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How to Use the Actor-Partner Interdependence Model (APIM) To Estimate Different Dyadic Patterns in MPLUS: A Step-by-Step Tutorial

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Abstract ■ Dyadic data analysis with distinguishable dyads assesses the variance, not only between dyads, but also within the dyad when members are distinguishable on a known variable. In past research, the Actor-Partner Interdependence Model (APIM) has been the statistical model of choice in order to take into account this interdependence. Although this method has received considerable interest in the past decade, to our knowledge, no specific guide or tutorial exists to describe how to test an APIM model. In order to close this gap, this article will provide researchers with a step-by-step tutorial for assessing the most recent advancements of the APIM with the use of structural equation modeling (SEM). The present tutorial will also utilize the statistical program MPLUS.

Keywords ■ Actor-Partner Interdependence Model; Dyadic data analysis; Tutorial.

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Introduction

Studies in social sciences often focus on the influence that individuals have on one another. However, when dealing with research questions involving interpersonal relationships, important errors and misinterpretations can be made when inappropriate statistical methods and tools are implemented. The Actor-Partner Interdependence Model (APIM) is the most popular model used to measure the influence that members of a dyad have on each other. With recent developments (i.e., the *k* parameter; which is a ratio of the partner and actor effects), the APIM can now be used to identify and compare different types of dyadic patterns that can characterize the interpersonal influences of actors and partners (Kenny & Ledermann, 2010). This article presents a step-by-step tutorial on how to test some of the recent developments of the APIM with the use of structural equation modeling (SEM). Before elaborating on our stepwise tutorial, key dyadic data assumptions and conceptual issues will be briefly presented. In addition, the APIM and its most recent developments will be described.

Dyadic Data Assumptions

A comprehensive and enriched examination of interpersonal processes requires that data of dyadic partners be considered as interdependent rather than independent. Nevertheless, researchers often consider or analyze their dyadic data as if partners were independent, even if such decisions potentially threaten the validity of the results and their interpretations. One fundamental principle with dyadic data is that members of a dyad share and/or develop similarities (i.e., emergence) in some of their psychological attributes, to the extent that their data cannot be considered totally independent from one another (Kenny, Kashy, & Cook, 2006).

As a result, the data in most studies implementing a dyadic design should be considered as violating the independence assumption. Most statistical analyses assume that participants are randomly sampled from the population. Clearly, the study of dyadic relationships violates this assumption because both members of a higher-order unit (i.e., dyad) are deliberately sampled to study the influence they may have on one another. Hence, analysis of dyadic data can be characterized, to a large extent, as the study of non-independence (Kenny et al., 2006). Furthermore, the term dyad represents a broad category of higher-order units that can either be indistinguishable or distinguishable. An indistinguishable dyad is composed of two individuals who cannot be meaningfully distinguished by a variable that has been shown to empirically differentiate the two members. In contrast, the members of a distinguishable dyad can be differentiated on a within-dyad variable (e.g., gender) that has substantial meaning to distinguish members from one another (Kenny & Cook, 1999). A description of how to test the APIM with indistinguishable dyads goes beyond the purposes of the current tutorial.

Conceptual and Measurement Issues in Dyadic Data

Dyadic data creates challenges but provides unique opportunities to investigate the intricate richness brought by the dependency between dyad members. In the early stages of dyadic data analysis, researchers were averaging the scores of the two members, thus obtaining one score for the dyad (Cook & Kenny, 2005). However, this method leads to errors in measure and no longer takes into account the score of each member; essentially, this is the same as analyzing the data at the group-level. Currently, two methods exist and are widely advocated for the analysis of dyadic data: multilevel modeling (MLM; Campbell and Kashy, 2002, Gaudreau, Fecteau, and Perreault, 2010, Woltman, Feldstain, MacKay, and Rocchi, 2012) and structural equation modeling (SEM). These methods treat the data of the two individuals as nested within the dyad, thus allowing researchers to examine the influence individuals have on themselves and on one another (Cook & Kenny, 2005).

Given that the body of research on dyadic data is growing and investigating more complex research questions, SEM seems to be the statistical technique of choice for researchers who want to investigate dyadic models. SEM can easily incorporate several dependent variables in one model; it also has the ability to correlate error terms, impose equality and/or restrictions on parameters in the model, which is extremely useful in dyadic data analysis. Also, it offers estimation procedures to correct for non-normality of the data while providing several statistical indicators needed to easily compare the tenability of nested alternative models. Although some researchers have tried to use SEM to assess indistinguishable dyads (Olsen & Kenny, 2006; Woody & Sadler, 2005), SEM is particularly easy to implement in the analysis of dyadic data when dyads are distinguishable.

