Issues in Solving the Problem of Effect Size Heterogeneity in Meta-Analytic Structural
Equation Modeling: A Commentary and Simulation Study on Yu, Downes, Carter, and
O'Boyle (2016)

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Abstract

Meta-analytic structural equation modeling (MASEM) is becoming increasingly popular for testing theoretical models from a pool of correlation matrices in management and organizational studies. One limitation of the conventional MASEM approaches is that the proposed structural equation models are only tested on the average correlation matrix. It remains unclear how far the proposed models can be generalized to other populations when the correlation matrices are heterogeneous. Recently, Yu, Downes, Carter, and O'Boyle (2016) proposed a full information MASEM approach to address this limitation by fitting structural equation models from the correlation matrices generated from a parametric bootstrap. However, their approach suffers from several conceptual issues and technical errors. In this study, we reran some of the simulations in Yu et al. by correcting all of the errors in their original studies. The findings showed that bootstrap credible intervals (CVs) work reasonably well, while test statistics and goodness-of-fit indices do not. We advise researchers on what they can and cannot achieve by applying the full information MASEM approach. We recommend fitting MASEM with the TSSEM approach, which works well for the simulation studies. If researchers want to inspect the heterogeneity of the parameters, they may use the bootstrap CVs from the full information MASEM approach. All of these analyses were implemented in the open-source R statistical platform; researchers can easily apply and verify the findings. This paper concludes with several future directions to address the issue of heterogeneity in MASEM.

Keywords: meta-analysis, structural equation modeling, meta-analytic structural equation modeling, parametric bootstrap

Issues in Solving the Problem of Effect Size Heterogeneity in Meta-Analytic Structural Equation Modeling: A Commentary and Simulation Study on Yu, Downes, Carter, and O'Boyle (2016)

Meta-analysis is the most popular tool for synthesizing research findings in management and organizational studies (Schmidt & Hunter, 2015). Most applications of meta-analysis focus on only one or a few effect sizes. Theories in management and organizational studies, however, usually involve multiple constructs. Researchers often formulate their theories in terms of measurement and structural models. Structural equation modeling (SEM) is then used to test these models. When there are enough studies on a particular topic, it is essential to meta-analyze these studies. These meta-analytic studies can advance theories by providing stronger tests of the proposed models (Bergh et al., 2016; Edwards & Christian, 2014).

The combination of meta-analysis and SEM to test theoretical models is widely known as meta-analytic structural equation modeling (MASEM). Becker (1992) and Viswesvaran and Ones (1995) were probably the first few scholars to provide a systematic treatment of this subject. Becker (1992) proposed a generalized least squares (GLS) approach to combining correlation matrices and to fitting regression models on the pooled correlation matrix. Viswesvaran and Ones (1995) outlined how to combine psychometric meta-analysis and SEM. They used Hunter and Schmidt's (1990) approach to meta-analyze correlation coefficients. Structural equation models are fitted on the average correlation matrix. Here, we call the approach used by Viswesvaran and One (1995) the univariate- r approach.¹ Cheung

¹ Some authors, e.g., Landis (2013) and Yu, Downes, Carter, and O'Boyle (2016), use the term MASEM to represent the statistical approach proposed by Viswesvaran and Ones (1995). We use the term MASEM broadly to refer to "methods for fitting or testing structural equation models for relations among several variables from multiple samples' correlation or covariance matrices for those variables" (Cheung & Hafdahl, 2016, p. 112).

and Chan (2005b, 2009) proposed a fixed-effects two-stage SEM (TSSEM) approach to conducting MASEM. Cheung (2014) extended the TSSEM approach to a random-effects model.²

There is evidence indicating that researchers are becoming increasingly interested in the applications and methodological development of MASEM. Sheng, Kong, Cortina, and Hou (2016) reviewed the current practices of MASEM. They traced all papers citing the methodological work of Becker (1992), Becker and Schram (1994), Viswesvaran and Ones (1995), and Cheung and Chan (2005b) and identified 153 papers. The univariate- r proposed by Viswesvaran and Ones (1995) was applied to more than 90% of these studies. Similarly, Rosopa and Kim (2017) summarized 94 published studies applying MASEM in human resource management, industrial-organizational psychology, organizational behavior, and allied fields. Again, the approach put forward by Viswesvaran and Ones (1995) was the most popular approach in these studies. Some examples of works that address critical substantive questions in management and organizational studies with MASEM are those by de Wit, Greer, and Jehn (2012), Monnot, Wagner, and Beehr (2011), Nahrgang, Morgeson, and Hofmann (2011), and Nohe, Meier, Sonntag, and Michel (2015).

Regarding methodological development, Bergh et al. (2016) and Landis (2013) reviewed issues related to applying MASEM in management and organizational studies. Cheung (2015a) produced a book-length treatment on how meta-analysis and SEM can be integrated into a single framework, which provides statistical justifications for the TSSEM approach. Jak (2015) provided a tutorial on how to conduct MASEM, focusing on the TSSEM approach. Cheung and Hong (2017) illustrated how to estimate functions of

Therefore, the approaches used by Becker (1992), Cheung (2014; Cheung & Chan, 2005b), and Viswesvaran and Ones (1995) are all MASEM approaches.

² Yu et al. (2016, pp. 1464 and 1470 and Table 1) mentioned that one weakness of the TSSEM approach is that one study must have a complete correlation matrix. This is not correct. Both the fixed- and random-effects TSSEM approaches implemented in the metaSEM package in R do not have such a requirement. This can be easily verified by running an example in the metaSEM package. The authors probably adapted this perception from Landis (2013, pp. 255 and 256, Table 1).

parameters, e.g., indirect effects, and their confidence intervals in MASEM. In a recent special issue of MASEM (Cheung & Hafdahl, 2016), various methodological and statistical issues in MASEM were addressed.

The most popular approach is *correlation-based MASEM* (Cheung & Cheung, 2016), which treats correlation coefficients as the effect sizes in a meta-analysis. Thus, the heterogeneity is quantified at the correlational level, whereas the parameters in the structural equation models remain fixed. However, researchers are sometimes interested in how the parameters, not correlations, vary across studies. Cheung and Cheung (2016) referred to this alternative approach as *parameter-based MASEM* because the parameters, e.g., regression coefficients and factor loadings, are the effect sizes in a meta-analysis.

Recently, Yu, Downes, Carter, and O'Boyle (2016) proposed a bootstrap approach to address the heterogeneity of the parameters in MASEM. They called their approaches the full information MASEM (FIMASEM), modified after the univariate- r approach, and the two-stage FIMASEM (TS-FIMASEM), modified after the TSSEM approach. By comparing the results of the conventional MASEM (univariate- r and TSSEM) with those of their new approaches, Yu et al. (2016) came to the conclusion that results based on the univariate- r and TSSEM approaches are likely to be misleading if the heterogeneity of the effect sizes is ignored.

If their findings and interpretations are correct, the implications for published works on MASEM and future methodological developments in MASEM are huge. This is because the findings in many published works on MASEM, such as those reviewed by Bergh et al. (2016), Sheng et al. (2016), and Rosopa and Kim (2017), are all based on correlation-based MASEM. Therefore, it is important to critically evaluate their work before recommending these approaches as the preferred methods for use in MASEM. Since the only difference

between the FIMASEM and TS-FIMASEM approaches relates to whether the inputs are from the univariate- r or the TSSEM approach, we do not differentiate between them in this paper.

The present study contributes to the literature in several ways. First, it highlights several critical issues and corrects some technical errors in Yu et al. (2016). These help the readers to fully understand the details behind the FIMASEM approach. Second, we reran some of the simulations in Yu et al. by correcting all of the errors in their original studies. The findings showed that bootstrap credible intervals (CVs) work reasonably well, while test statistics and goodness-of-fit indices do not. We advise researchers on what they can and cannot achieve by applying the FIMASEM approach. Third, after comparing the pros and cons of the TSSEM and FIMASEM approaches, we recommend fitting MASEM with the TSSEM approach. If researchers want to inspect the heterogeneity of the parameters, they may use the bootstrap CVs from the FIMASEM approach. Fourth, as all of these analyses were implemented in the open-source R statistical platform (R Development Core Team, 2017), researchers can easily apply and verify the findings.

