**Abstract:** The primary purpose of this manuscript is to provide an overview of multilevel modeling to readers and contributors to Psychosomatic Medicine. The manuscript begins with a general introduction to multilevel modeling. Multilevel regression modeling at two-levels is emphasized because of its prevalence in psychosomatic medicine research. Simulated datasets based on some core ideas from the Familias Unidas effectiveness study are used to illustrate key concepts including: communication of model specification, parameter interpretation, sample size and power, and missing data. Input and key output files from Mplus and SAS are provided. A cluster randomized trial with repeated measures (i.e., three-level regression model) is then briefly presented with simulated data based on some core ideas from a cognitive behavioral stress management intervention in prostate cancer.
Dr. Kop:

Enclosed is an invited Statistical Corner submission to *Psychosomatic Medicine* entitled: Multilevel Modeling in Psychosomatic Medicine Research.

Maria Llabre invited me to submit such a manuscript in April 2011. I came to understand that a main goal in seeking such a manuscript was that clinicians (who may not be used reading/writing such papers) could use this paper as a reference to interpret similar submissions/publications in *Psychosomatic Medicine*. I also came to understand that adding more detailed instructional Appendices that could be placed on the *Psychosomatic Medicine* website may be welcomed.

My co-authors and I, therefore, structured the manuscript as described below.

pp. 0-39 non-appendices (print copy)

- Word Count = 9293. Number of Tables = 2. Number of Figures = 2.
- Number of Appendices = 3.

- pp. 46-64 Appendix B, Supplemental path diagrams (38), equations, and text (website)
- pp. 65-93 Appendix C, Input and key output from *Mplus* and *SAS* (website)

I will serve as the corresponding author for this manuscript. Authors listed in the byline have agreed to the given order and to the submission of the manuscript in the current form. I assume responsibility for keeping the authors informed of our progress through the editorial review process, the content of the reviews, and any revisions made.

Thank you for considering our manuscript for publication in the Statistical Corner section of *Psychosomatic Medicine*.

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Multilevel Modeling in Psychosomatic Medicine Research


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Abstract

The primary purpose of this manuscript is to provide an overview of multilevel modeling to readers and contributors to *Psychosomatic Medicine*. The manuscript begins with a general introduction to multilevel modeling. Multilevel regression modeling at two-levels is emphasized because of its prevalence in psychosomatic medicine research. Simulated datasets based on some core ideas from the Familias Unidas effectiveness study are used to illustrate key concepts including: communication of model specification, parameter interpretation, sample size and power, and missing data. Input and key output files from *Mplus* and SAS are provided. A cluster randomized trial with repeated measures (i.e., three-level regression model) is then briefly presented with simulated data based on some core ideas from a cognitive behavioral stress management intervention in prostate cancer.

**Keywords:** mixed regression models; random coefficient models; hierarchical linear models; centering, power, missing data.

**MLM(s)** = multilevel model(s); **MLRM(s)** = multilevel regression model(s); **MLSMs** = multilevel structural equation model(s); **RAS** = raw score; **GMC** = grand mean centering; **CWC** = centering within cluster; **RSB** = risky sexual behavior; **PA** = perceived peer abstinence; **SF** = adolescent functioning in school; **GAP** = gap between parental and adolescents Americanism; **FAM** = family functioning; **ICC** = intraclass correlation coefficient; **ML** = maximum likelihood; **CBSM** = cognitive-behavioral stress management; **A** = time; **W** = treatment condition.
Multilevel Modeling in Psychosomatic Medicine Research

Multilevel data, sometimes referred to as hierarchical data, are common in psychosomatic research. A common hierarchical structure has repeated observations nested within participants (1,2). Time-varying data from the repeated observations constitute Level-1 variables, while time-invariant data from the individual participants constitute the Level-2 variables. A multilevel model (MLM) can be defined as a statistical model that has two or more distinct hierarchical levels, with variables at each of these levels, and a theoretical interest in relationships at one or more of, or across, these levels (3).

Cross-sectional data can also be viewed as multilevel. For example, data may be collected from patients who are receiving treatment for the same illness within different hospitals. Or, with respect to behavioral interventions, patients may receive a psychological treatment from different therapists. Suppose that the relevant population of hospitals (or therapists) was viewed as large and that some of the randomly sampled hospitals were assigned to an experimental treatment condition while other hospitals were assigned to the control condition (i.e., treatment as usual). From a conceptual perspective, variability in patient outcomes may be attributable to both patient-level characteristics (e.g., severity of condition) as well as hospital-level characteristics (e.g., experimental treatment versus control condition). A MLM enables researchers to partition variability in the outcome(s) by level (e.g., patient- and hospital-level) and allows for modeling within and across these levels simultaneously.

From a statistical perspective, a key concern is to what degree the assumption of independence of observations is violated. If the outcome measure for a patient who receives treatment at Hospital A is more similar to the outcome measures for other patients at Hospital A than to the outcomes for a patient at Hospital B, the independence assumption is violated. When this non-independence is non-trivial and is attributable to at least one cluster variable (e.g., the
hospital; the therapist), imposing a fixed effects model that ignores the non-independence is often problematic from both an empirical perspective (e.g., increased Type I error) and a theoretical perspective (e.g., inability to model relationships at, and across, different levels).

A review of *Psychosomatic Medicine* from 2006-2010 revealed that 33 studies utilized a MLM (see Appendix A). There is considerable variability within this set of studies, and across applications of MLMs in other disciplines (4), with regard to some core methodological issues: communication of model specification, parameter interpretation, sample size and power, and missing data. Modern approaches to address these core methodological issues are illustrated with example datasets in this manuscript (i.e., Example 1: Familias Unidas; Example 2: Stress Management). Prior to these illustrations we provide a brief general introduction to MLMs.

**MLMs: A Brief Introduction**

Researchers may recognize MLMs from multiple labels including mixed models, random coefficient models, covariance components models, and hierarchical linear and non-linear models. We adopt the nomenclature of Hox and Roberts (1) and classify MLMs into two groups: multilevel regression models (MLRM)s and multilevel structural equation models (MLSM)s. MLRM>s have an observed outcome or outcomes at Level-1, regression coefficients as outcomes at Level-2 and above, and generally observed independent variables. MLSM>s have latent or observed outcomes at each level, latent or observed independent variables, and greater flexibility than MLRM>s with regard to the path models that may be imposed. There are types of MLM>s, however, that do not fit neatly into either category (e.g., multilevel survival analysis).

Multilevel substantive theories predated the ability to estimate what are currently considered MLM>s (5-7). MLM>s were conceptualized only a few decades ago and initially based on MLRM>s (8-9). Initial algorithms that were implemented for the estimation of these models
followed (10-13). In the late 1980s and early 1990s, several MLM texts were presented (14-16). In each of these texts, a primary focus was given to cross-sectional and/or longitudinal two-level linear regression models. Application of this type of MLM is most common within Psychosomatic Medicine (see Appendix A). Therefore, this manuscript primarily focuses on this particular implementation of a MLRM unless otherwise noted.

**MLM Notation and Software**

As with any quantitative methodology with more than one set of contributors, notation, terminology, and software for MLM vary. Notation and terminology used in this manuscript are most consistent with Raudenbush and Bryk (17), which is consistent with the studies listed in Appendix A. The software used for demonstration is Mplus (18) and SAS (19) but many other software options are available (20).

Consider the notation for independent variables in MLMs. Independent variables at Level-1 are denoted $X_{qij}$, where $q$ identifies the variable (e.g., $X_{1ij}$, $X_{2ij}$, . . . , $X_{kij}$). The subscript $i$ denotes a particular observation at Level-1. The subscript $j$ denotes a particular cluster at Level-2. In the repeated measures example, $X_{111}$ identifies variable $X_1$ measured at time 1 for person 1. In a cross-sectional example, $X_{111}$ identifies variable $X_1$ measured for person 1 within hospital 1. Independent variables at Level-2 are often denoted in one of two ways. When a variable is measured at Level-2, it is denoted $W_{qsj}$, where $q$ communicates which Level-1 coefficient, $\beta_{qij}$, a given variable was specified to predict and $s$ uniquely identifies the variable (e.g., $W_{q1j}$, $W_{q2j}$, etc.). When a variable is measured at Level-1 and then aggregated at Level-2, it is denoted as $\bar{X}_{qs,j}$ to make clear that observations of the variable were aggregated across $i$ individuals within each $j$ group (or across $i$ time points within each $j$ person). Fixed effects at Level-2, $\gamma_{qs}$, adopt the
previously defined subscript notation. Subscripts are dropped in this manuscript when their function is redundant.

**Centering Predictors in MLMs**

Centering predictors is an important aspect of MLMs that has long been misunderstood (21). Manifestations of such misunderstanding include omission of centering decisions in published papers (rendering regression coefficients impossible to interpret) and basing centering decisions on only empirical information (e.g., trying various centering options in search of statistical significance). Centering Level-1 predictors should be informed by substantive multilevel theory, well-defined research questions, and empirical information. While a full review of centering Level-1 predictors is beyond the scope of this manuscript, thorough reviews are available elsewhere (22,23).

Parallel in time to the publication of initial texts on MLMs, a literature emerged on the consequences of centering Level-1 predictors within MLMs (24-28). Primary options debated were the use of raw scores (RAS; no centering), grand mean centering (GMC; subtracting the mean across all Level-1 observations from each observation), and centering within cluster (CWC; subtracting the group mean within each cluster from each observation within the relevant cluster). Within this manuscript, GMC will be communicated as follows $X_{qij} - \overline{X}_q$ at Level-1 and $\overline{X}_{qs,j} - \overline{X}_{qs}$ at Level-2, where a double bar indicates the mean of the group means. CWC will be denoted $X_{qij} - \overline{X}_{q\cdot j}$; CWC does not apply at Level-2 because there are no upper-level units for these observations to be nested within (i.e., Level-3).

Kreft, de Leeuw, and Aiken (29) mathematically defined conditions under which imposing different centering options (RAS, GMC, and CWC) for Level-1 predictors in two common specifications of MLMs resulted in theoretically equivalent models. The two models of
primary focus were (a) random coefficients regression and (b) intercepts and slopes as outcomes – both of these models are introduced in the subsequent section. Within both models, RAS and GMC are equivalent to each other and nonequivalent to CWC. That two parameterizations of a MLM, which differ only by centering decision(s), are statistically equivalent does not necessarily mean that both models do an equally good job of representing specific research questions and/or theory-driven hypotheses – a point that will be made clear in the Familias Unidas example.

**Example 1: Familias Unidas**

The HIV epidemic constitutes a major public health concern in the U.S. and around the globe. Although HIV has affected persons of all ages, from 2005 to 2008, the rates of HIV infection for those 15-19 years of age have increased (30). The prevalence of unprotected sexual intercourse among adolescents is one of the factors responsible for the high incidence of new HIV cases. Results from The CDC’s Youth Risk Behavior Surveillance Survey indicate that 46% of high school students reported having had sexual intercourse, and 13.8% reported four or more lifetime sexual partners (31). Although these national statistics are alarming, what may be even more disconcerting is that Hispanics, the largest and fastest growing minority group in the United States (31), appear to be at heightened risk for engaging in HIV risk behaviors, including unprotected sexual behavior, and consequently at disproportionate risk of HIV infection (32).

Ecodevelopmental theory is a conceptual framework that has been put forth to explain risk and protective processes linked to HIV risk behaviors in Hispanic youth (33-35). Risky sexual behavior (RSB) is a primary health outcome within an ecodevelopmental model predicting HIV risk behaviors. Theory-based predictors of RSB include perceived peer abstinence (PA), adolescent functioning in school (SF), parental and adolescent Americanism gap (GAP), and family functioning (FAM).
Ecodevelopmental theory data are often collected within middle schools and/or high schools, where only one adolescent per family is sampled. Sampling through schools provides researchers with access to a large number of adolescents but also introduces the possibility that the data collected may be non-independent. From a statistical perspective, risky sexual behavior is measured at Level-1 (i.e., adolescent) but these data may be non-independent based on the school (i.e., Level-2) that an adolescent is nested within. From a conceptual perspective, risky sexual behavior may be partially explained by independent variables at Level-1 (e.g., family functioning), Level-2 (e.g., average gap between parental and adolescents Americanism at the school-level), and cross-level interactions (e.g., family functioning* average gap between parental and adolescents Americanism at the school-level).

The first example dataset was simulated based on some core ideas from an ongoing randomized trial evaluating the relative effectiveness of Familias Unidas (36). In the Familias Unidas effectiveness study, a total of 744 Hispanic youth and their parents are being recruited from 24 middle schools in Miami-Dade County. Participants are assessed at baseline, randomized to either Familias Unidas or a Community Practice control condition, and reassessed at 6, 18, and 30-months post baseline. In a preliminary baseline dataset, adolescents \( N = 460 \) were nested within middle schools \( J = 16 \) and within-cluster size was unbalanced \( \bar{n}_j = 28.75 \) with the smallest school having 22 adolescents and the largest school having 32 adolescents.

A larger dataset using some characteristics from the Familias Unidas dataset was created because multilevel modeling generally is a large sample technique (37); a point that will be elaborated upon in the section on sample size and power. In the simulated dataset (i.e., dataset_1), adolescents \( N = 2869 \) were nested within schools \( J = 100 \) and within-cluster size
was unbalanced ($\bar{n}_j = 28.69$) with the smallest cluster having 22 observations and the largest cluster having 32 observations.¹

**MLRM and Familias Unidas**

The Familias Unidas simulated dataset is used to illustrate key concepts in a MLRM including: communication of model specification, parameter interpretation, sample size and power, and missing data. Model specification follows the general strategy outlined in Raudenbush and Bryk (17) where MLRMs are introduced by way of six “sub-models.” In practice, a single MLM may be fitted when sufficient a priori theory exists, but proceeding in this incremental way is consistent with the purpose of this manuscript. For spatial reasons, however, most of these sub-models (i.e., Model 2: Means as Outcomes Regression Model; Model 3: One-Way ANCOVA with Random Effects; Model 4: Non-Randomly Varying Slopes; Model 5: Random Coefficients Regression) are elaborated upon in Appendix B only (along with Equation 2, Equation 3, Equation 4, and Equation 5). The first four models are random intercept models. The final two models are random intercepts and slopes models.

Communication of model specification is provided in equation form and also via a path diagram. Each equation is written in uncombined form with variable acronyms (e.g., $RSB_{ij}$) and then in combined form with general notation (e.g., $Y_{ij}$) in Appendix B. The uncombined equation is a way to emphasize the meaning of the parameters by writing equations at each level. The combined equation is an equivalent, compact expression that collapses the uncombined equation across levels. An interpretation of only key terms (to reduce redundancy) follows each equation. The causal language used (e.g., effect) communicates the direction of the relationship assumed by the model specification. In practice, any causal inference would also need to account for design considerations and substantive theory in addition to the model specification. A path
diagram of each model specification (38) is also provided in Appendix B (see Figures 1-6).

