This is a chapter excerpt from Guilford Publications.
Monte Carlo Simulation Power Analysis Using Mplus and R, by James Peugh and Kaylee Litson.
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Preface

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So, why write a Monte Carlo simulation power analysis book? Why *now*? Two things still surprise us even after putting this book together: (1) the fact that the research that comprises the bulk of Chapter 1 shows sample sizes and statistical power levels really haven't changed much in 60 years, and (2) the fact that there hasn't been a Monte Carlo simulation power analysis book written in well over 20 years. The truly surprising part is that, during this same time span, there have been massive changes in the entire quantitative methodology landscape, far too many to mention. This book has been a work in progress for a very long time, but it all started with a "memorable" incident from way back in graduate school . . .

In the spring of 2004, the first author was in a Structural Equation Modeling class at the University of Nebraska–Lincoln taught by my dissertation chair (more on him in a minute . . .). One of the first topic lectures of that course introduced Sewall Wright's (1921, 1934) path tracing concepts and rules. I can recall we were all frantically drawing, labeling, and taking notes (or, maybe I should speak for myself) when suddenly, from the back of the room, we heard the unbelievable: "WHY ARE WE STUDYING THIS?!?!? THIS IS ARCHAIC!! DOES ANYONE EVEN **USE** THIS ANYMORE?!?!" While half the class sat motionless in stunned horror, the other half rubber-necked, if for no other reason, to catch a rare, live glimpse of graduate student verbal *seppuku*. My dissertation chair's immediate response was just as memorable: "Yeah, . . . I had a feeling I should have kept this class small . . ." That graduate student never returned to class and dropped the course a short time later. For me, the result of that spring day in 2004 was that Sewall Wright's path tracing rules were memorably stuck in my brain, but at that time, I had no idea when, why, or how to apply it.

The key to writing this book (20+ years later) was realizing three themes. The first theme arose from finally realizing that (quite opinionated) graduate student back in 2004 could not have been more wrong: Wright's rules enable the power analysis mission-critical calculation of residual variances even in the most complicated (see Chapter 11) research designs and data analytic models. The second theme came from a Special Topics class taught by my dissertation chair in graduate school a year later (eligibility for attendance was severely restricted this time): *standardization simplifies*. The third theme, the ability

to use the linear model algebra equations for longitudinal models offered by both Bollen and Curran (2006) and Grimm, Ram, and Estabrook (2017), is the key to obtaining Monte Carlo simulation power estimates as longitudinal designs increase in complexity (see Chapters 9–11). A global COVID-19 pandemic and lockdown provided the opportunity to write a 12-chapter plus four-appendix Monte Carlo simulation power analysis book we hope researchers worldwide will find helpful.

About This Book

The layout of this book moves from the simple to the more complex. The first six chapters describe cross-sectional power analyses; the next five chapters describe longitudinal power analyses. Within both sections of the book, examples begin with simpler analysis examples to illustrate foundational techniques such as Wright's path tracing rules (e.g., *t*-test and bivariate regression examples in Chapter 1, an unconditional growth model in Chapter 7) and move to the more complex analyses (SEMs in Chapter 4 and complex longitudinal mediation in Chapter 11). More importantly, although it appears to be a digressive tangent, incorporating missing data into a power analysis is shown in Chapter 6 immediately after logistic regression power analyses in Chapter 5 because logistic regression principles are used in Mplus and R to specify and control the amount of missing data incorporated into power estimates. In our opinion, incorporating missing data into power analysis estimates is a highlight of this book.

Researchers unfamiliar with Wright's path tracing rules, missing data specification, and incorporation, or both, would likely find the first six chapters of this book beneficial. With a firm grasp of both concepts, researchers can then choose from the longitudinal power analyses in Chapters 7–11 or the power analyses in Appendices A–D that best meet their needs. Although the supplemental power analyses shown in Appendices A–D could not be included in the book (it would have exceeded 800 pages), it is important to note those power analysis examples are available at the companion website:

- Appendix A. Statistical Power for Latent Variable Moderation Power Analysis
- Appendix B. Part I: Statistical Power for Survival Analysis
- Appendix C. Monte Carlo Simulation Power for Two-Level Models (Based on Arend & Schafer, 2019)
- Appendix D. Statistical Power for Moderated Mediation

Mplus and R syntax scripts and supplemental materials for Chapters 1–11, as well as text narrative, Mplus, and R syntax scripts, and supplemental materials for Appendices A–D mentioned above, are all available online at the following address: *www.guilford.com/peugh-materials.*

An Important Caveat

This book was originally intended to be a Monte Carlo simulation power analysis book that featured Mplus syntax examples only. Book proposal feedback from several anonymous

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reviewers was unanimous on one point: R syntax needed to be included. Again, special thanks to Kaylee Litson for doing a fantastic job following up the Mplus examples with equivalent R syntax specifications. It is important to note that for many of the chapters in the book, the Mplus and R sample size estimates are identical or reasonably close and the models are essentially equivalent. However, readers will see a notation that states for four of the chapters, equivalent R syntax for the Mplus example was not possible. In the second half of Chapter 8, as well as in Chapters 9 and 11, it was not possible in the R package simsem to covary the binary covariate (which is how the binary predictor variable needed to be simulated) with a continuous covariate in the presence of a complex SEM model. In Chapters 5 and 11, the inclusion of both a binary predictor and binary outcome was not possible to model in either lavaan or simsem. Readers will find the R code we were able to specify for these chapters in the supplemental online materials, but sample size estimates between that code and the Mplus code for the same example will not match because they reflect different underlying population and/or analysis models. When reading these chapters (and later conducting your own power analyses), it is important to note that even minor differences in the population and/or sample model, such as the inclusion or exclusion of a correlation among predictor variables, can *drastically* impact statistical power estimates.

Acknowledgments

From JP: I owe an enormous debt of gratitude, first and foremost, to my former mentoring professor and dissertation chair, Craig Enders. Your guidance and patience have made a huge difference in my professional development and this book would not have been possible without everything you've taught me. All I can say is that I will continue to try my best to pay it forward. You've shown me the difference one person can make.

I also would like to extend a big thank you to my good friend and colleague, David Feldon. Collaborations with you have always been enjoyable and productive, and the large dividends that resulted in the end have always been a very rewarding bonus. Most importantly, I am grateful that you allowed me to recruit (your then postdoctoral fellow) Kaylee Litson to provide the R syntax for all the power analyses in this book (more on that below).

Belated and long overdue thanks go to my University of Nebraska doctoral dissertation committee members (and a special thank you to both Rafael de Ayala, the department chair in my PhD program, and Calvin Garbin from the Psychology Department), all my former professors in the Quantitative PhD program in the Teacher's College, as well as to my postdoctoral fellowship supervisors from the Psychology Department: David DiLillo and Mario Scalora. I will always look back at graduate school and my postdoctoral fellowship with enormous personal satisfaction; my training was top-notch and I am grateful to you all.

