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Analyzing Dyadic Data With Multilevel Modeling Versus Structural Equation Modeling: A Tale of Two Methods

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Multilevel modeling (MLM) and structural equation modeling (SEM) are the dominant methods for the analysis of dyadic data. Both methods are extensively reviewed for the widely used actor–partner interdependence model and the dyadic growth curve model, as well as other less frequently adopted models, including the common fate model and the mutual influence model. For each method, we discuss the analysis of distinguishable and indistinguishable members, the treatment of missing data, the standardization of effects, and tests of mediation. Even though there has been some blending of the 2 methods, each method has its own advantages and disadvantages, thus both should be in the toolbox of dyadic researchers.

Keywords: multilevel modeling, structural equation modeling, dyadic data analysis, actor–partner interdependence model, dyadic growth curve model

Recently there has been an explosion of interest in the analysis of dyadic data. In part, this surge of interest has to do with the wide range of researchers who study dyads. Relationship researchers study married couples, family researchers study parent–child dyads and sibling relationships, social psychologists study interracial interactions, developmentalists study peer relations in schoolchildren, organizational psychologists study negotiation, sport psychologists study coach–athlete relationships, and communication researchers study speech patterns in friends, to name just a few examples.

Another reason for this explosion of interest is that a wide range of data-analytic models have been developed for the study of dyads, with two models dominating the dyadic landscape: the actor–partner interdependence model (APIM) proposed by Kenny (1996) and the dyadic growth curve model (GCM) of Raudenbush, Brennan, and Barnett (1995). As pointed out by Kenny, Kashy, and Cook (2006), as well as others, these two models can both be analyzed by either multilevel modeling (MLM) or structural equation modeling (SEM). Although both methods can be used, each has particular advantages and disadvantages. We believe that all too often researchers use one method and fail to realize the disadvantages of the adopted method and the potential advantages of the other method. The purpose of this paper is to review and contrast those advantages and disadvantages of MLM and SEM.

Because the two methods are very different in how they handle missing values, missing values are extensively discussed, and a new strategy is presented for standardizing effects in the APIM when missing values are present. We begin by briefly explaining MLM and SEM and then evaluate them for dyadic data analysis, concentrating on the APIM and dyadic GCM but also examining other dyadic models. Although not the central focus of this paper, in the final section, we discuss the rarely used multilevel SEM or MSEM, which combines both SEM and MLM.

An essential distinction for any type of dyadic data analysis is whether dyad members are *distinguishable* or *indistinguishable* (Kenny et al., 2006). Dyad members are distinguishable when the two members belong to two different classes, such as husbands and wives or mothers and children, which are distinguishable by gender and role, respectively. Dyad members are indistinguishable, sometimes called *exchangeable*, when there is no meaningful group variable and, thus, both members belong to the same class, such as homosexual partners or same-gendered twins. Sometimes in analyzing dyadic data with distinguishable members, the distinguishing variable may show no empirical effects, and it may then be preferable to treat the dyad members as if they were indistinguishable. All dyadic models can be used for both distinguishable and indistinguishable members, but for indistinguishable members, the models have fewer parameters and so have more power to detect effects than the models for distinguishable members. We shall see that often SEM is more straightforward for the analysis of distinguishable, whereas MLM is often more straightforward for indistinguishable members.

Description of MLM and SEM

MLM is a univariate method for a single outcome variable and was developed specifically for the analysis of clustered data. Clustered data occur when individuals are nested within groups, such as students nested within classes, or when individuals are observed at multiple occasions, with occasions being nested within

individuals. This method allows for multiple sources of variance, known as random effects, and correlated errors. For example, in over-time data, residuals of adjacent time points might be substantially correlated with each other. These days, most MLM software programs offer a wide range of different error and variance structures and a variety of estimation methods for continuous, ordinal, and binary outcomes. In terms of data entry, the observation for MLM with cross-sectional data is the individual (e.g., the student in a data set with students, teachers, and schools) and with over-time data, it is each individual's measurement at each time.

SEM is a multiequation technique in which some variables can be unmeasured or latent. The method began as a blending of path analysis and factor analysis. SEM can be used to compute the model's parameters, most importantly path coefficients, covariances, and factor loadings. Also, the estimated (model-implied) values of the means, variances, and covariances can be compared with the sample values generated from the raw data, which allows the evaluation of the model's goodness of fit when the number of estimated parameters is smaller than the number of sample values. In terms of data entry, each case is a single group that contains all the information of all members and time points. In addition to raw data, SEM can accept data in the form of a variance–covariance matrix.

MLM Advantages

Both MLM and SEM have their own strengths and weaknesses. MLM has the advantage that most statistical standard software packages have built-in routines for MLM analysis, including SPSS, SAS, STATA, and R and so, no new statistical program needs to be installed. (The software programs HLM and MLwiN are notable exceptions here.) Thus, with MLM no switch is necessary between MLM analysis and other analyses, such as descriptive statistics, creating new variables, or restructuring data, and no data need to be read in from an external source. Consequently, the learning curve for MLM is typically far less steep than for SEM, as researchers can remain within a software environment with which they are already familiar. Moreover, MLM is very similar in form to regression analysis. As most data analysts start with this knowledge, the use of MLM is more comfortable for many researchers than the use of SEM, and dyadic researchers are no exception.

In dyadic research, many of the early presentations of dyadic analysis used MLM for both the APIM (e.g., Campbell & Kashy, 2002) and the dyadic GCM (Raudenbush et al., 1995). The MLM notation and ideas of individual level, or Level 1, and group level, or Level 2, continue to dominate many presentations of dyadic analyses, where Level 1 is the individual and Level 2 the dyad. Thus, in some sense MLM is more "natural" for dyadic researchers, which may well explain its much greater popularity than SEM in dyadic research.