Providing path diagrams in addition to equations is done to provide future researchers with options for how to succinctly and clearly communicate model specification.

**Model 1: One-Way ANOVA with Random Effects**

A primary purpose of Model 1 is to partition the unconditional variance in the outcome(s) by level to assess the degree of non-independence of observations. Degree of non-independence is typically assessed by the intraclass correlation coefficient: \( ICC = \frac{\tau_{00}}{\tau_{00} + \sigma^2} \). Simulation research has shown potential consequences (e.g., inflated Type I) of ignoring the non-independence (e.g., imposing a fixed effects model) when the ICC is as small as .05 (39).

This model is fully unconditional in that there are no predictors at either level. This model can be written:

\[
\begin{align*}
RSB_{ij} &= \beta_{0j} + r_{ij} \\
\beta_{0j} &= \gamma_{00} + u_{0j}
\end{align*}
\]

(1)

- \( RSB_{ij} \) = observed risky sexual behavior for the \( i^{th} \) adolescent in the \( j^{th} \) school
- \( \beta_{0j} \) = mean risky sexual behavior in the \( j^{th} \) school
- \( \gamma_{00} \) = grand mean risky sexual behavior across schools
- \( r_{ij} \) = unique effect of the \( i^{th} \) adolescent on mean risky sexual behavior in the \( j^{th} \) school
- \( u_{0j} \) = unique effect of the \( j^{th} \) school on grand mean risky sexual behavior across schools
- \( \sigma^2 \) = unconditional adolescent-level variance in risky sexual behavior
- \( \tau_{00} \) = unconditional school-level variance in risky sexual behavior

Table 1 provides parameter estimates, standard errors, and model-data fit information for this model and all subsequent models. Appendix C provides input and key output for this model and all subsequent models. The ICC was equal to .064, which implied that 6.4% of the variance
in risky sexual behavior was attributable to school-level differences. The estimated grand mean risky sexual behavior across schools, \( \hat{\gamma}_{00} \), was equal to 0.04. The unconditional school-level variance estimate, \( \hat{\tau}_{00} \), around this average was equal to 0.07 and was statistically significant, \( p < 0.001 \). Table 2 provides descriptive statistics at Level-1 (i.e., “within” or adolescent-level) and Level-2 (i.e., “between” or school-level) due to evidence of non-independence by school. This information can be used to describe the bivariate associations that exist at each level.

**Model 6: Intercepts and Slopes as Outcomes**

Suppose that the interest is in modeling adolescent- and school-level effects on risky sexual behavior while specifying random intercepts and a mix of fixed, non-randomly varying, and random slopes. Level-1 predictors are specified to address research questions based on ecodevelopmental theory (e.g., what is the effect of perceived peer abstinence on risky sexual behavior at the adolescent-level?). Level-2 predictors of \( \beta_{0j} \) and \( \beta_{2j} \) are specified to address research questions based on ecodevelopmental theory (e.g., what is the effect of mean perceived peer abstinence on mean risky sexual behavior at the school-level?). For a fuller explanation of the wider array of research questions see Model 2 – Model 5 in Appendix B. Suppose further that there is reason to believe (1) that the magnitude of the within-school effect of family functioning on risky sexual behavior depends, in part, on the level of mean gap between parental and adolescents Americanism, and (2) that there will be substantial residual variance in the set of \( \beta_{1j} \) unaccounted for. This model can be written:
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\[ RSB_{ij} = \beta_{0j} + \beta_{1j}(PA_{ij} - \overline{PA}.) + \beta_{2j}(SF_{ij} - \overline{SF}.) + \beta_{3j}(GAP_{ij} - \overline{GAP}.) + \beta_{4j}(FAM_{ij} - \overline{FAM}.) + r_{ij} \]

\[ \beta_{0j} = \gamma_{00} + \gamma_{01}(PA_{ij} - \overline{PA}.) + \gamma_{02}(SF_{ij} - \overline{SF}.) + \gamma_{03}(GAP_{ij} - \overline{GAP}.) + \gamma_{04}(FAM_{ij} - \overline{FAM}.) + u_{0j} \] (6)

\[ \beta_{1j} = \gamma_{10} \]

\[ \beta_{2j} = \gamma_{20} + \gamma_{24}(FAM_{ij} - \overline{FAM}.) \]

\[ \beta_{3j} = \gamma_{30} \]

\[ \beta_{4j} = \gamma_{40} + \gamma_{43}(GAP_{ij} - \overline{GAP}.) + u_{4j} \]

\( u_{4j} = \text{residual within-school effect of risky sexual behavior regressed on family functioning (after controlling for the effect of peer abstinence, adolescent functioning in school, and gap between parental and adolescents Americanism at Level-1) after controlling for the effect of mean gap between parental and adolescents Americanism} \)

\( \tau_{44} = \text{residual variance of the } u_{4j} \)

As can be readily viewed in the combined form of Equation 6 (see Figure 6 in Appendix B), \( \gamma_{24} \) represents a cross-level interaction: \( \gamma_{24}(X_{240} - \overline{X}_{240}) * (\overline{X}_{4..} - \overline{X}_{4..}) \). One way to interpret this interaction is that the magnitude of the effect of adolescent functioning in school on risky sexual behavior depends on the level of mean family functioning. The statistical significance of this cross-level interaction, \( \hat{\gamma}_{24} = -0.009, p < .001 \) (see Table 1), supported rejection of the null hypothesis that the magnitude of the effect of adolescent functioning in school on risky sexual behavior did not depend on level of mean family functioning: \( H_0: \gamma_{24} = 0 \).

A question unanswered by testing \( H_0: \gamma_{24} = 0 \) was: at what values of mean family functioning (\( M = 0.00, SD = 1.13, Min = -2.13, Max = 3.45 \)) was the effect of adolescent functioning in school (\( Min = -42.19, Max = 38.11 \)) on risky sexual behavior statistically...
significant? More formally, what were the regions of significance of mean family functioning for the simple slope of risky sexual behavior on the effect of adolescent functioning in school (45,46)? Figure 1 plots simple slopes of risky sexual behavior on the effect of adolescent functioning in school on a few values of mean family functioning: -SD, M, +SD. The slope was positive when mean family functioning was low, -SD, but the slope became increasingly negative as mean family functioning increased.

Figure 2 identifies the regions of significance of mean family functioning where the effect of adolescent functioning in school on risky sexual behavior was statistically significant and non-significant. When mean family functioning was “low” (i.e., ≤-1.37) the effect of adolescent functioning in school on risky sexual behavior was statistically significant and positive. When mean family functioning was “low-average” (i.e., -1.37 < mean family functioning < -0.17) the effect of adolescent functioning in school on risky sexual behavior was not statistically significant. When mean family functioning was “average or greater” (i.e., ≥-0.17) the effect of adolescent functioning in school on risky sexual behavior was statistically significant and negative.

The interpretation of the cross-level interaction, γ_{43}, followed the same form as that of γ_{24}. As can be viewed in Table 1, mean gap between parental and adolescents Americanism was a statistically significant predictor of the within-school effect of risky sexual behavior regressed on family functioning: \( \hat{\beta}_{43} = 0.017, p < .001 \). The statistical significance of \( \hat{\gamma}_{44} = 0.015, p < .001 \) suggested that there was substantial residual variance in the \( \beta_{4j} \) slopes unaccounted for.

Determining explained variance in multilevel models, particularly when at least one Level-1 slope coefficient is not fixed, is a complex task and an active area of research. As can be
observed in Appendix C, in the current model, information regarding variance accounted for was not provided. When a slope is not fixed (i.e., TYPE = TWOLEVEL RANDOM) Mplus does not provide variance accounted for in the output. An ad hoc procedure for determining proportion of variance accounted for was detailed in Raudenbush and Bryk (17).

At Level-1 the relevant equation can be written:

\[ R^2_{\beta_j} = \frac{\sigma^2_{\text{baseline}} - \sigma^2_{\text{full}}}{\sigma^2_{\text{baseline}}} \]  \hspace{1cm} (7)

A key consideration is which model is designated the baseline model and which model is designated the full model. Using Model 1 as the baseline model and Model 6 as the full model, 32.8% of the Level-1 variance was accounted for by the set of Level-1 predictors.

At Level-2 relevant equations can be written:

\[ R^2_{\beta_{0j}} = \frac{\tau_{00_{\text{baseline}}} - \tau_{00_{\text{full}}}}{\tau_{00_{\text{baseline}}}} \]  \hspace{1cm} (8)

\[ R^2_{\beta_{4j}} = \frac{\tau_{44_{\text{baseline}}} - \tau_{44_{\text{full}}}}{\tau_{44_{\text{baseline}}}} \]  \hspace{1cm} (9)

Given that Level-2 predictors were specified for both \( \beta_{0j} \) and \( \beta_{4j} \), both Equation 8 and Equation 9 were used to determine variance accounted for at Level-2. Model 5 (see Appendix B) is used as the baseline model and Model 6 as the full model. Mean peer abstinence, mean adolescent functioning in school, mean gap between parental and adolescents Americanism, and mean family functioning jointly accounted for 12% of the variance in the unadjusted risky sexual behavior school means. Mean gap between parental and adolescents Americanism accounted for 3.75% of the variance in the within-school slopes of risky sexual behavior regressed on family functioning.

Sample Size and Power in MLRM
Three practical questions often arise when designing and/or analyzing data from an experiment: “what $N$ is needed in order to use a particular statistical method?”, “how much power ($\pi$) do I have with a fixed $N$?”, and “what $N$ is needed in order achieve a fixed level of $\pi$?”. A definitive answer to each of these somewhat under-defined questions is not possible across the myriad of model-data conditions observed in practice. Each of these questions is generally more difficult to answer under a MLRM as compared to a fixed effects linear regression model because there are multiple sample sizes to consider (i.e., $n_j$, $J$, and $N$) and the random part of the model is more complex (e.g., $u_{0j} + r_j$ in Equation 1 versus $r_i$ in Figure 2 of Appendix B).

**Sample Sizes in General**

Our response to the question, “what $N$ is needed in order to use a MLRM?”, is informed by summarizing the relevant simulation research (49). MLRM generally is a large sample technique that often uses maximum likelihood (ML) estimation. Results from full ML are summarized below. Estimation of the fixed effects, $\gamma$, is generally unbiased. Estimation of the standard errors for $\gamma$ have been shown to be negatively biased, increasing Type I error rate, when $J < 50$; although this bias generally is small when $J \approx 30$ (50-52). Accurate estimation of the random component at Level-1, $\sigma^2$, tends to be robust. Accurate estimation of the random component(s) at Level-2, $\mathbf{T}$, tends to be the most difficult, particularly when $J < 100$; although estimates may be adequate (if somewhat negatively biased) when $J \approx 50$ (50,53). Using restricted ML may markedly improve the estimation of $\mathbf{T}$ when $J$ is not large (50,53).

Increasing $J$ tends to be more important than increasing $n_j$ for the purpose of maximizing the possibility of producing precise and powerful estimates. This trend along with the more specific findings summarized in the previous paragraph has informed a set of general guidelines
The 30/30 \((i.e., \(J = 30\))/\(n_j = 30\)) guideline is offered for when the research questions are focused on \(\gamma\) without cross-level interactions. When the research questions are focused on cross-level interactions within \(\gamma\) the guideline is modified: 50/20. When the research questions are focused on \(T\) the guideline is 100/10. Like all sample size related guidelines, a limitation of the above guidelines is that they do not take fully into account study-specific characteristics.

**Sample Sizes and Power in a Specific Study**

Our response to the questions, “how much \(\pi\) do I have with fixed values of \(n_j\) and \(J\)?” and “what \(n_j\) and/or \(J\) is/are needed in order achieve a fixed level of power (\(\pi\))?”, is demonstrated by using a flexible two-step Monte Carlo approach in *Mplus* (see Appendix C). A full accounting of this approach, input and output, is available elsewhere (18,54). The first step is referred to as a real data analysis. The second step is referred to as a Monte Carlo simulation. This approach fits within the more general framework of using Monte Carlo methods in data analysis (55). The contribution of using Monte Carlo methods (e.g., simulating data) for a clinical trial with real data is toward improved application of a particular statistical model (e.g., MLRM) for a particular clinical trial, and hence resultant conclusions, and not to statistical theory per se (56).

Returning to the Familias Unidas study, another dataset (i.e., dataset_2) was generated following the same protocol used to generate dataset_1 with the exception that \(N = 633, J = 25\), and \(\overline{n_j} = 25.32\), which probably more closely resembles sample sizes in many trials due to budgetary constraints. Suppose that Model 6 is of interest (see Equation 9) and that answering the question “how much \(\pi\) do I have with fixed values of \(n_j\) and \(J\)?” for each parameter of interest is desired. Parameters of interest, \(\theta_i\), were all statistically significant parameter estimates, except main effects of cross-level interactions, from Model 6 in Table 1. In Step 1 dataset_2 was fitted
to Model 6 and parameter estimates were saved. In Step 2 these parameter estimates were then treated as population values for a Monte Carlo simulation where 10,000 datasets were simultaneously generated and analyzed. Observed power for \( \theta_i, \hat{\pi}_i \) was defined as the percentage of replications that rejected \( H_0 : \theta_i = 0 \). A commonly used desired \( \hat{\pi}_i \) of 80% was adopted (57).

As displayed in Table 1, \( \hat{\pi}_i \) for \( \hat{\gamma} \) ranged from 33.4% to 97.5%. Two fixed effects, \( \gamma_{03}, \gamma_{43} \), had low power and in both cases the simulation suggested that there was less than 50/50 chance that the relevant null hypothesis would be rejected. Three fixed effects, \( \gamma_{10}, \gamma_{24}, \gamma_{30} \), were sufficiently powered and in all cases the simulation suggested that there was a very good chance that the relevant null hypothesis would be rejected. A similar range of \( \hat{\pi}_i \) was observed for the variance components: from 53.6% to 100%. Clearly, in this example and most examples in practice, an answer to the question “how much \( \pi \) do I have with fixed values of \( n_j \) and \( J \)” will be complex (e.g., sufficiently powered for primary research questions while insufficiently powered for non-primary research questions). Providing an answer to this question, however, may provide a useful context for evaluating results from a trial (e.g., chance of committing a Type II error).

Given the results summarized in the previous paragraph, and assuming that \( n_j \) is fixed, suppose the following question is asked: “what \( J \) is needed in order achieve \( \hat{\pi}_i \geq 80\% \) for each \( \theta_i \)?”. Through relatively minor manipulation of input for Step 2 it is determined that the answer to the question is \( J \approx 115 \). Because sampling more Level-2 units groups often requires more resources than sampling more Level-1 units, however, derivation of an optimal design in practice frequently considers trade-offs (in addition to \( \hat{\pi}_i \)) due to budgetary constraints and other study-specific characteristics (58-60). Software has been developed for this purpose (e.g., 61).
Missing Data in MLRM

A key to understanding the missing data literature is to comprehend Rubin’s taxonomy of missing data (62). Missing completely at random (MCAR) is when the propensity for missing data on a variable, $G$, is unrelated to values of other variables in the model and is also unrelated to values of $G$ itself. Missing at random (MAR) is when the propensity for missing data on $G$ is related to values of one or more other variables in the model but unrelated to values of $G$ itself. Missing not at random (MNAR) is when the propensity for missing data on $G$ is related to values of $G$ itself. Which mechanism the missing data actually follow is typically impossible to identify with relative certainty because MCAR is the only missing data mechanism for which a statistical test exists (63). Modern approaches which address missing data generally assume MAR (64) although approaches that assume MNAR are beginning to be used with more frequency (65-67).