The Actor-Partner Interdependence Model

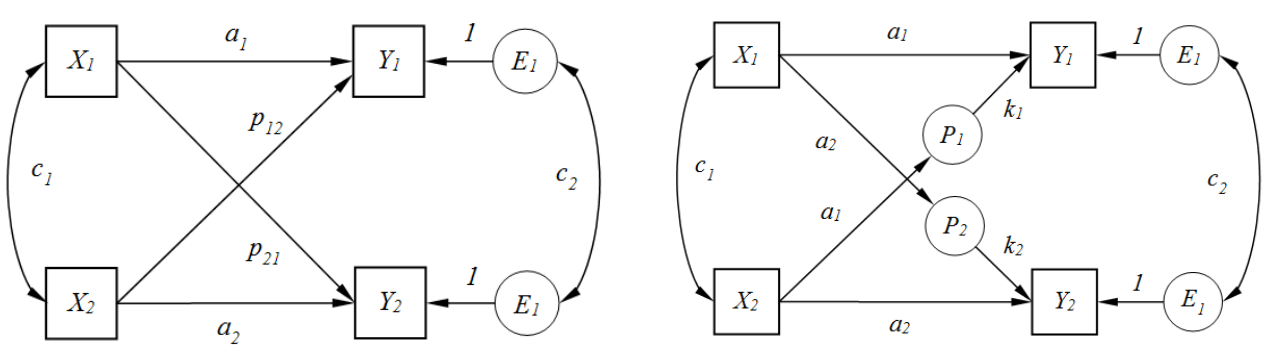
A growing number of researchers are using the Actor-Partner Interdependence Model (APIM) in social sciences. A PsychINFO search using APIM as a keyword from the past five years generated 319 articles. The APIM can be defined as a "model of dyadic relationships that integrates a conceptual view of interdependence with the appropriate statistical techniques for measuring and testing it" (Cook & Kenny, 2005, , p101). As displayed in Figure 1, the APIM can estimate the extent to which the independent variable of a person influences his or her score on the dependent variable ($X1 \rightarrow Y1$ for the male, or $X2 \rightarrow Y2$ for the female). This is known as the actor effect - denoted as a. For the present article we have attributed the male with the identifier of 1 and the female with the identifier of 2; however, it should be noted that this choice is an arbitrary identification process. The APIM can also estimate the extent to which the independent variable of a person influences the dependent variable of his or her partner. This partner effect — denoted as p ($X1 \rightarrow Y2$ for the female partner effect, or $X2 \rightarrow Y1$ for the male partner effect) — enables researchers to move beyond traditional analyses by exploring the richness of the dependency across partners of a dyad. Two correlations are also estimated in the APIM. The first indicates the correlation between $X1$ and $X2$ ($c1$), which might be due to a compositional effect (i.e., when shared attributes become more similar than randomly selected individuals in a given population). The second correlation between $E1$ and $E2$ indicates the residual non-independence of $Y1$ and $Y2$ ($c2$). The latter is a common practice used in SEM because endogenous variables cannot directly correlate with one another. As such, the correlations between the error terms of the dependent variables take into account the correlations of $Y1$ and $Y2$ not accounted by the predictors, as well as the compositional effect over and beyond what can be explained by the partner and actor effects included in the model. It represents the correlation between the scores of the two partners on the dependent variables.

Dyadic patterns

Interestingly, the actor and partner effects can be compared with the use of dyadic patterns proposed and defined by Kenny and Cook (1999). The APIM provides an empirically accessible platform to help researchers in assessing and comparing a variety of conceptually and theoretically meaningful dyadic patterns. Specifically, testing dyadic patterns allows the comparison of dyad member's respective influence on psychological outcomes and, in turn, enables a proper evaluation of emerging and existing theories hypothesizing the respective and/or combined roles of actor and partner. Four prototypical types of patterns can be readily tested with the APIM which comprises two patterns to be determined - one for each partner. In order to uncover a pattern, a ratio is computed with the partner and actor effect that are regressed on the same outcome (i.e., $Y1$ or $Y2$). The specific steps to calculate these ratios will be described later on in the tutorial. In order to best describe and illustrate these patterns, let us consider a typical example of a distinguishable dyad consisting of a male and a female from a heterosexual romantic relationship.

A first pattern, the couple pattern Kenny and Cook (1999) or the couple-oriented pattern (Kenny et al., 2006) is represented by $a = p$. This pattern considers that the effect of the male on his outcome (i.e., $X1 \rightarrow Y1$) is the same as the effect that the female has on the male's outcome (i.e., $X2 \rightarrow Y1$). This also applies for the opposite scenario, that is, when the effect of the female on her outcome (i.e., $X2 \rightarrow Y2$) is the same as the effect that the male has on the female's outcome (i.e., $X1 \rightarrow Y2$). For example,

Figure 1 ■ The actor-partner interdependence model (APIM) for Model 1 (a) and Model 2 (b) with the k parameter.



(a) The basic APIM

(b) APIM with phantom variable

the size of the association between the male's relationship satisfaction and the male's life satisfaction would be the same as the association between the female's relationship satisfaction and the male's life satisfaction (e.g., $X1 \to Y1 = X2 \to Y1$). A second pattern, known as the contrast pattern (Kenny & Ledermann, 2010) or the social comparisons pattern (Kenny et al., 2006), is represented by $a + p = 0$. In this case, the effect that the male has on his own outcome (i.e., male actor effect) is the opposite of the effect the female has on the male's outcome (i.e., male partner effect). A prototypical example of a contrast pattern might be envisioned in the study of solitary leisure activities. For example, the male participation in solitary leisure activities might be positively associated with his level of happiness. However, the male's rate of participation in solitary leisure activities might be negatively associated with the female's level of happiness. Thus, the directions of the actor and partner effects are in opposition (i.e., one positive, one negative) whereas their absolute strengths are quite comparable. The third pattern, the actor-only pattern (Kenny & Ledermann, 2010) or the actor-oriented pattern (Kenny et al., 2006) is represented by $a \neq 0$, $p = 0$. In this case, the male and female's independent variable has a significant effect on his or her own dependent variable (i.e., actor effect), whereas none of the partner effects reach statistical significance. For example, the male and the female's occupational success could have a significant positive impact on his or her own life satisfaction whereas the male's occupational success may fail to significantly influence the female's life satisfaction. Likewise, the female's occupational success may fail to significantly influence the male's life satisfaction. The fourth pattern, which is the rarest, is the partner-only pattern (Kenny & Ledermann, 2010) or the partner-oriented pattern (Kenny et al., 2006). This pattern can be represented by $a = 0$, $p \neq 0$. Each member of the dyad only has an effect on the outcome of his/her partner but none of the actor effects are statistical significant. For example, the fact that the male is giving a gift to the female could positively influence the female's satisfaction without significantly impacting the male's satisfaction.