Another strength is that MLM can be used to estimate models with small samples using restricted maximum likelihood (REML). Currently, SEM uses maximum likelihood (ML) estimation, which requires larger sample sizes, perhaps as many as 100 cases when all variables are measured and 200 cases for models with latent variables. Recall that, for SEM, the sample size is the number of dyads, not persons, and so achieving 200 dyads can be difficult. On a related note, as MLM uses REML, estimates of variances are

unbiased, whereas SEM estimates are downwardly biased; however, asymptotically, they are identical. This is because in MLM, the variance estimates are obtained by dividing the sum of squares by the degrees of freedom (df), whereas SEM divides by the sample size. Although the standard errors differ, if only slightly, several studies have demonstrated that the estimates of unstandardized fixed effects are identical for the two approaches (e.g., Chou, Bentler, & Pentz, 1998; Wendorf, 2002). In addition, some MLM programs provide df for tests for model coefficients, enabling t tests, as opposed to the approximate z test used in SEM.

SEM Advantages

Although SEM falls short in some respects to MLM, it has several key strengths. One is that it provides estimates of the whole model, including regression weights, means, intercepts, variances, and covariances, as well as their standard errors, whereas MLM primarily focuses on the regression weights. SEM can also handle a wide range of models, including models with latent variables. The latent variable might be the causal variable, the outcome variable, or an intermediary variable. In latent variable models, factor loadings can be estimated, fixed to a particular value, or set equal to one another, and errors can be correlated to allow for shared variance. The ability to have latent variables in the model allows the researcher to include the effects of unreliability of measurement. In addition to reflective measurement models, where the measured variables serve as indicators of latent variables, SEM can handle a formative latent variable (Bollen & Lennox, 1991), an unmeasured variable that is determined by a set of measured variables.

Another advantage of SEM over MLM is that SEM is a multiequation approach. Many analyses require more than one outcome, one being example is mediation, where the mediator is an "outcome" of the predictor. Another one is the APIM for distinguishable members, where each member has his or her own outcome. Although MLM can be adapted to handle multiequation models, it does so with some awkwardness that gets more complicated the more outcomes a model has (Goldstein, 1995).

Further, a distinct advantage of SEM over MLM is the direct evaluation of how well a particular model fits the data. For most structural equation models, the goodness of absolute fit can be assessed. This SEM advantage might be considered a "pseudoadvantage" for MLM, in that one can be deluded to have a good model, thereby not having to make changes, when in fact, the model is not consistent with the data. If the same model were estimated using SEM, the researcher would notice that the model did not fit the data using fit indices and would then have to revise that model to make it a good fitting model (see Wendorf, 2002, for an example). Thus, with SEM, one knows after one has estimated the model whether it is statistically a "good" or "bad" model, whereas with MLM, additional analyses must be conducted to determine whether the model is good or bad. We note that these "additional analyses" are not typically done in practice, or are only done partially.

On a related note, SEM is flexible in specifying the parameters being estimated in a particular model because it allows researchers to fix parameters to specific values, set one parameter equal to another parameter, or have that parameter freely estimated. This is a key feature of SEM, and it allows researchers to include unmea-

sured confounders, which affect some variables (e.g., Hernán & Robins, 2016), and instrumental variables (Bollen, 2012), which have an effect on one variable but not on another, to remove possible specification errors (e.g., measurement or reverse causation). A related advantage is that several SEM programs allow for the defining of new parameters, which are a function of other parameters, something particularly useful in tests of mediation (e.g., the ratio of the indirect to the total effect).

Another unique feature of SEM is its ability to analyze data from multiple independent groups, which allows the assessment of measurement invariance across populations and time points (Meredith, 1993). This strategy for accommodating multiple groups is easier and more flexible than the use of indicator variables to represent the groups, which must be used in MLM. Also available in most SEM programs is mixture modeling (e.g., McLachlan & Peel, 2004), which allows for the estimation of the same model for multiple latent groups.

A further advantage is that with SEM, it is relatively easy to conduct sensitivity or "what if" analyses (Saltelli, Chan, & Scott, 2000). Consider a mediational model in which there is worry that the mediator might have measurement error. One can re-estimate the model to determine what the paths would be if the mediator had a certain degree of reliability, say .80. Still another advantage of SEM is that it can handle "nonstandard" models, such as higher-order latent variable models and nonrecursive or feedback models, both of which MLM is unable to estimate. We detail some of these models in the next section.

Comparison of MLM and SEM for Dyadic Data Analysis

Here we focus on differences between MLM and SEM for specific dyadic models, including the APIM and dyadic GCM. We discuss how they can each be estimated using both MLM and SEM and what are the advantages and disadvantages. A distinct difference between MLM and SEM is the structure of the data. For SEM, the data need to be in wide format, where each record has the information of all members of a group and all time points. In dyadic data analysis, this format is known as *dyad data structure* (Kenny et al., 2006). Using MLM, the data need to be in what is called *long format*, such that each row has the information of one member and for over-time data, one time point (Singer & Willett, 2003). For the APIM, this data format is known as *pairwise data structure*, which is explained below.

