.7 to include a single continuous predictor x instead of the dichotomous predictor c used earlier. Specifically, we can express the model–implied mean of y_t at time a_t as a function of continuous predictor x as

$$\mu_{y_t} = [\mu_\alpha + \gamma_1 x] + [\mu_\beta + \gamma_2 x] a_t, \tag{4.14}$$

in which all else holds as before, but now x is a continuously distributed predictor variable.[8]

Although the extension of the conditional HLM from a categorical to a continuous predictor is analytically trivial (i.e., Equation 4.7 vs.

[8]Although we are focusing on predictors that are continuously distributed, just as in multiple regression, we are not concerned about the shape of these exogenous distributions.

4.14), the corresponding interpretations are not. Whereas we were able to express the conditional equations for the simple trajectories at each of the two discrete values $c = 0$ and $c = 1$, x encompasses a range of infinite potential values, with each value resulting in a uniquely different simple trajectory describing the relation between y_t and time. That is, there is an entire *family* of simple trajectories between y_t and time across all levels of x. Although choosing specific values of x on which to compute the simple trajectory is often arbitrary, it has been recommended in standard regression to select values at one standard deviation above and below the mean of x (Aiken & West, 1991, p. 13). We will utilize these same guidelines here, although we stress that any value of x might be chosen depending on the theoretical question of interest.

Recall from the dichotomous predictor model that the intercept terms in the regression of the random trajectories on the dichotomous measure c (i.e., μ_α and μ_β in Equation 4.7) represented the model–implied means of the random trajectories when the predictor variable was equal to zero. In the presence of a continuously distributed predictor, the intercept term similarly reflects the mean of the random trajectories when the predictor equals 0, although the value 0 may or may not be interpretable with respect to the raw metric of x (i.e., a value of 0 may lie outside the logical range of x). We can "center" our predictor x so that the mean of x is equal to 0, thus increasing the interpretability of several of our model parameters. By centering, we simply deviate each individual x from the mean of x, such that $x'_i = x_i - \bar{x}$ where x_i represents the measure on variable x for individual i, $\bar{x}$ represents the mean of x over all individuals, and x'_i is the centered x. Given $\Sigma x'_i = 0$, then $\bar{x}' = 0$. Because the mean of a centered variable is by definition zero, the intercept terms of the random trajectories when regressed on the centered x'_i represent the model–implied mean initial value and mean slope of y_{it} assessed at the mean of the predictor variable x'_i. There are interpretive and sometimes computational advantages to using centered predictors in conditional trajectory models. Because of this, we will assume that all continuous predictor variables are mean centered. For ease of notation, we will refer to the centered, continuous predictor as x_i.

To demonstrate these modeling strategies, we regressed the intercept and slope trajectory components of the perceived health problems on a single continuous measure of social support (from relatives) that had been centered around the mean. In contrast to our expectations, the effect of relative support was nonsignificant in the prediction of both intercepts ($\hat{\gamma}_1 = .01$; $t(437) = .17$, $p = .87$) and slopes ($\hat{\gamma}_2 = -.002$; $t(539) = -.81$, $p = .42$). Thus, there is no statistical evidence that social support provided by relatives meaningfully predicts either initial levels of health or changes in health over time.

Because no main effect of social support was found in the prediction of the random trajectories, there is of course no need to probe this effect further. If such a main effect had been identified, it could have been probed further in precisely the same way as with the dichotomous predictor. In the next section, we describe how such a main–effect predictor of the trajectories would be further probed, but we do not demonstrate these procedures given the lack of a significant effect associated with social support. However, at the risk of spoiling the surprise, we do find an effect associated with social support in the presence of gender, and we demonstrate how to probe this in greater detail later.

4.1.6 Probing Simple Trajectories with a Single Continuous Predictor

As we described earlier, regarding the simple trajectories of y_t regressed on time within discrete group c, we can analytically derive point estimates and standard errors for simple trajectories of y_t at specific values of x. Again, we can use standard HLM software packages to compute these estimates, and we can derive regions of significance for the simple trajectories across levels of x.