In the following sections, we first briefly review correlation- and parameter-based MASEM. This review gives the background to the issues and explains the difficulties of addressing the heterogeneity in MASEM. In the next section, we summarize the procedures of the FIMASEM approach and illustrate the analyses with an empirical example. We then discuss the critical issues and technical errors in Yu et al. We empirically compare the performance of the FIMASEM and the TSSEM approaches by using a computer simulation. Finally, we discuss future directions on how to address the heterogeneity in MASEM.

Correlation- and Parameter-Based MASEM

Since the conceptualization of the heterogeneity is directly relevant to the issue of correlation- vs. parameter-based MASEM, we first briefly review the two approaches to MASEM.

Correlation-based MASEM

Most existing MASEM approaches, e.g., the univariate- r (Viswesvaran & Ones, 1995), GLS (Becker, 1992), and TSSEM (Cheung, 2014), are correlation-based MASEM. In the first stage of the analysis, correlation-based MASEM combines the correlation matrices into an average correlation matrix. In the second stage of the analysis, structural equation models are fitted on the average correlation matrix. Correlation-based MASEM has two features: (1) only one structural equation model is fitted on the average correlation matrix, and (2) the heterogeneity (the random effects) appears at the correlations SD_{ρ} rather than at the parameters SD_{θ} .³

Correlation-based MASEM has several strengths. First, missing correlation coefficients in the studies can be easily handled in the first stage of the analysis (Furlow & Beretvas, 2005). When the TSSEM approach is used, the maximum likelihood (ML) estimation can be used to efficiently handle the missing correlations (Cheung, 2015a). Second, alternative structural equation models can be compared in the second stage of the analysis.

However, there are also a few limitations to correlation-based MASEM. The most critical one is that the proposed structural equation model is fitted to the average correlation matrix. It is hard to tell whether the proposed model also fits well in all populations when the effect sizes are heterogeneous. Second, correlation-based MASEM only informs us about the heterogeneity of correlation coefficients SD_{ρ} . It does not give us any information on how heterogeneous the parameters SD_{θ} are.

Parameter-based MASEM

³ We use SD_{ρ} and SD_{θ} to represent the variation (standard deviation) on the correlation coefficients and on the parameters in SEM, respectively.

Parameter-based MASEM conceptualizes the heterogeneity on the parameters rather than on the correlations. In the first step of the analysis, a regression model, path model, or structural equation model is fitted on each study. In the second stage of the analysis, the parameter estimates, e.g., regression coefficients or factor loadings, are treated as effect sizes in a meta-analysis. Since parameter estimates are used in the meta-analysis, this approach is called parameter-based MASEM. This approach has been applied in only a handful of studies (e.g., Becker & Wu, 2007; Cheung & Jak, 2016; Gasparrini, Armstrong, & Kenward, 2012; Paul, Lipps, & Madden, 2006).

The strengths and weaknesses of parameter-based MASEM are essentially the opposite of those of correlation-based MASEM. The primary strength of parameter-based MASEM is that researchers can study the heterogeneity of the parameters SD_{θ} across studies. On the other hand, parameter-based MASEM has several weaknesses that may limit its usefulness. Since the proposed models are fitted on each study, parameter-based MASEM is not applicable when there are many missing correlations in the studies. Thus, previous applications of parameter-based MASEM assume that there are no missing correlations (Becker & Wu, 2007; Cheung & Jak, 2016; Gasparrini et al., 2012; Paul et al., 2006).

Another limitation of parameter-based MASEM is that in the case of over-identified models it is unclear how this approach can be used to test for model fit. Suppose that researchers fit an over-identified path model on 50 studies using parameter-based MASEM. If the proposed model fits well in some of these studies, say 20, but not in the other studies, it would be hard to draw a general conclusion. Moreover, if this path model does not fit those 30 other studies, the parameter estimates are questionable because the model is misspecified. Therefore, previous applications of parameter-based MASEM all employed regression models, which are just-identified models. Yu et al. (2016) proposed an index of generalizability to address this issue. The simulation studies reported in this paper, however,

do not support the use of such an index. We will discuss these various issues in more detail later.

Several researchers have previously put forward ideas similar to parameter-based MASEM. Hafdahl (2009) proposed several sophisticated statistical methods to address the heterogeneity of the functions of correlation matrices. His approach can be extended to parameter-based MASEM. Edwards and Christian (2014) suggested a simple method to address the uncertainty of population parameters. Their proposal consists of two steps. First, they calculate the credible intervals (CVs) of the correlation coefficients based on conventional meta-analysis. Suppose that there are five variables in a meta-analysis; there would then be a total of 20 upper and lower CVs on the correlation matrix. In the second step, the proposed structural equation model is fitted 20 times by replacing the average correlation matrix with their lower and upper CVs one at a time. They interpreted these values as the upper and lower CVs of the parameters.

Summary and Illustrations of the FIMASEM Approach

In this section, we first provide a summary of the procedures of the FIMASEM approach. Following that, we illustrate the procedures and interpretations with an empirical example.

Summary of the FIMASEM Approach

Although Yu et al. (2016) did not use the term parameter-based MASEM, their approach falls into this category. Specifically, both parameter-based MASEM and FIMASEM assume that the population parameters are random variables with means and standard deviations (SD_{θ}). There are several strengths to their approaches that may address some of the abovementioned weaknesses in parameter-based MASEM. First, the average correlations are used to generate parametric bootstrap correlation matrices. This practice addresses the problem of missing correlations. Second, they propose to evaluate the model fit

by using an index of generalizability. Doing so may address the issue of how to handle fit indices across different studies. In the following section, we summarize their procedures for ease of reference and discussion.

1. The first step is to conduct either a univariate- r or a random-effects TSSEM approach with the sample correlation matrices and the sample sizes. After the analysis, we have an estimate of the $p^* \times 1$ with $p^* = p(p-1)/2$ average population correlation vector $\hat{\boldsymbol{\rho}}$. If the univariate- r approach is used, the correlations are meta-analyzed individually. Thus, the variance component of the heterogeneity $\hat{\mathbf{D}}$ is a $p^* \times p^*$ diagonal matrix. The diagonal elements indicate the heterogeneity variances of the population correlation vector. If the TSSEM approach is used, researchers may estimate either the full $p^* \times p^*$ variance component of the heterogeneity $\hat{\mathbf{\Omega}}$ or the diagonal matrix $\hat{\mathbf{D}}$. Regardless of whether or not $\hat{\mathbf{\Omega}}$ is available, the FIMASEM and TS-FIMASEM approaches only use the diagonal matrix $\hat{\mathbf{D}}$ in the following steps.
2. Once we have estimated $\hat{\boldsymbol{\rho}}$ and $\hat{\mathbf{D}}$, the next step is to apply a parametric bootstrap to generate $\boldsymbol{\rho}_i \sim N(\hat{\boldsymbol{\rho}}, \hat{\mathbf{D}})$ from a multivariate normal distribution.⁴ The $p^* \times 1$ correlation vector $\boldsymbol{\rho}_i$ in the i th bootstrap sample is converted to the $p \times p$ population correlation matrix $\mathbf{P}_i$. If $\mathbf{P}_i$ is non-positive definite, it is resampled until it is positive definite. Alternatively, $\mathbf{P}_i$ can be converted to a near positive definite matrix with the Matrix package (Bates & Maechler, 2016).
3. The $\mathbf{P}_i$ correlation matrix is then used to fit a structural equation model $\mathbf{P}_i(\boldsymbol{\theta}_i) = \mathbf{P}_i$ by treating $\mathbf{P}_i$ as a sample covariance matrix. An arbitrary sample size, say the harmonic

⁴ With a slight abuse of notation, we keep the “hats” in $\boldsymbol{\rho}_i \sim N(\hat{\boldsymbol{\rho}}, \hat{\mathbf{D}})$, although they are used as fixed values to generate the data. This reminds us that they are estimated rather than true population values.

mean of the sample sizes in averaging the correlation coefficients, is used as the sample size in fitting the structural equation model. The parameter estimates $\hat{\theta}_i$ and the various statistics and fit indices such as the chi-square statistic χ^2 , comparative fit index (CFI), and standardized root mean square residual (SRMR) are saved.