In addition to the faculty members in the Behavioral Medicine Clinical Psychology division of the Cincinnati Children's Hospital Medical Center, I need to extend much thanks to several more individuals within my division and outside the hospital for allowing the use of their quotable comments, power analyses, and pilot data for the contents included in this book: Scott Powers (Chater 1), Kevin Hommel (Chapter 2), Zarina Vakhitova (Chapter 5), Julia Carmody (Chapter 7), Nina M. Tauber and Rosalie Corona (Chapter 8), Stephen Becker (Chapter 10), Sarah Beal (Chapter 11), Pin-Lun Kuo, Judd Walson, and my two

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trusted colleagues and friends Michael Toland and David Dueber (Appendix B, Parts 1 and 2), Matthias Arend and Thomas Schafer (Appendix C), and Nurit Tal-Or (Appendix D).

I must give a very big and well overdue thank you to the Mplus support group. I have tested your patience for decades. Thank you.

Thank you also to C. Deborah Laughton, Katherine Sommer, Jared Greenberg, and all at The Guilford Press for your help and support. Thank you also to Chia-Lin Tsai, Statistics Department, University of North Colorado; Fred L. Oswald, Psychology Department, Rice University; and Guilford's other anonymous reviewers willing to give their time and offer their suggestions to make this book the best product it could be. Special thanks also to Ryne Estabrook for his excellent answers to all of my linear model equation questions.

Finally, and most importantly, I want to dedicate this book to my wife, Jennifer (who challenged me to write this book), my daughter, Mary Catherine, who keeps me company at times in my new post-COVID-19 office in the basement of my home, and my infant son, Gerard. Everything I do is always for the three of you.

From KL: Although I came to this book much later in the game, I have had an incredible, educational, experience writing it. First and foremost, thank you to my good friend and colleague David Feldon, who connected me with James and helped me see that the translation of quantitative work into practice is where my passion lies. Second, I want to thank the many, many scholars and programmers who have contributed to and continue contributing to open-source SEM software packages, such as lavaan and simsem. I hope these packages continue to be developed and receive funding to make them more accessible to researchers as well as more robust to different research designs and applications. I also would like to thank those who have fielded my questions in online forums, particularly Terrence Jorgensen, whose email responses to my questions about simsem and lavaan have been immensely helpful as I grappled with how to translate Mplus syntax to R across some more complex research designs.

Thank you also to C. Deborah Laughton and all at The Guilford Press for your support and advice as I've navigated writing this book. Although I feel I should have heeded your warning about not taking on a book project so early in my career, I couldn't have had a better first book writing experience. And finally, a huge thank you to James Peugh, for trusting me and bringing me on to this project. It has been an uphill battle at times, and I couldn't have done it without your support and continued collaboration.

On a personal note, I'd like to thank my mom, my siblings, and my grandma (who has since passed away). All of these individuals listened to me talk, complain, and rejoice as I worked through some of the more difficult parts of this book. You all got to see moments where I was frustrated because R froze or I had a minor error in code that led to unexpected problematic results. Each of you also saw joyful moments when I finally figured out the solution to my problem or came to the realization that I wasn't in the position to solve the problem I had encountered. My grandma was one who was very excited for me having this opportunity, and I spent many nights working on this book while spending time with her in her last years. For this reason, I dedicate the work I did in this book to her.

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2

A Multivariate, Two-Group, Pretest–Posttest Power Analysis

Pretest–posttest research designs involving random assignment to a treatment or a control condition are both a budgetary cost-effective and statistically efficient means for testing a treatment intervention in which (1) participants are recruited and pretest data are collected on all response variables of interest, (2) participants are then randomly assigned to a treatment condition to receive the intervention to be tested, or to a control condition to receive a "treatment as usual" or another inert procedure, and (3) following an acceptable amount of exposure to the treatment or control conditions, posttest data are again collected on all response variables of interest. A pretest–posttest randomized design allows for posttest scores to be compared against "baseline" pretest scores both within the treatment and control groups, and between the treatment and control conditions at posttest. Furthermore, both the comparative-based and relationship-based power analysis examples shown in Chapter 1 dealt with a single (univariate) response variable. However, researchers are likely to be interested in changes in multiple related (multivariate) response variables operating simultaneously.

Researchers would, understandably, be tempted to analyze changes in multiple related response variables from a pretest–posttest random assignment design with a mixed-factorial (within factor: pretest vs. posttest; between factor: treatment vs. control) multivariate analysis. However, a mixed-factorial multivariate comparative design only optimizes statistical power if the correlation between pretest and posttest response variable scores is $r_{\text{Pretest,Posttest}} > .50$. Treating such a research design as purely cross-sectional by analyzing posttest mean differences between the independent variable groups after controlling for pretest scores as covariates in a multivariate *co*variance analysis is a more statistically powerful option. Compared to a mixed-factorial design, statistical power is optimized in a covariate inclusion design for *any nonzero* pretest–posttest correlation. However, a covariate design assumes homogeneity of the covariate regression slope coefficients, which means the effects of any pretest covariate on any posttest response variable must be equivalent across the indepen-

dent variable groups. If the assumption of homogeneity of covariate regression slopes is not met, a covariate is essentially functioning as an additional independent variable in analysis. This means that any significant effect for the treatment of interest could be due to treatment efficacy or could be due to a violation of the homogeneity of covariate regression slopes assumption.

For a multivariate, cross-sectional comparative statistical power analysis example, let's consider a specific medical research scenario (this specific scenario will prove very helpful in explaining how to specify and incorporate missing data into Monte Carlo simulation power analyses in Chapter 6). Let's assume a researcher wishes to use a pretest/posttest data collection design with random assignment to a treatment condition or a control condition (independent variable) to test an intervention believed to improve medication adherence (`ADH`), medical disease activity (`DA`), daily functional activity (`FA`) and overall health-related quality of life (`QOL`) ratings, all of which are assumed to be correlated. Let's further assume that, to maximize statistical power, the medical researcher plans to use the four-response variable pretest scores as covariates in a multivariate data analysis design. Let's also finally assume that the medical researcher suspects, based on a review of previous publications, that the intervention will produce an effect size difference (Δ) between the treatment and control groups for all four response variables at posttest of $\Delta d = 0.45$. A model for this data analysis design is shown in Figure 2.1.

The multivariate covariance analysis model is presented separately for the treatment (upper pane) and control (lower pane) groups to indicate that the same multiple group approach in both Mplus and R used for the independent samples *t*-test power analysis from Chapter 1 will again be used for this example. The curved, double-headed arrows on the left and right sides of the analysis model indicate correlated pretest and posttest response variables. The question marks (?) both within the circles above the posttest response variables and on the single-headed regression arrows indicate unknown but related quantities that must be specified. The amount of posttest variable variance left unexplained (question marks within the circles) is contingent upon the amount of posttest variance explained by the pretest scores as predictors (question marks on the regression slopes).