Computation of standard errors for simple slopes

Equation 4.14 expressed the model–implied mean of y_t as a function of x. If using a centered predictor, $x = 0$ represents the mean of x, and thus $\hat{\mu}_\alpha$ (the intercept term of the intercept equation) and $\hat{\mu}_\beta$ (the intercept term of the slope equation) in Equation 4.14 represent the model–implied simple trajectory at the mean of x. Although there is an infinite number of simple trajectories defined at every value of x, we will focus on the simple trajectories that exist for specific conditional values of x (denoted cv_x). The sample estimates of the

model–implied intercept and slope of the simple trajectory at $x = cv_x$ is

$$\begin{aligned} \hat{\alpha}|_{cv_x} &= \hat{\mu}_\alpha + \hat{\gamma}_1 cv_x \\ \hat{\beta}|_{cv_x} &= \hat{\mu}_\beta + \hat{\gamma}_2 cv_x \end{aligned} \tag{4.15}$$

with standard errors

$$\begin{aligned} SE(\hat{\alpha}|_{cv_x}) &= [VAR(\hat{\mu}_\alpha) + 2cv_x COV(\hat{\mu}_\alpha, \hat{\gamma}_1) + \\ &\quad cv_x^2 VAR(\hat{\gamma}_1)]^(1/2) \\ SE(\hat{\beta}|_{cv_x}) &= [VAR(\hat{\mu}_\beta) + 2cv_x COV(\hat{\mu}_\beta, \hat{\gamma}_2) + \\ &\quad cv_x^2 VAR(\hat{\gamma}_2)]^(1/2), \end{aligned} \tag{4.16}$$

where VAR and COV again represent the appropriate variance and covariance elements from the asymptotic covariance matrix of sample parameter estimates. As before, the ratios of these point estimates to their corresponding standard errors follow a t distribution allowing for formal tests of significance of the intercept and slope of the simple trajectory at any given cv_x.

Using Equations 4.15 and 4.16, the sample estimates and corresponding standard errors for the simple trajectories can be computed for any desired cv_x. As in the dichotomous case, however, these same point estimates and standard errors can be obtained using any standard HLM software package. To accomplish this, we would create new variables based on our original x variable at each specific cv_x of interest such that $x_{new} = x - cv_x$. For example, when using centered predictors, our new measure of x at one standard deviation above the mean is $x_{high} = x - (1sd_x)$, at the mean is x_{medium}=$x - (0sd_x)$, and at one standard deviation below the mean is $x_{low} = x - (-1sd_x)$.[9] We then simply estimate three separate conditional HLMs, one regressing the random trajectories on x_{high}, one on x_{medium}, and one on x_{low}. As in OLS regression, each of these models will fit the data precisely the same, but the intercept terms and associated standard errors for

[9]Note that it is correct that one SD is subtracted to compute x_{high} and that one SD is added to compute x_{low}. This is because we take advantage of the fact that the intercepts of the regression equations predicting the intercept and slope factors represents the model–implied mean when all predictors are equal to zero. Thus, by *adding* one SD to all x scores, a value of zero on x represents one SD *below* the mean, and vice versa.

each of the trajectory equations represent the simple trajectory of y on time at the given level of x_{new}. As before, the resulting parameter estimates and standard errors are equal to the values that would be obtained using Equations 4.15 and 4.16.

Regions of significance for simple slopes

Just as we did for the dichotomous predictor, we can calculate regions of time over which the effect of the continuous predictor is or is not statistically significant. To demonstrate this, we can choose any arbitrary levels of the continuous predictor, say x_{high} and x_{low}, and determine the model–implied mean levels of y as a function of time:

$$\mu_{y_t}|_{x=x_{high}} = (\mu_\alpha + \gamma_1 x_{high}) + (\mu_\beta + \gamma_2 x_{high}) a_t \tag{4.17}$$

$$\mu_{y_t}|_{x=x_{low}} = (\mu_\alpha + \gamma_1 x_{low}) + (\mu_\beta + \gamma_2 x_{low}) a_t. \tag{4.18}$$