4. Repeat Steps 2 and 3 B , say $B=500$, times.
5. The parameter estimates and the fit indices over the B bootstrap samples are used to construct the CVs on the parameter estimates, the mean and the SD of χ^2 , and several indices of generalizability by counting the proportion of studies that have a CFI score of $> .9$ and an SRMR score of < 0.1 .

Illustrations of the FIMASEM and TSSEM Approaches

We illustrate the FIMASEM and the TSSEM approaches using a real dataset from the published literature so that readers may compare and contrast the findings from these two approaches.

Methods. The dataset reported by Nohe et al. (2015) was used for illustration. Nohe et al. studied the relationship between work-family conflict and strain measured during at least two waves of measurement in a panel design. In their Table A1, they extracted 32 studies on work conflict at times 1 and 2 (W_1 and W_2) and on strain at times 1 and 2 (S_1 and S_2). The sample sizes varied from 66 to 2,235 with a median of 248. All of the studies were complete without any missing variables.

They fitted several theoretical models. One was a cross-lagged model with two equality constraints on the same variables ($W_1 \rightarrow W_2$ and $S_1 \rightarrow S_2$) and different variables ($W_1 \rightarrow S_2$ and $S_1 \rightarrow W_2$), labeled “Same” and “Cross” respectively in Figure 1. This model, which was over-identified with two degrees of freedom (dfs), was chosen in this illustration because we could inspect the fit indices. We used the metaSEM package (Cheung, 2015b) implemented in the R statistical platform (R Development Core Team, 2017) to conduct the

analyses. The R code and the output are in the Online Supplemental Materials #1 accompanying this paper.

Results and Discussion. We used 500 bootstrap replications with a medium sample size ($N=248$) in fitting structural equation models in the FIMASEM. Forty-four out of 500 bootstrap samples (~9%) were non-positive definite. These samples were resampled until they were positive definite. The mean and *SD* of the chi-square test ($dfs=2$) were 738.40 and 851.48, respectively. The proposed model was rejected in 99.4% of the 500 bootstrapped samples. The percentages of the 500 bootstrap replications with $CFI > .9$ and $SRMR < .1$ were 92.4 and 86.6, respectively. The chi-square statistic shows that the proposed model fits the data extremely poorly (mean=738 for $dfs=2$), even though the input sample size is not very large ($N=248$). On the other hand, the fit indices seem to suggest that the proposed model fits the populations reasonably well. Using the interpretations of Yu et al., the proposed model can be generalized to about 90% of these studies.

Regarding the TSSEM approach, the first stage of the analysis revealed that the population heterogeneity of the correlation coefficients varied from $SD_{\rho}=.09$ to .12. There is a small degree of heterogeneity on the correlation coefficients. The fit indices on the path model in the second stage of the analysis were $\chi^2(df=2)=0.23$, $p=.89$, $CFI=1.00$, $SRMR=.0033$, and the root mean square error of approximation (RMSEA)=0.00. These fit indices show that the cross-lagged model with the equality constraints fits the average correlation matrix well.

Table 1 shows the parameter estimates of these two approaches. The means of the parameter estimates of the FIMASEM are very similar to the parameter estimates of the TSSEM fitted on the average correlation matrix. The SD_{θ} of the path coefficients in the FIMASEM vary from .10 to .18. On the other hand, the TSSEM approach reports the standard errors (*SEs*) of the parameter estimates. The estimated *SEs* vary from .02 to .03. It

should be noted that SD_{θ} and SE are fundamentally different. The SD_{θ} refers to the variation in the population parameter, whereas the SE quantifies the precision of the parameter estimates due to sampling errors. Since the analyses are based on real data, whether the interpretations on the FIMASEM are correct remained unclear.

Critical Evaluations of and Simulation Study on the FIMASEM Approach

After summarizing the procedures and illustrating them with an example, we now discuss the critical issues in FIMASEM. We group these under five issues. A computer simulation study will be conducted to evaluate how serious these issues are.

Critical Issues in FIMASEM

Issue 1: Are $\hat{\rho}$ and $\hat{\mathbf{D}}$ stable enough to represent the “population” values in Step 2? The approach proposed by Yu et al. is similar to a conventional parametric bootstrap (e.g., Davison & Hinkley, 1997; Efron & Tibshirani, 1993). The samples (or the sample statistics $\hat{\rho}$ and $\hat{\mathbf{D}}$) are treated as population values to generate the bootstrap samples. Although it is the convention to use sample estimates in place of population parameters in a bootstrap, the sample sizes in the data should be large enough to obtain reliable results.

Let us consider Study 14 (Monnot et al., 2011) in Yu et al. (2016) as an example. The number of studies involved in calculating the average correlations varies from 3 to 71, with a median of 25 in averaging the correlations (Monnot et al., 2011, Table 1). There is substantial uncertainty in estimating the heterogeneity variances or SD_{ρ} because of the small numbers of studies. We may quantify the variability by constructing 95% confidence intervals (CIs) on the estimated heterogeneity variances. Researchers may get some idea of how stable these estimated heterogeneity variances are by inspecting these CIs.

Let us illustrate how uncertain the heterogeneity variances are in small samples. To simplify the discussion, we assume that the sampling variances are nearly the same for all

studies. Under this scenario, the estimated heterogeneity variance is similar to the sample variance of the effect sizes (Demidenko, 2013). Suppose that the estimated heterogeneity variance equals 1 ($SD_{\rho}^2 = 1$ in the notation of Yu et al.). Figure 2 displays the 95% CI on $SD_{\rho}^2 = 1$ with various numbers of studies in a meta-analysis (see Freund, 1992 for the formula).⁵

If we consider the number of studies (k) in Study 14, the 95% CIs on the estimated variance =1 for $k=3$ (minimum), 25 (median), and 71 (maximum) are (0.27; 39.50), (0.61; 1.94), and (0.74; 1.44), respectively. Even if there are 25 studies, the true variance varies from 0.61 to 1.94. Hence, if we use the estimated SD_{ρ} to generate the data, the results would likely be inaccurate. The situation becomes worse when the number of variables increases. As there are 15 dimensions (correlation coefficients in the correlation matrix) in Study 14, the number of studies required to make the estimated variances stable is huge (Gupta & Gupta, 1987). The results of FIMASEM can be highly unstable unless there are enough studies, which is typically not the case in MASEM.

Issue 2: What is the impact of the non-positive definite matrices on the bootstrap data? Do the bootstrap correlation matrices $\mathbf{\rho}_i$ follow the pre-defined population values with a mean vector of $\hat{\mathbf{\rho}}$ and a variance-covariance matrix of $\hat{\mathbf{D}}$? Perhaps not. This is because $\mathbf{\rho}_i$ is converted into a correlation matrix $\mathbf{P}_i$, which must be positive definite. Non-positive definite correlation matrices mean that the data do not exist in reality. Yu et al. briefly mentioned this limitation in their Limitations and Future Directions. However, they did not investigate how this issue affected their results. When there are non-positive definite

⁵ The formula listed in Freud (1992) is exact when the known sampling variances in a meta-analysis are 0. It is only an approximation in the presence of known sampling variances in a meta-analysis. But it is already sufficient to demonstrate the variability of the estimated heterogeneity variances. We reported variances SD_{ρ}^2 (τ^2 in other writings on meta-analysis) instead of SD_{ρ} because variances are usually used in statistics, e.g., in the assumption of the homogeneity of variances in ANOVA. Readers can easily convert them into SD_{ρ} .

correlation matrices, they are either replaced by resampling other matrices in the FIMASEM approach or converted by some near positive definite matrices (Bates & Maechler, 2016) in the TS-FIMASEM approach. For ease of reference, we refer to these two approaches as the replacement method and the nearPD method.