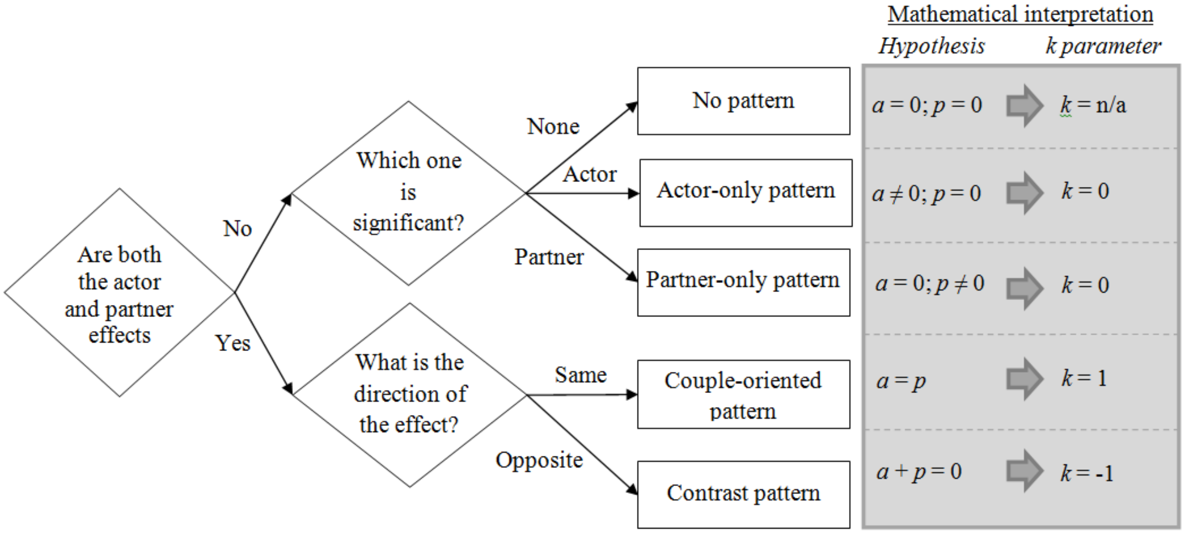
These patterns not only help researchers understand their data, but also allow an in-depth interpretation of the results based on a priori hypothesis. Therefore, assessing dyadic patterns offers an essential tool to clearly identify the exact form and nature of dependency in interpersonal dyadic processes, while taking full advantage of the richness of the distinct sources of variance encompassed in the data.

Uncovering the dyadic patterns

As previously mentioned, dyadic patterns can be examined through a computed ratio of the partner and actor effect. To do this type of computation, phantom variables, which are latent variables with no meaning or disturbance, are utilized within the SEM framework (Kenny & Ledermann, 2010). The phantom variable method creates a new parameter named k, which reveals the underlying dyadic pattern at play. In each APIM, two dyadic patterns can be found, one for each member of the dyad. How should one proceed in the interpretation of the k parameter? We have created a flowchart that depicts the different decisions to be made when interpreting the model with dyadic patterns (Figure 2) in order to help with this decisional process. All possible scenarios that might come up when computing the k parameter are described in the flowchart.

The first information to take into consideration when interpreting the APIM results is the significance of the actor and partner effects. If both actor and partner effects are significant, regardless of their directionality, the actor-only and partner-only dyadic patterns are no longer considered. However, if at least one of the effects (i.e., actor or partner for both partners) is not significant, the inter-

Figure 2 ■ Flow chart for interpreting the k parameters



pretation of the k parameters can no longer be a couple-oriented pattern or a contrast pattern. If we follow this decision, three scenarios remain possible: no pattern, actor-only, and partner-only. Based on the significance of the effect and with a computed k of near 0, we could proceed to interpret the presence of an actor-only or partner-only pattern. However, when both actor and partner effects are significant, we have to verify the directionality of the effect; whether they are of same or opposite direction. If the directionalities are identical, the results would be interpreted as a couple-oriented pattern; opposite directions would be interpreted as a contrast or social comparison pattern.

Furthermore, we can describe the overall findings of an APIM with a new nomenclature for describing both interpreted dyadic patterns. There are four possible types of dyadic patterns, four for each member. When placing them in a 4 × 4 table, different combinations emerge (Table 1). Diagonally, we can observe all the dyadic patterns that are mirrored between the members of the dyad (e.g. double actor-only pattern). In the rare case in which one couple-oriented pattern and one contrast pattern is found, we may describe this as a mixed dyadic pattern. At the top left of this table, two unique patterns are described as the sole predictor patterns. The sole predictor patterns denote that only one member of the dyad has his independent variable actually predicting the outcomes in the APIM. The four other patterns - two at the top right and two at the bottom left of the table - are described with the effect that is missing in the identified dyadic pattern. For example, the pattern "no partner effect from female partner" is either a combination of a couple-oriented or contrast pattern from the male partner and an actor-only pattern from the female, leaving the partner effect from the female partner to be the only non-significant effect.