The Actor–Partner Interdependence Model

The details of the APIM are discussed in Kashy and Kenny (2000); Kashy and Snyder (1995); Kenny (1996), and Kenny and Cook (1999). Figure 1 shows a path diagram of the APIM for Member A and Member B and two variables, *x* and *y*, both measured in both dyad members. The path from the person's *x* to that person's *y* is called *actor effect* and the path to the other person's *y* is called *partner effect*. With distinguishable members, the APIM has two actor effects, one for each type of dyad member, as well as two partner effects, whereas with indistinguishable members, the two actor effects and the two partner effects are set equal. For both MLM and SEM, we discuss the differences in how each is estimated when dyad members are distinguishable versus indistinguishable, the treatment of missing data, the standardiza-
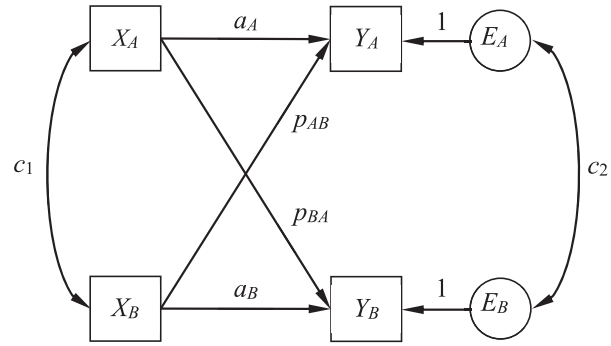

Figure 1. Path diagram of the APIM for two members, A and B.

tion of the effects, specialized models that are simpler and often have more power than the standard APIM, and tests of mediation.

The use of MLM. A pairwise data structure is needed when using MLM (e.g., Ledermann & Kenny, 2015), which has not only the individual's response (actor variable), but also the partner's response (partner variable), both of which affect the actor's outcome. The setup of the model for indistinguishable members is relatively straightforward. The program simply needs to be told to estimate the effect of an actor variable and its partner variable on the outcome. The effect of the actor variable on the outcome is the actor effect and the effect of the partner variable on the outcome is the partner effect.

Distinguishable and indistinguishable members. For distinguishable members, the analysis becomes a little more cumbersome. Two different strategies have been proposed (see Kenny et al., 2006). One strategy uses the distinguishing variable, and has that variable interact with both the actor and the partner variables. In essence, the distinguishing variable is treated as a moderator. This strategy is known as *interaction APIM* and allows researchers to test whether the two actor effects and the two partner effects vary significantly between the two types of dyad members. The other strategy involves "tricking" MLM to make a single-equation model into a multiequation model by using an indicator variable for each outcome (Goldstein, 1995). With dyads, it uses two indicator variables, one whose value is 1 for Member A and 0 for Member B, and another whose value is 1 for Member B and 0 for Member A (Newsom, 2002). These two indicator variables are then multiplied separately with the actor and partner variables and added to the model. This setup is known as *two-intercept APIM* (Kenny et al., 2006) and provides separate estimates of the two intercepts, the two actor effects, and the two partner effects. In contrast to indistinguishable members, for distinguishable members, the error variances may be different for memeber A and member B.

Missing data. If there are missing data on the actor's score on *x*, the partner's score on *x*, or either person's *y*, then the case is lost. Sometimes one member of the dyad may have complete data, but the other not, which results in a *single*. A single occurs in MLM analysis when a dyad has both of the *x* scores, but a *y* score from only one person. Table 1 presents the pairwise data from five dyads used in a multilevel analysis. For Dyad 1, both members have complete data and so both members' data are used. For the remaining dyads, there are missing data, and one or both cases are

Table 1

Five Hypothetical Cases From a Data Set With Singles (Dyads 2 and 3)

Dyad	Member	Actor x	Partner x	y	Included[a]
1	1	5	8	3	Yes
1	2	8	5	4	Yes
2	1	3	7	5	Yes
2	2	7	3		No
3	1	9	4		No
3	2	4	9	8	Yes
4	1		6	7	No
4	2	6		4	No
5	1	3	6		No
5	2	6	3		No

[a] Case included in the multilevel analysis.

lost. For Dyads 2 and 3, the missing case is on y for one member, so only one member is used (i.e., both members are treated as singles). For Dyad 4, there is a missing datum on x which results in missing data for both members, so the dyad is lost. The same is true for Dyad 5, where both members have a missing value on y.

If there are singles, complications arise in the computation of means and standard deviations. For each dyad, x serves as both an actor and a partner variable. But for data sets with singles, there are different x scores for the actor and partner variables and, thus, the resulting descriptive statistics are likely different for the actor and partner variables. Returning to Table 1, for Dyad 2, a score of 3 contributes to the actor x variable but not the partner x variable, because Member B of Dyad 2 is excluded, whereas a score of 7 contributes to the partner x variable but not the actor x variable. Most analysts ignore or are unaware of this complication, and simply report the mean and standard deviations of the individual scores. We suggest computing the means and variances separately for the actor and partner x variables, and then pooling the two values to obtain a single mean and standard deviation for x, which can then be used for descriptive statistics and standardization.

MLM essentially uses a form of listwise deletion to handle missing data, a strategy that has been well documented to lead to biased estimates of parameter estimates (Enders, 2010). As suggested by Schoemann and Sakaluk (2016), dyad researchers using MLM should begin to employ more advanced solutions, in particular, multiple imputation (Enders, 2010).

Standardization. Standardization of actor and partner effects is accomplished by standardizing both the x and y variables prior to the analysis. The estimates then represent the standardized effects. Alternatively, the standardized actor and partner effects can be calculated by multiplying the unstandardized effects by the ratio of standard deviation (*SD*) of x to the *SD* of y. When dyad members are distinguishable, it is advisable to use a common *SD* for x and y across members (Kenny et al., 2006), which is the pooled *SD* of the *SD*s computed separately within levels of the distinguishing variables (Ackerman, Donnellan, & Kashy, 2011).

Specialized models. MLM can also be used to estimate specialized models, such as models implying a specific dyadic pattern (Kenny & Cook, 1999) and models involving multiple types of dyads. Specifically, Kenny et al. (2006) discuss how to test the hypothesis that actor and partner effects are equal (known as a couple pattern), or that the two effects are equal, but opposite in

sign (known as a contrast pattern), by using the sum of the members' scores or the difference of the members' scores, respectively. A more parametric alternative to the estimations of patterns is to employ the estimate of the ratio of the partner effect to the actor effect, which is known as k (Kenny & Ledermann, 2010). Although the use of sum or difference scores is straightforward in MLM, no current MLM program provides an estimate of the standard error or confidence interval of k, which has been found useful in assessing patterns within the APIM (Kenny & Ledermann, 2010). However, it is possible to use parametric bootstrapping or the Monte Carlo method, which is done in the online app APIM_MM (Kenny, 2015). Another type of specialized model is the analysis of group composition within the APIM when there are multiple types of dyads, such as mother–son dyads and mother–daughter dyads. The analysis of such multiple types of dyads is straightforward for both distinguishable and indistinguishable members using MLM (West, Popp, & Kenny, 2008).