To demonstrate how the non-positive definite matrices affect the means and variances of the generated data, we reran the analysis for Study 14 using the two methods employed in the FIMASEM and TS-FIMASEM approaches.⁶ We used 10,000 bootstrap samples so that we could minimize the simulation error. The R code for this analysis is given in the Online Supplemental Materials #2 accompanying this paper.

In Study 14, the non-positive matrix occurred in 75% and 43% of the bootstrap samples in the replacement and the nearPD methods, respectively. The bias (the mean of the bootstrap samples minus the true value) of the correlations for the replacement and the nearPD methods ranged from -20.35% to 13.95% and from -11.32% to 8.25%, respectively. Regarding the SD_ρ , the bias for the replacement and the nearPD methods ranged from -27.40% to -5.10% and from -18.55% to -3.11%, respectively. The replacement method was slightly worse than the nearPD method. These findings suggest that the generated bootstrap samples may not follow the specified model $\boldsymbol{\rho}_i \sim N(\hat{\boldsymbol{\rho}}, \hat{\mathbf{D}})$ because of the truncation of the non-positive definite matrices. There are substantial biases in both the means and the variances of the generated data. These biases may affect the performance of the proposed approaches.

Issue 3: Do the bootstrap $\boldsymbol{\rho}_i$ (and $\boldsymbol{\Sigma}_i$) represent the population or the sample correlation matrices in Step 3? Before addressing this issue, it is of relevance to review

⁶ It is important to note that there was a programming error in Yu et al.'s Online Supplemental Material #1. In their R code, users are required to specify the SD_ρ of the effect sizes (p. 2, lines 21-27). The `mvnrnorm` function from the MASS package (Venables & Ripley, 2002) was then used to generate multivariate normal data. The authors incorrectly specified SD_ρ to represent the variances (p. 3, lines 7-11) to generate the data. For example, when the users specify $SD_\rho = .3$, their function actually generates data from $SD_\rho = .55$.

what SEM is. In SEM, we fit a proposed model $\Sigma(\theta)$ against the sample covariance matrix S with a sample size N via a fit (or discrepancy) function $F(\Sigma(\theta), S)$. The parameter estimates $\hat{\theta}$ are obtained at the minimum of the fit function $\hat{F}(\Sigma(\hat{\theta}), S)$. If the proposed model is correct, the test statistic, $X^2 = (N - 1)\hat{F}$, approximately follows a chi-square distribution with the appropriate *dfs* under some regularity conditions (Mulaik, 2009). We would seldom expect the proposed model to be correct even in the population because some of these assumptions may be violated. Researchers have proposed various goodness-of-fit indices to assess the approximate fit of the model (e.g., Hu & Bentler, 1999; Marsh, Hau, & Wen, 2004).

We now return to the issue of whether the generated data are populations or samples. Yu et al. have said that one of the main strengths of their proposed method is its ability to address the heterogeneity of population parameters. A parametric bootstrap is used to generate the “population” correlation matrices. Based on the generated “population” correlation matrices, CVs on the parameters and indices of generalizability, e.g., $CFI > .9$ and $SRMR < .1$, can be formed. Even though the authors focused only on CFI and SRMR, they claimed that “[a]lthough we focus on the three fit indices, the online software outputs 16 fit indices, and the logic we propose can be applied to any fit index” (p. 1461).

There are several fundamental problems with this approach. Yu et al. used the harmonic mean of the correlation coefficients in their analyses. They suggested that it does not matter what sample sizes are used. However, they reported and interpreted the mean and the *SD* of the chi-square statistics. It is clear that the chi-square statistic is a function of the sample size used in the analysis. The reported chi-square statistic is arbitrary and misleading. Users can easily get a large (or small) chi-square statistic by plugging in a different sample size.

Nearly all goodness-of-fit indices have been developed for sample covariance matrices. Most of the goodness-of-fit indices are sensitive to sample sizes (Bollen, 1990). If we were to use a different sample size in FIMASEM, the values of many fit indices would be different. One exception is the SRMR, which is not sensitive to sample size. However, the SRMR is also not sensitive to the complexity of the model that is used. We can make the SRMR arbitrarily small by adding more and more paths to the model. Moreover, the SRMR that is calculated in most SEM packages including lavaan (Rosseel, 2012) and OpenMx (Neale et al., 2016), and that are used in Yu et al., assume that the input matrices are covariances. Therefore, the standardized residuals on the diagonals are also included in the formula. This is inappropriate for MASEM, as the diagonals are always ones because the inputs are correlation matrices (see Cheung, 2015a for a modified SRMR for MASEM).

Another issue is that $CFI > .9$ and $SRMR < 0.1$ were arbitrarily selected as the indices for generalizability. That the cut-off for CFI is $> .9$ is, in fact, a statistical myth (Lance, Butts, & Michels, 2006). On the other hand, it remains unclear why RMSEA, a popular fit index in SEM, was excluded. There was no theoretical justification for why and how these indices and cut-offs would be valid for measuring the model fit for “population” correlation matrices.

To get a better sense of what these goodness-of-fit indices look like, we re-analyzed Study 14 using 10,000 bootstrap samples (see the Online Supplemental Materials #2). Only in a respective 9.71%, 20.51%, and 0.07% of bootstrap samples was $CFI > .9$, $SRMR < 0.1$, and the $RMSEA < 0.05$.⁷ Table 2 displays a summary of the statistics of various fit indices. Astonishingly, the RMSEA and SRMR show a maximum of 1.19 and 34.83, respectively. Since the SRMR is the mean of the standardized residuals, it is strange to have an SRMR of close to 1 in applied research. A value of $SRMR=34.83$ (and $RMSEA=1.19$) indicates that something is wrong in either the bootstrap samples or the proposed model. In Yu et al.

⁷ The values of CFI and SRMR are different from those reported in Yu et al. One possible reason for the difference is that Yu et al. used 500 bootstrap samples, while we used 10,000 bootstrap samples.

(2016), the authors took these exceptionally poor values as evidence that the proposed path model was not generalizable to different populations. In light of the issues observed in the present study, a more reasonable interpretation is that the proposed approach is questionable.

Issue 4: Should we interpret the CVs of the parameters when the proposed model is misspecified in Step 5? Another advertised strength of Yu et al.'s approach is that we can study the heterogeneity of the parameters through the CVs of the parameters. If the CV is very wide, the parameter may vary significantly across studies. If the CV is short, the parameter is said to be stable across studies.

There are two critical assumptions behind this approach. The first one is that the estimated SD_{θ} is an unbiased estimator of the heterogeneity of the population. If the estimated SD_{θ} is biased, the constructed CVs are also biased. We will evaluate this assumption in the later simulation study. Another assumption is that the proposed model is correctly specified. If the proposed model is misspecified, the parameter estimates are likely to be biased (e.g., Mulaik, 2009). Although many researchers argue that the proposed model is almost misspecified in some (minor) ways, most researchers agree that we should interpret the parameter estimates only if the proposed model has either a good "exact" fit with the chi-square test or a good "approximate" fit with some goodness-of-fit indices.