A Step by Step Guide for Testing the APIM with SEM

Participants Used for the Example

To illustrate our step-by-step tutorial of the APIM, we used a sample of 252 individuals from 126 adult heterosexual couples aged between 21 and 80 years old for male (M = 33.49, SD = 11.18) and between 20 and 79 years old for female (M = 31.18, SD = 9.76). This data set is available on the journal's website. Participants were community-based couples who had been involved in their romantic relationship with their partner for at least one year. We used data collected through questionnaires answered by these couples to examine whether one's own and partner's sexual satisfaction could predict life satisfaction. Sexual satisfaction was measured using the Sexual Satisfaction Questionnaire on a 7-point Likert scale (Lawrance & Byers, 1995). The questionnaire assesses the level of sexual satisfaction of partners according to different perceived qualities of the sexual relationship (Male α = .92; Female α = .94). Life satisfaction was measured using the validated Satisfaction with Life Scale on a 7-point Likert scale (Diener, Emmons, Larsen, & Griffin, 1985). The SWLS is widely used to assess a person's global judgment of life satisfaction. An example of an item would be ”In most ways my life is close to ideal?” (Male α = .91; Female α = .92). In the following tutorial,

Table 1 ■ 4 × 4 table describing all the possible combinations of dyadic patterns in a distinguishable dyad

	Female patterns			
Male patterns	Actor-only	Partner-only	Couple-oriented	Contrast
Actor-only	Double actor-only pattern	Male as the sole predictor	No *partner effect* from male partner	
Partner-only	Female as the sole predictor	Double partner-only pattern	No *actor effect* from male partner	
Couple-oriented	No *partner effect* from female partner	No *actor effect* from female partner	Double couple-oriented pattern	mixed dyadic pattern
Contrast			mixed dyadic pattern	Double contrast pattern

we used the MPLUS 6.12 program (L. K. Muthén & Muthén, 2012) to conduct all analyses; all analyses could also be implemented in other SEM modeling programs.

Basics of MPLUS

MPLUS is a statistical program created by L. K. Muthén and Muthén (2012) and offers a free program demo that allows the testing of the basic APIM. This program offers a syntax platform that can test a broad array of models with different types of estimators. Mainly, the program is recognized as being flexible and particularly useful for structural equation modeling (SEM). Many important benefits of MPLUS exist such as it allows you, for example, to test bootstrapping with missing data and test models with dichotomous outcomes.

Over the course of this tutorial, different MPLUS syntaxes will be used. Therefore, to better follow the tutorial and the application of the APIM in MPLUS we suggest readers to have preliminarily read chapter 2 in (Byrne, 2012) and/or chapter 2 of the MPLUS user guide (http://statmodel.com/download/usersguide/Chapter2.pdf) . Simply put, there are ten different commands in MPLUS (title, data, variable, define, analysis, model, output, savedata, plot, montecarlo) and all of them have different subcommands. However, as mentioned, for a complete coverage of the existing sub-commands in MPLUS one should rely on the user guide of this program (L. K. Muthén & Muthén, 2012).

Importing Data in MPLUS. MPLUS only reads .dat format files. Most of the statistical programs (e.g., SPSS) will offer a save as function that can be used for converting the format of your data. Different formats of .dat can be chosen; the FIXED format uses the same display as in the original software, for example if only 2 decimals were displayed in the data, the .dat format will be the same. This can pose as a problem if different data points use different numbers of decimals (e.g., $2.66 \neq 2.66666666667$). However, the TAB delimited format keeps all the information from the original dataset and uses TABS between data point for their differentiation. This option should be prioritized in order to not compromise the data itself and the quality of subsequent analyses. In SPSS, researchers have to uncheck the "write variable names to spreadsheet" button. We recommend researchers to shorten the number of variables in the new .dat format by including only the ones needed for the analysis. Also, please note that your database should be structured at the couple level (i.e., each line is one couple) for performing dyadic data analysis with SEM. Before creating the .dat file, all missing data should be flagged with a particular number (e.g., 999) that you will later define in the MPLUS analysis. While performing the analyses, MPLUS will generate different files. Therefore, we recommend that researchers create one folder that will hold the new .dat file you have just created and the MPLUS syntax that will be written during the analysis. By putting both the syntax file and the .dat in the same folder, linking the syntax file to the data will be easier in the syntax language. Finally, decimals should be represented with dots not with commas in the .dat file, as MPLUS reads the dots as decimal and commas as separation of data points.

Title, data, and variable commands. Once the .dat file is created, you can open a new MPLUS syntax file by clicking the blank page button called new in MPLUS. The first command to write is TITLE (optional). This command allows you to give a title to your analysis. The second command is DATA. Under this command you must specify the location of your data and the name of the file. The simple subcommand file is xxxx.dat will identify your .dat file in the syntax, if the syntax and the .dat file are in the same folder. However, if the syntax and the .dat file are not in the same folder you would have to name the entire system path of your .dat file. This is why we encourage researchers to put all the files under the same folder for better organization. The last command to write for this section is VARIABLE. Under this command you have to name your variables and specify which ones you wish to use for a particular analysis. The first sub-command is `names are`; each variable name should be separated by a space. The second sub-

Listing 1 ■ Title, Data and Variable commands

```
TITLE:       actor-partner interdependence model;
DATA:        file is apim.dat;           !created file with SPSS
VARIABLE:    names are X1 Y1 X2 Y2;
             usevariables are X1 Y1 X2 Y2;
             missing is all (999);       ! For missing flag
```

command is `usevariables are` and it operates like the names are sub-command. Finally, the missing data flag is also specified in the VARIABLE command. Listing 1 shows an example; note that each line of sub-commands should end with a semi-colon. The symbol "!" can also be used to insert personal comments in the syntax file; everything after the "!" is not considered in the analysis.