Incomplete data has long been a difficult issue in MLRM when a non-trivial proportion (e.g., $\geq 5\%$; 64) of data are missing for both the outcome(s) and at least one predictor (68,69). Common default approaches in many statistical packages are to delete Level-1 observations with any incomplete Level-1 data (especially predictors), and, to delete all observations within a cluster if any Level-2 data (especially predictors) are missing within that cluster. These defaults may inefficiently use the observed data, assume MCAR, and may yield untrustworthy results (70,71). The use of a few simple strategies that directly provide a single set of observations for missing data, such as last observation carried forward and class mean imputation, has generally been discouraged (72,75).

Likelihood-based methods for handling missing data in MLRM address the missing data and fit the MLRM in a single step. Likelihood-based methods are preferred when the missing data are in the outcome(s) only, the specification of the MLRM is correct, and MAR can reasonably be assumed (69). Missing data in the predictors generally cannot be handled in
likelihood-based methods (with typical model commands) although some programs (e.g., *Mplus*) do allow missing data on auxiliary variables (74). Likelihood-based methods can, however, handle missing data in the predictors if the predictors are brought into the model by specifying additional model commands that make distributional assumptions regarding the predictors (see Appendix C). A current and thorough review of likelihood-based methods for handling missing data in medical research is available elsewhere (75).

Multiple imputation methods for handling missing data in MLRM address the missing data and fit the MLRM in separate steps. The first step addresses the missing data problem by imputing multiple datasets while acknowledging the multilevel structure of the data. The second step fits the complete datasets to the MLRM and combines the results to provide a single set of parameter estimates and standard errors (76,77). Multiple imputation of multilevel data is generally the preferred approach in MLRM (under the MAR assumption) because of its greater flexibility than likelihood-based approaches (69). It should be noted, however, that much methodological research remains to be done with regard to exploring the full range of possible missing data scenarios (and the relative performance of likelihood-based versus multiple imputation approaches) in MLRM.

Multiple imputation of multilevel data can be performed in *Mplus* under Bayesian estimation (78). Both unrestricted and restricted models can be used for imputation but for multilevel data specifying a restricted model may increase the likelihood of convergence under model-data conditions frequently observed in practice (e.g., a large number of variables, continuous and categorical variables, and a non-large number of Level-2 units). A review of the unrestricted model options available in *Mplus* is available elsewhere (78).
Returning to the Familias Unidas study, dataset_2 was altered (i.e., dataset_2_md) such that approximately 10% of cases were missing data on both RSB (i.e., the outcome) and FAM (i.e., a predictor). Using the default setting of most statistical packages, 323 cases would have been ignored when fitting Model 6 to dataset_2_md. Instead, prior to fitting Model 6 to the incomplete dataset, five imputed datasets were generated in Mplus (i.e., Step 1) under a restricted approach (i.e., Model 6 - see Appendix C). Generating five imputed datasets was consistent with the small amount of missing data (64). In Step 2, the five imputed datasets were then fitted to Model 6 in Mplus (see Appendix C) and the results were consistent with those previously listed in Table 1.

**Example 2: Stress Management**

Three-level MLRMs occasionally appear in the literature (see Appendix A). When three-level MLRMs are used the data structure often is repeated measures nested within people who are nested within Level-3 units (e.g., treatment provider, dyads, etc.). Thus, for example 2, we briefly present a cluster randomized trial with repeated measures based on some core ideas from a real intervention: cognitive behavioral stress management in prostate cancer (79). Fuller treatments of three-level MLRMs are available elsewhere (17).³

Prostate cancer is the most common cancer among men in the United States, excluding skin cancer. There are over 2.2 million current survivors of prostate cancer, with over 240,000 new diagnoses estimated each year (80). Radical prostatectomy and radiation therapy are the standard treatment options for localized disease. Although both treatments are highly effective in disease management and extending survival, men often experience chronic and debilitating treatment-related side effects, such as urinary and/or bowel incontinence and erectile dysfunction, that challenge quality of life (81,82). Sexual dysfunction, for example, is associated with increased distress, depression and anxiety, and lowered self-esteem, quality of
marital/partner relationships and general QOL (83-86). Psychosocial interventions tailored specifically for post-treatment prostate cancer survivors have been shown to have positive effects on survivors’ ability to adjust to and cope with disease- and treatment-related changes.

The CBSM intervention is a manualized, 10-week, group-based intervention designed to improve quality of life through improvements in cognitive-behavioral stress management skills. It was modified from the original protocol designed by Antoni et al. (87) in order to address the specific needs and concerns of men coping with localized prostate cancer. A review of the CBSM intervention has been reported elsewhere (88). Briefly, intervention groups met once per week for approximately 2 hours, which consisted of a 90-minute didactic component and 30-minute relaxation training. Participants were instructed in a number of stress management skills, including identifying distorted or irrational thoughts, effective coping strategies, anger management, assertiveness training, and eliciting social support. The control condition consisted of a group-based, one-day seminar that lasted for approximately 4 hours during which participants were instructed in the same stress management skills that were taught in the CBSM intervention sessions.

Suppose that the CBSM intervention example summarizes a relatively controlled and large trial. Treatment is randomly assigned at the cluster-level, where 50 therapists are to administer the control condition and 50 therapists are to administer the experimental condition ($J = 100$). Participants are randomly assigned to a therapist, with 10 participants assigned to each therapist ($I = 1000$). A quality of life measure is taken repeatedly from each participant at four equally-spaced measurement occasions ($M = 4$) that are common across participants: immediately prior to the trial (i.e., baseline); 1-week into the trial; 2-weeks into the trial; and three weeks into the trial. The nesting structure can be conceptualized as repeated quality of life
measures (i.e., Level-1) within participants (i.e., Level-2) within therapists (i.e., Level-3). The hypothesis is that the average difference in linear change in quality of life will be greater for patients in the treatment condition compared to those in the control condition, after accounting for the cluster (“therapist”) effect. This model can be written:

\[
\text{quality of life}_{mij} = \pi_{0ij} + \pi_{1ij}A_{mij} + e_{mij}
\]

\[
\begin{align*}
\pi_{0ij} &= \beta_{00j} + r_{0ij} \\
\pi_{1ij} &= \beta_{10j} + r_{1ij} \\
\beta_{00j} &= \gamma_{000} + \gamma_{001}W_j + u_{00j} \\
\beta_{10j} &= \gamma_{100} + \gamma_{101}W_j + u_{10j}
\end{align*}
\]

where, \(A\) represents time (and is coded 0 at baseline, 1 at week-1, 2 at week-2, and 3 at week-3) and \(W\) is a dummy variable for treatment condition (0 = one-day educational intervention, 1 = CBSM intervention). A dataset was generated (i.e., dataset_3) consistent with this example. Equation 10 was fitted to dataset_3 (see Appendix C for input and key output). Interpretation of a few key results follows but a fuller set of interpretations and the relevant path model are both available in Appendix B.

The fixed effects are typically emphasized in three-level MLRMs. In this example, the estimate of \(\gamma_{001}\) was not statically significant, \(\hat{\gamma}_{001} = 1.44, p = .207\). This result provided evidence that the difference in expected quality of life at baseline for participants in the experimental condition as compared to the control condition was not greater than what we would expect by chance, which was consistent with the random assignment of participants to therapists. The estimate of \(\gamma_{100}\) was statically significant, \(\hat{\gamma}_{100} = 1.21, p < .001\). This result provided evidence that the expected rate of weekly linear change in quality of life for participants in the control condition was greater than what we would expect by chance, which was consistent with the one-day educational seminar that this group received (i.e., the control group received a standard
Perhaps most importantly, the estimate of $\gamma_{101}$ was statically significant, $\hat{\gamma}_{101} = 0.84$, $p = .004$. This result provided evidence that the difference in the expected rate of weekly linear change in quality of life for participants in the experimental condition as compared to the control condition was greater than what we would expect by chance, which was consistent with the CBSM intervention that this group received (i.e., in addition to the standard treatment received by the control group).

The random part of three-level MLRMs also is important. In this example, the variance of the level-1 error term, $e_{mij}$, was statically significant, $\hat{\sigma}^2 = 46.82$, $p < .001$. This result provided evidence for residual within-participant heterogeneity and thus the possibility of adding time-varying covariates (e.g., urinary incontinence, erectile dysfunction, pain) to the model if theoretically defensible. The variance of each Level-2 error term, $r_{ij}$ and $r_{iij}$, was statistically significant, $\tau_{\eta_{0i}} = 125.03$, $p < .001$, and, $\tau_{\eta_{ii}} = 4.96$, $p < .001$. This result provided support for allowing each participant to have her/his own change trajectory relative to other participants within the same therapist. The observed level of between-participant heterogeneity would support adding participant-level covariates (e.g., age, comorbid medical conditions, pre-treatment physical functioning) to the model if theoretically defensible. The variance of each Level-3 error term, $u_{00j}$ and $u_{10j}$, was statically significant, $\tau_{\beta_{00}} = 19.17$, $p < .001$ and $\tau_{\beta_{01}} = 0.53$, $p = .043$. This result provided support for allowing each therapist to have her/his own average participant trajectory relative to the other therapists – even after controlling for the effect of the treatment condition. The observed level of between-therapist heterogeneity would support adding therapist-level covariates to the model (e.g., gender, years of experience) if theoretically defensible.
It may have been ideal if evidence had been observed to support treating $\beta_{00j}$ as fixed (i.e., dropping $W_j$ and $u_{00j}$) and $\beta_{10j}$ as non-randomly varying based on treatment condition (i.e., dropping $u_{10j}$). Treating $\beta_{00j}$ as fixed, $\beta_{00j} = \gamma_{000}$, would have suggested that mean participant quality of life at baseline was relatively constant across therapists. Conceptually, such a result could have been interpreted as the result of successful random assignment of participants to therapists – giving each therapist a similar patient profile, with regard to mean quality of life, at baseline. Treating $\beta_{10j}$ as non-randomly varying, $\beta_{10j} = \gamma_{100} + \gamma_{101}W_j$, would have suggested that mean participant rate of weekly linear change in quality of life was relatively constant across therapists after controlling for the effect of treatment condition. Conceptually, such a result could have been interpreted as the average rate of linear change in quality of life being independent of which therapist a participant was assigned to, after adjusting for the effect of treatment condition. What may be theoretically ideal may not observed in practice and the complex error structure of three-level MLRMs allow for flexible modeling of complex phenomenon often observed in cluster randomized trials with repeated measures.

**Summary**

Multilevel data, sometimes referred to as hierarchical data, are common in psychosomatic research. A common hierarchical structure has repeated observations nested within participants (e.g., Example 2: Stress Management) but cross-sectional data can also be viewed as multilevel (e.g., Example 1: Familias Unidas). When non-independence in the data is non-trivial and is attributable to at least one cluster variable (e.g., adolescents nested within schools; repeated measures nested within participants who are nested within therapists), imposing a model that ignores the non-independence is often problematic from both an empirical perspective (e.g.,
increased Type I error) and a theoretical perspective (e.g., inability to model relationships at, and across, different levels).

MLMs, particularly MLRMs, are beginning to appear with some frequency in psychosomatic research (see Appendix A). Some core methodological issues within applications of MLMs that require careful attention include: communication of model specification, parameter interpretation, sample size and power, and missing data. Examples of how to communicate the model specified and how to interpret the model parameters were provided in Example 1, Example 2, and Appendix B. Special sections were dedicated to both sample size and power in MLRM, and, to missing data in MLRM. Appendix C provides annotated input and key output from Mplus and SAS. While MLRMs were emphasized in this manuscript, we note that MLMs have also been implemented within a more general latent variable framework that may be used with considerable frequency in future research (e.g., MLSMs; 89-91).
References


Footnotes

1 Because dataset_1 through dataset_3 were simulated, the results that follow should be viewed as only a means for providing a relevant context for understanding multilevel modeling.

2 A brief review of the parallel fixed effects linear regression model is provided following Figure 1b in Appendix B as a contrast to Equation 1.

3 Results reported in the text of this manuscript are from Mplus output.

4 The alpha for all hypothesis tests was set equal to .05.

5 There are limitations (e.g., possibility of negative variance accounted for) to this approach to variance explained (47). Other approaches, including a single index of explained variance for the entire model, are beginning to emerge (48).

6 The problem generally is considerably easier to address if incomplete data are confined to the outcome(s) and the missing data can reasonably be viewed as MAR.  

7 Addressing the missing data problem by imputing multiple datasets, while ignoring the multilevel structure of the data, can be described as multiple imputation-flat file. There is evidence that multiple imputation of multilevel data outperforms multiple imputation-flat file for handling missing data that follow a multilevel structure (69).

8 The Monte Carlo approach in Mplus for sample size and power determination described previously in the Familias Unidas example could be extended to this example (18,54).

9 Mplus takes a multivariate (not univariate as in some dedicated MLRM software) approach to change modeling. Thus, the program considers a three-level MLRM to be a two-level model.