Recall that Wright's (1921, 1934) path tracing rules and general form equation [Equation (1.2) from Chapter 1] for computing variance explained (R^2_Y) in any posttest response variable (Y) are given as follows:

1. A path tracing cannot involve the same variable twice.
2. A path tracing can involve only one correlation (i.e., double-headed curved arrow).
3. A path tracing can involve tracing both backward (from the arrowhead of a regression arrow back to its source) and forward (from the source of the arrow to its arrowhead), but once a forward trace is made, additional backward traces are prohibited.
4. A path tracing can involve as many backward and forward tracings as is permissible.

$$R^2_Y = \text{Direct path} * (\text{Direct path} + [\text{Indirect path product}])$$

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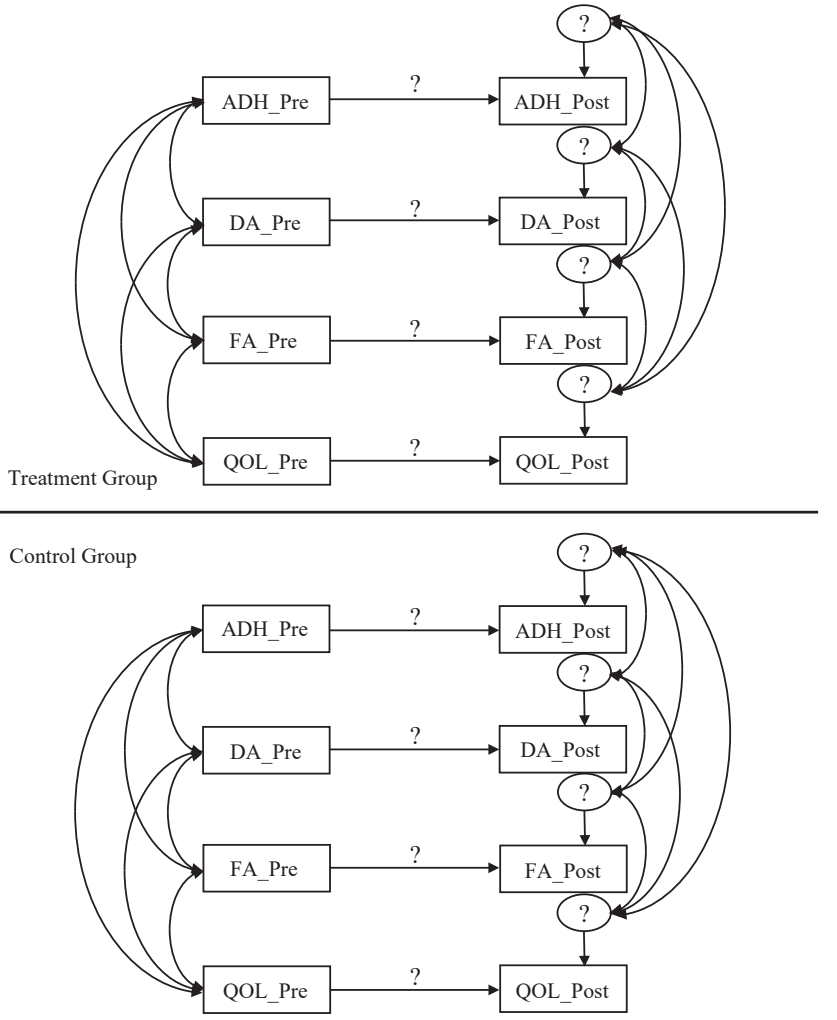

FIGURE 2.1. A multivariate two-group model.

Furthermore, assuming standardization, residual variance ($\sigma^2_{\text{RESIDUAL}}$) for each posttest response variable is calculated as ($\sigma^2_{\text{RESIDUAL}} = 1 - R^2_Y$). Equation 1.2 from Chapter 1 for calculating variance explained can be simplified further because, for the MANCOVA example, the direct path for each posttest response variable is the regression slope for its respective pretest as a predictor. Note, there are no admissible indirect paths because any indirect path tracing for the relationship between any pretest variable and its respective posttest variable would involve more than one correlation (curved, double-headed arrow) path, which is inadmissible. To illustrate, assume an indirect path tracing for pretest adherence predicting posttest adherence (`ADH_Pre` → `ADH_Post`) is needed. Starting at pretest adherence, a researcher could use any curved, double-headed arrow as a path to any other pretest variable, and then follow the regression arrow forward to the pretest variable's

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respective posttest variable. But getting from any posttest variable back to posttest adherence would require taking a second curved, double-headed arrow path, which is inadmissible under path tracing rule #2. The residual variance calculation for any posttest response variable then reduces to exclude the indirect path ($\sigma^2_{RESIDUAL} = 1 - [\text{Direct path}^2]$). Suppose that after a literature search, the medical researcher is willing to assume that a standardized regression slope of $\beta = 0.40$ best quantifies the prediction of all posttest variables by their respective pretest scores. This implies that ($R^2_{Post-test} = [0.40]^2 = 0.16$) 16% of posttest variance is explained by pretest scores across both groups and ($\sigma^2_{RESIDUAL} = 1 - [0.40^2] = 0.84$) 84% of posttest variance remains unexplained. Using these now known values, it is possible to conduct a Monte Carlo simulation power analysis in either Mplus or R (see Figure 2.2).

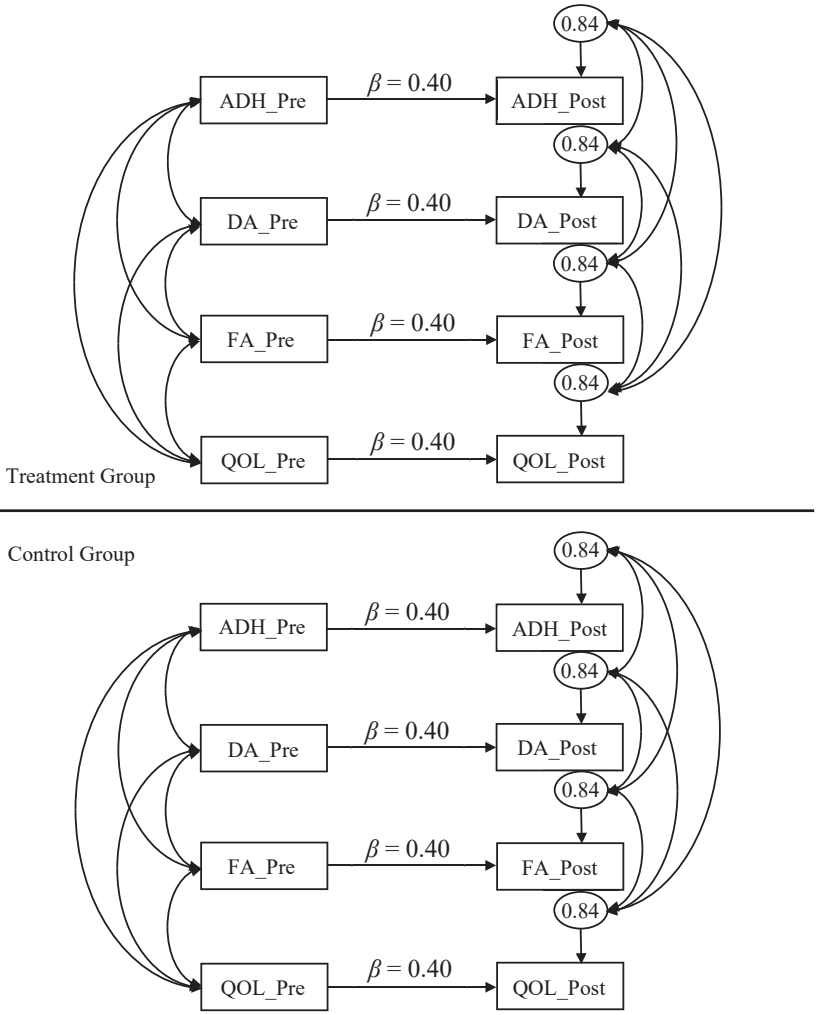

FIGURE 2.2. A fully specified multivariate two-group model.