Define, analysis, model, and output commands. Firstly, the DEFINE command allows the transformation of your variable, which creates new variables that can be used in the analysis. For example, if you import raw item scores into MPLUS you would have to use the DEFINE command to create mean score variables. Secondly, the ANALYSIS command allows you to specify the type of analysis you wish to run and the estimators you want to use for doing the analysis. By default full information maximum likelihood estimator is always estimated in MPLUS. Thirdly, the MODEL command allows you to specify the model you wish to estimate. To create/specify models in MPLUS you have to use three different sub-commands: BY (to define a latent variable), ON (to define a regression relation) and WITH (to define a correlation). Within this command you can constrain parameters. With "@", you force a parameter to be equal to the value of your choice; with "( )", you can label parameters, thus forcing equality; and with "*", you can estimate the chosen parameter freely and bypass some default functions in MPLUS. Finally, the OUTPUT command allows you to generate outputs. For example, if you want to obtain descriptive statistics for your sample you must write `SAMPSTAT;`, for standardized solutions `STDYX;`, and for confidence intervals when bootstraping is used `CINTERVAL(BCBOOTSTRAP);`. Listing 2 shows the commands. In all of the commands we described above, many sub-commands exist. However, as we have previously mentioned, the purpose of this short introduction was not to elaborate on the details of the program functions but to ensure that readers know the basic commands in MPLUS and understand and follow the tutorial below.

Overview of the Current APIM Procedure

The sequence in which the models are presented is the sequence we recommend researchers should use to analyse the APIM. Each step gives insight on the nature of the relations between the variables. Skipping steps in the sequence may hinder your comprehension of the data at hand and, consequently, the validity and reliability of your results and interpretation. To better illustrate this process, each step will be accompanied with an example from our data. In order to test dyadic patterns in the APIM, Kenny and Ledermann (2010) proposed a sequence of steps that could lead to two different applications: one for distinguishable dyads and one for indistinguishable dyads. These steps are as follows: (1) Estimate the saturated model; (2) test the distinguishability of the dyads; (3) estimate the k parameters; and (4) interprete the k parameters. The first step is always required whether the data involves distinguishable dyads or not. In the second step, it has been proposed to test the distinguishability (Kenny, 2013a) of dyads by constraining the male actor effect with the female actor effect and the male partner effect with the female partner effect. Distinguishability is unquestionably an important issue to address whenever performing dyadic data analysis. However, the aforementioned test should not be taken as a test of whether or not the members of the dyads are *ipso facto* distinguishable.[1] Several streams of research have tried to specify the specific roles of husbands and of wives in shaping their own and their partner's psychological adjustment (Gambles, Lewis, & Rapoport, 2006, e.g.,). Husbands and wives can be analyzed as distinguishable even in APIM

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[1] Why step 2 does not test distinguishability: In the case of the APIM if no distinction is made prior to the estimation, then the order in which the data is entered, which is an order that has no meaning (i.e., random), will be the variable of distinction. Let's say that members of dyads are given 1 or 0 at random in a sample of 100 dyads, accordingly, there is a finite number of possible permutations with repetition (i.e. $1-0, 1-0, 1-0 \ldots n$). More precisely, with a sample of 100 dyads with two possible choices at each n (01 or 10) there is 2^{100} possible arrangements of the data. Interestingly, estimates of the effects are not liable to the value attributed to the dyads (1-0 or 0-1); chi-square value will however vary depending on the arrangement, which will consequently affect other fit indices (Kenny et al., 2006). We argue that if effects are not liable on the possible permutation within the dyadic data; constraining equality on the actor and partner effects does not test the distinguishability quality of the dyads in the sample. We could infer from this demonstration that empirical tests of distinguishability does not always concord with the natural distinction (e.g., gender) and/or theorized distinction (e.g., dominance) and thus are not to be mixed with the definition of distinguishability.

Listing 2 ■ Define, Analysis, Model and Output commands

```
DEFINE:      X1 = MEAN (i1 i2 i3 i4);!example
ANALYSIS:    estimator = ml;
             bootstrap = 5000;
MODEL:       Y1 on X1(a);            ! "On" statement for regression
             Y1 on X2(p);            !label use for equality constraint
             Y2 on X1(p);
             Y2 on X2(a);
             X1 with X2;             !"with" statement for correlation
             Y1 with Y2;
OUTPUT:      stand;                  !for standardized estimation
             sampstat;               !for descriptive statistics
             cinterval(bcbootstrap); !for confidence intervals
```

models in which the effects of $X1$ and $X2$, and $Y1$ and $Y2$ are not distinguishable - as evidenced by their statistical invariance (i.e., test of distinguishability). Statistical invariance of the effects should not be taken as evidence to suggest that male and female are, de facto, members of an indistinguishable dyad. Rather, distinguishability should be seen as a conceptual matter that needs to be resolved a priori on the basis of whether the members can be clearly distinguished from one another using a theoretically defendable defining characteristic (e.g., gender, senior vs. junior in dyadic work unit, backcourt vs. net players in a badminton double team). As a result, we decided not to incorporate the test of distinguishability in our tutorial. Therefore, our tutorial relies on a three-step approach to test the APIM.

Model 1: The basic saturated APIM

In this model, there are two actor effects — one male actor effect $a1$ ($Y1$ on $X1$) and one female actor effect a2 ($Y2$ on $X2$) — and two partner effects — one male partner effect $p12$ ($Y1$ on $X2$) and one female partner effect $p21$ ($Y2$ on $X1$) (Figure 1). The basic APIM has 14 parameters (4 regressions effects, 2 correlations, 2 means, 2 intercepts, 2 variances, and 2 residual variances), thus if one estimates all of them, as in any common SEM model, the model is said to be saturated with a χ^2 equal to zero and with zero df (Kenny & Ledermann, 2010). Two steps are proposed to estimate the basic APIM.