10 Note that $\gamma_{101}$ is a cross-level interaction (e.g., the magnitude of the linear effect of time in trial on quality of life depends on treatment condition). The regions of significance approach described previously in the Familias Unidas example could be extended to this example (45,46).
Table 1

*Familias Unidas: Parameter Estimates, (Standard Errors), Observed Power, and Model-Data Fit*

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Model 1</th>
<th>Model 2</th>
<th>Model 3</th>
<th>Model 4</th>
<th>Model 5</th>
<th>Model 6</th>
<th>Power</th>
<th>Power</th>
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<td></td>
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<td></td>
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<td></td>
<td>$J = 25$</td>
<td>$J = 100$</td>
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<td><strong>Fixed Effects</strong></td>
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<td></td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>$\gamma_{00}$</td>
<td>0.040 (0.033)</td>
<td>0.039 (0.031)</td>
<td>0.039 (0.032)</td>
<td>0.030 (0.036)</td>
<td>0.040 (0.033)</td>
<td>0.039 (0.031)</td>
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<tr>
<td>$\gamma_{01}$</td>
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<td>0.023 (0.032)</td>
<td>0.016 (0.034)</td>
<td>0.025 (0.031)</td>
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<tr>
<td>$\gamma_{02}$</td>
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<td>0.037 (0.044)</td>
<td>0.025 (0.046)</td>
<td>0.037 (0.041)</td>
<td>-----</td>
<td>-----</td>
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<tr>
<td>$\gamma_{03}$</td>
<td>0.036* (0.014)</td>
<td>0.035* (0.014)</td>
<td>0.036* (0.015)</td>
<td>0.037* (0.014)</td>
<td>33.4%</td>
<td>79.7%</td>
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<td></td>
</tr>
<tr>
<td>$\gamma_{04}$</td>
<td>-0.007 (0.047)</td>
<td>-0.010 (0.048)</td>
<td>-0.005 (0.048)</td>
<td>-0.009 (0.048)</td>
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<td>$\gamma_{10}$</td>
<td>-0.017*** (0.003)</td>
<td>-0.016*** (0.003)</td>
<td>-0.015*** (0.003)</td>
<td>-0.015*** (0.003)</td>
<td>80.8%</td>
<td>100.0%</td>
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<tr>
<td>$\gamma_{20}$</td>
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<td>-0.008* (0.003)</td>
<td>-0.008* (0.003)</td>
<td>-0.007* (0.003)</td>
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<td>$\gamma_{24}$</td>
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<td>-0.009*** (0.002)</td>
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### Multilevel Modeling

#### γ-Parameters

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<td></td>
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<td>(0.002)</td>
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<tr>
<td></td>
<td>(0.016)</td>
<td>(0.016)</td>
<td>(0.014)</td>
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<td>γ43</td>
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<td></td>
<td>(0.004)</td>
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#### Variance Components

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<th>1.058***</th>
<th>1.012***</th>
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<th>0.747***</th>
<th>0.711***</th>
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<tr>
<td></td>
<td>(0.053)</td>
<td>(0.053)</td>
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<td>(0.047)</td>
<td>(0.019)</td>
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<td>0.061***</td>
<td>0.065***</td>
<td>0.070***</td>
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<td>0.073***</td>
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<td></td>
<td>(0.013)</td>
<td>(0.011)</td>
<td>(0.012)</td>
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<td>(0.011)</td>
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<tr>
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<td>0.015***</td>
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<td>96.9%</td>
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<td></td>
<td>(0.003)</td>
<td>(0.002)</td>
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#### Model-Data Fit

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*Note.* *p* < .05; **p** < .01; ***p** < .001; # par = number of parameters estimated.
Table 2

Descriptive Statistics at Level-1 and Level-2

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<td>0.02</td>
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<tr>
<td></td>
<td>0.04</td>
</tr>
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</table>
Figure 1. Simple slopes of risky sexual behavior on the effect of adolescent functioning in school on a few values of mean family functioning.
Figure 2. Regions of significance of mean family functioning ($-1.37 \geq \text{mean parental stressors} \geq -0.17$) where the effect of adolescent functioning in school on risky sexual behavior was statistically significant.
Appendix A

Multilevel articles, 2006-2010: *Psychosomatic Medicine*

<table>
<thead>
<tr>
<th>Article</th>
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<th>Level-2</th>
<th>Level-3</th>
<th>Type</th>
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<td>Diary entries</td>
<td>Individuals</td>
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<tr>
<td>(93) Dierckx et. al., 2009</td>
<td>Children</td>
<td>Mothers</td>
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<td>(94) Ditzen et. al., 2008</td>
<td>Repeated measures</td>
<td>Individuals</td>
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*Note.* MLRM = multilevel regression model; MLSM = multilevel structural equation model.


Appendix B

Supplemental path diagrams (38), equations, and text

Curran and Bauer’s system of path diagrams for MLRMs contains a number of components. A box represents an observed variable. Font within a box communicates the centering decision: no centering (plain font), group-mean centered (italicized font), grand-mean centered (bold italic font). A triangle labeled with the number “1\_level” defines an intercept term where the subscript denotes the level at which the intercept is specified. A circle represents a random coefficient, where the particular coefficient is declared within the circle. A straight single-headed arrow represents a regression parameter which is taken as fixed unless superimposed within a circle. A multiheaded arrow indicates a covariance that is estimated as a model parameter.

For indexing purposes, let \( y = RSB_{ij}, X_{1ij} = PA_{ij}, X_{2ij} = SF_{ij}, X_{3ij} = GAP_{ij}, \) and \( X_{4ij} = FAM_{ij}. \) Adolescent-level independent variables were aggregated to the school-level to create Level-2 predictors that adopted the relevant acronym while altering subscript notation (e.g., \( PA_{ij} \) changed to \( \overline{PA} j \) from Level-1 to Level-2). For indexing purposes, let \( \overline{X}_{1j} = \overline{PA} j, \overline{X}_{2j} = \overline{SF} j, \overline{X}_{3j} = \overline{GAP} j, \) and \( \overline{X}_{4j} = \overline{FAM} j. \)
Figure 1a. One-way ANOVA with random effects: $Y_{ij} = \gamma_{00} + u_{0j} + r_{ij}$. 
Figure 1b. Unconditional fixed effects linear regression model: $Y_i = \gamma_0 + r_i$.

This model can also be written:

$$RSB_i = \beta_0 + r_i$$

$RSB_i$ = observed risky sexual behavior for the $i^{th}$ adolescent

$\beta_0$ = mean risky sexual behavior

$r_i$ = unique effect of the $i^{th}$ adolescent on mean risky sexual behavior

$\sigma^2$ = unconditional total variance in risky sexual behavior

As can viewed in Appendix C the intercept was mean risky sexual behavior, 0.04, and not the grand mean because group-level means were not specified (i.e., school was ignored). An incorrect assumption of the residual was that the observations were independent (e.g., risky sexual behavior was independent of school). Variance in risky sexual behavior was not partitioned by level and the estimate provided, 1.13, was a composite composed of both adolescent- and school-level variance. Had a correlation matrix been provided parallel to Table 2, but ignoring high school, each value would have been a composite: a blended estimate of the Level-1 and Level-2 correlation. A third modeling option that resides between a MLM and a fixed effects linear regression is to model only at Level-1 while applying a correction for the non-independence by cluster (40,41). This option was not pursued in this manuscript but examples are available elsewhere (42).
Model 2: Means as Outcomes Regression Model

Suppose that the interest is in modeling unadjusted mean risky sexual behavior at the school-level. This model will be unconditional at Level-1 and conditional at Level-2. If each Level-2 predictor is GMC then the interpretation of $\gamma_{00}$ is the same as in the previous model (where there also was no adjustment to the school-level means, $\beta_{0,j}$). This model can be written:

$$R_{SB_j} = \beta_{0_j} + r_j$$

$$\beta_{0_j} = \gamma_{00} + \gamma_{01}(PA_j - \overline{PA}) + \gamma_{02}(SF_j - \overline{SF}) + \gamma_{03}(GAP_j - \overline{GAP}) + \gamma_{04}(FAM_j - \overline{FAM}) + u_{0j}$$

(2)

$\gamma_{01} = \text{change in mean risky sexual behavior given a one-unit increase in mean perceived peer abstinence after controlling for the effect of mean adolescent functioning in school, mean gap between parental and adolescents Americanism, and mean family functioning.}$

The text following “after controlling” for is denoted … for the remaining terms. Interpretation of $\gamma_{02}$ through $\gamma_{04}$ follows the same form as the interpretation of $\gamma_{01}$.

$u_{0j} = \text{residual mean risky sexual behavior for the } j^{th} \text{ school after controlling for …}$

$\tau_{00} = \text{residual school-level variance in mean risky sexual behavior after controlling for …}$

From this point forward all Level-2 independent variables are GMC.

As can be viewed in Table 1, mean gap between parental and adolescents Americanism at the school-level was the only statistically significant predictor of the intercepts (i.e., school-mean risky sexual behavior), $\hat{\gamma}_{03} = 0.04$, $p = .011$. The set of predictors combined to explain 15.3% of the variance in the intercepts. The italicized text emphasizes that in a MLM the notion of variance accounted for can be complex due to the fact that the variance in the outcome(s) can be conceptualized as being partitioned by level. Because the independent variables were specified as predictors of only the intercepts, variance explained can be focused at Level-2. That $\hat{\tau}_{00} = 0.06$, ...
\( p < .001 \) suggested there was substantial residual variance in the intercepts unaccounted for by the set of predictors.
Figure 2. Means as outcomes regression model:

\[ Y_{ij} = \beta_{0j} = \gamma_{00} + \gamma_{01} \left( \bar{X}_{1,j} - \bar{X}_{1..} \right) + \gamma_{02} \left( \bar{X}_{2,j} - \bar{X}_{2..} \right) + \gamma_{03} \left( \bar{X}_{3,j} - \bar{X}_{3..} \right) + \gamma_{04} \left( \bar{X}_{4,j} - \bar{X}_{4..} \right) + u_{0j} + r_{ij}. \]
Model 3: One-Way ANCOVA with Random Effects

Suppose there are theoretical reasons to believe that school means need to be adjusted for some adolescent-level variables because students are not randomly assigned to schools; thereby making comparisons of unadjusted school means misleading. The goal then is to model adjusted mean risky sexual behavior at the school-level. This model will be conditional at both Level-1 and Level-2. Suppose further that there is reason to believe that each Level-1 slope coefficient should be treated as fixed (i.e., the relationship between each Level-1 predictor and the outcome is believed to be homogenous across schools). In this case it is appropriate to GMC (or RAS) each Level-1 predictor because CWC results in unadjusted school means. This model can be written:

\[
RSB_j = \beta_{00} + \beta_{1j}(PA_j - \overline{PA}) + \beta_{2j}(SF_j - \overline{SF}) + \beta_{3j}(GAP_j - \overline{GAP}) + \beta_{4j}(FAM_j - \overline{FAM}) + r_j
\]

\[
\beta_{0j} = \gamma_{00} + \gamma_{01}(PA_j - \overline{PA}) + \gamma_{02}(SF_j - \overline{SF}) + \gamma_{03}(GAP_j - \overline{GAP}) + \gamma_{04}(FAM_j - \overline{FAM}) + u_{0j}
\]

\[
\beta_{1j} = \gamma_{10}
\]

\[
\beta_{2j} = \gamma_{20}
\]

\[
\beta_{3j} = \gamma_{30}
\]

\[
\beta_{4j} = \gamma_{40}
\]

\[
\gamma_{01} = \text{change in adjusted mean risky sexual behavior given a one-unit increase in mean perceived peer abstinence after controlling for the effect of mean adolescent functioning in school, mean gap between parental and adolescents Americanism, and mean family functioning.}
\]

Interpretation of \(\gamma_{02}\) through \(\gamma_{04}\) follows the same form as the interpretation of \(\gamma_{01}\).

\[
u_{0j} = \text{residual adjusted mean risky sexual behavior for the } j^{th} \text{ school after controlling for } \ldots
\]

\[
\tau_{00} = \text{residual school-level variance in adjusted mean risky sexual behavior after controlling for } \ldots
\]
\( \gamma_{20} \) = average change in expected risky sexual behavior across schools given a one-unit increase in Adolescent functioning in school after controlling for the effect of perceived peer abstinence, gap between parental and adolescents Americanism, and family functioning. Interpretation of

\( \gamma_{10}, \gamma_{30}, \text{ and } \gamma_{40} \) follow the same form as the interpretation of \( \gamma_{20} \).

\( r_{ij} \) = residual risky sexual behavior of the \( i \)th adolescent in the \( j \)th school after controlling for …

\( \sigma^2 \) = residual adolescent-level variance in risky sexual behavior after controlling for …

Each Level-1 predictor had a statistically significant direct effect on adolescent-level (or “within school”) risky sexual behavior (see Table 1). The set of Level-1 predictors combined to explain 4.3% of the adolescent-level variance. Note that the set of Level-2 predictors explained less of the variance in the intercepts than in the previous model (i.e., from 15.3% to 13.8%). This can largely be explained by the differing definition of the intercepts between the two models (i.e., unadjusted versus adjusted means). If the Level-1 predictors had been CWC the explained variance in the intercepts would have been nearly identical (i.e., from 15.3% to 15.0%). Finally, the statistical significance of both residual variances, \( \hat{\sigma}^2 = 1.01, p < .001 \) and \( \hat{\tau}_{00} = 0.06, p < .001 \), suggested that there was substantial unexplained variance at both levels.

The centering decision at Level-1 (GMC) along with including the means for each Level-1 predictor at Level-2, allowed \( \hat{\gamma}_{10}, \hat{\gamma}_{20}, \hat{\gamma}_{30}, \text{ and } \hat{\gamma}_{40} \) to each be interpreted as the relevant estimated within effect (e.g., the effect of school functioning at the adolescent-level), while \( \hat{\gamma}_{01}, \hat{\gamma}_{02}, \hat{\gamma}_{03}, \text{ and } \hat{\gamma}_{04} \) are interpreted as the relevant estimated contextual effect. The contextual effect is defined as the difference between the within effect and the between effect (17). It should be noted that this same distinction (i.e., the possibility for three different “types” of effects of an
observed Level-1 predictor: within, between, contextual) could also be viewed from a latent variable perspective (43,44).

The estimated effect of each Level-1 predictor \( (\hat{\gamma}_{10}, \hat{\gamma}_{20}, \hat{\gamma}_{30}, \hat{\gamma}_{40}) \) was listed under the “Within Level” results of the output (see Appendix C). Treating each Level-1 slope as homogenous across schools (i.e., fixed) was akin to ignoring the nesting of the data for these effects; thereby relegating each effect to Level-1. For example, \( \hat{\gamma}_{20} = -0.009 \), \( p = .009 \), within the context of the fuller model implied that the effect of school functioning on risky sexual behavior was negative and constant across schools (and therefore adolescents).
Figure 3. One-way ANCOVA with random effects:

\[
Y_{ij} = \gamma_{00} + \gamma_{01}(X_{1i} - \bar{X}_{1..}) + \gamma_{02}(X_{2i} - \bar{X}_{2..}) + \gamma_{03}(X_{3i} - \bar{X}_{3..}) + \gamma_{04}(X_{4i} - \bar{X}_{4..}) \\
+ \gamma_{10}(X_{1ij} - \bar{X}_{1..}) + \gamma_{20}(X_{2ij} - \bar{X}_{2..}) + \gamma_{30}(X_{3ij} - \bar{X}_{3..}) + \gamma_{40}(X_{4ij} - \bar{X}_{4..}) + u_{0j} + r_{ij}.
\]
Model 4: Non-Randomly Varying Slopes

Suppose that the previous model is altered to reflect the belief that the within-school effect (i.e., slope) of risky sexual behavior regressed on the adolescent functioning in school, $\beta_{2j}$, should be changed from fixed, $\beta_{2j} = \gamma_{20}$, to non-randomly varying based on mean family functioning: $\beta_{2j} = \gamma_{20} + \gamma_{24}\left(\overline{FA_{jFU}} - \overline{FA_{FU.}}\right)$. Conceptually, the slope for risky sexual behavior regressed on adolescent functioning in school in each school can now vary based on the mean family functioning value in each school (assuming $\hat{\gamma}_{24} \neq 0$). Note the continued absence of a random component for this within-school slope (i.e., the absence of a $u_{2j}$ term). This model can be written:

$$
RSB_{ij} = \beta_{0j} + \beta_{1j}\left(PA_{ij} - \overline{PA.}\right) + \beta_{2j}\left(SF_{ij} - \overline{SF.}\right) + \beta_{3j}\left(GAP_{ij} - \overline{GAP.}\right) + \beta_{4j}\left(FAM_{ij} - \overline{FAM.}\right) + r_{ij}
$$

$$
\beta_{0j} = \gamma_{00} + \gamma_{01}\left(PA_{ij} - \overline{PA.}\right) + \gamma_{02}\left(SF_{ij} - \overline{SF.}\right) + \gamma_{03}\left(GAP_{ij} - \overline{GAP.}\right) + \gamma_{04}\left(FAM_{ij} - \overline{FAM.}\right) + u_{0j}
$$

$$
\beta_{1j} = \gamma_{10}
$$

$$
\beta_{2j} = \gamma_{20} + \gamma_{24}\left(FAM_{ij} - \overline{FAM.}\right)
$$

$$
\beta_{3j} = \gamma_{30}
$$

$$
\beta_{4j} = \gamma_{40}
$$

$\gamma_{20}$ = change in expected risky sexual behavior given a one-unit increase in adolescent functioning in school (after controlling for the effect of peer abstinence, gap between parental and adolescents Americanism, and family functioning for schools that have a mean family functioning value equal to the grand mean family functioning value) across schools.