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Mplus Monte Carlo Power Analysis: Multivariate Two-Group Comparison

The complete multivariate two-group comparison Monte Carlo simulation power analysis Mplus input syntax is shown next.

```
TITLE: Mplus 2.1 Multivariate Two-Group Comparison

MONTECARLO:
NAMES ARE
ADH_pre  DA_pre  FA_pre  HRQ_pre
ADH_post DA_post FA_post HRQ_post;
NOBSERVATIONS = 66 66;
NGROUPS = 2;
NREPS = 5000;
SEED = 10127;

! IV: Control Group;
MODEL POPULATION:

[ADH_pre*0];
[DA_pre*0];
[FA_pre*0];
[HRQ_pre*0];
ADH_pre*1;
DA_pre*1;
FA_pre*1;
HRQ_pre*1;

[ADH_post*0.16];
[DA_post*0.16];
[FA_post*0.16];
[HRQ_post*0.16];

ADH_post*.84;
DA_post*.84;
FA_post*.84;
HRQ_post*.84;

ADH_post DA_post FA_post WITH DA_post*0.3 FA_post*0.3 HRQ_post*0.3;
ADH_pre DA_pre FA_pre WITH DA_pre*0.3 FA_pre*0.3 HRQ_pre*0.3;

ADH_post ON ADH_pre*.4(1);
DA_post ON DA_pre*.4(2);
FA_post ON FA_pre*.4(3);
HRQ_post ON HRQ_pre*.4(4);

! IV: Treatment Group;
MODEL POPULATION-g2:

[ADH_pre*0];
[DA_pre*0];
[FA_pre*0];
[HRQ_pre*0];
```

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```
ADH_pre*1;
DA_pre*1;
FA_pre*1;
HRQ_pre*1;

[ADH_post*0.61];
[DA_post*0.61];
[FA_post*0.61];
[HRQ_post*0.61];

ADH_post*.84;
DA_post*.84;
FA_post*.84;
HRQ_post*.84;

ADH_post DA_post FA_post WITH DA_post*0.3 FA_post*0.3 HRQ_post*0.3;
ADH_pre DA_pre FA_pre WITH DA_pre*0.3 FA_pre*0.3 HRQ_pre*0.3;

ADH_post ON ADH_pre*.4(1);
DA_post ON DA_pre*.4(2);
FA_post ON FA_pre*.4(3);
HRQ_post ON HRQ_pre*.4(4);

MODEL:!IV: Control Group;
ADH_post DA_post FA_post WITH DA_post*0.3 FA_post*0.3 HRQ_post*0.3;

ADH_post ON ADH_pre*.4(1);
DA_post ON DA_pre*.4(2);
FA_post ON FA_pre*.4(3);
HRQ_post ON HRQ_pre*.4(4);

[ADH_post*0.16](E);
[DA_post*0.16](F);
[FA_post*0.16](G);
[HRQ_post*0.16](H);

ADH_post*.84;
DA_post*.84;
FA_post*.84;
HRQ_post*.84;

MODEL g2:! IV: Treatment Group;
ADH_post DA_post FA_post WITH DA_post*0.3 FA_post*0.3 HRQ_post*0.3;

ADH_post ON ADH_pre*.4(1);
DA_post ON DA_pre*.4(2);
FA_post ON FA_pre*.4(3);
HRQ_post ON HRQ_pre*.4(4);

[ADH_post*0.61](A);
[DA_post*0.61](B);
[FA_post*0.61](C);
[HRQ_post*0.61](D);

ADH_post*.84;
DA_post*.84;
```

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```
FA_post*.84;
HRQ_post*.84;

MODEL CONSTRAINT:
NEW (ADH_DIFF*.45 DA_DIFF*.45 FA_DIFF*.45 HRQ_DIFF*.45);
ADH_DIFF = A-E;
DA_DIFF = B-F;
FA_DIFF = C-G;
HRQ_DIFF = D-H;
```

To facilitate ease of learning, the Mplus syntax above is presented in later sections.

```
MONTECARLO:
NAMES ARE
ADH_pre  DA_pre  FA_pre  HRQ_pre
ADH_post DA_post FA_post HRQ_post;
NGROUPS = 2;
NOBSERVATIONS = 66 66;
NREPS = 5000;
SEED = 10127;
```

Rather than list a single response variable for a univariate independent samples *t*-test power analysis, as was done in Chapter 1, the names of the four pretest covariate variables and their respective posttest variables are all listed after `NAMES ARE`. The `NGROUPS = 2` indicates a two-group (treatment vs. control) comparison, the `NOBSERVATIONS = 66 66` specification indicates that the medical researcher is testing an $N = 132$ ($n = 66$ per independent variable group; group-specific sample sizes are entered separately on the '`NOBSERVATIONS =`' line separated by a space and can be adjusted as needed) sample size for power ≥ .80 to detect a posttest difference between the treatment and control groups of $\Delta d = 0.45$.

```
! IV: Control Group;
MODEL POPULATION:
[ADH_pre*0];
[DA_pre*0];
[FA_pre*0];
[HRQ_pre*0];

ADH_pre*1;
DA_pre*1;
FA_pre*1;
HRQ_pre*1;

[ADH_post*0.16];
[DA_post*0.16];
[FA_post*0.16];
[HRQ_post*0.16];

ADH_post*.84;
DA_post*.84;
FA_post*.84;
HRQ_post*.84;
```

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As shown near the top of the MODEL POPULATION: data generation statement, all pretest response variables are assumed to be standardized with means equal to zero and variances equal to one. In the lower portion of the MODEL POPULATION: statement, the means of the posttest response variables in the control condition are specified to be 0.16 based on meta-analysis research that shows control condition participants experience a response variable improvement of $d = 0.16$, on average (Kahana, Drotar, & Frazier, 2008). Finally, as shown, posttest response variable variances are specified as 0.84 based on the above residual variance calculations.

```
ADH_post DA_post FA_post WITH DA_post*0.3 FA_post*0.3 HRQ_post*0.3;
ADH_pre DA_pre FA_pre WITH DA_pre*0.3 FA_pre*0.3 HRQ_pre*0.3;
```

The next two statements are a shortcut method for specifying all pretest and posttest response variable correlations at $r = .30$. These values can be adjusted based on previous research or length of time between pretest and posttest assessments. Shorter time intervals between assessments tend to dictate higher correlations among response variables.

```
ADH_post ON ADH_pre*.4(1);
DA_post ON DA_pre*.4(2);
FA_post ON FA_pre*.4(3);
HRQ_post ON HRQ_pre*.4(4);
```