Mediation. MLM estimation of mediation is generally not simple. The essential challenge is that MLM is a single outcome procedure, whereas in mediation, the mediator is also an outcome. One strategy is to run separate MLM analyses and then piece together the results (Kenny, Korchmaros, & Bolger, 2003). Alternatively, the method described by Bauer, Preacher, and Gil (2006) to restructure the data could be used to estimate all effects. A related drawback of current MLM programs is that there is no simple way to obtain bootstrap estimates of the indirect effect. One possibility is to perform parametric bootstrapping to test effects.

The use of SEM. In contrast to MLM, SEM is very straightforward for the analysis of distinguishable dyad members. The model in Figure 1 can be directly estimated with an SEM software program. One advantage of SEM is that it gives all the estimates of the model, including the path coefficient, means, intercepts, variances, and covariances of the predictor variables and the residuals. Note that with SEM there are no actor and partner variables in the data set. Rather each x variable has an actor effect when it affects the response from the same person, and a partner effect when it affects the response from the other person.

Distinguishable and indistinguishable members. The analysis of indistinguishable members is more awkward in SEM than it is in MLM, because it requires the imposition of equality constraints on all parameters that come in pairs (i.e., variances, actor effects, partner effects, means, and intercepts) and an adjustment of the model fit statistic (Olsen & Kenny, 2006). Imposing these constraints, Olsen and Kenny call this model the I_Sat model, which has 6 *df* with two variables measured in both members. Adjustments need to be made to the χ^2 fit statistic, the *df* of the estimated model, and the null model for fit indices that require it.

Missing data. One major advantage of SEM over MLM is how it deals with missing data. The standard estimation method SEM uses with missing data is called Full Information Maximum Likelihood (FIML). It uses all the data, and even dyads in which both members do not provide a score on the outcome are included in the analysis, assuming that at least one of them provides an x score. As such, for the cases in Table 1, it would keep all five dyads, even Dyads 4 and 5. Moreover, most SEM programs can use *auxiliary variables* (i.e., variables not in the model but correlated with variables in the model) to improve estimation in cases with missing data (Graham, 2003).

When there are missing data, we can also use FIML to provide estimates of descriptive statistics (i.e., means and variances) using the saturated model, in which all the measured variables are correlated. These FIML estimates are statistically better estimates than the sample statistics from the individual data, especially when observations are missing not at random, and the model includes the variables that lead to the nonrandom missing data as predictor variables. However, we do note that the estimates of variance are the sum of squares divided by the sample size rather than the *df*, and so they are slightly downwardly biased. In the indistinguishable case, one advantage of FIML is that it gives a single estimate of descriptive statistics for each variable measured in both members, whereas with MLM, there can be different values for actor *x* and partner *x* variables.

Standardization. Most SEM software programs provide standardized estimates, but they are wrong in the indistinguishable case, and misleading for the distinguishable case. With indistinguishable members, the variables need to be standardized before conducting the analysis, either using the individual data to obtain the means and standard deviations, or in the case of missing data, using the FIML estimates from the saturated model. With distinguishable members, the SEM "standardized" estimates are done within each type of dyad member, and because variances are very likely to differ to some degree, the differences between standardized actor or partner effects across different members are not meaningful, because the same metric is not used for each. Again, we need to standardize across all members using pooled means and standard deviations, or the FIML values from the saturated model for both indistinguishable and distinguishable members when data are missing.

Specialized models. The estimation of specialized models suggesting specific dyadic patterns (e.g., actor-only, partner-only, couple, or contrast pattern) is relatively straightforward using SEM (Kenny & Ledermann, 2010). Moreover, specific hypotheses can be tested, such as the partner effect from the older sibling to the younger sibling is twice as strong as the partner effect from the younger to the older sibling, using phantom variables (Rindskopf, 1984). However, the analysis of multiple types of dyads using interaction terms can be laborious when some members are indistinguishable (e.g., homosexual and heterosexual couples); multiple group analysis is an alternative that is more flexible, but requires larger samples (Ledermann, Rudaz, & Grob, in press).

Mediation. The analysis of mediation within the APIM is especially straightforward using SEM (Ledermann, Macho, & Kenny, 2011) because it allows the estimation of the full model in one run. Most SEM computer programs can produce estimates of direct, indirect, and total effects, and contrasts of effects, as well as perform bootstrap confidence interval estimates of those effects.

Summary. We see MLM as more compatible with indistinguishable members, whereas SEM is more compatible with distinguishable members. An SEM APIM with many variables and indistinguishable members has a slew of equality constraints (Olsen & Kenny, 2006). For instance, if there were four variables each measured in both members and three dyad-level (between-dyads) covariates, a total of 96 constraints need to be imposed in the indistinguishable case. Imposing these constraints is difficult, and MLM might well be the more prudent course of action for models with a large number of variables. However, should the investigator wish to conduct mediational analysis or has significant amounts of missing data, we see SEM as far superior. Moreover, if the

investigator wants to compute *k* and test for specific patterns or analyze multiple groups, it is easier to do so with SEM.