$\gamma_{24}$ = change in the change in expected risky sexual behavior given a one-unit increase in school functioning (conditional on all other Level-1 predictors) given a one-unit increase in mean
family functioning.
Figure 4. Non-randomly varying slopes:

\[
Y_{ij} = \gamma_{00} + \gamma_{01}(\bar{X}_{1j} - \bar{X}_{1..}) + \gamma_{02}(\bar{X}_{2j} - \bar{X}_{2..}) + \gamma_{03}(\bar{X}_{3j} - \bar{X}_{3..}) + \gamma_{04}(\bar{X}_{4j} - \bar{X}_{4..})
\]

\[
+ \gamma_{10}(X_{1ij} - \bar{X}_{1..}) + \gamma_{20}(X_{2ij} - \bar{X}_{2..}) + \gamma_{23}(X_{2ij} - \bar{X}_{2..})(\bar{X}_{4j} - \bar{X}_{4..})
\]

\[
+ \gamma_{30}(X_{3ij} - \bar{X}_{3..}) + \gamma_{40}(X_{4ij} - \bar{X}_{4..}) + u_{0j} + r_{ij}.
\]
Model 5: Random Coefficients Regression

Suppose that the interest is in modeling adolescent-level effects on risky sexual behavior while specifying random intercepts, a mix of both random and fixed slopes, and no school-level predictors. This model will be conditional at Level-1 and unconditional at Level-2. The effect of family functioning on risky sexual behavior is believed to be heterogeneous across schools, justifying the inclusion of the $u_{4j}$ term, while each of the other within-school slopes is believed to be homogenous across schools. CWC each Level-1 predictor is appropriate because the interest is estimating pure adolescent-level effects (i.e., $\gamma_{10}, \gamma_{20}, \gamma_{30}, \gamma_{40}$). Failing to CWC would yield estimates of total effects (i.e., $\gamma_{10}, \gamma_{20}, \gamma_{30}, \gamma_{40}$) that are a blend of the relevant adolescent-level (or within) effect and school-level (or between) effect (17). This model can be written:

$$RSB_{yj} = \beta_{0j} + \beta_{1j} \left( PA_{yj} - \bar{PA}_{j} \right) + \beta_{2j} \left( SF_{yj} - \bar{SF}_{j} \right) + \beta_{3j} \left( GAP_{yj} - \bar{GAP}_{j} \right) + \beta_{4j} \left( FAM_{yj} - \bar{FAM}_{j} \right) + r_{yj}$$

$$\beta_{0j} = \gamma_{00} + u_{0j}$$
$$\beta_{1j} = \gamma_{10}$$
$$\beta_{2j} = \gamma_{20}$$
$$\beta_{3j} = \gamma_{30}$$
$$\beta_{4j} = \gamma_{40} + u_{4j}$$

$u_{0j} =$ unique effect of the $j^{th}$ school on grand mean risky sexual behavior across schools

$u_{4j} =$ unique effect of the $j^{th}$ school on the average change in expected risky sexual behavior across schools given a one-unit increase in family functioning (after controlling for the effect of peer abstinence, adolescent functioning in school, and gap between parental and adolescents Americanism at Level-1).

$\tau_{44} =$ unconditional variance of the $u_{4j}$ (or equivalently, the $\beta_{4j}$).
\( \tau_{04} = \) unconditional school-level covariance between the \( u_{0j} \) and the \( u_{4j} \) (or equivalently, the \( \beta_{0j} \) and the \( \beta_{4j} \), respectively).

As can be viewed in Table 1, while the average change in expected risky sexual behavior across schools given a one-unit increase in family functioning was statistically non-significant, \( \hat{\tau}_{40} = -0.026, p = .068 \), the variance around this average was statistically significant, \( \hat{\tau}_{44} = 0.018, p < .001 \). The statistical significance of \( \hat{\tau}_{44} \) suggested that there was substantial variance in this set of within-school slopes that may be explained by the Level-2 predictors (i.e., treating this slope as an outcome – see Model 6). The covariance between the set of unadjusted risky sexual behavior school means and the set of within-school risky sexual behavior on family functioning slopes was not statistically significant, \( \hat{\tau}_{04} = 0.001, p = .900 \).
Figure 5. Random coefficients regression:

\[ Y_{ij} = \gamma_{00} + \gamma_{10} (X_{1ij} - \bar{X}_{1}^{*j}) + \gamma_{20} (X_{2ij} - \bar{X}_{2}^{*j}) + \gamma_{30} (X_{3ij} - \bar{X}_{3}^{*j}) + \gamma_{40} (X_{4ij} - \bar{X}_{4}^{*j}) \\
+ u_{ij} + u_{4j} (X_{4ij} - \bar{X}_{4}^{*j}) + r_{ij}. \]
Figure 6. Intercepts and slopes as outcomes:

\[
Y_{ij} = \gamma_{00} + \gamma_{01}(\bar{X}_{1,i} - \bar{X}_{1..}) + \gamma_{02}(\bar{X}_{2,i} - \bar{X}_{2..}) + \gamma_{03}(\bar{X}_{3,i} - \bar{X}_{3..}) + \gamma_{04}(\bar{X}_{4,i} - \bar{X}_{4..}) \\
+ \gamma_{10}(X_{1ij} - \bar{X}_{1,j}) + \gamma_{20}(X_{2ij} - \bar{X}_{2,j}) + \gamma_{24}\left((X_{2ij} - \bar{X}_{2,j})^* (\bar{X}_{4,j} - \bar{X}_{4..})\right) \\
+ \gamma_{30}(X_{3ij} - \bar{X}_{3,j}) + \gamma_{40}(X_{4ij} - \bar{X}_{4,j}) + \gamma_{43}\left((X_{4ij} - \bar{X}_{4,j})^* (\bar{X}_{3,j} - \bar{X}_{3..})\right) \\
+ u_{0j} + u_{4j}(X_{4ij} - \bar{X}_{4,j}) + r_{ij}.
\]
**Figure 7. Stress Management Example:**

\[
Y_{mij} = \gamma_{000} + \gamma_{001}W_j + \gamma_{100}A_{mij} + \gamma_{101}(A_{mij} \times W_j) \\
+ u_{00j} + u_{10j}A_{mij} + r_{0ij} + r_{1ij}A_{mij} + e_{mij}.
\]
\[ Y_{mij} = \text{observed quality of life at time } m \text{ for the } i^{th} \text{ participant in the } j^{th} \text{ therapist} \]

\[ e_{mij} = \text{residual quality of life at time } m \text{ for the } i^{th} \text{ participant in the } j^{th} \text{ therapist} \]

\[ r_{0ij} = \text{unique effect of the } i^{th} \text{ participant on mean expected quality of life at baseline in the } j^{th} \text{ therapist} \]

\[ r_{1ij} = \text{unique effect of the } i^{th} \text{ participant on mean expected rate of weekly linear change in quality of life in the } j^{th} \text{ therapist} \]

\[ \gamma_{00} = \text{expected quality of life at baseline for participants in the control condition} \]

\[ \gamma_{01} = \text{difference in expected quality of life at baseline for participants in the experimental condition as compared to the control condition} \]

\[ u_{0ij} = \text{residual quality of life at baseline in the } j^{th} \text{ therapist after controlling for the treatment effect} \]

\[ \gamma_{10} = \text{expected rate of weekly linear change in quality of life for participants in the control condition} \]

\[ \gamma_{11} = \text{difference in expected rate of weekly linear change in quality of life for participants in the experimental condition as compared to the control condition} \]

\[ u_{10j} = \text{residual rate of weekly linear change in quality of life in the } j^{th} \text{ therapist after controlling for the treatment effect} \]
Appendix C

Input and key output from Mplus and SAS
(some brief annotations, ! or /*, of input are provided below)

Mplus Input for Model 1: One-Way ANOVA with Random Effects

TITLE: Model 1 1WARE
DATA: FILE = dataset_1.dat;
VARIABLE: NAMES ARE RSB PA SF GAP FAM
          PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;
          USEARIABLES = RSB;
          CLUSTER = CLUSTER;
! Identifies the name of the cluster variable(s) in the dataset
ANALYSIS: TYPE = TWOLEVEL;
! Allows for multilevel model with random intercepts
MODEL:  %WITHIN%
          RSB;
! Describes the Level-1 part of a two-level model
%BETWEEN%
          RSB;
! Describes the Level-2 part of a two-level model

Key Mplus Output for Model 1: One-Way ANOVA with Random Effects

Estimated Intraclass Correlations for the Y Variables
RSB  0.064

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<tr>
<td>RSB</td>
<td>1.058</td>
<td>0.053</td>
<td>20.142</td>
<td>0.000</td>
</tr>
<tr>
<td>Between Level Means</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.040</td>
<td>0.033</td>
<td>1.215</td>
<td>0.224</td>
</tr>
<tr>
<td>Variances</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.072</td>
<td>0.013</td>
<td>5.620</td>
<td>0.000</td>
</tr>
</tbody>
</table>
**Mplus Input for Parallel Fixed Effects Linear Regression Model**

```
TITLE:     Model 1 linear regression
DATA:      FILE = Dataset_1.dat;
VARIABLE:  NAMES ARE RSB PA SF GAP FAM
           PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;
           USEVARIABLES = RSB;
MODEL:     RSB;
```

**Key Mplus Output for Parallel Fixed Effects Linear Regression Model**

```
MODEL RESULTS

Means
   RSB          0.041     0.020     2.060   0.039

Variances
   RSB          1.130     0.030    37.878   0.000
```
SAS Input for Model 1: One-Way ANOVA with Random Effects

/*Invoking glimmix which subsumes mixed*/
/*empirical requests empirical sandwich estimator*/
/*noclprint prevents printing of class level information*/
Proc glimmix data=dataset_1 empirical noclprint;
  class school;
  /* The /solution requests print estimates of fixed effects*/
  model RSB= / solution;
  /*Random statement to indicate random effects*/
  random intercept / subject=school type=un;
run;

Key SAS Output for Model 1: One-Way ANOVA with Random Effects

<table>
<thead>
<tr>
<th>Cov Parm</th>
<th>Subject</th>
<th>Estimate</th>
<th>Standard Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>UN(1,1)</td>
<td>school</td>
<td>0.07301</td>
<td>0.01566</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>1.0580</td>
<td>0.02843</td>
</tr>
</tbody>
</table>

| Effect   | Estimate | Standard Error | DF | t Value | Pr > |t| |
|----------|----------|----------------|----|---------|------|---|
| Intercept| 0.04013  | 0.03302        | 99 | 1.22    | 0.2271 |
SAS Input for Parallel Fixed Effects Linear Regression Model

```
proc reg data=mlrmcomplete;
model RSB=;
run;
```

Key SAS Output for Parallel Fixed Effects Linear Regression Model

<table>
<thead>
<tr>
<th>Cov Parm</th>
<th>Estimate</th>
<th>Standard Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>0.000552</td>
<td></td>
</tr>
<tr>
<td>Residual</td>
<td>1.1304</td>
<td>0.02985</td>
</tr>
</tbody>
</table>

| Variable | Label     | DF | Parameter Estimate | Standard Error | t Value | Pr > |t| |
|----------|-----------|----|--------------------|----------------|---------|-------|
| Intercept| Intercept | 1  | 0.04088            | 0.01985        | 2.06    | 0.0395 |
### Mplus Input for Model 2: Means as Outcomes Regression Model

```
TITLE: Model 2 Means as outcomes
DATA:  FILE = dataset_1.dat;
VARIABLE: NAMES ARE RSB PA SF GAP FAM
PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;
USEVARIABLES = RSB PA_L2 SF_L2 GAP_L2 FAM_L2;
CLUSTER = CLUSTER;
! Identifies the name of the cluster variable(s) in the dataset
BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2;
! Identifies variables observed at Level-2
CENTERING = GRANDMEAN (PA_L2 SF_L2 GAP_L2 FAM_L2);
! Identifies variables to be centered at the grand mean
ANALYSIS: TYPE = TWOLEVEL;
! Allows for multilevel model with random intercepts
MODEL:  %WITHIN%
RSB;
! Describes the Level-1 part of a two-level model
%BETWEEN%
RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
! Describes the Level-2 part of a two-level model
```

### Key Mplus Output for Model 2: Means as Outcomes Regression Model

<table>
<thead>
<tr>
<th>MODEL RESULTS</th>
<th>Estimate</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>Two-Tailed P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Within Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Variances</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>1.058</td>
<td>0.053</td>
<td>20.139</td>
<td>0.000</td>
</tr>
<tr>
<td><strong>Between Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB ON</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PA_L2</td>
<td>0.020</td>
<td>0.031</td>
<td>0.657</td>
<td>0.511</td>
</tr>
<tr>
<td>SF_L2</td>
<td>0.030</td>
<td>0.042</td>
<td>0.716</td>
<td>0.474</td>
</tr>
<tr>
<td>GAP_L2</td>
<td>0.036</td>
<td>0.014</td>
<td>2.548</td>
<td>0.011</td>
</tr>
<tr>
<td>FAM_L2</td>
<td>-0.007</td>
<td>0.047</td>
<td>-0.158</td>
<td>0.874</td>
</tr>
<tr>
<td><strong>Intercepts</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.039</td>
<td>0.031</td>
<td>1.253</td>
<td>0.210</td>
</tr>
<tr>
<td><strong>Residual Variances</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.061</td>
<td>0.011</td>
<td>5.618</td>
<td>0.000</td>
</tr>
</tbody>
</table>

### R-SQUARE

<table>
<thead>
<tr>
<th>Between Level</th>
<th>Estimated</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>Two-Tailed P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Observed</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.153</td>
<td>0.086</td>
<td>1.780</td>
<td>0.075</td>
</tr>
</tbody>
</table>
SAS Input for Model 2: Means as Outcomes Regression Model