Step 1: Looking for significant actor and partner effects. Because one of our later goals will be to add phantom variables that will estimate the ratio of the partner to actor effect - referred hereafter as the k parameter ($k = p/a$) - it has been suggested by Kenny and Ledermann (2010) to examine the value of the actor effects: $a1$ and $a2$. According to their recommendation, computing the k parameters should be avoided if the absolute standardized values of the actor effects are less than 0.10. Dividing the partner effect with a near 0 actor effect ($k = p/a$) will result in a ratio that will tend toward infinity and will be ultimately non interpretable. Therefore, weak actor effects (<0.10) combined with strong partner effects would suggest the presence of a partner-only pattern. This rare occurrence can also be tested with the k parameter by inverting the ratio when estimating the model ($k = a/p$ instead of $k = p/a$). Although existing literature on the assessment of this pattern is limited, (Kenny & Ledermann, 2010) have been paving the way to a clearer understanding of this analysis. Small modifications would be required in the next step if a partner-only pattern was hypothesized or discovered during the first step. In our example, only the actor effects were statistically significant and estimates were higher than 0.10 (male $a1 = 0.41$, $p21 = -0.06$; female $a2 = 0.35$, $p12 = 0.02$). Actor effects are significant, thus ensuring that k parameters in subsequent steps will be interpretable. However, the magnitude of the actor and partner effects cannot be interpreted as one being greater than the other.

Model 2: The saturated APIM with k

Step 2: Adding the k parameters to estimate dyadic patterns. The k parameter, introduced by Kenny and Ledermann (2010), was created to test the different patterns of interdependence explained earlier. As already mentioned, the k parameter is a ratio of the partner effect on the actor effect, which is computed separately for each member when studying distinguishable dyads. Consequently, there are two different k parameters to be estimated: $k1 = p12/a1$ for male and $k2 = p21/a2$ for female. The k parameter's values will provide information about the type of dyadic pattern that characterizes the effects reported in the model. If we have significant actor effects and non-significant partner effects then, as mentioned, we would specify the ratio to $k = p/a$. If we then obtained a k param-

Listing 3 ■ Model command

```
MODEL:      Y1 on X1;      !actor effect for males
            Y1 on X2;      !partner effect for males
            Y2 on X1;      !actor effect for females
            Y2 on X2;      !partner effect for males
            X1 with X2;    !X construct correlation
            Y1 with Y2;    !Y construct correlation
```

eter with a value near 0, this would suggest the presence an actor-only pattern ($a \neq 0$, $p = 0$). Alternatively, if we obtain significant partner effects and non-significant actor effects, we would then specify the ratio to $k = a/p$. In this scenario, if we have a k parameter with a value near 0, this would suggest the presence of a partner-only pattern ($a = 0$, $p \neq 0$). A k parameter near 1 would provide evidence for a couple-oriented pattern ($a = p$). Finally, a k parameter near -1 would lend credence for a contrast pattern in which the actor and partner effects are of comparable strength but in opposite direction ($a + p = 0$).

In order to estimate the k parameters, two phantom variables are added in the model. Phantom variables have been proposed by Rindskopf (1984) to be a valuable tool in SEM in order to incorporate more complex model constraints. Phantom variables are defined as latent variables that have no meaning or disturbance because no observed measures are linked to them. In our model, both phantom variables ($P1$ and $P2$) are defined as latent variables with the "BY" statement. However, we want this new path to be estimated; by default MPLUS always sets the first observed variable on a latent variable to be equal to 1.0. For this reason, you will have to add an asterisk on each of the Ys. Then, to correctly estimate the k parameters you will have to force equality between $a1$ and $p12$, and $a2$ and $p21$, which will incorporate the ratio inside the estimated model. The phantom variables, in this case, act as mediators of the relationship between predictor and outcome variables.[2] Also, both phantom variables' residual variances will have to be fixed to 0.0. Last thing to do in the MODEL command is to set the correlation between the two phantom variables (P1 and P2) to be 0.0. Finally, bootstraps for confidence intervals (CIs) are suggested by Kenny and Ledermann (2010) to better interpret the k parameters. You can now run this syntax and look at the results.

It is important to outline that model 1 (basic APIM) and model 2 (with k) are statistically equivalent models because they are both saturated models (MacCallum, Wegener, Uchino, & Fabrigar, 1993). Statistically equivalent models are indistinguishable based on their goodness of fit. Additionally, bias-corrected bootstrap 95% CIs (hereafter referred to as CIs) are suggested by Kenny and Ledermann (2010) to better interpret the k parameters considering that the distribution of the ratio is likely to be skewed due to its mathematical nature. In our example, the male's k parameter, $k1$, equalled -0.17, CI $[-0.56, 0.24]$. The female's k parameter, $k2$, was 0.06. CI $[-0.40, 0.70]$. These results must then be interpreted using the provided flowchart and the method described below. However, earlier, we discussed the possibility of testing a partner-only pattern if the results of the analysis at step 1 revealed non-significant actor effects and significant partner effects. As already mentioned in step 1, this hypothesis would require the estimation of $k = a/p$ rather than $k = p/a$. All of the manipulations explained for adding the phantom variables could be done, but instead of placing the phantom variables on the partner effect paths, like you would for an actor-only pattern hypothesized ratio, the phantom variables must be placed on the actor effect paths ($a1$ and $a2$). After making these model specifications, $k = 0$ would now denote a partner-only pattern ($a = 0$, $p \neq 0$) instead of an actor-only pattern ($a \neq 0$, $p = 0$). However, in this case, based on the results from step 1, no partner-only pattern was hypothesized, accordingly, a ratio of $k = p/a$ was calculated.

Model 3: Finding the best fit

Step 3: Interpreting the k parameters. As explained by (Kenny, 2013b), the confidence intervals are important to allow researchers to determine if any interpretable k values (-1, 0, or 1) are included within the boundaries of the 95% CIs. In our example, the CIs were of $k1 = -0.17$ $[-0.56, 0.24]$ and $k2 = 0.06$ $[-0.40, 0.70]$. Based on those results, we fixed $k1$ to 0 and $k2$ to 0, which freed 2 degrees of freedom, making the model overidentified. With these new specifications, we can then compare the overidentified model with the saturated model. In our example, the two constraints added to the new model did not significantly worsen the fit of the model (see step 3 in Table 1).