The advantage that SEM can determine if the model is correct by a goodness-of-fit test is not relevant for most APIM analyses because the model with measured *x* and *y* variables is a saturated model and so it exactly reproduces the variance–covariance matrix. Most of the tests of a specialized APIM model (e.g., a model with distinguishable dyads in which both partner effects are set to zero and the two actor effects are set equal) that can be conducted within SEM could also be accomplished by a deviance difference test within MLM. However, the comparison of models differing in their fixed effects requires the use of the ML estimation method rather than REML, which only allows the comparison of models differing in their random effects.

The major advantage that MLM has over SEM is that the APIM can be used in models with smaller sample sizes, whereas SEM requires larger sample sizes. The usual rule of thumb for SEM analyses is 200 cases for latent-variable models, which for dyadic research implies a study with 400 people. However, we suspect that this standard is too high for an APIM analysis, as there are no latent variables in a traditional APIM analysis. We suspect that between 80 and 100 dyads might be a better minimum for SEM APIM analyses, but we await a more definitive analysis.

The Dyadic Growth Curve Model

Figure 2 shows a diagram of the dyadic GCM for a single variable, *y*, measured at three points in time for members A and B. In this model, a person's score is a function of the intercept or *i*, the linear slope (trajectory) or *s*, and a time specific error, *e*. The intercept is generally where dyad members start on average at the first time point (given that time equals zero at that point), whereas the slope is the average rate of linear change for each type of member. These slope and intercept factors can vary across members and are correlated both within and between members. There is also a correlation between the errors of the two dyad members' scores measured at the same time. We now compare MLM and SEM, focusing on the issues of distinguishability, testing of fit, ease of estimation, and missing data.

The use of MLM. We first note there is the myth of a three-level dyadic GCM (Laurenceau & Bolger, 2005): Dyadic growth can be appropriately modeled by a three-level GCM comprised of observations nested in persons nested in dyads. Almost always it is much more appropriate to estimate growth in dyads by a two-level model with observations nested within dyads (Raudenbush et al., 1995, see also Atkins, 2005). To model systematic change, the analysis requires the creation of two indicator variables (one that has 1 for Member A and otherwise 0 and one that has 1 for Member B and otherwise 0). These indicator variables are used to create the two equations, one for each member. With MLM, time is a variable in the data set and is treated as a predictor of the outcome, and so time is multiplied by each indicator variable to measure the effect of time, the slope effect.

Distinguishability. With distinguishable members, the effects of the indicator variables and their interactions with time are allowed to vary for the dyad members to allow for different intercept and slope estimates for each of the two members. The two intercepts and slopes from this prediction equation are treated
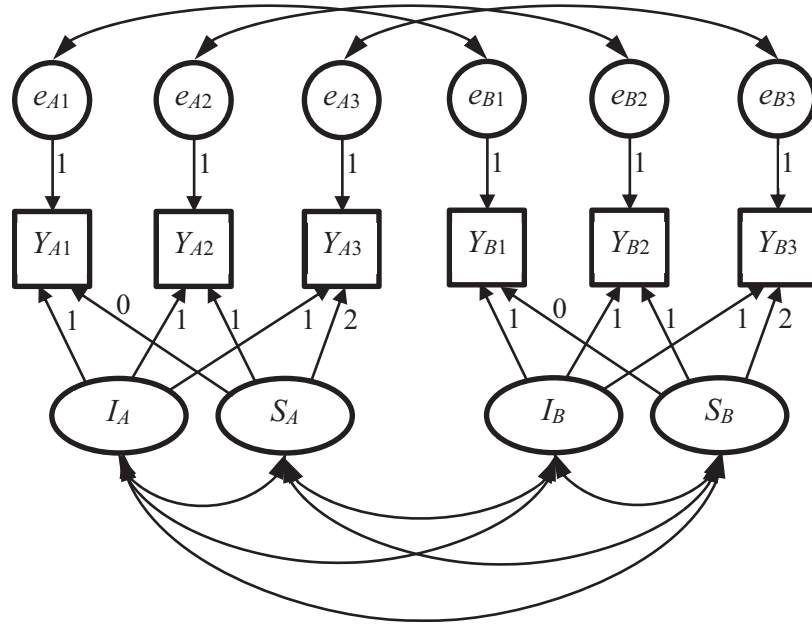
Figure 2. Path diagram of the dyadic GCM for Members A and B and three equally spaced time points.

as random variables with their own variance and correlations between each pair.

With indistinguishable members, there is just one fixed intercept and one slope effect. For the random effects, we need to impose equality constraints on the residual and random variances, and the covariances of these random effects (Kashy, Donnellan, Burt, & McGue, 2008). For instance, we want the slope variances to be the same for member A and member B. Imposing this constraint appears not to be currently possible for most MLM software programs (e.g., SPSS and R's lmer package), but can be accomplished somewhat awkwardly for other programs (e.g., SAS and MLwiN).

Ease of estimation. Often in these models, there is what is called a time-varying covariate. For instance, in measuring how much life satisfaction changes over time, we might want to adjust for the person's income at that time. This is relatively easy to do in MLM, as we simply add income to the equation. If we are interested in the moderating role of a predictor, we just add the product of that predictor and time to the equation.

One major advantage of MLM is that many time points is not especially problematic—the MLM equation is essentially the same regardless of the number of time points. Another major advantage is that MLM can deal with time points as well as time intervals that vary between and within dyads without increasing the number of missing values.

Missing data. Missing a few values on the outcome for each member presents no difficulties in estimation for MLM. However, if a person is missing a predictor or covariate value, all of that person's data are excluded from the analysis.

The use of SEM. Using SEM, the model shown in Figure 1 can be directly estimated. Again, as with the APIM, the analysis of distinguishable members is straightforward. The model with indistinguishable members requires the imposition of a series of equality constraints on all parameters that come in pairs (a total of 12 for the model in Figure 1) and an adjustment of the fit (see Kashy et al., 2008, for details).