/*Invoking glimmix which subsumes mixed*/
/*empirical requests empirical sandwich estimator*/
/*noclprint prevents printing of class level information*/
proc glimmix data=dataset_1 empirical noclprint;
class school;
/*ddfm=bw asks SAS to use the between/within method for computing denominator
degrees of freedom for tests of fixed effects*/
model RSB=PA.\_\_\_PA. SF.\_\_\_SF. GAP.\_\_\_GAP. FAM.\_\_\_FAM. / solution ddfm=bw;
/*type=un asks SAS to treat the variance-covariance matrix as unstructured*/
random intercept / subject=school type=un;
run;

Key SAS Output for Model 2: Means as Outcomes Regression Model

<table>
<thead>
<tr>
<th>Covariance Parameter Estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cov Parm</td>
</tr>
<tr>
<td>----------</td>
</tr>
<tr>
<td>UN(1,1)</td>
</tr>
<tr>
<td>Residual</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Solutions for Fixed Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td>Effect</td>
</tr>
<tr>
<td>--------</td>
</tr>
<tr>
<td>Intercept</td>
</tr>
<tr>
<td>PA.___PA.</td>
</tr>
<tr>
<td>SF.___SF.</td>
</tr>
<tr>
<td>GAP.___GAP.</td>
</tr>
<tr>
<td>FAM.___FAM.</td>
</tr>
</tbody>
</table>
**Mplus Input for Model 3: One-Way ANCOVA with Random Effects**

TITLE:  Model 3 ANCOVA random int  
DATA:  FILE = dataset_1.dat;  
VARIABLE:  NAMES ARE RSB PA SF GAP FAM  
          PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;  
USEVARIABLES = RSB PA SF GAP FAM  
               PA_L2 SF_L2 GAP_L2 FAM_L2;  
CLUSTER = CLUSTER;  
! Identifies the name of the cluster variable(s) in the dataset  
CENTERING = GRANDMEAN (PA SF GAP FAM  
               PA_L2 SF_L2 GAP_L2 FAM_L2);  
! Identifies variables to be centered at the grand mean  
WITHIN = PA SF GAP FAM;  
! Identifies variables observed at Level-1  
BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2;  
! Identifies variables observed at Level-2  
ANALYSIS:  TYPE = TWOLEVEL;  
! Allows for multilevel model with random intercepts  
MODEL:  %WITHIN%  
      RSB ON PA SF GAP FAM;  
! Describes the Level-1 part of a two-level model  
%BETWEEN%  
      RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;  
! Describes the Level-2 part of a two-level model
## Key Mplus Output for Model 3: One-Way ANCOVA with Random Effects

### MODEL RESULTS

<table>
<thead>
<tr>
<th>Within Level</th>
<th>Estimate</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>RSB ON PA</td>
<td>-0.017</td>
<td>0.003</td>
<td>-4.935</td>
<td>0.000</td>
</tr>
<tr>
<td>RSB ON SF</td>
<td>-0.009</td>
<td>0.003</td>
<td>-2.630</td>
<td>0.009</td>
</tr>
<tr>
<td>RSB ON GAP</td>
<td>0.011</td>
<td>0.002</td>
<td>5.970</td>
<td>0.000</td>
</tr>
<tr>
<td>RSB ON FAM</td>
<td>-0.034</td>
<td>0.016</td>
<td>-2.167</td>
<td>0.030</td>
</tr>
</tbody>
</table>

### Residual Variances

| RSB | 1.012 | 0.048 | 21.134 | 0.000 |

<table>
<thead>
<tr>
<th>Between Level</th>
<th>Estimate</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>RSB ON PA L2</td>
<td>0.023</td>
<td>0.032</td>
<td>0.704</td>
<td>0.482</td>
</tr>
<tr>
<td>RSB ON SF L2</td>
<td>0.037</td>
<td>0.044</td>
<td>0.841</td>
<td>0.400</td>
</tr>
<tr>
<td>RSB ON GAP L2</td>
<td>0.035</td>
<td>0.014</td>
<td>2.458</td>
<td>0.014</td>
</tr>
<tr>
<td>RSB ON FAM L2</td>
<td>-0.010</td>
<td>0.047</td>
<td>-0.206</td>
<td>0.837</td>
</tr>
</tbody>
</table>

### Intercepts

| RSB | 0.039 | 0.032 | 1.230 | 0.219 |

### Residual Variances

| RSB | 0.065 | 0.012 | 5.490 | 0.000 |

### R-SQUARE

<table>
<thead>
<tr>
<th>Within Level</th>
<th>Two-Tailed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>Estimate</td>
</tr>
<tr>
<td>RSB</td>
<td>0.043</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Between Level</th>
<th>Two-Tailed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>Estimate</td>
</tr>
<tr>
<td>RSB</td>
<td>0.138</td>
</tr>
</tbody>
</table>
SAS Input for Model 3: One-Way ANCOVA with Random Effects

/*Invoking glimmix which subsumes mixed*/
/*empirical requests empirical sandwich estimator*/
/*noclprint prevents printing of class level information*/
proc glimmix data=dataset_1 empirical noclprint;
    class school;
    /*ddfm=bw asks SAS to use the between/within method for computing denominator
degrees of freedom for tests of fixed effects*/
    model RSB= PA_{j}..SF_{j}..GAP_{j}..FAM_{j}..PA_{ij}..SF_{ij}..GAP_{ij}..FAM_{ij}.. / solution ddfm=bw;
    /*type=un asks SAS to treat the variance-covariance matrix as unstructured*/
    random intercept / subject=school type=un;
run;

Key SAS Output for Model 3: One-Way ANCOVA with Random Effects

<table>
<thead>
<tr>
<th>Covariance Parameter Estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cov Parm</td>
</tr>
<tr>
<td>UN(1,1)</td>
</tr>
<tr>
<td>Residual</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Solutions for Fixed Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td>Effect</td>
</tr>
<tr>
<td>Intercept</td>
</tr>
<tr>
<td>PA_{j}..PA_{j}..</td>
</tr>
<tr>
<td>SF_{j}..SF_{j}..</td>
</tr>
<tr>
<td>GAP_{j}..GAP_{j}..</td>
</tr>
<tr>
<td>FAM_{j}..FAM_{j}..</td>
</tr>
<tr>
<td>PA_{ij}..PA_{ij}..</td>
</tr>
<tr>
<td>SF_{ij}..SF_{ij}..</td>
</tr>
<tr>
<td>GAP_{ij}..GAP_{ij}..</td>
</tr>
<tr>
<td>FAM_{ij}..FAM_{ij}..</td>
</tr>
</tbody>
</table>
**Mplus Input for Model 4: Non-Randomly Varying Slopes**

**TITLE:** Model 4 Non-randomly varying slopes_2  
**DATA:** FILE = dataset_1.dat;  
**VARIABLE:** NAMES ARE RSB PA SF GAP FAM  
PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;  
USEVARIABLES = RSB PA SF GAP FAM  
PA_L2 SF_L2 GAP_L2 FAM_L2;  
CLUSTER = CLUSTER;  
! Identifies the name of the cluster variable(s) in the dataset  
CENTERING = GRANDMEAN (PA SF GAP FAM  
PA_L2 SF_L2 GAP_L2 FAM_L2);  
! Identifies variables to be centered at the grand mean  
WITHIN = PA SF GAP FAM;  
! Identifies variables observed at Level-1  
BETWEEN = PA L2 SF L2 GAP L2 FAM L2;  
! Identifies variables observed at Level-2  
**ANALYSIS:** TYPE = TWOLEVEL RANDOM;  
! Allows for multilevel model with random intercepts and slopes  
**MODEL:**  
%WITHIN%  
RSB ON PA GAP FAM;  
slope_2 | RSB ON SF;  
! Describes the Level-1 part of a two-level model  
%BETWEEN%  
RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;  
slope_2 ON FAM_L2;  
slope_2@0;  
! Describes the Level-2 part of a two-level model  
**OUTPUT:** tech1 tech3;  
! Provides some information necessary for calculations of regions of significance  
**SAVEDATA:** TECH3 IS tech3.dat;  
! Provides some data necessary for calculations of regions of significance
Key *Mplus* Output for Model 4: Non-Randomly Varying Slopes

<table>
<thead>
<tr>
<th>MODEL RESULTS</th>
<th>Estimate</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Within Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB ON PA</td>
<td>-0.016</td>
<td>0.003</td>
<td>-4.858</td>
<td>0.000</td>
</tr>
<tr>
<td>RSB ON GAP</td>
<td>0.010</td>
<td>0.002</td>
<td>5.653</td>
<td>0.000</td>
</tr>
<tr>
<td>RSB ON FAM</td>
<td>-0.033</td>
<td>0.016</td>
<td>-2.153</td>
<td>0.031</td>
</tr>
<tr>
<td>Residual Variances</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.961</td>
<td>0.047</td>
<td>20.398</td>
<td>0.000</td>
</tr>
<tr>
<td><strong>Between Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLOPE_2 ON FAM_L2</td>
<td>-0.011</td>
<td>0.002</td>
<td>-6.878</td>
<td>0.000</td>
</tr>
<tr>
<td>SLOPE_2 ON RSB</td>
<td>0.016</td>
<td>0.034</td>
<td>0.472</td>
<td>0.637</td>
</tr>
<tr>
<td>SLOPE_2 ON SF_L2</td>
<td>0.025</td>
<td>0.046</td>
<td>0.541</td>
<td>0.588</td>
</tr>
<tr>
<td>SLOPE_2 ON GAP_L2</td>
<td>0.036</td>
<td>0.015</td>
<td>2.437</td>
<td>0.015</td>
</tr>
<tr>
<td>SLOPE_2 ON FAM_L2</td>
<td>-0.003</td>
<td>0.048</td>
<td>-0.067</td>
<td>0.947</td>
</tr>
<tr>
<td>Intercepts</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.037</td>
<td>0.032</td>
<td>1.142</td>
<td>0.253</td>
</tr>
<tr>
<td>SLOPE_2</td>
<td>-0.008</td>
<td>0.003</td>
<td>-2.548</td>
<td>0.011</td>
</tr>
<tr>
<td>Residual Variances</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.070</td>
<td>0.013</td>
<td>5.239</td>
<td>0.000</td>
</tr>
<tr>
<td>SLOPE_2</td>
<td>0.000</td>
<td>0.000</td>
<td>999.000</td>
<td>999.000</td>
</tr>
</tbody>
</table>
SAS Input for Model 4: Non-Randomly Varying Slopes

/*Invoking glimmix which subsumes mixed*/
/*empirical requests empirical sandwich estimator*/
/*noclprint prevents printing of class level information*/
proc glimmix data=dataset_1 empirical noclprint noitprint;
  class school;
  model RSB=PA_{ij}-PA_{..} SF_{ij}-SF_{..} GAP_{ij}-GAP_{..} FAM_{ij}-FAM_{..} PA_{ij}-PA_{..} SF_{ij}-SF_{..} GAP_{ij}-GAP_{..} FAM_{ij}-FAM_{..} SF_{ij}-SF_{..} FAM_{ij}-FAM_{..} / solution ddfm=bw;
  random intercept / subject=school type=un;
run;

Key SAS Output for Model 4: Non-Randomly Varying Slopes

<table>
<thead>
<tr>
<th>Covariance Parameter Estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cov Parm</td>
</tr>
<tr>
<td>UN(1,1)</td>
</tr>
<tr>
<td>Residual</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Solutions for Fixed Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td>Effect</td>
</tr>
<tr>
<td>Intercept</td>
</tr>
<tr>
<td>PA_{ij}-PA_{..}</td>
</tr>
<tr>
<td>SF_{ij}-SF_{..}</td>
</tr>
<tr>
<td>GAP_{ij}-GAP_{..}</td>
</tr>
<tr>
<td>FAM_{ij}-FAM_{..}</td>
</tr>
<tr>
<td>PA_{ij}-PA_{..}</td>
</tr>
<tr>
<td>SF_{ij}-SF_{..}</td>
</tr>
<tr>
<td>GAP_{ij}-GAP_{..}</td>
</tr>
<tr>
<td>FAM_{ij}-FAM_{..}</td>
</tr>
<tr>
<td>SF_{ij}-SF_{..} FAM_{ij}-FAM_{..}</td>
</tr>
</tbody>
</table>
**Mplus Input for Model 5: Random Coefficients Regression**

**TITLE:** Model 5 Random coefficients regression_2  
**DATA:** FILE = dataset_1.dat;  
**VARIABLE:** NAMES ARE RSB PA SF GAP FAM  
  PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;  
  USEVARIABLES = RSB PA SF GAP FAM;  
  CLUSTER = CLUSTER;  
  ! Identifies the name of the cluster variable(s) in the dataset  
  CENTERING = GROUPMEAN (PA SF GAP FAM);  
  ! Identifies variables to be centered at the cluster mean  
  WITHIN = PA SF GAP FAM;  
  ! Identifies variables observed at Level-1  
**ANALYSIS:** TYPE = TWOLEVEL RANDOM;  
  ! Allows for multilevel model with random intercepts and slopes  
**MODEL:**  
  %WITHIN%  
  RSB ON PA SF GAP;  
  slope_4 | RSB ON FAM;  
  ! Describes the Level-1 part of a two-level model  
  %BETWEEN%  
  RSB WITH slope_4;  
  ! Describes the Level-2 part of a two-level model

**Key Mplus Output for Model 5: Random Coefficients Regression**

<table>
<thead>
<tr>
<th>MODEL RESULTS</th>
<th>Estimate</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>Two-Tailed P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Within Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB ON PA</td>
<td>-0.015</td>
<td>0.003</td>
<td>-4.820</td>
<td>0.000</td>
</tr>
<tr>
<td>RSB ON SF</td>
<td>-0.008</td>
<td>0.003</td>
<td>-2.551</td>
<td>0.011</td>
</tr>
<tr>
<td>RSB ON GAP</td>
<td>0.010</td>
<td>0.002</td>
<td>6.346</td>
<td>0.000</td>
</tr>
<tr>
<td>Residual Variances</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.747</td>
<td>0.019</td>
<td>38.904</td>
<td>0.000</td>
</tr>
<tr>
<td><strong>Between Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB WITH SLOPE_4</td>
<td>0.001</td>
<td>0.005</td>
<td>0.126</td>
<td>0.900</td>
</tr>
<tr>
<td>Means</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.040</td>
<td>0.033</td>
<td>1.212</td>
<td>0.225</td>
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<tr>
<td>SLOPE_4</td>
<td>-0.026</td>
<td>0.014</td>
<td>-1.825</td>
<td>0.068</td>
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<tr>
<td>Variances</td>
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<td></td>
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<tr>
<td>RSB</td>
<td>0.083</td>
<td>0.013</td>
<td>6.396</td>
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</tr>
<tr>
<td>SLOPE_4</td>
<td>0.018</td>
<td>0.003</td>
<td>6.276</td>
<td>0.000</td>
</tr>
</tbody>
</table>
SAS Input for Model 5: Random Coefficients Regression

```sas
/*Invoking glimmix which subsumes mixed*/
/*empirical requests empirical sandwich estimator*/
/*noclprint prevents printing of class level information*/
proc glimmix data=dataset_1 empirical noclprint noitprint;
class school;
  /*ddfm=bw asks SAS to use the between/within method for computing denominator
degrees of freedom for tests of fixed effects*/
model RSB = PA_ij - PA_.j SF_ij - SF_.j GAP_ij - GAP_.j FAM_ij - FAM_.j / solution ddfm=bw;
  /*type=un asks SAS to treat the variance-covariance matrix as unstructured*/
random intercept FAM_ij - FAM_.j / subject=school type=un;
run;
```