The syntax lines shown above indicate a standardized regression slope coefficient of $\beta = 0.40$ for each pretest response variable predicting its respective posttest counterpart. Notice also that integer values between 1 and 4 are listed in parentheses after each ON statement. Integer values listed in parentheses indicate *equality constraints*. Recall that for any univariate or multivariate covariance analysis, the assumption of homogeneity of covariate regression slope coefficients must be met. Recall also that the asterisk (*) indicates that the covariate regression slope values will differ randomly around the 0.40 specified slope value consistent with central limit theorem. The integer values listed in parentheses, together with asterisks, indicate that the standardized regression slope values can vary separately for each response variable, but such variation must be constrained to equality between the treatment and control conditions for each response variable to meet the homogeneity of covariate regression slopes assumption. For example, within the treatment group for a given replication of simulated data, the slope for the effect of adherence pretest scores (ADH_Pre) as a predictor of adherence posttest (ADH_Post) scores could be $\beta = 0.43$, while the effect of disease activity pretest scores (DA_Pre) as a predictor of disease activity posttest scores could be $\beta = 0.37$ (DA_Post). The integer values in parentheses specify that, within the same dataset replication, the effects of adherence pretest scores (ADH_Pre) as a predictor of adherence posttest (ADH_Post) scores and disease activity pretest scores (DA_Pre) as a predictor of disease activity posttest scores must also be $\beta = 0.43$ and $\beta = 0.37$, respectively, in the control condition for that specific dataset replication. The data-generating syntax for the treatment condition is exactly the same as the syntax specified above for the control condition, with one exception.

```
! IV: Treatment Group;
MODEL POPULATION-g2:
```

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```
[ADH_post*0.61];
[DA_post*0.61];
[FA_post*0.61];
[HRQ_post*0.61];
```

The posttest means for the four response variables in the treatment condition are specified as $d = 0.61$. Recall that the medical researcher expected a treatment ($d = 0.61$) versus control ($d = 0.16$) response variable effect size difference at posttest of (0.61 – 0.16 =) $\Delta d = 0.45$.

The data analysis statements for the control group (`MODEL:`) and the treatment group (`MODEL g2:`) are the same as the data-generating `MODEL POPULATION:` and `MODEL POPULATION-g2:` statements with one exception.

```
! IV: Control Group;
MODEL:

[ADH_post*0.16](E);
[DA_post*0.16](F);
[FA_post*0.16](G);
[HRQ_post*0.16](H);

! IV: Treatment Group;
MODEL g2:

[ADH_post*0.61](A);
[DA_post*0.61](B);
[FA_post*0.61](C);
[HRQ_post*0.61](D);
```

As shown in the `MODEL g2:` statement above, the treatment group response variable intercept values (0.61; not means, because posttest scores are predicted by their respective pretest counterparts) for adherence (`ADH_post`), disease activity (`DA_post`), functional activity (`FA_post`), and health-related quality of life (`HRQ_post`) are assigned to variables `A-D`, respectively. Similarly, in the `MODEL:` statement, the control group response variable intercept values (0.16) for adherence (`ADH_post`), disease activity (`DA_post`), functional activity (`FA_post`), and health-related quality of life (`HRQ_post`) are assigned to variables `E-H`, respectively.

```
MODEL CONSTRAINT:
NEW
(ADH_DIFF*.45 DA_DIFF*.45 FA_DIFF*.45 HRQ_DIFF*.45);
ADH_DIFF = A-E;
DA_DIFF = B-F;
FA_DIFF = C-G;
HRQ_DIFF = D-H;
```

As shown above, the MODEL CONSTRAINT: command together with the NEW specification allows treatment group minus control group intercept difference (‘ `_DIFF’`) variables to be created from the group-specific intercept values assigned to variables `A-H`. Each of the

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four difference variables are assigned the value (`.45`) to indicate the medical researcher's hypothesized (0.61 – 0.16 =) $\Delta d = 0.45$ posttest treatment effect difference. The abbreviated results produced from the above syntax (Mplus 2.1) are shown below.

```
MODEL RESULTS
```

		ESTIMATES		S. E.	M. S. E.	95%	% Sig
	Population	Average	Std. Dev.	Average		Cover	Coeff
New/Additional Parameters							
ADH_DIFF	0.450	0.4476	0.1576	0.1582	0.0248	0.949	**0.808**
DA_DIFF	0.450	0.4509	0.1600	0.1581	0.0256	0.943	**0.809**
FA_DIFF	0.450	0.4482	0.1594	0.1580	0.0254	0.947	**0.804**
HRQ_DIFF	0.450	0.4474	0.1584	0.1580	0.0251	0.946	**0.808**

As shown in the results above, a sample size of ($n_{Treatment} = n_{Control} = 66$; $N = 132$) is needed for power ≥ .80 to detect any treatment group minus control group intercept difference of $\Delta d = 0.45$ at posttest. Also, the Monte Carlo simulation power analysis was conducted assuming that both response variable pretest scores and posttest scores were correlated at $r = .30$. Response variable pretest and posttest correlations represent information a researcher may not have. However, additional sensitivity simulation power analyses showed that assuming response variable correlations as low as $r = .10$ or as high as $r = .50$ produced no appreciable change in the sample size needed for power ≥ .80.

With quick, simple adjustments to the above syntax, a quick admissibility verification check can be conducted in two steps. The previous Monte Carlo simulation power analysis was conducted in a single step, sometimes referred to as an *internal* power analysis. An admissibility verification involves a two-step, or *external* power analysis. In the first step, the following two lines (**bolded**) are added to the previous '`NAMES ARE:`' syntax as follows:

```
TITLE: Mplus 2.2 Admissibility Check, Part 1

MONTECARLO:
NAMES ARE
ADH_pre  DA_pre  FA_pre  HRQ_pre
ADH_post DA_post FA_post HRQ_post;
NOBSERVATIONS = 66 66;
NGROUPS = 2;
NREPS = 5000;
SEED = 10127;
REPSAVE = ALL;
SAVE = NAME_*.dat;
```

The '`REPSAVE = ALL;`' syntax results in Mplus writing out all 5,000 Monte Carlo simulation data files. The '`SAVE = NAME_*.dat;`' syntax allows the researcher to assign any name to the replication datasets, and the '`_*`' specification automatically assigns a value from 1 to 5,000 for all datasets. For example, if a researcher specified

```
REPSAVE = ALL;
SAVE = MANCOVA_*.dat;
```

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Mplus would write out 5,000 datasets named MANCOVA_1.dat, MANCOVA_2.dat,. . . MANCOVA_5000.dat. and also, by default, Mplus will write out an additional file named 'MANCOVA_list.dat'. The 'MANCOVA_list.dat' file contains the names of all 5,000 datasets in a single column.

```
MANCOVA_1.dat
MANCOVA_2.dat
…
MANCOVA_5000.dat
```

As will be shown, the '`_list.dat`' file is used by Mplus to automate the process of reading in and analyzing the 5,000 datasets. In addition, at the bottom of the output file in the '`SAVEDATA INFORMATION`' section, Mplus will print the '`Order of variables`' for the 5000 datasets as shown.