Model fit. One major advantage of SEM is that almost every GCM is overidentified (i.e., one with positive *df*) and so it allows the researcher to determine if, in fact, the model is consistent with data. If a particular model is inconsistent with the data, the researcher can make changes in the model to improve its fit. Those changes are of two major types: One is that the researcher can weaken the assumption of linearity to allow for nonlinear change, for example, by adding a quadratic slope or a second intercept, when there are four or more time points. Also some of the fixed factor loadings of the slope component can be freed, which then reflect the relative growth across time and so allow the estimation of nonlinear change (Meredith & Tisak, 1990). The other type of respecification is that the errors may be correlated over time, both within and across persons.

Ease of estimation. Another major advantage of SEM over MLM is that one can have paths directly to intercept and growth curve factors, thereby determining how much variance is accounted for by explanatory variables. Moreover, one can look at effects of each of those latent growth variables on other variables. For example, SEM users can combine the dyadic growth curve approach with the APIM to address how the change in one variable is related to change in another variable both within and between partners (e.g., how stress after the birth of a child in both members is related to the changes in satisfaction in both members).

SEM, as demonstrated by Chou et al. (1998), is very flexible in testing whether error variances change over time. MLM does allow researchers to choose from a number of predefined covariance structures, but the researcher has almost complete control with SEM.

Missing data. Another advantage of SEM is that it can include cases with missing data in the analysis as long as the dyad has at least one observation. For instance, a dyad might have covariate information but no outcome values, yet the case can still be included in the analysis. Moreover, if cases are missing not at random, there is evidence that SEM with FIML is superior to

estimates from MLM (Enders, 2011). (MLM could be adapted to use multiple imputation in this case, but this is rarely ever done.)

The one major weakness with SEM is that there is not one equation but rather an equation for each observed outcome variable (i.e., one for each person at each time point). The sheer number of variables can be overwhelming. Imagine a study with one outcome and two time-varying covariates, each measured once a day in both members for 2 weeks. The total number of variables in the SEM model would be 84 variables (2 people $\times$ 14 days $\times$ 3 variables). Additionally, if we were to treat dyad members as indistinguishable, we would need to impose over a thousand constraints on parameters. Thus, models with a large number of time points are virtually impossible to work with in SEM, especially in the indistinguishable case.

Another weakness of SEM is the estimation of interaction effects involving the trajectory. Although possible, the way to estimate such interactions is much less straightforward in SEM than in MLM because of the necessity of including many new variables and paths in the model. However, as demonstrated by Li, Duncan, and Acock (2000), SEM allows researchers to test interaction effects between two growth trajectories that predict an outcome, which cannot be done using MLM.

Summary. Although both MLM and SEM can estimate a dyadic growth curve model, we feel that the use of MLM is again more straightforward when dyad members are indistinguishable. Moreover, the use of MLM is superior to SEM when there are many time points, the spaces between the time points vary across and within dyad members, the number of time points varies, and time-varying covariates and interactions between predictors and the growth curve components should be included. The advantage here is practical, as SEM becomes incredibly cumbersome in these cases.

SEM has the advantage that more complex models can be estimated, including models with a Level-2 outcome, such as relationship success, or models involving multiple growth processes (e.g., Cheong, MacKinnon, & Khoo, 2003). Moreover, SEM includes persons with missing values that are excluded when using MLM. However, should MLM be used, the researcher needs to estimate alternative models to show that the proper model of growth and error structure has been chosen.

Other Dyadic Models

Although APIM and dyadic GCM analyses dominate the dyadic landscape, they are not the only dyadic methods. Here we briefly detail a few of them and discuss their analysis using SEM or MLM. One important class of models is latent variable models, which include confirmatory factor analysis (CFA), the common fate model (CFM), the dyadic latent congruence model (LCM), and the dyadic latent-difference score (LDS) model. We also briefly consider the mutual influence model (MIM), which is a nonrecursive model.

The use of SEM. A latent variable model is the prototypical model for SEM, and so it should then come as no surprise that dyadic models have been developed involving latent variables. We start with the modeling of measurement error in the APIM and then discuss the models mentioned above.

An assumption of the APIM when actor and partner effects are to be interpreted as causal is that the x-variable measures

have no measurement error, but measurement error in the x variables can lead to biased results. Moreover, measurement error is often correlated in dyads and these correlations lead to further biases in the estimates of the actor and partner effects (Orth, 2013). By adding latent variables to an APIM analysis with self-report and partner report as indicators, estimates could be dramatically improved.

CFA is an especially useful technique that has become very important in the development and refinement of psychological tests. In dyadic research, one important use of CFA is to demonstrate measurement equivalence across distinguishable members and to assess the intradyadic association in both the distinguishable and indistinguishable case. For example, South, Krueger, and Iacono (2009) estimated a CFA model to test invariance across partners for Spanier's (1976) Dyadic Adjustment Scale.

The CFM introduced by Kenny and La Voie (1985) is shown in Figure 3A and enables the analysis of associations at the dyadic level. It is the best known latent variable model used in dyadic data analysis. Basic introductions to this model are given in Ledermann and Kenny (2012) and Galovan, Holmes, and Proulx (2016), and the model has been extended to study both mediation (Ledermann & Macho, 2009) and systematic growth (Ledermann & Macho, 2014) at the level of the dyad. Erol and Orth (2014) used this dyadic growth curve approach to assess the relation between partners' self-esteem and change in relationship satisfaction at the couple level.

Another model that can be estimated by SEM but not by MLM is the MIM. This model was introduced by Kenny (1996) and is displayed in Figure 3B. It resembles the APIM (see Figure 1), but instead of partner effects, there are reciprocal effects between the two y variables, which makes the model nonrecursive (see also Woody & Sadler, 2005). Due to the reciprocal effects, the analysis of this model is limited to SEM. An excellent example of MIM, combined with a latent variable analysis, is Sadler and Woody (2003) who examined the effects of personality on behavior in dyadic interactions.