Key SAS Output for Model 5: Random Coefficients Regression

### Covariance Parameter Estimates

<table>
<thead>
<tr>
<th>Cov Parm</th>
<th>Subject</th>
<th>Estimate</th>
<th>Standard Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>UN(1,1)</td>
<td>school</td>
<td>0.07297</td>
<td>0.01566</td>
</tr>
<tr>
<td>UN(2,1)</td>
<td>school</td>
<td>0.001018</td>
<td>0.001736</td>
</tr>
<tr>
<td>UN(2,2)</td>
<td>school</td>
<td>7.01E-24</td>
<td></td>
</tr>
<tr>
<td>Residual</td>
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<td>1.0589</td>
<td>0.02848</td>
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</tbody>
</table>

### Solutions for Fixed Effects

<table>
<thead>
<tr>
<th>Effect</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>DF</th>
<th>t Value</th>
<th>Pr &gt;</th>
<th>t</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>0.04018</td>
<td>0.03301</td>
<td>99</td>
<td>1.22</td>
<td>0.2264</td>
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<tr>
<td>PA_ij - PA_.j</td>
<td>0.002003</td>
<td>0.002798</td>
<td>2765</td>
<td>0.72</td>
<td>0.4741</td>
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</tr>
<tr>
<td>SF_ij - SF_.j</td>
<td>0.003107</td>
<td>0.002451</td>
<td>2765</td>
<td>1.27</td>
<td>0.2049</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP_ij - GAP_.j</td>
<td>0.000289</td>
<td>0.001858</td>
<td>2765</td>
<td>0.16</td>
<td>0.8766</td>
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<td></td>
</tr>
<tr>
<td>FAM_ij - FAM_.j</td>
<td>0.002538</td>
<td>0.005917</td>
<td>2765</td>
<td>0.43</td>
<td>0.6680</td>
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<td></td>
</tr>
</tbody>
</table>
**Mplus Input for Model 6: Intercepts and Slopes as Outcomes**

```
TITLE:    Model 6 Intercepts and slopes as outcomes
DATA:     FILE = dataset_1.dat;
VARIABLE: NAMES ARE RSB PA SF GAP FAM
          PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;
USEVARIABLES = RSB PA SF GAP FAM
          PA_L2 SF_L2 GAP_L2 FAM_L2;
CLUSTER = CLUSTER;
! Identifies the name of the cluster variable(s) in the dataset
CENTERING = GROUPMEAN (PA SF GAP FAM);
! Identifies variables to be centered at the cluster mean
CENTERING = GRANDMEAN (PA_L2 SF_L2 GAP_L2 FAM_L2);
! Identifies variables to be centered at the grand mean
WITHIN = PA SF GAP FAM;
! Identifies variables observed at Level-1
BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2;
! Identifies variables observed at Level-2
ANALYSIS: TYPE = TWOLEVEL RANDOM;
! Allows for multilevel model with random intercepts and slopes
MODEL:    %WITHIN%
          RSB ON PA GAP;
          slope_2 | RSB ON SF;
          slope_4 | RSB ON FAM;
! Describes the Level-1 part of a two-level model
%BETWEEN%
          RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
          slope_2 ON FAM_L2;
          slope_4 ON GAP_L2;
          RSB WITH slope_4;
          slope_2@0;
! Describes the Level-2 part of a two-level model
```
### Key Mplus Output for Model 6: Intercepts and Slopes as Outcomes

**MODEL RESULTS**

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Within Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB ON</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PA</td>
<td>-0.015</td>
<td>0.003</td>
<td>-4.756</td>
<td>0.000</td>
</tr>
<tr>
<td>GAP</td>
<td>0.010</td>
<td>0.002</td>
<td>6.105</td>
<td>0.000</td>
</tr>
<tr>
<td>Residual Variances</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.711</td>
<td>0.019</td>
<td>36.964</td>
<td>0.000</td>
</tr>
<tr>
<td><strong>Between Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLOPE_2 ON</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FAM_L2</td>
<td>-0.009</td>
<td>0.001</td>
<td>-6.416</td>
<td>0.000</td>
</tr>
<tr>
<td>SLOPE_4 ON</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP_L2</td>
<td>0.017</td>
<td>0.004</td>
<td>4.028</td>
<td>0.000</td>
</tr>
<tr>
<td>RSB ON</td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>PA_L2</td>
<td>0.025</td>
<td>0.031</td>
<td>0.801</td>
<td>0.423</td>
</tr>
<tr>
<td>SF_L2</td>
<td>0.037</td>
<td>0.041</td>
<td>0.888</td>
<td>0.374</td>
</tr>
<tr>
<td>GAP_L2</td>
<td>0.037</td>
<td>0.014</td>
<td>2.572</td>
<td>0.010</td>
</tr>
<tr>
<td>FAM_L2</td>
<td>-0.009</td>
<td>0.048</td>
<td>-0.186</td>
<td>0.853</td>
</tr>
<tr>
<td>RSB WITH SLOPE_4</td>
<td>-0.005</td>
<td>0.004</td>
<td>-1.223</td>
<td>0.221</td>
</tr>
<tr>
<td><strong>Intercepts</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.039</td>
<td>0.031</td>
<td>1.238</td>
<td>0.216</td>
</tr>
<tr>
<td>SLOPE_2</td>
<td>-0.007</td>
<td>0.003</td>
<td>-2.523</td>
<td>0.012</td>
</tr>
<tr>
<td>SLOPE_4</td>
<td>-0.027</td>
<td>0.013</td>
<td>-2.012</td>
<td>0.044</td>
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<tr>
<td><strong>Residual Variances</strong></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.073</td>
<td>0.011</td>
<td>6.657</td>
<td>0.000</td>
</tr>
<tr>
<td>SLOPE_2</td>
<td>0.000</td>
<td>0.000</td>
<td>999.000</td>
<td>999.000</td>
</tr>
<tr>
<td>SLOPE_4</td>
<td>0.015</td>
<td>0.002</td>
<td>6.137</td>
<td>0.000</td>
</tr>
</tbody>
</table>
SAS Input for Model 6: Intercepts and Slopes as Outcomes

/*Invoking glimmix which subsumes mixed*/
/*empirical requests empirical sandwich estimator*/
/*noclprint prevents printing of class level information*/
proc glimmix data=dataset_1 empirical noclprint noitprint;
  class school;
  /*ddfm=bw asks SAS to use the between/within method for computing denominator
degrees of freedom for tests of fixed effects*/
  /*type=un asks SAS to treat the variance-covariance matrix as unstructured*/
  random intercept FAM,.j - FAM.. / subject=school type=un;
run;

SAS Output for Model 6: Intercepts and Slopes as Outcomes

<table>
<thead>
<tr>
<th>Cov Parm</th>
<th>Subject</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Z Value</th>
<th>Pr Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>UN(1,1)</td>
<td>school</td>
<td>0.06576</td>
<td>0.01497</td>
<td>4.39</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>UN(2,1)</td>
<td>school</td>
<td>0.000226</td>
<td>0.001727</td>
<td>0.13</td>
<td>0.8957</td>
</tr>
<tr>
<td>UN(2,2)</td>
<td>school</td>
<td>0</td>
<td>.</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>1.0588</td>
<td>0.02849</td>
<td>37.17</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

| Effect    | Estimate | Standard Error | DF | t Value | Pr > |t|  |
|-----------|----------|----------------|----|---------|------|------|
| Intercept | 0.03922  | 0.03132        | 95 | 1.25    | 0.2136|
| PA,.j - PA.. | 0.02064  | 0.03106        | 95 | 0.66    | 0.5079|
| SF,.j - SF.. | 0.03049  | 0.04235        | 95 | 0.72    | 0.4734|
| GAP,.j - GAP.. | 0.03626  | 0.01418        | 95 | 2.56    | 0.0121|
| FAM,.j - FAM.. | -0.00718 | 0.04710        | 95 | -0.15   | 0.8792|
| PA,.j - PA.. | 0.002165 | 0.002785       | 2763| 0.78    | 0.4370|
| SF,.j - SF.. | 0.003324 | 0.002449       | 2763| 1.36    | 0.1748|
| GAP,.j - GAP.. | 0.000223 | 0.001848       | 2763| 0.12    | 0.9039|
| FAM,.j - FAM.. | 0.002588 | 0.005838       | 2763| 0.44    | 0.6576|
| SF,.j - SF.. * FAM,.j - FAM.. | -0.00099 | 0.001363       | 2763| -0.72   | 0.4688|
| FAM,.j - FAM.. * GAP,.j - GAP.. | 0.002135 | 0.002125       | 2763| 1.00    | 0.3151|
**Mplus Input for Model 6 with Regard to Sample Sizes and Power: Step 1 Real Data Analysis**

```plaintext
TITLE: Model 6 with Regard to Sample Sizes and Power: Step 1 Real Data Analysis
DATA: FILE = dataset_2.dat;
VARIABLE: NAMES ARE RSB PA SF GAP FAM PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;
USEVARIABLES = RSB PA SF GAP FAM PA_L2 SF_L2 GAP_L2 FAM_L2;
CLUSTER = CLUSTER;
! Identifies the name of the cluster variable(s) in the dataset
CENTERING = GROUPMEAN (PA SF GAP FAM);
! Identifies variables to be centered at the cluster mean
CENTERING = GRANDMEAN (PA_L2 SF_L2 GAP_L2 FAM_L2);
! Identifies variables to be centered at the grand mean
WITHIN = PA SF GAP FAM;
! Identifies variables observed at Level-1
BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2;
! Identifies variables observed at Level-2
ANALYSIS: TYPE = TWOLEVEL RANDOM;
! Allows for multilevel model with random intercepts and slopes
MODEL: %WITHIN%
  RSB ON PA GAP;
  slope_2 | RSB ON SF;
  slope_4 | RSB ON FAM;
! Describes the Level-1 part of a two-level model
%BETWEEN%
  RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
  slope_2 ON FAM_L2;
  slope_4 ON GAP_L2;
  RSB WITH slope_4;
  slope_2@0;
! Describes the Level-2 part of a two-level model
SAVEDATA: ESTIMATES = Step_1.dat;
! Save parameter estimates for subsequent use in Step 2
```
Mplus Input for Model 6 with Regard to Sample Sizes and Power: Step 2 Monte Carlo Simulation ($J = 25$)

TITLE: Model 6 with Regard to Sample Sizes and Power Step 2 Monte Carlo Simulation ($J = 25$)
MONTECARLO: NAMES ARE RSB PA SF GAP FAM 
  PA_L2 SF_L2 GAP_L2 FAM_L2; 
  NOBSERVATIONS = 713; 
! Identifies the number of Level-1 observations 
  NREPS = 10000; 
! Identifies the number of replications 
  SEED = 58459; 
! Identifies the starting point for data generation 
  NCSIZES = 7; 
! Identifies the number of unique within-group sizes 
  CSIZES = 2 (22) 2 (26) 6 (27) 3 (29) 5 (30) 6 (31) 1 (32); 
! Identifies the number of clusters for each unique (within-group size) 
  WITHIN = PA SF GAP FAM; 
! Identifies variables observed at Level-1 
  BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2; 
! Identifies variables observed at Level-2 
  POPULATION = Step_1.DAT; 
! Identifies the file containing the population values 
  COVERAGE = Step_1.DAT; 
! Identifies the file containing population values used to compute coverage 
ANALYSIS: TYPE = TWOLEVEL RANDOM; 
! Allows for multilevel model with random intercepts and slopes 
MODEL POPULATION: 
! Identifies the model used to generate the data 
  %WITHIN% 
  RSB ON PA GAP; 
  slope_2 | RSB ON SF; 
  slope_4 | RSB ON FAM; 
! Describes the Level-1 part of a two-level model 
  %BETWEEN% 
  RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2; 
  slope_2 ON FAM_L2; 
  slope_4 ON GAP_L2; 
  RSB WITH slope_4; 
  slope_2@0; 
! Describes the Level-2 part of a two-level model 
MODEL: 
! Identifies the model used to fit the generated data 
  %WITHIN% 
  RSB ON PA GAP; 
  slope_2 | RSB ON SF; 
  slope_4 | RSB ON FAM; 
! Describes the Level-1 part of a two-level model 
  %BETWEEN% 
  RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2; 
  slope_2 ON FAM_L2; 
  slope_4 ON GAP_L2; 
  RSB WITH slope_4; 
  slope_2@0; 
! Describes the Level-2 part of a two-level model
Key *Mplus* Output for Model 6 with Regard Sample Sizes and Power: Step 2 Monte Carlo Simulation ($J = 25$)

<table>
<thead>
<tr>
<th>MODEL RESULTS</th>
<th>ESTIMATES</th>
<th>S. E.</th>
<th>M. S. E.</th>
<th>95% Cover Coeff</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Within Level</strong></td>
<td>Population Average</td>
<td>Std. Dev. Average</td>
<td>M. S. E.</td>
<td>% Sig</td>
</tr>
<tr>
<td>RSB ON PA</td>
<td>-0.14</td>
<td>-0.0141</td>
<td>0.0050</td>
<td>0.0048</td>
</tr>
<tr>
<td>RSB ON GAP</td>
<td>0.01</td>
<td>0.0110</td>
<td>0.0031</td>
<td>0.0029</td>
</tr>
<tr>
<td>Residual Variances</td>
<td>RSB</td>
<td>0.705</td>
<td>0.7011</td>
<td>0.0394</td>
</tr>
<tr>
<td><strong>Between Level</strong></td>
<td>SLOPE_2 ON</td>
<td>FAM_L2</td>
<td>-0.012</td>
<td>-0.0120</td>
</tr>
<tr>
<td>SLOPE_4 ON GAP_L2</td>
<td>0.013</td>
<td>0.0130</td>
<td>0.0090</td>
<td>0.0080</td>
</tr>
<tr>
<td>RSB ON PA_L2</td>
<td>0.022</td>
<td>0.0216</td>
<td>0.0515</td>
<td>0.0413</td>
</tr>
<tr>
<td>RSB ON SF_L2</td>
<td>0.092</td>
<td>0.0917</td>
<td>0.0709</td>
<td>0.0570</td>
</tr>
<tr>
<td>RSB ON GAP_L2</td>
<td>0.033</td>
<td>0.0331</td>
<td>0.0294</td>
<td>0.0243</td>
</tr>
<tr>
<td>RSB ON FAM_L2</td>
<td>-0.014</td>
<td>-0.0138</td>
<td>0.0683</td>
<td>0.0560</td>
</tr>
<tr>
<td>RSB WITH SLOPE_4</td>
<td>-0.009</td>
<td>-0.0082</td>
<td>0.0063</td>
<td>0.0055</td>
</tr>
<tr>
<td><strong>Intercepts</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSB</td>
<td>0.11</td>
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<td>0.0591</td>
<td>0.0518</td>
</tr>
<tr>
<td>SLOPE_2</td>
<td>-0.009</td>
<td>-0.0090</td>
<td>0.0051</td>
<td>0.0049</td>
</tr>
<tr>
<td>SLOPE_4</td>
<td>-0.018</td>
<td>-0.0182</td>
<td>0.0231</td>
<td>0.0217</td>
</tr>
<tr>
<td>Residual Variances</td>
<td>RSB</td>
<td>0.046</td>
<td>0.0334</td>
<td>0.0186</td>
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<tr>
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<td>0.0000</td>
<td>0.0000</td>
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</tr>
<tr>
<td>SLOPE_4</td>
<td>0.010</td>
<td>0.0090</td>
<td>0.0033</td>
<td>0.0029</td>
</tr>
</tbody>
</table>
**Title:** Model 6 with Regard Sample Sizes and Power Step 2 Monte Carlo Simulation