Suppose that we accept the authors' approach to evaluating the generalizability of the proposed model (Issue 3) with $CFI > .9$ and $SRMR < 0.1$. In Study 14 in Yu et al.'s Table 5, $CFI > .9$ in only 2% of the studies and $SRMR < 0.1$ in only 21% of the studies. According to the authors, the proposed model does not generalize to the majority of the population. The calculated CVs of the parameter estimates in Table 3 of Yu et al. are thus based on a majority of misspecified models (79% to 98%) and a minority of correctly specified models (2% to 21%). The validity of these CVs is questionable.

Issue 5: Some technical errors related to the simulation study (Study 1 in Yu et al.). Besides the conceptual problems in the proposed methods, there were also several technical errors in the simulation study (Study 1). Checking the R code in their simulation studies uncovered three fatal programming errors. The first was that the population correlation matrices used to generate the data were incorrect (that is, different from what the authors intended); the second was that the models used to analyze the data were incorrectly specified. We discuss these errors in more detail.

A path coefficient of .3 was intended to be used to generate data in Figures 1 and 2 in Yu et al. (2016). From their descriptions of the simulation study and by checking the R code used in their simulation studies, it appears that a path coefficient was incorrectly used to represent a Pearson correlation in the paper. Let us consider the model in Figure 1 in Yu et al. (2016). Some path coefficients are the same as those in the model implied correlation matrix,

$$\rho_{x \bullet m_1} = \beta_{x \rightarrow m_1} \text{ and } \rho_{x \bullet m_2} = \beta_{x \rightarrow m_2}, \text{ whereas others are different, in that } \rho_{m_1 \bullet y} \neq \beta_{m_1 \rightarrow y},$$

$$\rho_{m_2 \bullet y} \neq \beta_{m_2 \rightarrow y}, \text{ and } \rho_{x \bullet y} \neq \beta_{x \rightarrow y} .^8$$

For example, in their paper a specification of 0 was given for the population correlation between x and y ($\rho_{x \bullet y} = 0$) because there was no direct effect between x and y ($\beta_{x \rightarrow y} = 0$). However, there are still indirect effects via m_1 and m_2 between x and y . The correct correlation between x and y is $\rho_{x \bullet y} = .3 \times .3 + .3 \times .3 = .18$. Tables 3 and 4 display the incorrect (actually used) and the correct (intended) correlation matrices for the models in Figures 1 and 2 in Yu et al. (2016). Figures 3 and 4 in this paper display the incorrect (actually used) and the correct (intended) models for generating the data in Yu et al. (2016).

Another programming error was that the models used to analyze the data in their R code were incorrectly specified. The RAM specification (McArdle & McDonald, 1984) was

⁸ $\rho_{x \bullet m_1}$ and $\beta_{x \rightarrow m_1}$ are used to represent the population correlation between x and m_1 and the path coefficient from x to m_1 , respectively.

used in the model specification in the univariate-*r* and the TSSEM approaches using the OpenMx and metaSEM packages. The RAM specification uses three matrices to specify a structural equation model. The **A** matrix specifies the asymmetric paths, e.g., regression coefficients and factor loadings. The element $\mathbf{A}_{ij}$ in the *i*th row and *j*th column represents the regression coefficient from the *j*th column variable to the *i*th row variable. The roles of independent and dependent variables were incorrectly reversed in the paper. Therefore, when a model is specified from *x* to *y*, the actual analysis was from *y* to *x*. Figures 5 and 6 in this paper display the incorrect (actually used) and correct (intended) models for Figures 1 and 2 in Yu et al.

The third programming error was that all of the error variances in their Figures 1 and 2 were incorrectly fixed at 1.0 in their **S** matrix, which specifies the variance-covariance matrix of the variables. An explanation of how to compute the correct matrices and model specifications is given in the Online Supplemental Materials #3 accompanying this paper.

In standard simulation studies, researchers generate a large amount of data from a pre-defined population. Since the generated data are also subject to sampling errors, we have to generate a large number of replications, say 1,000, to minimize the simulation error. After running the analyses, researchers summarize the findings by studying the bias and efficiency of various estimators (e.g., Paxton, Curran, Bollen, Kirby, & Chen, 2001). In the simulation studies in Yu et al., there was only one replication in the simulation study—i.e., the 500 bootstrap samples were only run within one replication in the simulation study. Strictly speaking, Study 1 is an illustration with some artificial data rather than a simulation study to assess the empirical performance of various statistical methods. Thus, the results are likely to have been captured by chance. Because of these programming errors, the correctness of their findings is highly questionable.

A Simulation Study of the FIMASEM and TSSEM Approaches

As a result of the above critical issues and technical errors, it remains unclear how the FIMASEM works in simulated data with known properties. The present simulation study attempts to address these concerns by empirically evaluating the performance of the FIMASEM under conditions similar to those of Yu et al., except that the technical errors will be corrected. We also included the TSSEM for comparison, so that the readers may make an informed decision when choosing between the new approach and the conventional MASEM.

Methods. Artificial data were generated from the model with two specific mediators used in Yu et al.'s Figure 1, which was also reported on the right-hand side of Figure 3 in this paper. There were four variables with no missing variables. As there is no direct effect from x to y and no correlation between m_1 and m_2 , the dfs of this model are 2 when it is correctly specified. To make the simulations manageable, we mostly followed the settings of Yu et al. We set the means of all path coefficients (except for the two paths with 0) at .3. The sample size per study was set at 200. The following factors were manipulated.

Number of studies. Yu et al. only used 50 studies in their simulation studies. We expanded this to three levels (10, 20, and 50) in the present simulation study. These levels should be representative enough to give us some insights into how the methods work in typical settings.

Population SD. Three levels were selected: 0, .1, and .3. The level of 0 was used to represent the condition of the homogeneity of correlation matrices (and path coefficients). The levels of .1 and .3 are similar to those observed in applied research in Bosco et al. (2015).

Types of heterogeneity. As elaborated in the section on correlation- vs. parameter-based MASEM, there are two types of random effects in MASEM. We may conceptualize the random effects on the correlation coefficients. This approach is consistent with conventional MASEM. Two stages are required to generate the sample correlation matrices for the analyses. Let us illustrate how the sample correlation matrices are generated under this

condition. Since all of the path coefficients are .3, the model implied correlation matrix is shown in the upper triangle in Table 3. We take the off-diagonal correlations as the population means. Suppose that the population SD_{ρ} is .1; we generate normal data from these means and $SDs=.1$ and convert them into the population correlation matrices. If the population correlation matrices are non-positive definite, we resample them until the generated correlation matrices are positive definite. These population correlation matrices are then used to generate sample correlation matrices ($N=200$) for the meta-analysis. Here, this condition is termed the *Random Correlation Matrices*.

Another condition is to conceptualize the random effects on the structural parameters. This approach is consistent with the FIMASEM approach proposed by Yu et al. and with parameter-based MASEM. It works as follows. There are four path coefficients in the model ($x \rightarrow m_1$, $x \rightarrow m_2$, $m_1 \rightarrow y$, and $m_2 \rightarrow y$). Suppose that the population SD_{θ} is .1; we generate four normal scores from the mean=.3 and $SDs=.1$. These path coefficients are converted to the model implied correlation matrices using the tracing rules. If the population matrices are non-positive definite, they are resampled until the generated matrices are positive definite. These population correlation matrices are then used to generate sample correlation matrices ($N=200$) for the meta-analysis. Here, this condition is termed the *Random Path Coefficients*.

There are some points to note on the combination of this factor and the population SD . When the population $SD=0$, the model generating the data is the same for both the random correlation matrices and the random path coefficients because there is no heterogeneity on the population correlation matrices and the path coefficients. Second, the degree of the heterogeneity of the data can be different between the random correlation matrices and the random path coefficients even under the same level of population SD . Take population $SD=.1$ as an example. For the condition of random correlation matrices, the population correlation between x and y is generated from the mean=.18 and $SD=.1$. For the condition of random path

coefficients, the same population correlation between x and y is generated from

$\beta_{x \rightarrow m1} \beta_{m1 \rightarrow y} + \beta_{x \rightarrow m2} \beta_{m2 \rightarrow y}$, where β is generated from the mean=.3 and $SD=.1$.