The dyadic LCM (Cheung, 2009) is a latent variable model with two indicators, one for each dyad member, that load on two factors. One factor has both loadings fixed to 1 and represents the level or the average of the dyad members' measures. The other one has one loading fixed to -0.5 and the other loading fixed to 0.5 and represents the difference between the two members. Figure 3C illustrates how this type of model can be used to study the effects of level (l) and difference (d) on an outcome. Schaffhuser, Allemand, Werner, and Martin (2016) build on this approach to study the relative effect of the partners' ratings. in couples and found that the more positive a person rated his or her partner's personality relative to the partner's self-rated personality, the more satisfied both partners were with their relationship.

Researchers have also applied the LDS model (McArdle, 2001; McArdle & Nesselroade, 1994) to study change in dyadic longitudinal data (e.g., Hilpert, Bodenmann, Nussbeck, & Bradbury, 2016; Kouros & Cummings, 2011). The dyadic LDS model is also known as Latent Change Score Model and is illustrated in Figure 4 for a variable y measured in both members at four equidistant time points. For each type of dyad member, there is a common factor score, l, and a unique score, e, at each time point. At each time point after Time 1, each common factor score, l_t, is the sum

A: Common Fate Model
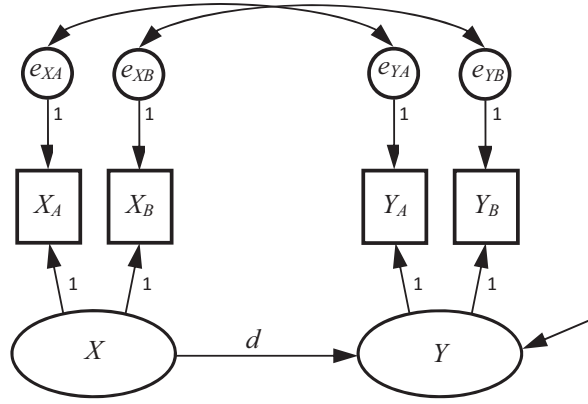
B: Mutual Influence Model
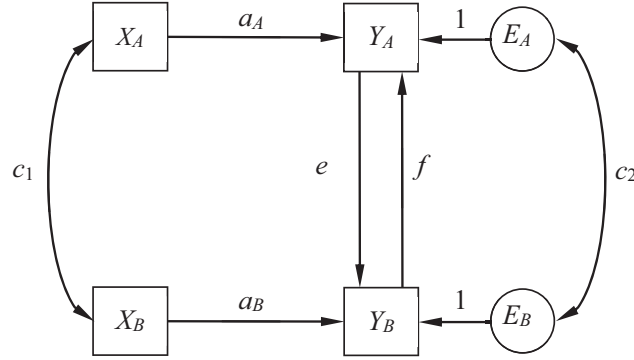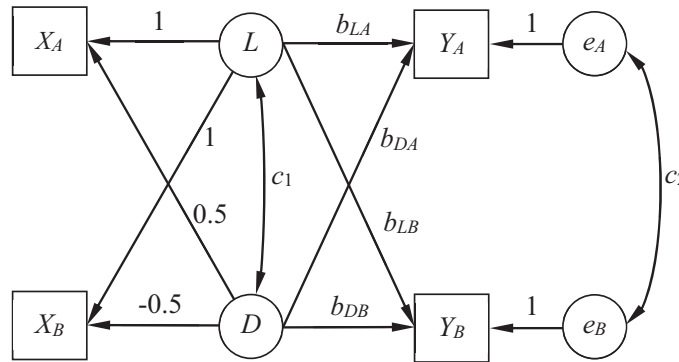
C: Dyadic Latent Congruence Model

Figure 3. Path diagram of the common fate model and the mutual influence model.

of the previous factor score, l_{t-1}, and a latent change score, d_t. There is also an initial score, I, and a latent change score, S, that both have a mean and a variance. As in the GCM, there is also a variance for each unique score. This type of model allows the researcher to address whether there is a statistically significant average change or s.

The use of MLM. MLM has rather limited capabilities to construct and test models with latent variables. It is possible to use MLM to estimate a latent variable model, but such models are limited to a measurement model in which the factor loadings are all fixed (see Wendorf, 2002). For this reason, MLM can be used with dyadic GCM and LCM because those models have factors with fixed loadings. For dyadic LCM, x_A and x_B are dropped from the model and replaced by $x_A + x_B$ for l and $x_A - x_B$ for d. Another key limitation is that latent variables can have only correlational relationships between them and not causal or predictive (i.e., no path can be drawn from one latent variable to another), which precludes the estimation of many dyadic models,
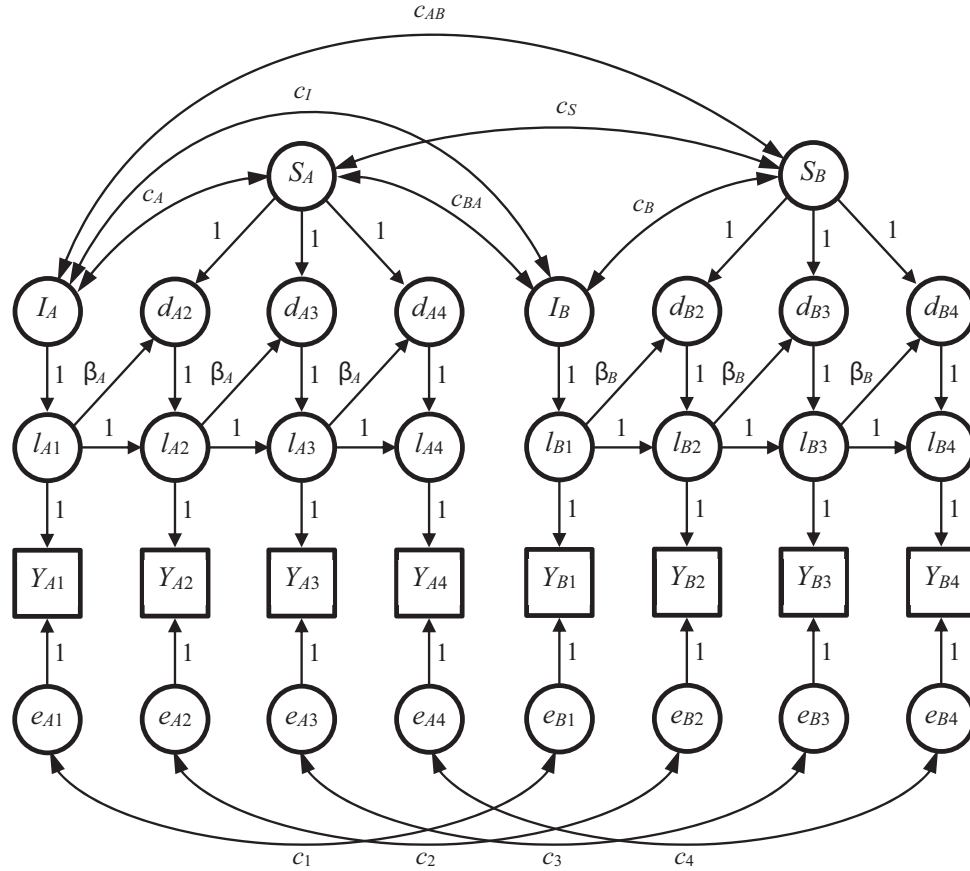
Figure 4.   Path diagram of a dyadic latent-difference score model with four equally spaced time points.