**MONTECARLO**:
- NAMES ARE RSB PA SF GAP FAM PA_L2 SF_L2 GAP_L2 FAM_L2;
- NOBSERVATIONS = 3281;
- NREPS = 10000;
- SEED = 58459;
- NCSIZES = 7;
- CSIZES = 9 (22) 9 (26) 28 (27) 14 (29) 23 (30) 27 (31) 5 (32);
- WITHIN = PA SF GAP FAM;
- BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2;
- POPULATION = Step_1.DAT;
- COVERAGE = Step_1.DAT;
- ANALYSIS: TYPE = TWOLEVEL RANDOM;
- MODEL POPULATION:
  - %WITHIN%
    - RSB ON PA GAP;
    - slope_2 | RSB ON SF;
    - slope_4 | RSB ON FAM;
  - %BETWEEN%
    - RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
    - slope_2 ON FAM_L2;
    - slope_4 ON GAP_L2;
    - RSB WITH slope_4;
    - slope_2@0;
- MODEL:
  - %WITHIN%
    - RSB ON PA GAP;
    - slope_2 | RSB ON SF;
    - slope_4 | RSB ON FAM;
  - %BETWEEN%
    - RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
    - slope_2 ON FAM_L2;
    - slope_4 ON GAP_L2;
    - RSB WITH slope_4;
    - slope_2@0;
- MODEL POPULATION:
### Key Mplus Output for Model 6 with Regard Sample Sizes and Power: Step 2 Monte Carlo Simulation ($J = 115$)

<table>
<thead>
<tr>
<th>MODEL RESULTS</th>
<th>Population</th>
<th>ESTIMATES</th>
<th>S. E.</th>
<th>M. S. E.</th>
<th>95% Cover</th>
<th>% Sig</th>
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<tbody>
<tr>
<td><strong>Within Level</strong></td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>RSB ON</td>
<td></td>
<td></td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>PA</td>
<td>-0.014</td>
<td>-0.0140</td>
<td>0.0023</td>
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<tr>
<td>GAP</td>
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<td>0.0110</td>
<td>0.0014</td>
<td>0.0014</td>
<td>0.0000</td>
<td>0.948</td>
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<tr>
<td>SLOPE_2 ON</td>
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<tr>
<td>FAM_L2</td>
<td>-0.012</td>
<td>-0.0120</td>
<td>0.0013</td>
<td>0.0013</td>
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<tr>
<td>SLOPE_4 ON</td>
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<tr>
<td>GAP_L2</td>
<td>0.013</td>
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<tr>
<td>RSB</td>
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<tr>
<td>PA_L2</td>
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<tr>
<td>SF_L2</td>
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<td>0.0285</td>
<td>0.0274</td>
<td>0.0008</td>
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<tr>
<td>GAP_L2</td>
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<td>0.0331</td>
<td>0.0121</td>
<td>0.0117</td>
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<td>-0.0142</td>
<td>0.0282</td>
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<td>0.0110</td>
<td>0.0255</td>
<td>0.0248</td>
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<td>-0.0090</td>
<td>0.0024</td>
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<td>-0.0178</td>
<td>0.0105</td>
<td>0.0104</td>
<td>0.0001</td>
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<tr>
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<td>0.0094</td>
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<td>0.0001</td>
<td>0.888</td>
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<td>0.0000</td>
<td>0.0000</td>
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<td>SLOPE_4</td>
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<td>0.0016</td>
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<td>0.923</td>
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</table>
**Mplus Input for Model 6 with Regard to Missing Data under Likelihood-Based Approach**

**TITLE:** Model 6 with Regard to Missing Data under Likelihood-Based Approach

**DATA:** FILE = dataset_2_md.dat;

**VARIABLE:** NAMES ARE
- RSB
- PA
- SF
- GAP
- FAM
- PA_L2
- SF_L2
- GAP_L2
- FAM_L2

USEVARIABLES = RSB PA SF GAP FAM  
- PA_L2
- SF_L2
- GAP_L2
- FAM_L2;

CLUSTER = CLUSTER;

! Identifies the name of the cluster variable(s) in the dataset
CENTERING = GROUPMEAN (PA SF GAP FAM);

! Identifies variables to be centered at the cluster mean
CENTERING = GRANDMEAN (PA_L2 SF_L2 GAP_L2 FAM_L2);

! Identifies variables to be centered at the grand mean
WITHIN = PA SF GAP FAM;

! Identifies variables observed at Level-1
BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2;

! Identifies variables observed at Level-2
MISSING ARE ALL (999);

**ANALYSIS:** TYPE = TWOLEVEL RANDOM;

! Allows for multilevel model with random intercepts and slopes
ALGORITHM = INTEGRATION;
INTEGRATION = MONTE;

**MODEL:**

%WITHIN%
- RSB ON PA GAP;
- slope_2 | RSB ON SF;
- slope_4 | RSB ON FAM;
- PA SF GAP FAM;
- [PA@0 SF@0 GAP@0 FAM@0];
- PA WITH SF;
- PA WITH GAP;
- PA WITH FAM;
- SF WITH GAP;
- SF WITH FAM;
- GAP WITH FAM;

! Describes the Level-1 part of a two-level model
%BETWEEN%
- RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
- slope_2 ON FAM_L2;
- slope_4 ON GAP_L2;
- RSB WITH slope_4;
- slope_2@0;

! Describes the Level-2 part of a two-level model
TITLE: Step 1 with Regard to Missing Data in MLRM under Multiple Imputation
DATA: FILE = dataset_2_md.dat;
VARIABLE: NAMES ARE RSB PA SF GAP FAM
          PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;
USEVARIABLES = RSB PA SF GAP FAM
          PA_L2 SF_L2 GAP_L2 FAM_L2;
CLUSTER = CLUSTER;
! Identifies the name of the cluster variable(s) in the dataset
MISSING ARE ALL (999);
CENTERING = GROUPMEAN (PA SF GAP FAM);
! Identifies variables to be centered at the cluster mean
CENTERING = GRANDMEAN (PA_L2 SF_L2 GAP_L2 FAM_L2);
! Identifies variables to be centered at the grand mean
WITHIN = PA SF GAP FAM;
! Identifies variables observed at Level-1
BETWEEN = PA_L2 SF_L2 GAP_L2 FAM_L2;
! Identifies variables observed at Level-2
ANALYSIS: TYPE = TWOLEVEL RANDOM;
! Allows for multilevel model with random intercepts and slopes
ESTIMATOR = BAYES;
MODEL: %WITHIN%
RSB ON PA GAP;
slope_2 | RSB ON SF;
slope_4 | RSB ON FAM;
! Describes the Level-1 part of a two-level model
%BETWEEN%
RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
slope_2 ON FAM_L2;
slope_4 ON GAP_L2;
RSB WITH slope_4;
slope_2@0;
! Describes the Level-2 part of a two-level model
DATA IMPUTATION:
IMPUTE = RSB FAM;
! Identifies names of variables for which missing values will be imputed
SAVE = dataset_*..dat;
! Identifies names of files where imputed datasets will be stored
**Mplus Input for Model 6, Step 2, with Regard to Missing Data under Multiple Imputation**

**TITLE:**    Model 6, Step 2, with Regard to Missing Data under Multiple Imputation

**DATA:**    FILE = dataset_list.dat;
              TYPE = IMPUTATION;

**VARIABLE:** NAMES ARE  RSB PA SF GAP FAM
              PA_L2 SF_L2 GAP_L2 FAM_L2 CLUSTER;

**USEVARIABLES =** RSB PA SF GAP FAM
              PA_L2 SF_L2 GAP_L2 FAM_L2;

**CLUSTER =** CLUSTER;

! Identifies the name of the cluster variable(s) in the dataset
**CENTERING = GROUPMEAN (PA SF GAP FAM);**
! Identifies variables to be centered at the cluster mean
**CENTERING = GRANDMEAN (PA_L2 SF_L2 GAP_L2 FAM_L2);**
! Identifies variables to be centered at the grand mean
**WITHIN =** PA SF GAP FAM;
! Identifies variables observed at Level-1
**BETWEEN =** PA_L2 SF_L2 GAP_L2 FAM_L2;
! Identifies variables observed at Level-2
**MISSING ARE ALL (999);**

**ANALYSIS:** TYPE = TWOLEVEL RANDOM;

! Allows for multilevel model with random intercepts and slopes
**MODEL:**

%WITHIN%
  RSB ON PA GAP;
  slope_2 | RSB ON SF;
  slope_4 | RSB ON FAM;

! Describes the Level-1 part of a two-level model
%BETWEEN%
  RSB ON PA_L2 SF_L2 GAP_L2 FAM_L2;
  slope_2 ON FAM_L2;
  slope_4 ON GAP_L2;
  RSB WITH slope_4;
  slope_2$@0$;

! Describes the Level-2 part of a two-level model
Mplus Input for Three-Level MLRM: Cluster Randomized Trial with Repeated Measures

TITLE: Three-Level MLRM: Cluster Randomized Trial with Repeated Measures
DATA: FILE IS dataset_3.dat;
VARIABLE: NAMES ARE QOL_0 QOL_1 QOL_2 QOL_3 cond therap;
USEVARIABLES ARE cond QOL_0 QOL_1 QOL_2 QOL_3;
! Identifies variables observed at Level-3
! Identifies the name of the cluster variable(s) in the dataset
ANALYSIS: TYPE IS TWOLEVEL RANDOM;
! Allows for multilevel model with random intercepts and slopes
ESTIMATOR IS MLR;
MITERATIONS = 10000;
MODEL:
%WITHIN%
pie_0 pie_1 | QOL_0 QOL_1 QOL_2 QOL_3;
QOL_0 - QOL_3 (1);
%BETWEEN%
beta_00 beta_10 | QOL_0 QOL_1 QOL_2 QOL_3;
beta_10 ON cond;
beta_00 ON cond;
beta_10 WITH beta_00;
QOL_0 - QOL_3;
! Describes the Level-3 part of a three-level model
# Key Mplus Output for Three-Level MLRM: Cluster Randomized Trial with Repeated Measures

## MODEL RESULTS

<table>
<thead>
<tr>
<th>Within Level</th>
<th>Estimate</th>
<th>S.E.</th>
<th>Est./S.E.</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>PIE 0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PIE 0</td>
<td>1.000</td>
<td>0.000</td>
<td>999.000</td>
<td>999.000</td>
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<tr>
<td>PIE 1</td>
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<td>999.000</td>
</tr>
<tr>
<td>PIE 1 WITH</td>
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<td></td>
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<td>PIE 0</td>
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<td>PIE 0</td>
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<td></td>
</tr>
<tr>
<td>QOL 0</td>
<td>46.823</td>
<td>1.512</td>
<td>30.977</td>
<td>0.000</td>
</tr>
<tr>
<td>QOL 1</td>
<td>46.823</td>
<td>1.512</td>
<td>30.977</td>
<td>0.000</td>
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<td>QOL 2</td>
<td>46.823</td>
<td>1.512</td>
<td>30.977</td>
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<td>1.512</td>
<td>30.977</td>
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<td>Between Level</td>
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<tr>
<td>BETA 00</td>
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<td>0.531</td>
<td>0.263</td>
<td>2.018</td>
<td>0.044</td>
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</table>

## Intercepts

<table>
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<th>Est./S.E.</th>
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<tbody>
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<td>999.000</td>
<td>999.000</td>
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<td>0.531</td>
<td>0.263</td>
<td>2.018</td>
<td>0.044</td>
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## Residual Variances

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<th>P-Value</th>
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</thead>
<tbody>
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<td>QOL 0</td>
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<td>0.000</td>
<td>999.000</td>
<td>999.000</td>
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<tr>
<td>QOL 1</td>
<td>0.000</td>
<td>0.000</td>
<td>999.000</td>
<td>999.000</td>
</tr>
<tr>
<td>QOL 2</td>
<td>0.000</td>
<td>0.000</td>
<td>999.000</td>
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<tr>
<td>QOL 3</td>
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<td>999.000</td>
</tr>
<tr>
<td>BETA 00</td>
<td>19.168</td>
<td>3.843</td>
<td>4.988</td>
<td>0.000</td>
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<tr>
<td>BETA 10</td>
<td>0.531</td>
<td>0.263</td>
<td>2.018</td>
<td>0.044</td>
</tr>
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</table>
SAS Input for Three-Level MLRM: Cluster Randomized Trial with Repeated Measures

/*Invoking GLIMMIX with empirical sandwich estimator*/
PROC glimmix DATA = dataset_3A empirical noclprint noitprint;
CLASS subject therap;
MODEL QOL = A W A*W/ SOLUTION ddfm=bw;
/*Level three variable*/
RANDOM Intercept A/ TYPE = UN SUBJECT = therap;
/*Level two within level three variable*/
RANDOM Intercept A/ TYPE = UN SUBJECT = subject(therap);
RUN ;
SAS Output for Three-Level MLRM: Cluster Randomized Trial with Repeated Measures

<table>
<thead>
<tr>
<th>Cov Parm</th>
<th>Subject</th>
<th>Estimate</th>
<th>Standard Error</th>
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<td>therap</td>
<td>20.2341</td>
<td>5.1952</td>
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<tr>
<td>UN(2,1)</td>
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<td>1.0231</td>
</tr>
<tr>
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### Solutions for Fixed Effects

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<th>t Value</th>
<th>Pr &gt;</th>
<th>t</th>
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<tbody>
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<tr>
<td>A</td>
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<td>3898</td>
<td>5.18</td>
<td>&lt;.0001</td>
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<tr>
<td>W</td>
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