Criteria for Assessments. In the FIMASEM approach, what are calculated are the relative percentage bias of the means of the estimated path coefficients and the estimated SD_{θ} . In the TSSEM approach, it is the relative percentage bias of the estimated path coefficients and the SEs that are calculated. It is important to note that when the data are generated from the condition of random correlation matrices, the correct population value of SD_{θ} is unknown, although the data are generated from $SD_{\rho}=.3$. We empirically generated 10,000 random samples and used them to calculate the population values in the assessments. This approach also applies to the TSSEM approach when the data are generated from the condition of random path coefficients. This step ensures that the biases of FIMASEM and TSSEM are calculated from the correct population values. Since the population values are the same for the four path coefficients (.3), we reported the average biases among these four paths for ease of interpretation. When the individual biases were not in the same signs, i.e., some were positive while others were negative, we indicated the ranges in the table.

Besides the parameter estimates, we also summarized the chi-square statistics and the various goodness-of-fit indices. Since the data are generated from multivariate normal data and the models are correctly specified with 2 dfs , the χ^2 statistic provides the correct statistic for assessing the performance of the methods. We also reported the fit indices to judge whether the proposed SEM has a good approximate fit to the data.

Results and Discussion. Table 5 displays the relative percentage biases of the parameter estimates. When the correlation matrices (and the path coefficients) are homogeneous, both the FIMASEM and the TSSEM approaches are unbiased. The FIMASEM is accurate in recovering the mean path coefficients and their SD_{θ} , which are

essentially zero. Similarly, the TSSEM approach is also accurate in recovering the path coefficients and their *SEs*.

When the data are generated under the condition of random correlation matrices, both approaches are accurate in recovering the path coefficients under the condition of population $SD=.1$. The bias of the parameter estimates becomes slightly more substantial when the degree of heterogeneity gets larger at population $SD=.3$. The estimated SD_{θ} in the FIMASEM is slightly under-estimated (-3 to -14%), especially when the number of studies is 10. The *SEs* in the TSSEM are also slightly under-estimated (-2% to -11%).

Regarding the condition of the random path coefficients, the parameter estimates of the TSSEM are unbiased in all conditions ($< 1\%$). The parameter estimates of the FIMASEM are unbiased only when the population $SD=.1$, whereas the parameter estimates are slightly under-estimated (about 13%) when the population $SD=.3$. Both the *SDs* of the FIMASEM and the *SEs* of the TSSEM are under-estimated. The bias of the *SEs* of the TSSEM (-12% to -20%) is slightly larger than that of the *SDs* in the FIMASEM (-1% to -17%). Regardless of the type of heterogeneity, the number of studies plays a vital role in the accuracy of estimating SD_{θ} in FIMASEM and *SE* in TSSEM.

Before going through the results of the test statistics and goodness-of-fit indices, it is helpful to recall the model generating the data (the model on the right-hand side of Figure 3 in this study). As there is no direct effect from x to y and no correlation between m_1 and m_2 , the proposed model should fit the data well in the FIMASEM with 2 *dfs*, even though the coefficients are random across the population correlation matrices. If we refer to the exact fit with the test statistic, it should follow a chi-square distribution with 2 *dfs* in the simulation study. If we use a close fit with the goodness-of-fit indices, they should also show that the proposed model fits well in nearly ALL simulated studies – that is, the percentage of studies

with $\text{CFA} > .9$ and $\text{SRMR} < .1$ should be close to 100% because the proposed model exactly fits in these populations.

Table 6 shows the test statistic and goodness-of-fit indices of the FIMASEM and TSSEM approaches. Under the condition of the homogeneity of correlation matrices (and of path coefficients), the means of the χ^2 statistic of the FIMASEM will vary from 5.87 to 13.79, which are larger than the expected value of 2. When the data are generated under random correlation matrices and random path coefficients, the means of the χ^2 statistic of the FIMASEM will vary from 33.33 to 3,737.66. The findings here provide clear evidence that the FIMASEM does not follow the statistical theory of SEM.

Using the proposed cut-offs by Yu et al. ($\text{CFI} > .9$ and $\text{SRMR} < .1$), almost all bootstrap correlation matrices are classified as being of good fit under the condition of the homogeneity of correlation matrices (and path coefficients), which is correct. When the data become heterogeneous under either the random correlation matrices or the random path coefficients, the proposed model fits more poorly in the bootstrap correlation matrices. When the population $SD=.3$, the percentages of the bootstrap correlation matrices vary from 20% to 44% under the random correlation matrices and from 36% to 69% under the random path coefficients for $\text{CFI} > .9$ and $\text{SRMR} < .1$. In theory, the FIMASEM should identify almost all bootstrap samples as well-fitted samples because the data are generated from models with 2 *dfs*. However, the FIMASEM failed to identify most of these studies. We also included $\text{RMSEA} < .05$ in the simulation study. The findings are even worse.

One reviewer wondered whether it might be possible to modify the conventional cut-offs in SEM to identify the percentage of studies that the proposed model fits in the population. To answer this question, we reran the above simulation by saving more information on the fit indices. Specifically, we calculated the 0th (minimum), 10th, 20th, 50th, 80th, 90th, and 100th (maximum) percentiles of the goodness-of-fit indices among each 500

bootstrap samples. We then calculated the means of the percentiles across the 1,000 replications in each condition. The profile of these percentiles may give us some ideas about the revised cut-offs that may be required in the FIMASEM. Since a larger CFI means a better model fit while a larger RMSEA and SRMR means a poorer model fit, we reversed the percentiles of the CFI in the figures for ease of interpretation. Therefore, higher percentiles, e.g., 90th and 100th, are always associated with a poorer model fit (lower CFI and larger RMSEA and SRMR).

Figures 7, 8, and 9 display the heat maps of these cut-offs. The x-axis shows the 0th to 100th percentiles of the fit indices. The left and right y-axes indicate the number of studies (10, 20, and 50) and the (type of) heterogeneity ($SD=0$, .1, and .3 in random correlation matrices and random path coefficients), respectively. The color indicates the “heat” of the values. When the values are above or below the ranges ($CFI < .9$, $RMSEA > 0.1$, and $SRMR > .1$), the color becomes gray.

When inspecting the patterns of the heat maps, it can be seen that the proposed model fit becomes poorer when the population parameters become more heterogeneous. We focus on the condition of $SD=.3$ in random path coefficients, which gives us the cases for large heterogeneity. We may recall that the proposed model is correctly specified with 2 *dfs* in all conditions. Thus, it is expected that these goodness-of-fit indices should identify 100% of the studies that the proposed model fits in the population. If we want to be 100% correct in identifying the models, the cut-offs in the 100th percentile in the condition can be as low as .06 for CFI, as high as .84 for SRMR, and as high as 1.52 for RMSEA. If we aim to identify 90% of studies correctly, the cut-offs in the 90th percentile can be as low as .35 for CFI, as high as .21 for SRMR, and as high as .67 for RMSEA. Suppose that we are comfortable with the 50th percentile (correctly identifying 50% of studies and misclassifying the other 50% of

studies); the cut-offs for the CFI, SRMR, and RMSEA would be .72, .11, and .32, respectively. Based on the current SEM literature, it is difficult to defend these cut-offs.

As discussed in Issue 3, these fit indices, e.g., CFI, SRMR, and RMSEA, were developed to evaluate sample covariance matrices. They were not meant to be used to evaluate population correlation matrices. The findings in this simulation study provide clear evidence that these cut-offs should not be used to identify the percentage of population studies for which the proposed model can be generalized. The follow-up simulation study also shows that we have to apply unreasonable cut-offs if we want to use them in FIMASEM.