```
SAVEDATA INFORMATION

  Order of variables

    ADH_POST
    DA_POST
    FA_POST
    HRQ_POST
    ADH_PRE
    DA_PRE
    FA_PRE
    HRQ_PRE
    GROUP
```

In the second step, and using the '`Order of variables`' and the '*`NAME`*`_list.dat`' file, Mplus can automate the reading-in and analysis of all data files with the following syntax commands:

```
TITLE: Mplus 2.3 Admissibility Check, Part 2
DATA:
File = MANCOVA_list.dat;
Type = MONTECARLO;
```

Notice how the '`MANCOVA_list.dat;`' file is given as the input file in the first line. This specification, followed on the next line by the '`Type = MONTECARLO;`' specification automates the reading-in and analyzing of all 5,000 datasets.

```
VARIABLE:

NAMES =

ADH_POST
DA_POST
FA_POST
```

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```
HRQ_POST
ADH_PRE
DA_PRE
FA_PRE
HRQ_PRE
GROUP;
```

The order of the variable names given in the '`NAMES =`' specification *must* be in the same order given in the output file that generated the 5,000 datasets.

```
GROUPING IS GROUP (1=Control 2 = Treat);
```

The 5,000 datasets were generated using the multiple-group format, so the last variable generated, as shown above, is '`GROUP`'. Based on the syntax that generated the datasets, the first group specified ('`MODEL POPULATION`') was the control condition, the second ('`MODEL POPULATION-g2`') group was the treatment condition. To analyze the 5,000 datasets in a multiple-group model, the values in the '`GROUP`' variable are assigned the labels '`(1=Control 2 = Treat);`' so that the '`MODEL:`' statement refers to the control group, and '`MODEL TREAT:`' refers to the treatment group as follows:

```
MODEL: !IV: Control Group;

ADH_post WITH DA_post*0.3 FA_post*0.3 HRQ_post*0.3;
DA_post WITH FA_post*0.3 HRQ_post*0.3;
FA_post WITH HRQ_post*0.3;

ADH_post ON ADH_pre*.4(1);
DA_post ON DA_pre*.4(2);
FA_post ON FA_pre*.4(3);
HRQ_post ON HRQ_pre*.4(4);

[ADH_post*0.16](E);
[DA_post*0.16](F);
[FA_post*0.16](G);
[HRQ_post*0.16](H);

ADH_post*.84;
DA_post*.84;
FA_post*.84;
HRQ_post*.84;

MODEL Treat: !IV: Treatment Group;

ADH_post WITH DA_post*0.3 FA_post*0.3 HRQ_post*0.3;
DA_post WITH FA_post*0.3 HRQ_post*0.3;
FA_post WITH HRQ_post*0.3;

ADH_post ON ADH_pre*.4(1);
DA_post ON DA_pre*.4(2);
FA_post ON FA_pre*.4(3);
HRQ_post ON HRQ_pre*.4(4);
```

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```
[ADH_post*0.61](A);
[DA_post*0.61](B);
[FA_post*0.61](C);
[HRQ_post*0.61](D);

ADH_post*.84;
DA_post*.84;
FA_post*.84;
HRQ_post*.84;

MODEL CONSTRAINT:
NEW (ADH_DIFF*.45 DA_DIFF*.45 FA_DIFF*.45 HRQ_DIFF*.45);

ADH_DIFF = A-E;
DA_DIFF = B-F;
FA_DIFF = C-G;
HRQ_DIFF = D-H;
```

After running the above syntax (Mplus 2.2 and 2.3), and also by default, Mplus will print to the output file model-reproduced correlation matrices for both the treatment and control groups averaged across the 5,000 datasets, as shown:

```
SAMPLE STATISTICS

NOTE: These are average results over 5000 data sets.

     SAMPLE STATISTICS FOR CONTROL
          ADH_POST DA_POST  FA_POST HRQ_POST ADH_PRE  DA_PRE  FA_PRE  HRQ_PRE
          ________ _______ ________ ________ _______ _______ _______ _______
 ADH_POST     1
  DA_POST    0.350     1
  FA_POST    0.348   0.350     1
 HRQ_POST    0.349   0.347   0.349     1
  ADH_PRE    0.403   0.124   0.124   0.123     1
   DA_PRE    0.123   0.401   0.122   0.120   0.301     1
   FA_PRE    0.119   0.123   0.403   0.123   0.300   0.302     1
  HRQ_PRE    0.122   0.121   0.122   0.402   0.302   0.302   0.302     1

      SAMPLE STATISTICS FOR TREAT
          ADH_POST DA_POST  FA_POST HRQ_POST ADH_PRE  DA_PRE  FA_PRE  HRQ_PRE
          ________ _______ ________ ________ _______ _______ _______ _______
 ADH_POST     1
  DA_POST    0.351     1
  FA_POST    0.348   0.348     1
 HRQ_POST    0.349   0.348   0.346     1
  ADH_PRE    0.398   0.120   0.119   0.116     1
   DA_PRE    0.121   0.401   0.117   0.119   0.299     1
   FA_PRE    0.118   0.119   0.399   0.118   0.298   0.298     1
  HRQ_PRE    0.120   0.120   0.120   0.400   0.297   0.300   0.298     1
```

As shown above, the model-reproduced correlation matrices are *admissible*, which is defined as both matrices showing values of exactly one on the main diagonal elements, and correlations between zero and one on the off-diagonal elements. However, this was a post hoc model admissibility check, performed in a two-step external process after having obtained Monte Carlo statistical power estimates. In all subsequent chapters, model

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admissibility checks will be performed *prior to* Monte Carlo simulation power estimation to ensure model admissibility. Rather than performing the somewhat cumbersome external or two-step admissibility check using Mplus, a priori model admissibility checks will be performed using matrix syntax in base R and show how to compute even simpler admissibility checks using lavaan syntax.

R Monte Carlo Power Analysis: Multivariate Two-Group Comparison

The first step in evaluating the multivariate two-group comparison Monte Carlo simulation power analysis in R, specifically by using the combination of lavaan and simsem packages, is to specify and save the population model.

```
PopulationModel_Ch2 <- "
  ADH_pre ~ 0                                  # means are set to 0 for documentation
  DA_pre ~ 0
  FA_pre ~ 0
  HRQ_pre ~ 0
  ADH_pre ~~ 1*ADH_pre                         # variances are constrained to 1
  DA_pre ~~ 1*DA_pre
  FA_pre ~~ 1*FA_pre
  HRQ_pre ~~ 1*HRQ_pre

  ADH_post ~ c(0.16, 0.61)*1                   # mean values differ across populations
  DA_post ~ c(0.16, 0.61)*1
  FA_post ~ c(0.16, 0.61)*1
  HRQ_post ~ c(0.16, 0.61)*1
  ADH_post ~~ 0.84*ADH_post                    # residual variances are constrained to .84
  DA_post ~~ 0.84*DA_post
  FA_post ~~ 0.84*FA_post
  HRQ_post ~~ 0.84*HRQ_post

  ADH_post ~~ 0.3*DA_post + 0.3*FA_post + 0.3*HRQ_post
  DA_post ~~ 0.3*FA_post + 0.3*HRQ_post
  FA_post ~~ 0.3*HRQ_post
  ADH_pre ~~ 0.3*DA_pre + 0.3*FA_pre + 0.3*HRQ_pre
  DA_pre ~~ 0.3*FA_pre + 0.3*HRQ_pre
  FA_pre ~~ 0.3*HRQ_pre