By simple subtraction, we can calculate the difference in these simple trajectories as

$$\Delta_y = (x_{high} - x_{low})(\gamma_1 + \gamma_2 a_t) \tag{4.19}$$

We can then test the magnitude of the sample estimate of this difference by calculating the ratio of the estimate to the corresponding standard error such that

$$t_{\hat{\Delta}_y} = \frac{(x_{high} - x_{low})(\hat{\gamma}_1 + \hat{\gamma}_2 a_t)}{\sqrt{(x_{high} - x_{low})^2 (VAR(\hat{\gamma}_1) + 2a_t COV(\hat{\gamma}_1, \hat{\gamma}_2) + a_t^2 VAR(\hat{\gamma}_2))}}, \tag{4.20}$$

which simplifies to

$$t_{\hat{\Delta}_y} = \frac{\hat{\gamma}_1 + \hat{\gamma}_2 a_t}{\sqrt{VAR(\hat{\gamma}_1) + 2a_t COV(\hat{\gamma}_1, \hat{\gamma}_2) + a_t^2 VAR(\hat{\gamma}_2)}}. \tag{4.21}$$

This is equivalent to Equation 4.13 and illustrates that the arbitrarily chosen values of the predictor (i.e., x_{high} and x_{low}) are unimportant for the test because they simply cancel out of the test of significance.

As before, we can set the left side of Equation 4.20 to any desired critical t value (e.g., $t = 1.96$ to define $\alpha = .05$) and then solve for a_t. This will identify the specific points in time at which the continuous predictor x does and does not significantly affect μ_{y_t}. Equation 4.13

is a quadratic expression, the solution of which involves two roots (see Curran et al., 2004, for further details). The lesser and greater roots reflect the lower and upper time points at which μ_{y_t} significantly differs as a function of x, respectively.

Again, because the interaction of social support with time was not significant in predicting health perceptions, we do not demonstrate these methods here. However, we will demonstrate these techniques in the next section when we probe the interaction of social support with gender in the prediction of health perceptions over time.

4.1.7 Categorical by Continuous Interactions in the Prediction of the Random Trajectories

Up to this point, we have only considered the estimation and testing of a single categorical or a single continuous predictor variable within the conditional HLM. We could easily extend this model to include two or more correlated predictor variables. The resulting regression parameters would be interpreted in precisely the same fashion as previously done, but these parameters would represent the unique effect of that predictor and *not* the influences of all other predictors. Our ultimate goal here, however, is not to simply estimate main effects in the prediction of the random trajectories, but to estimate higher–order interactions among our explanatory variables. We will begin by exploring the two–way interaction between a single dichotomous variable and a single continuous variable in the prediction of the random intercepts and slopes. Given that we just described how a main–effect predictor of random slopes should be treated as a two–way interaction with time, an interaction between two predictors of slopes should then logically be treated as a three–way interaction with time.

To estimate interactions between two level 2 exogenous variables in the prediction of the random intercepts and slopes, the level 1 equation (i.e., Equation 4.1) remains as before. Whereas we incorporated just main effects in the previous level 2 equations (Equation 4.7 for a dichotomous predictor and Equation 4.14 for a continuous predictor), we now add higher–order terms to represent these interactions. For example, say that we were interested in estimating the two–way interaction between a dichotomous measure c and a continuous measure x in the prediction of the random intercepts and slopes. We would expand the level 2 equations to contain these higher–order interactions such that

$$\begin{aligned} \alpha_i &= \mu_\alpha + \gamma_1 c_i + \gamma_2 x_i + \gamma_3 c_i x_i + \zeta_{\alpha_i} \\ \beta_i &= \mu_\beta + \gamma_4 c_i + \gamma_5 x_i + \gamma_6 c_i x_i + \zeta_{\beta_i}, \end{aligned} \tag{4.22}$$

Just as we substituted the level 2 equations into the level 1 equation to derive the reduced form expressions earlier, we can do this same substitution here. The reduced form equation, however, is becoming an increasingly unwieldy expression in scalar terms, and we will thus not present this here. The important point to recognize is that although we are estimating a two–way interaction between c and x in the prediction of β_i, we substitute this level 2 equation back into the level 1 equation in the prediction of y. Thus, the entire equation for β_i is multiplied by time, resulting in the three–way interaction term $\gamma_6 c_i x_i a_{it}$. This, of course, is the standard cross–level interaction in general HLMs. It is important to remember, however, that the two–way interaction between the level 2 variables in the prediction of the random trajectories must be treated as a three–way interaction between the level 2 variables and time.