Regarding the TSSEM approach shown in Table 6, it can be seen that it performs close to the theoretical value under the condition of the homogeneity of correlation matrices. The means of the χ^2 statistic of the TSSEM vary from 1.95 to 2.09, which are very close to the expected value of 2. When the data are heterogeneous in the condition of random correlation matrices, the χ^2 statistic is slightly over-estimated. The largest one is 4.05 when the population $SD_\rho = .3$ and $k=50$. On the other hand, the χ^2 statistic is under-estimated under the condition of random path coefficients. The under-estimation is more serious when the population $SD_\rho = .3$. The fit indices (CFI, SRMR, and RMSEA) are excellent because the data were generated from true models.

General Discussion

Yu et al. (2016) addressed an important topic on both the methodological development and applications of MASEM. Due to some critical issues and technical errors, it was unclear whether their findings and interpretations were valid. The present study clarified the conceptual issues and corrected the technical errors in their paper. We further extended their study by evaluating the FIMASEM approach with a simulation study. The findings provide some empirical evidence of how the FIMASEM approach works on simulated data. We summarize the key findings here: (1) the means of the parameter estimates are generally

unbiased (or slightly biased) when the degree of heterogeneity is small (or large); (2) the estimated SD_{θ} is slightly under-estimated (-1% to -17%) in both the conditions of random correlation matrices and random path coefficients. Therefore, the constructed CVs on the parameters are also slightly under-covered; (3) the chi-square test statistic is severely over-estimated and does not follow the expected chi-square distribution; and (4) the proposed cut-offs ($CFI > .9$ and $SRMR < .1$) are inaccurate in identifying the percentage of studies that can be generalized by the proposed model. Further simulation results have shown that it is hard to find modified cut-offs to use.

Regarding the issues that we discussed previously, Issue 5 is the most critical but has been fixed in the present simulation study. Both Issues 1 and 2 may affect the accuracy of the parameter estimates. Based on the simulation study, the bias of the parameter estimates does not seem to be critical. Issues 1, 2, and 4 may impact the accuracy of the estimated SD_{θ} . The findings of the simulation study also show that the bias of SD_{θ} is quite mild. The most critical concern is the appropriateness of using the cut-offs to interpret the percentage of studies that can be generalized by the proposed model. The findings of the simulation study put into question the correctness of the test statistics and the proposed cut-offs (Issue 3).

Table 7 summarizes the conceptual differences and empirical findings between the FIMASEM and the TSSEM approaches. It may help readers to choose between these two approaches. The statistical theory of the TSSEM is well known. The present simulation study also shows that the TSSEM has good statistical properties. Based on the current evidence, we recommend the TSSEM approach to conducting MASEM for general analyses and model comparisons. If researchers want to explore the effects of heterogeneity on the parameter estimates, they may use the bootstrap CVs suggested by Yu et al. (2016). However, researchers are cautioned to neither apply the chi-square test nor any cut-offs to check the generalizability of the proposed model. To promote open science and facilitate research, we

implemented these procedures in the metaSEM package in the R statistical platform.

Researchers may easily verify and improve on the methods.

Future Directions

Since we attempted to replicate the conditions in Yu et al., several factors were not manipulated in this simulation study. These factors should be addressed in future simulation studies. Different studies may contribute different numbers of correlation coefficients in applied research. For example, the number of studies varies from 3 to 71, with a median of 25, in Study 14 (Monnot et al., 2011) in Yu et al. (2016). The presence of missing variables may make the statistical analysis challenging for both the FIMASEM and conventional MASEM. Another factor affecting the performance is the complexity of the models. We only used a simple model with four variables. Models in applied MASEM are much more complicated (cf. the numbers of paths in Table 4, Yu et al.). Further simulation studies should explore models that are more complex with larger *dfs*.

Another direction concerns the impact of Issues 1, 2, and 4. The findings of the present simulation study seem to suggest that these issues only have a minimal impact on the performance of the bootstrap CV in the FIMASEM. It is not clear whether this is true or whether the findings are specific to the particular conditions used in the simulation study. It should be noted that all of the proposed models have been correctly specified in the present simulation studies. Although MASEM can be considered a special case of SEM, there are more complications in MASEM. Future simulation studies are required to explore how these methods work in more complicated models. When designing simulation studies, it is important to manipulate the factors in such a way as to ensure that they are similar to realistic settings (Paxton et al., 2001). This ensures that the findings in the simulation studies can be generalized to real-world applications. Sheng et al. (2016) provided a review of the current

practice in MASEM. Their findings will be useful for guiding realistic simulations in MASEM.

The indices of generalizability proposed by Yu et al. did not work well in simulation studies. As suggested by an anonymous reviewer, another possible direction for addressing issues of heterogeneity in MASEM is to identify homogenous clusters of correlations. For example, Cheung and Chan (2005a) suggested using cluster analysis to group correlation matrices into relatively homogeneous subgroups. The same model or different models can be fitted in each subgroup. Moreover, study characteristics may be used to predict the classifications. This approach can be a viable alternative to address the heterogeneity in MASEM. Future studies may compare the advantages and limitations of using cluster analysis and mixture models to address heterogeneity in MASEM.

To conclude, MASEM is a complicated technique that has inherited issues from both meta-analysis and SEM. A unified statistical model is required to account for the complexity of MASEM correctly. Yu et al. (2016) and the present study have highlighted further complications to conceptualizing random effects in MASEM. We hope that the further development of MASEM may lead to better applications and to the development of theories in management and organizational studies.

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Table 1

Parameter Estimates of the FIMASEM and the TSSEM Approaches in Nohe et al. (2015)

	FIMASEM		TSSEM	
	Mean ^a	SD ^a	Parameter estimates ^b	SE ^b
Same lagged coefficient ($S_1 \rightarrow S_2$; $W_1 \rightarrow W_2$)	0.6079	0.1032	0.5826	0.0155
Cross lagged coefficient ($S_1 \rightarrow W_2$; $W_1 \rightarrow S_2$)	0.0833	0.1536	0.0869	0.0204
Correlation between S_1 and W_1	0.3950	0.1408	0.3891	0.0229
Correlation between S_2 and W_2	0.1652	0.1752	0.1699	0.0258

Note. ^aThey are the means and SDs of the estimated coefficients across 500 bootstrap replications. ^bThey are the parameter estimates and their SEs on the average correlation matrix.

Table 2

Summary statistics of the 10,000 bootstrap samples in Study 14 (Monnot et al., 2011) in Yu et al. (2016)

	mean	<i>SD</i>	median	min	max	Q10	Q25	Q50	Q75	Q90
Test statistic (<i>df</i> =2)	201.12	167.14	151.99	4.83	1995.53	56.78	90.52	151.99	254.54	408.70
CFI	0.72	0.15	0.74	0.11	1.00	0.51	0.63	0.74	0.84	0.90
RMSEA	0.34	0.14	0.32	0.00	1.19	0.19	0.24	0.32	0.42	0.54
SRMR	0.14	0.36	0.13	0.03	34.83	0.09	0.10	0.13	0.16	0.19

Note. Q10 to Q90 refer to the 10th to 90th percentiles.

Table 3

Incorrect (Actually Used) and Correct (Intended) Population Correlation Matrices to Generate the Data in Runs 1 to 5 in Study 1 in Figure 1 in Yu et al.

	<i>x</i>	<i>m1</i>	<i>m2</i>	<i>y</i>
<i>x</i>	1.0000	.3000	.3000	.1800
<i>m1</i>	.3000	1.0000	.0900	.3270
<i>m2</i>	.3000	.0000	1.0000	.3270
<i>y</i>	.0000	.3000	.3000	1.0000

Note. The lower and upper triangles represent the incorrect correlation matrix used in Runs 1 to 5 in Figure 1 in Yu et al. and the correct correlation matrix, respectively. The values in bold font highlight the elements that differ between these two matrices.