  ADH_post ~ 0.4*ADH_pre + a1*ADH_pre   # constrain parameters equal across groups
  DA_post ~ 0.4*DA_pre + a2*DA_pre
  FA_post ~ 0.4*FA_pre + a3*FA_pre
  HRQ_post ~ 0.4*HRQ_pre + a4*HRQ_pre

  ADH_DIFF := .45                              # set population value mean difference
  DA_DIFF := .45
  FA_DIFF := .45
  HRQ_DIFF := .45 "
```

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Within this set of code that is used to define the population model, multiple sections are explained. The first section:

```
ADH_pre ~ 0                 # means are set to 0 for documentation
DA_pre ~ 0
FA_pre ~ 0
HRQ_pre ~ 0
ADH_pre ~~ 1*ADH_pre        # variances are constrained to 1
DA_pre ~~ 1*DA_pre
FA_pre ~~ 1*FA_pre
HRQ_pre ~~ 1*HRQ_pre
```

constrains all pretest means and variances to 0 and 1, respectively. The second section:

```
ADH_post ~ c(0.16, 0.61)*1      # mean values differ across groups
DA_post ~ c(0.16, 0.61)*1
FA_post ~ c(0.16, 0.61)*1
HRQ_post ~ c(0.16, 0.61)*1
ADH_post ~~ 0.84*ADH_post       # residual variances are set to .84
DA_post ~~ 0.84*DA_post
FA_post ~~ 0.84*FA_post
HRQ_post ~~ 0.84*HRQ_post
```

establishes the posttest means and variances across the two groups. The first group is assigned posttest mean values of 0.16 while the second group is assigned posttest mean values of 0.61. Both groups are assigned posttest residual variances of 0.84. The third section of code:

```
ADH_post ~~ 0.3*DA_post + 0.3*FA_post + 0.3*HRQ_post
DA_post ~~ 0.3*FA_post + 0.3*HRQ_post
FA_post ~~ 0.3*HRQ_post
ADH_pre ~~ 0.3*DA_pre + 0.3*FA_pre + 0.3*HRQ_pre
DA_pre ~~ 0.3*FA_pre + 0.3*HRQ_pre
FA_pre ~~ 0.3*HRQ_pre
```

designates correlation values among the posttest scores and the pretest scores, separately, while the fourth section of code:

```
ADH_post ~ 0.4*ADH_pre      # regression estimates are set to 0.4 across groups
DA_post ~ 0.4*DA_pre
FA_post ~ 0.4*FA_pre
HRQ_post ~ 0.4*HRQ_pre
```

sets the regression between each pre- and posttest score at 0.4. Finally, the last section of the population model code:

```
ADH_DIFF := .45 # set population value mean difference
DA_DIFF := .45
FA_DIFF := .45
HRQ_DIFF := .45
```

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provides the expected difference value between pre- and posttest scores to indicate the medical researcher's hypothesized (0.61 – 0.16 =) $\Delta d = 0.45$ posttest treatment effect difference.

Once the population model is defined, the analysis model can now be written.

```
AnalysisModel_Ch2 <- "
  ADH_pre ~~ ADH_pre
  DA_pre ~~ DA_pre
  FA_pre ~~ FA_pre
  HRQ_pre ~~ HRQ_pre

  ADH_post ~ c(E, A)*1          # mean label across groups
  DA_post ~ c(F, B)*1
  FA_post ~ c(G, C)*1
  HRQ_post ~ c(H, D)*1
  ADH_post ~~ ADH_post
  DA_post ~~ DA_post
  FA_post ~~ FA_post
  HRQ_post ~~ HRQ_post

  ADH_post ~~ DA_post + FA_post + HRQ_post
  DA_post ~~ FA_post + HRQ_post
  FA_post ~~ HRQ_post
  ADH_pre ~~ DA_pre + FA_pre + HRQ_pre
  DA_pre ~~ FA_pre + HRQ_pre
  FA_pre ~~ HRQ_pre

  ADH_post ~ a1*ADH_pre          # label parameter and constrain equal across groups
  DA_post ~ a2*DA_pre
  FA_post ~ a3*FA_pre
  HRQ_post ~ a4*HRQ_pre

  #Creating mean difference values
  ADH_DIFF := A-E
  DA_DIFF := B-F
  FA_DIFF := C-G
  HRQ_DIFF := D-H "
```

There are three primary differences between the analysis model and the population model. First, parameter values are not specified in the analysis model since doing so sets the parameter equal to that exact value in all sample analyses (equivalent to the Mplus `@` specification). Second, parameter *labels* are included in two sections of the analysis model code:

```
  ADH_post ~ c(E, A)*1 # mean labels across groups
  DA_post ~ c(F, B)*1
  FA_post ~ c(G, C)*1
  HRQ_post ~ c(H, D)*1
```

and

```
  ADH_post ~ a1*ADH_pre # label a parameter and constrain it equal across groups
  DA_post ~ a2*DA_pre
```

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```
FA_post ~ a3*FA_pre
HRQ_post ~ a4*HRQ_pre
```

The first set of parameter labels, denoted c(E, A) through c(H, D), name each posttest mean value according to its group, where, for example, the mean value of ADH_post in group 1 will be named E and the mean value of ADH_post in group 2 will be named A. The second set of parameter labels, denoted a1 through a4, label the pre–post regression estimates, constraining them equal across groups in the analysis phase of the simulation. The last difference between the population and analysis model is shown as follows:

```
ADH_DIFF := A-E
DA_DIFF := B-F
FA_DIFF := C-G
HRQ_DIFF := D-H
```

Unlike the population model, which provided exact difference values for the difference variables, the analysis model uses parameter labels to estimate the difference found within each sample model. In the power analysis simulation, these sample difference estimates will be compared to the previously specified population difference parameters.

Because of the multigroup nature of this dataset, a two-step approach was used to conduct the simulation analysis, where sample datasets were first generated using the simulateDatasets(),

```
SampleDatasets_Ch2 <- simulateDataSets(PopulationModel_Ch2,
                                       nIterations = 5000,
                                       nObservations = c(66, 66),
                                       seed = 10127)
```

then output was evaluated using sim().

```
output_Ch2 <- sim(model = AnalysisModel_Ch2,
                  rawData = SampleDatasets_Ch2,
                  group = "group",
                  silent = TRUE)
```

Initial examination of the output summary showed that all replications converged, and provided the following power estimates:

ADH_DIFF	DA_DIFF	FA_DIFF	HRQ_DIFF
0.82	0.82	0.86	0.83

Statistical power is above .80, so a sample size of ($n_{\text{Treatment}} = n_{\text{Control}} = 66$; $N = 132$) is adequate for power ≥ .80 to detect any treatment group minus control group intercept difference of $\Delta d = 0.45$ at posttest. Additional smaller sample sizes could be estimated, if desired, yet those will not be shown here for brevity.