As with our usual regression model, we test the interaction between our two predictors by examining the unique contribution of the multiplicative term above and beyond the contribution of the two corresponding main effects (see Cohen, 1978, for a detailed exposition on this). If the interaction between c and x is significant, it must be probed to fully understand the nature of this relation. Given that this two–way interaction itself interacts with time, we must probe this effect as we would with a standard three–way interaction. The statistical question that we are asking is, "What is the relation between y_t and a_t as a function of x within group c?" The corresponding substantive question that we are asking is, "Do trajectories of perceived health status vary over time as a function of social support, and does the magnitude of this relation depend on whether the individual is male or female?" To answer these questions, we must extend the methods for probing simple trajectories to incorporate these higher–order interactions.

Conceptually, this extension involves probing the relation between a continuous measure x and the random trajectories (as we discussed, but did not demonstrate, earlier), but we are now going to probe

these effects within each group c. So, there will be one set of simple trajectories between y_t and a_t across levels of x for $c = 0$, and one set of simple trajectories between y_t and a_t across levels of x for $c = 1$. The model–implied mean of y at time t is thus

$$\mu_{y_t} = (\mu_\alpha + \gamma_1 c + \gamma_2 x + \gamma_3 cx) + (\mu_\beta + \gamma_4 c + \gamma_5 x + \gamma_6 cx)\, a_t. \quad (4.23)$$

Expansion and rearrangement of terms highlights that the simple trajectories between y_t and a_t as a function of x within group c are

$$\begin{aligned} \mu_{y_t}|_{c=0} &= (\mu_\alpha + \gamma_2 x) + (\mu_\beta + \gamma_5 x)\, a_t \\ \mu_{y_t}|_{c=1} &= ((\mu_\alpha + \gamma_1) + (\gamma_2 + \gamma_3)\, x) + \\ &\quad ((\mu_\beta + \gamma_4) + (\gamma_5 + \gamma_6)\, x)\, a_t. \end{aligned} \quad (4.24)$$

Note that within group $c = 0$, the relation between y_t and a_t varies as a function of x in precisely the same way as expressed in Equation 4.14. However, in group $c = 1$, additional influences are incorporated (i.e., γ_1, γ_3, γ_4, and γ_6) to account for the interaction between x and time as a function of membership in group $c = 1$. In other words, there is a two–way interaction between x and time in the prediction of y_t, and this interaction itself interacts with group membership c. Our goal now is to test and probe this three–way interaction.

The formal test of the interaction is simply the test of γ_3 and γ_6. The significance of these terms implies that the relation between x and the growth trajectories depends, in part, on group membership c. To demonstrate this, we regressed the intercept and slope parameters of the health trajectories on three predictors: the dichotomous variable sex; the centered, continuous measure of social support from relatives; and the multiplicative interaction between these two measures. Importantly, the two–way interaction between sex and social support from relatives significantly predicted both the intercept and slope parameters ($p < .05$). These parameter estimates are presented in Table 4.1. We must now probe this interaction further to better understand the nature of this effect, bearing in mind that this two–way interaction itself interacts with time in the reduced form equation and must thus be treated as a three–way interaction.

To formally probe these effects, we need to compute the sample estimates for the intercept and the slope of the model–implied simple trajectories of y on a_t at the conditional level of x (i.e., cv_x) within the

Table 4.1: Parameter Estimates From the Main Effects and Two–Way Interaction Predicting the Random Intercepts and Slopes.

Predictor Variable	*Random Intercept*	*Random Slope*
Sex	−2.31	.082
Time 1 Support From Relatives	**.043**	**−.005**
Sex by Relative Support	−.342	.018
Intercept Term of the Prediction Equation	2.289	.124

Note: Model results are based on $n = 439$. All effects are significant at $p < .05$ except for the two parameters presented in bold.

conditional level of group c (i.e., cv_c). Re–expressing Equation 4.23, given conditional values of cv_x and cv_c, results in the sample estimates of the intercept and slope of the simple trajectory as

$$\begin{aligned} \hat{\alpha}|_{cv_x, cv_c} &= \hat{\mu}_\alpha + \hat{\gamma}_1 cv_c + \hat{\gamma}_2 cv_x + \hat{\gamma}_3 cv_c cv_x \\ \hat{\beta}|_{cv_x, cv_c} &= \hat{\mu}_\beta + \hat{\gamma}_4 cv_c + \hat{\gamma}_5 cv_x + \hat{\gamma}_6 cv_c cv_x, \end{aligned} \quad (4.25)$$

respectively. The standard errors for these point estimates are complex and are presented in Curran et al. (2004). As before, the ratio of the point estimate to standard error follows a t distribution allowing for the usual tests of significance.