---

[2] This last specification may seem unusual but is central to the computation of the k parameter ratio. In sum, when this specification is applied, the partner effect is now defined as the product of the actor effect (constrained as equal) and the new k parameter ($p = a * k$). For a more elaborate explanation of the constrained effect and the implication of the phantom variable see Kenny and Ledermann (2010, p. 362).

Listing 4 ■ Analysis, Model and Output commands for step 2

```
ANALYSIS:   estimator = ml;
            bootstrap = 5000;
MODEL:      P1 by Y1*(k1);  ! "*" is use for freeing the estimate
            P2 by Y2*(k2);
            Y1 on X1 (a1);  !Label used for constraining parameters to equality
            Y2 on X2 (a2);
            P1 on X2 (a1);
            P2 on X1 (a2);
            P1@0;           !residual variance fixed to 0.0
            P2@0;
            X1 with X2;
            Y1 with Y2;
            P1 with P2@0;   !correlation fixed to 0.0
OUTPUT:     stand;          !for standardized estimation
            sampstat;       !for descriptive statistics
            cinterval(bcbootstrap);!for confidence intervals
```

Listing 5 ■ Model syntax for partner-only pattern with $k = a/p$

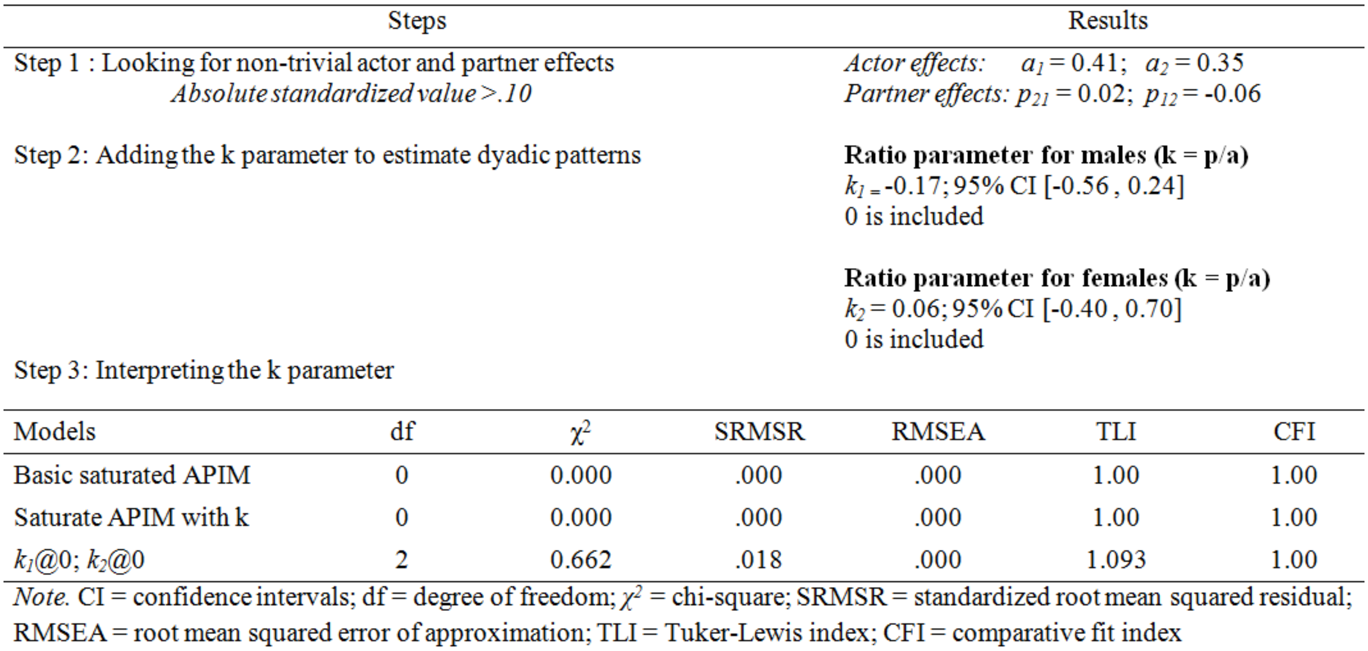
```
MODEL:      P1 by Y1*(k1);
            P2 by Y2*(k2);
            P1 on X1(a1);
            P2 on X2(a2);
            Y1 on X2(a1);
            Y2 on X1(a2);
            P1@0;
            P2@0;
            X1 with X2;
            Y1 with Y2;
            P1 with P2@0;
```

How should we interpret these results with dyadic patterns? One should consider multiple aspects when interpreting the k parameters such as the significance of the actor and partner effects found in step 1 and the value obtained for the k. The numbers are summarized in Figure 3. If we follow our flowchart, we can find the dyadic patterns present in our example. The female actor effect ($a2 = 0.35$) was significant whereas the male partner effect ($p21 = 0.02$) was non-significant, thus implying an actor-only pattern. The ratio ($k2$) was also found to be 0, thus indicating the presence of an actor-only for females. Similarly, the male actor ($a1 = 0.40$) and female partner ($p12 = -0.06$) effects presented a same interpretable ratio of 0 ($k1$). The significance of the latter effects revealed an actor-only pattern for males.