including the CFM. MLM is also unable to estimate the MIM because it is a feedback model, which is limited to SEM analysis. Quite clearly MLM is very limited in estimating and testing many nonstandard dyadic models.

Summary.   SEM is clearly the hands-down winner when it comes to estimating nonstandard dyadic models. Although MLM can estimate some latent variable models, SEM is far superior.

Multilevel Structural Equation Modeling

A promising development is the combination of both world SEM and MLM, known as multilevel SEM or MSEM (e.g., Goldstein & McDonald, 1988; Lee, 1990; Muthén, 1989), which has been incorporated in the software program Mplus. Like SEM, MSEM allows for latent variables, estimation of nonrecursive models, and multiple group analysis. As with MLM, the analysis of over-time data with a larger number of time points is not a problem and varying time intervals within and between groups do not increase the number of missing values. In contrast to MLM, which requires that the outcome variable needs to be Level 1, MSEM allows the analysis of an outcome that operates at a higher level. For example, MSEM might be used to predict couples' relationship success by spouses' stress levels measured at several occasions. As in SEM, missing data in a case does not preclude analysis. However, like MLM, there is no test of the model's absolute fit. Although MSEM can be used for CFM analysis

(Ledermann & Kenny, 2012) and dyadic growth curve models (Ledermann & Macho, 2014), Mplus does currently not have the wide array of possibilities for complicated error structures that most MLM programs have. Yet, for complex models, such as latent variable models with longitudinal mediation, MSEM looks to be very beneficial (e.g., Preacher, Zyphur, & Zhang, 2010). However, given that MSEM analysis is currently limited to Mplus, which is costly for most potential users and may not be readily accessible, it is perhaps unsurprising that MSEM has not been widely adopted by relationship researchers.

Overall Summary and Conclusion

Curran (2003) was perhaps the first to argue that there is a parallelism between MLM and SEM, and that eventually they would blend together. Although there has been some activity in such a blending, it has been slow to come, and as our review shows, the two methods have still distinct advantages and disadvantages. Specifically, our review revealed that to be an accomplished dyadic data analyst, one needs to know both modeling methods. Moreover, it would be clearly beneficial for teams to have skills in both MLM and SEM, because each method has its advantages, and if the research team knows only one method, they would often find themselves unable to do the optimal analysis.

We also believe that some domains in relationship science have suffered because MLM dominates dyadic data analysis. With SEM, one can relatively easily conduct sensitivity analyses that would allow for confounds and see how much the effect estimates would change. Another researcher may be interested in modeling change at the dyadic level. These types of analyses belong to the standard repertoire of SEM. Using MLM, such analyses would be much more difficult, or perhaps even impossible to conduct. No doubt the opposite happens, too: The research group only knows SEM and they fail to conduct analyses that would be more appropriate using MLM. For instance, SEM researchers may fail to estimate models with indistinguishable members because of many and cumbersome constraints that need to be imposed, as well as to analyze hierarchical data in an APIM framework.

Likely the overwhelming popularity of the APIM over CFM and MIM is due to the fact that the majority of dyadic analysts prefer to use MLM over SEM. If more dyadic researchers knew SEM, we believe there would be many more CFM and MIM analyses, as well as combinations of models (e.g., models in which one variable is a dyad-level variable).

That said, MLM has some distinct advantages, including the analysis of small samples, the many estimation methods available in software packages, the testing of group composition within the APIM when there are three types of dyads (e.g., gay, lesbian, and heterosexual couples), and the analysis of indistinguishable members. For dyadic GCM analysis, MLM is superior when there are numerous time points and the time points or intervals vary and when there are time-varying covariates and interactions involving the time variable. However, if MLM is to be used, especially for dyadic GCM, more careful attention must be paid to make sure a proper model is estimated using alternative models (e.g., nonlinear growth and alternative error structures). By doing so, SEM's advantage of being able to determine absolute fit is partially offset.

In conclusion, it is crucial to be aware of the strengths and limitations that both MLM and SEM have. To be able to address as many research questions as possible in the most appropriate way, relationship researchers should have a basic understanding of both methods or have a collaborator who knows the other method. For our field to advance, both methods should be in the repertoire of not only, but especially, dyadic research teams.

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