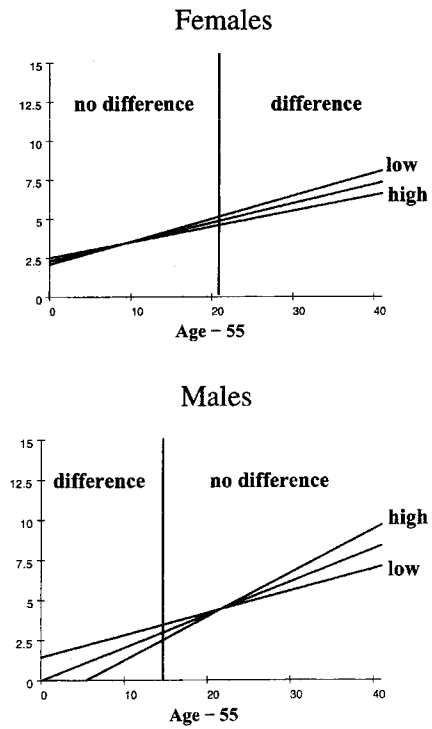
We can also compute these point estimates and standard errors using the computer methods described earlier in this chapter. Specifically, to probe the simple trajectories of y_t at plus and minus 1 standard deviation around the mean of x within each of the two groups c, we would estimate a total of six conditional HLMs. Three HLMs would estimate the effect of x_{low}, x_{medium}, and x_{high} with group 1 coded as $cv_c = 0$, and three would repeat the process with group 2 coded as $cv_c = 0$. A model would be estimated for each combination of conditional main effects and their interaction (e.g., the main effect of cv_c, the main effect of cv_x, and the interaction between cv_c and cv_x). From each of these models, the sample estimates of the intercept terms of the random trajectory equations (i.e., $\hat{\mu}_\alpha$ and $\hat{\mu}_\beta$) represent the model–implied simple trajectory and appropriate standard error for each combination of conditional cv_c and cv_x values.

Using this technique, we probed the simple trajectories of health perceptions one standard deviation above and below the mean of social support from relatives within each sex. The simple trajectories for each combination are plotted in Fig. 4.4. Several interesting characteristics are evident. First, for women, we see that family support appears to have little effect either on intercepts or slopes. That is, trajectories of health problems are significantly increasing over time, but the starting point and rate of change does not appear to vary as a function of family support within females. In contrast, there is greater evidence that the trajectories of health problems in men do vary as a function of support from relatives. Specifically, men with higher levels of social support from relatives showed steeper increases in self–reported physical health problems than those with lower levels of social support.

Thus, although there was not evidence for an overall main effect of family support in the prediction of trajectories of health problems, evidence was found when considering the interactive effects of family support and gender. There are two interesting issues here, however. First, although nonsignificant, the intercepts of two of the simple trajectories for males are negative, which, given the scaling of the measure, are impossible values. This might imply some model misfit of the growth trajectory function for males or reflect unreliable estimation in this part of the trajectory; either way, these negative intercepts would not have been identified without the further probing of this relation. Second, it is potentially theoretically inconsistent to conclude that males reporting higher levels of social support also report greater increases in health problems when the opposite relation holds in females. To better understand both of these issues, we can probe this interaction one step further by computing regions of significance.

The computational formulae for the regions of significance are more complex with the additional terms involved, but represent a direct extension of Equation 4.20, so we do not present them here (see Curran et al., 2004, technical appendix, for further details). For females, the lower and upper boundaries of the region of significance are 21.10 and 35.35. Because our coding of time ranges from 0 to 41 (corresponding to the age range of 55 to 96), these results imply that relative support significantly reduces the perceived health

Figure 4.4: Model–implied simple trajectories for high, medium, and low values of social support as a function of gender.



problems of women between ages 76.10 and 90.35 years of age. After this point, our estimate of the effect of social support is too imprecise (i.e., the standard error is too large) to be statistically significant. For males, the lower and upper boundaries of the region of significance are -447.09 and 13.14. Given our coding of time, these results imply that social support significantly reduces the perceived health problems of men between ages 55 and 68.14 years of age. This additional information helps us understand the earlier apparent contradiction. Specifically, higher levels of social support are associated with better overall health for women *later* in the aging process, whereas higher levels of social support are associated with better overall health for men *earlier* in the aging process. From the point of view of substantive theory, this is critical information that would not be available without these additional analyses.