Discussion

The main goal of this tutorial was to present and demonstrate a step-by-step tutorial for the APIM with distinguishable dyads using SEM in the MPLUS statistical program. Although the APIM has received great attention and conceptual growth in the past decade, novice researchers still express the need for basic and concrete explanations for the specific execution of the APIM. Hopefully this tutorial will make dyadic data analyses more accessible and help researchers with basic SEM knowledge to easily test an APIM. Moreover, this tutorial simplifies current APIM steps by eliminating steps we deemed unnecessary. Although there is a great need to develop existing dyadic data analyses procedures, it is also of great importance to clearly communicate statistical procedures to researchers wishing to learn new statistical methods. Without these types of tu-

Figure 3 ■ Summary of the APIM results for each step based on our example



Steps	Results
Step 1 : Looking for non-trivial actor and partner effects *Absolute standardized value >.10*	*Actor effects:* $a_1 = 0.41$; $a_2 = 0.35$ *Partner effects:* $p_{21} = 0.02$; $p_{12} = -0.06$
Step 2: Adding the k parameter to estimate dyadic patterns	**Ratio parameter for males (k = p/a)** $k_1 = -0.17$; 95% CI [-0.56 , 0.24] 0 is included **Ratio parameter for females (k = p/a)** $k_2 = 0.06$; 95% CI [-0.40 , 0.70] 0 is included
Step 3: Interpreting the k parameter	

Models	df	χ^2	SRMSR	RMSEA	TLI	CFI
Basic saturated APIM	0	0.000	.000	.000	1.00	1.00
Saturate APIM with k	0	0.000	.000	.000	1.00	1.00
k_1@0; k_2@0	2	0.662	.018	.000	1.093	1.00

Note. CI = confidence intervals; df = degree of freedom; χ^2 = chi-square; SRMSR = standardized root mean squared residual; RMSEA = root mean squared error of approximation; TLI = Tuker-Lewis index; CFI = comparative fit index

torials, not only are researchers limited in their own statistical analyses but the field of dyadic research is limited in the processing and interpretation of rich and available data.

Recent and Future Applications of the APIM

In recent years, the APIM methodology has been used and proposed to accommodate research questions of increasing complexity. For example, Ledermann, Macho, and Kenny (2011) have expanded the APIM presented by Kenny and Ledermann (2010) to enable the assessment of mediating manifest variables and guidelines have been developed by West, Popp, and Kenny (2008) for investigating different types of moderation effects in dyadic data, while others have investigated moderation with SEM (Kivlighan, Marmarosh, & Hilsenroth, 2014; Maleck & Papp, 2015; Papp, Kouros, & Cummings, 2010, e.g.m,). Wickham and Knee (2012) have also suggested the calculation of an interaction term between $X1$ and $X2$ (i.e., moderation) and have added two other ratios ($h = a/x1x2$; $c = p/x1x2$) in order to improve the methodological-substantive synergy between the APIM and interdependence theory. Marsh, Wen, and Hau (2004) have investigated different strategies for testing interaction terms in SEM; results of simulation studies indicate that the unconstrained approach performs just as well as the more traditional and technically demanding constrained approach (Marsh, Wen, Nagengast, & Hau, 2012). In light of these new advances, future research could also use latent rather than manifest variables because interactions with latent variables have the advantage of controlling for measurement error in the interaction term in order to increase the statistical power associated with the interaction effect. Moreover, the different ratios that are proposed by Wickham and Knee (2012) could be computed with more advanced mathematical constraints (i.e., MODEL CONSTRAINT function in MPLUS) and a new parameter may be computed for bootstrapped 95% CIs. On a final note, a study of Sagan and Kowalska-Musial (2010) has recently used a Bayesian approach in their APIM analyses of dyadic data. The Bayesian estimator could be particularly useful in dyadic data insofar as it generally allows researchers to analyze smaller samples of dyads, while minimizing the risk of improper solutions and convergence problems (Hox, van de Schoot, & Matthijsse, 2012). As noted by Fife, Weaver, Cook, and Stump (2013), this estimation technique offers great advantages like obtaining better estimations of parameters, calculating confidence intervals more accurately, and having better performance of rejecting a model with a small sample. Before integrating the "Bayesian revolution" into their own research, researchers should try to gain knowledge on the numerous advantages and applications of the Bayesian estimation. As such, the user friendly guide of Zyphur and Oswald (2013) offers a

Listing 6 ■ Model command for step 3

```
MODEL:      P1 by Y1@0(k1);  !"@" is used for fixing a parameter with a value
            P2 by Y2@0(k2);
            Y1 on X1 (a1);   !Label used for constraining parameters to equality
            Y2 on X2 (a2);
            P1 on X2 (a1);
            P2 on X1 (a2);
            P1@0;
            P2@0;
            X1 with X2;
            Y1 with Y2;
            P1 with P2@0;
```

good introductory resource for researchers willing to explore the specificities of Bayesian statistics.

Invariance testing and advanced notions in APIM

Although the APIM procedure presented in this tutorial offers readers a clear step-by-step methodology to test a basic APIM, one important issue was not discussed. It could be essential to consider the fact that measured variables (X and Y) could bear a different meaning between males and females in a given sample. To test the hypothesis of equality of constructs, or factorial equality it could be of great importance to use the measurement of invariance methodology (Van De Schoot, Schmidt, De Beuckelaer, Lek, & Zondervan-Zwijnenburg, 2015). The solution for such an important question is known as the measurement of equivalence/invariance (ME/I). In a subsequent tutorial, we will present new elements to the APIM analytic procedure by incorporating a measurement component to the model and by testing the invariance across dyad members. Following the footprints of (Kenny, 2013b), this new tutorial will extend the interpretation of the k parameters with valuable information that will help researchers to better interpret their data.

Conclusion

Over the last decade, there has been great progress in the development of APIM analysis methods. Despite recent efforts to widen the potential applications of the APIM (e.g., incorporating ratio parameters, mediators, and moderating effects), most researchers in the general field of psychology have yet to take full advantage of these advancements in their respective research program. It was our intention to bridge the gap between methodological and applied research by offering this tutorial to explain how to estimate the APIM with the aid of dyadic patterns in structural equation model.

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