Table 4

Incorrect (Actually Used) and Correct (Intended) Population Correlation Matrices to Generate the Data in Run 6 in Study 1 in Figure 2 in Yu et al.

	x_1	x_2	x_3	m_1	m_2	y_1	y_2
x_1	1.0000	.0000	.0000	.3000	.3000	.1800	.1800
x_2	.0000	1.0000	.0000	.3000	.3000	.1800	.1800
x_3	.0000	.0000	1.0000	.3000	.3000	.1800	.1800
m_1	.3000	.3000	.3000	1.0000	.2700	.3810	.3810
m_2	.3000	.3000	.3000	.0000	1.0000	.3810	.3810
y_1	.0000	.0000	.0000	.3000	.3000	1.0000	.2286
y_2	.0000	.0000	.0000	.3000	.3000	.0000	1.0000

Note. The lower and upper triangles represent the incorrect correlation matrix used in Runs 1 to 5 in Figure 2 in Yu et al. and the correct correlation matrix, respectively. The values in bold font highlight the elements that differ between these two matrices.

Table 5

Relative Percentage Biases of the Means of the Parameter Estimates, the Standard Deviations of the FIMASEM, and the Standard Error of the TSSEM Approaches.

No. of Studies	Population <i>SD</i>	FIMASEM		TSSEM	
		Relative percentage bias of estimated mean	Relative percentage bias of estimated <i>SD</i>	Relative percentage bias of estimated mean	Relative percentage bias of estimated <i>SE</i>
Homogeneity of Correlation Matrices (and Path Coefficients)					
10	0.0	-0.26	0.01 ^a	0.19 ^c	1.14 ^e
20	0.0	-0.22 ^b	0.01 ^a	0.20 ^d	-1.46
50	0.0	-0.15	0.01 ^a	0.27	-3.07
Random Correlation Matrices					
10	0.1	-0.43	-14.39	0.03 ^f	-11.19
20	0.1	-0.68	-5.95	-0.15 ^g	-4.32
50	0.1	-0.62	-2.87	-0.33	-2.00
10	0.3	-5.96	-13.24	-7.46	-10.90
20	0.3	-6.13	-9.54	-8.10	-5.67
50	0.3	-6.47	-7.68	-8.17	-3.03
Random Path Coefficients					
10	0.1	-0.29	-12.45	-0.10 ^h	-19.84 ⁿ
20	0.1	-0.27	-5.19	-0.16 ⁱ	-14.02
50	0.1	-0.15	-0.71 ^o	-0.08 ^j	-11.54
10	0.3	-12.59	-16.69	-0.16 ^k	-17.95
20	0.3	-13.28	-12.83	-0.48 ^l	-13.37
50	0.3	-13.08	-11.08	-0.10 ^m	-13.15

Note. ^aThey are the absolute bias because the relative bias is not defined for population *SD*=0.

The ranges of the relative percentage biases are ^bfrom -0.53 to 0.13, ^cfrom -0.17 to 0.33,

^dfrom -0.19 to 0.19, ^efrom -1.18 to 3.83, ^ffrom -0.50 to 0.43, ^gfrom -0.45 to 0.12, ^hfrom -0.26

to 0.39, ⁱfrom 0.59 to 0.32, ^jfrom -0.77 to 0.38, ^kfrom -1.63 to 1.12, ^lfrom -1.42 to 0.11, ^mfrom

-0.39 to 0.46, ⁿfrom -1.18 to 3.83, and ^ofrom -2.39 to 1.24.

Table 6

Fit Indices of the FIMASEM, and the Standard Error of the TSSEM Approaches.

No. of Studies	Population <i>SD</i>	FIMASEM			TSSEM				
		Mean of $\chi^2(df=2)$	Percentage of CFI > .9	Percentage of SRMR < .1	Percentage of RMSEA < .05	Mean of $\chi^2(df=2)$	Mean of CFI	Mean of SRMR	Mean of RMSEA
Homogeneity of Correlation Matrices (and Path Coefficients)									
10	0	5.87	99.84	100.00	87.70	1.95	1.00	0.01	0.01
20	0	8.47	99.95	100.00	90.68	2.08	1.00	0.01	0.01
50	0	13.79	99.99	100.00	94.17	2.09	1.00	0.00	0.00
Random Correlation Matrices									
10	0.1	77.96	76.48	95.84	19.47	2.78	1.00	0.02	0.01
20	0.1	158.04	74.89	96.00	16.63	2.29	1.00	0.01	0.01
50	0.1	392.27	74.35	96.34	14.90	2.15	1.00	0.01	0.00
10	0.3	720.52	22.13	43.68	2.51	2.84	0.98	0.05	0.01
20	0.3	1471.92	21.22	42.48	2.19	2.87	0.99	0.04	0.01
50	0.3	3737.66	20.54	41.58	1.98	4.05	0.99	0.03	0.01
Random Path Coefficients									
10	0.1	33.33	93.50	99.55	43.74	1.38	1.00	0.01	0.00
20	0.1	68.22	93.23	99.68	38.49	1.26	1.00	0.01	0.00
50	0.1	175.15	92.94	99.75	34.24	1.25	1.00	0.00	0.00
10	0.3	467.32	39.90	68.85	5.85	0.79	1.00	0.02	0.00
20	0.3	976.55	37.07	66.40	4.64	0.68	1.00	0.01	0.00
50	0.3	2468.55	35.75	65.26	4.01	0.64	1.00	0.01	0.00

Table 7

Summary of the Conceptual Differences and Simulation Findings between FIMASEM and TSSEM

	FIMASEM	TSSEM
	Model	
Target population of the model	Population correlation matrices in each study $\mathbf{P}_i$	Average population correlation matrix $\bar{\mathbf{P}}$
Definition of heterogeneity (random effects)	Random path coefficients SD_θ	Random correlations SD_ρ
Statistical theory	Unclear	SEM with maximum likelihood estimation and weighted least squares
Model comparisons of alternative models	Unclear	Standard SEM approach
Major limitations	Issues discussed in this study	Do not quantify the heterogeneity of the parameters SD_θ
	Findings in the simulation study	
Parameter estimates	Biased up to 13%	Biased up to 8%
SD_θ in FIMASEM (SE in TSSEM)	Biased up to -17% in SD_θ	Biased up to -20% in SE
Chi-square test statistic	Seriously over-estimated (depends on the sample size used)	Slightly over-estimated (and under-estimated) in the condition of random correlation matrices (and random path coefficients)
Goodness-of-fit indices and proposed cut-offs	Cannot identify most studies	Very good values

Figure 1. The path model ($df=2$) used in the simulation study.

Figure 2. The 95% confidence intervals on the estimated variance=1 when ($k=5$ to 100). The solid and dotted lines represent the 95% lower and upper confidence intervals, respectively.

Figure 3. Incorrect (actually used) and correct (intended) models to generate the correlation matrices in Figure 1 in Yu et al. The models on the left and right are the incorrect and correct models, respectively.

Figure 4. Incorrect (actually used) and correct (intended) models to generate the correlation matrices in Figure 2 in Yu et al. The models on the left and right are the incorrect and correct models, respectively.

Figure 5. Incorrect (actually used) and correct (intended) models to analyze the correlation matrices in Figure 1 in Yu et al. The models on the left and right are the incorrect and the correct models, respectively.

Figure 6. Incorrect (actually used) and correct (intended) models to analyze the correlation matrices in Figure 2 in Yu et al. The models on the left and right are the incorrect and the correct models, respectively.

Figure 7. Mean CFI in different conditions. Random cors: random correlation matrices; Random paths: random path coefficients. Values in gray color are smaller than .9.

Figure 8. Mean SRMR in different conditions. Random cors: random correlation matrices;

Random paths: random path coefficients. Values in gray color are larger than .1.

Figure 9. Mean RMSEA in different conditions. Random cors: random correlation matrices;

Random paths: random path coefficients. Values in gray color are larger than .1.