4.1.8 Continuous by Continuous Interactions in the Prediction of the Random Trajectories

Whereas our previous discussion focused on the interaction between a continuous predictor x and a dichotomous predictor c, we can instead consider the interaction between two continuous predictors denoted x and w. In this case, the model–implied mean of y at time t is

$$\begin{aligned} \mu_{y_t} &= (\mu_\alpha + \gamma_1 w + \gamma_2 x + \gamma_3 wx) + \\ &\quad (\mu_\beta + \gamma_4 w + \gamma_5 x + \gamma_6 wx)\, a_t. \end{aligned} \tag{4.26}$$

Whereas previously we probed the simple trajectories at conditional values of x_{low}, x_{medium}, and x_{high} within each of two groups cv_c, we now consider these same simple trajectories between y_t and time at conditional values of x (i.e., cv_x; namely, x_{low}, x_{medium}, x_{high}) across conditional values of w (i.e., cv_w; namely, w_{low}, w_{medium}, w_{high}). To accomplish this, we modify Equation 4.25 such that the sample estimates for the model–implied intercept and slope of the simple trajectory at a given conditional value of cv_x and cv_w is

$$\begin{aligned} \hat{\alpha}|_{cv_x, cv_w} &= \hat{\mu}_\alpha + \hat{\gamma}_1 cv_w + \hat{\gamma}_2 cv_x + \hat{\gamma}_3 cv_w cv_x \\ \hat{\beta}|_{cv_x, cv_w} &= \hat{\mu}_\beta + \hat{\gamma}_4 cv_w + \hat{\gamma}_5 cv_x + \hat{\gamma}_6 cv_w cv_x \end{aligned} \tag{4.27}$$

The standard errors for these sample estimates are similar to those with a dichotomous–by–continuous interaction and are presented in (Curran et al., 2004).

As with the earlier case, we can calculate these point estimates and standard errors using any standard HLM software package. Here, however, we must estimate nine separate conditional HLMs, three for each cv_x of interest evaluated at each cv_w of interest (e.g., x_{low} evaluated at w_{low}, w_{medium}, and w_{high}, etc.). The resulting sample estimates and standard errors for the simple trajectories will correspond to those derived in Curran et al. (2004).

We could extend the results from the two–way interaction in a number of interesting and straightforward ways. For example, we could again compute the regions of significance for the simple trajectory between y_t and time across values of x within each group membership c or across continuous values of w. To accomplish this, we would create the ratio of the point estimate of the simple trajectory to the appropriate standard error and solve for cv_x or cv_w. Further, we could test the equality of intercepts or slopes from any two simple trajectories taken at any conditional value of cv_x, cv_w, or cv_c. For example, we might like to formally test the equality of the slopes of the simple trajectory of perceived health at low levels of social support for males compared with females. We could easily include one or more control variables in the model, and all of these procedures could be directly applied to test and probe simple trajectories above and beyond the influence of covariates. Finally, all of these values can be computed using online calculators described in Preacher, Curran, and Bauer (in press).

4.2 Conclusion

Hierarchical linear modeling provides a powerful and flexible method for testing a variety of theoretical questions about individual differences in developmental trajectories over time. A set of particularly intriguing applications is the incorporation of one or more explanatory variables used to predict the random trajectory components. Of course, it has long been known in the HLM literature that the main–effect prediction of the random trajectories often involves a cross–level interaction with time. There is less evidence, however,

that the presence of this interaction has been fully capitalized in HLM applications. Specifically, we are aware of no published literature that has drawn on classic methods to test and probe interactions in HLM that are commonly used in standard OLS regression. Here we have demonstrated that the methods used to probe interactions in OLS regression can be generalized directly to HLM as well. Further, our empirical example has highlighted what we believe to be significant advantages associated with the use of these techniques in practice. Indeed, based on our own experiences with these models, we recommend these methods be used anytime one or more explanatory variables are used in HLM growth models. This will not only enhance our ability to more fully understand complex models, but will also allow for the formal testing of additional types of research hypotheses in ways not possible without the use of such techniques.

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