To evaluate the model-reproduced correlation matrices and determine admissibility, a much simpler approach in R is available than that shown in Mplus. In single group models, only one additional line of code (shown below) will be necessary to determine admissi-

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bility. However, in the multigroup approach, minimal additional coding is necessary to first specify each population group model separately before examining admissibility within each group. Instead of writing the multigroup model as a single object, specify each group as its own object. For the control group,

```
Population1_Ch2 <- "
  ADH_pre ~ 0
  DA_pre ~ 0
  FA_pre ~ 0
  HRQ_pre ~ 0
  ADH_pre ~~ 1*ADH_pre
  DA_pre ~~ 1*DA_pre
  FA_pre ~~ 1*FA_pre
  HRQ_pre ~~ 1*HRQ_pre

  ADH_post ~ 0.16*1
  DA_post ~ 0.16*1
  FA_post ~ 0.16*1
  HRQ_post ~ 0.16*1
  ADH_post ~~ 0.84*ADH_post
  DA_post ~~ 0.84*DA_post
  FA_post ~~ 0.84*FA_post
  HRQ_post ~~ 0.84*HRQ_post

  ADH_post ~~ 0.3*DA_post + 0.3*FA_post + 0.3*HRQ_post
  DA_post ~~ 0.3*FA_post + 0.3*HRQ_post
  FA_post ~~ 0.3*HRQ_post
  ADH_pre ~~ 0.3*DA_pre + 0.3*FA_pre + 0.3*HRQ_pre
  DA_pre ~~ 0.3*FA_pre + 0.3*HRQ_pre
  FA_pre ~~ 0.3*HRQ_pre

  ADH_post ~ 0.4*ADH_pre
  DA_post ~ 0.4*DA_pre
  FA_post ~ 0.4*FA_pre
  HRQ_post ~ 0.4*HRQ_pre "
```

and for the treatment group,

```
Population2_Ch2 <- "
#Treatment Group
  ADH_pre ~ 0
  DA_pre ~ 0
  FA_pre ~ 0
  HRQ_pre ~ 0
  ADH_pre ~~ 1*ADH_pre
  DA_pre ~~ 1*DA_pre
  FA_pre ~~ 1*FA_pre
  HRQ_pre ~~ 1*HRQ_pre

  ADH_post ~ 0.61*1
  DA_post ~ 0.61*1
  FA_post ~ 0.61*1
  HRQ_post ~ 0.61*1
```

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```
ADH_post ~~ 0.84*ADH_post
DA_post ~~ 0.84*DA_post
FA_post ~~ 0.84*FA_post
HRQ_post ~~ 0.84*HRQ_post

ADH_post ~~ 0.3*DA_post + 0.3*FA_post + 0.3*HRQ_post
DA_post ~~ 0.3*FA_post + 0.3*HRQ_post
FA_post ~~ 0.3*HRQ_post
ADH_pre ~~ 0.3*DA_pre + 0.3*FA_pre + 0.3*HRQ_pre
DA_pre ~~ 0.3*FA_pre + 0.3*HRQ_pre
FA_pre ~~ 0.3*HRQ_pre

ADH_post ~ 0.4*ADH_pre
DA_post ~ 0.4*DA_pre
FA_post ~ 0.4*FA_pre
HRQ_post ~ 0.4*HRQ_pre "
```

The accuracy of the model-implied covariance matrices and mean vectors can then be evaluated by calling the function combination fitted(sem()), as follows:

```
fitted(sem(Population1_Ch2))
fitted(sem(Population2_Ch2))
```

which produces covariance matrices and mean vectors for each group.

```
$cov
           ADH_ps DA_pst FA_pst HRQ_ps ADH_pr DA_pre FA_pre HRQ_pr
ADH_post        1
DA_post     0.348      1
FA_post     0.348  0.348      1
HRQ_post    0.348  0.348  0.348      1
ADH_pre       0.4   0.12   0.12   0.12      1
DA_pre       0.12    0.4   0.12   0.12    0.3      1
FA_pre       0.12   0.12    0.4   0.12    0.3    0.3      1
HRQ_pre      0.12   0.12   0.12    0.4    0.3    0.3    0.3      1

$mean
           ADH_post DA_post FA_post HRQ_post ADH_pre DA_pre FA_pre HRQ_pre
                0.16    0.16    0.16     0.16       0      0      0       0

$cov
           ADH_ps DA_pst FA_pst HRQ_ps ADH_pr DA_pre FA_pre HRQ_pr
ADH_post        1
DA_post     0.348      1
FA_post     0.348  0.348      1
HRQ_post    0.348  0.348  0.348      1
```

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ADH_pre	0.4	0.12	0.12	0.12	1			
DA_pre	0.12	0.4	0.12	0.12	0.3	1		
FA_pre	0.12	0.12	0.4	0.12	0.3	0.3	1	
HRQ_pre	0.12	0.12	0.12	0.4	0.3	0.3	0.3	1
$mean								
	ADH_post	DA_post	FA_post	HRQ_post	ADH_pre	DA_pre	FA_pre	HRQ_pre
	0.61	0.61	0.61	0.61	0	0	0	0

As shown above, the model-reproduced correlation matrices are *admissible*, defined as both matrices showing values of exactly one on the main diagonal elements, and correlations between zero and one on the off-diagonal elements. Although this admissibility check was conducted post hoc, admissibility checks can be conducted before completing the power analysis.

Simulation Power Analysis Write-Up: Multivariate Two-Group Comparison

Finally, an example of a Monte Carlo simulation power analysis write-up is shown below and consists of four sections: (1) a statement of the power analysis question; (2) a description of how power was calculated, including the data analysis model assumed, and the statistical software package and version used; (3) a clear statement of all power analysis assumptions, including specific parameter estimate values; and (4) a clear answer to the power analysis question that includes the number of simulated dataset replications requested, the effect size assumed, and the sample size needed to achieve power ≥.80. Here, the write-up is shown using the Mplus results.

> "The power analysis question involves the smallest sample size needed to achieve power ≥.80 to detect a posttest mean effect size difference (Δd) between the treatment and control conditions of $\Delta d = 0.45$ after controlling for pretest scores as covariates. A Monte Carlo simulation power analysis was conducted using Mplus (version 8.6) assuming: (1) a multivariate covariance data analysis model where pretest response variables are included as covariates for each of their respective posttest variables (adherence, disease activity, functional activity and health-related quality of life); (2) standardization of all pretest and posttest response variables; (3) random assignment results in equivalent groups across the four response variables at the pretest assessment; (4) the control condition will experience a minimal pretest to posttest difference ($\Delta d = 0.16$; Kahana et al., 2008); (5) the treatment condition will experience a pretest to posttest difference of ($\Delta d = 0.61$), resulting in a treatment versus control group difference of ($\Delta d = 0.61 - 0.16 = 0.45$) at posttest; (6) the assumption of homogeneity of covariate regression slopes (i.e., the effect of each posttest response variable regressed onto their respective pretest counterparts is equal across the treatment and control groups) will be ensured via parameter estimate equality constraints; (7) the use of pretest scores as

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covariates will explain ($R^2 = 0.16$) 16% of response variable error variance; and (8) all four response variables will be correlated at a medium effect size (i.e., $r_{Pearson} = 0.30$) at both the pretest and posttest assessments. Monte Carlo simulation power analysis results aggregated over 5,000 replications showed power ≥.80 for the anticipated treatment versus control posttest difference ($\Delta d = 0.45$) if $N = 132$ ($n_{Treatment} = n_{Control} = 66$) is available for analysis."

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