

Latent Class Moderated Mediation in Structural Equation Mixture Models:

Applications and Limitations

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Abstract

Latent class moderated mediation in structural equation models can describe individual differences in psychological processes across latent groups. This method could be most useful where two latent classes have indirect paths of equal magnitude, but opposite signs. Global model fit indices often failed to detect misfit when a one-class model was fit to data from a two-class population with latent class moderated mediation. Under this misfitted one-class model, significant indirect effects were rarely found, even with strong indirect effects in each subpopulation. Information criteria only reliably selected the correct number of classes with a strong population indirect effect and measurement invariance. Violations of assumed strong measurement invariance led to selecting more classes than in the population.

Introduction

Psychology aims to empirically validate directional, causal mechanisms that influence human behavior. However, it can be challenging to model relationships between multiple constructs. Methodologists have developed a number of models that represent fundamental notions of causal sequencing. For example, consider the simple diagram in Figure 1 that represents causal *mediation* in the relationships among three variables. Variable X affects variable Y directly, but also affects Y indirectly through its influence on a *mediator* M that also has an effect on Y . The effect of X on Y through its influence on M is an *indirect effect*. Methodologists have developed a number of models and designs to support the testing of such indirect effects.

Mediation remains the most popular model for modeling indirect relationships in psychology. Developed by Baron and Kenny, this approach describes the indirect effect and direct effect through linear relationships between the exogenous variable (X), the outcome variable (Y) and the mediator (M) (Baron & Kenny, 1986; D. MacKinnon & Lockwood, 2002) as

$$M = \beta_0 + aX + r_0 \quad (1)$$

and

$$y = \beta_1 + cX + bM + r_1 \quad (2)$$

In the above equations, β_0 and β_1 are intercepts; a , b , and c are weights; and r_0 and r_1 are residuals (Figure 1). The indirect effect, or how much X predicts Y through M , is then quantified as ab . We can test the significance of this effect in a number of ways. Relying on the asymptotic normality of the product ab , traditional methods

utilize estimates of the standard error of ab to conduct Wald tests within a traditional null hypothesis significance testing (NHST) framework (Goodman, 1960; Sobel, 1982). More modern bootstrapping procedures (e.g., Preacher, Rucker, & Hayes, 2007) do not rely on the normality of ab . Simulation studies have demonstrated that using Wald tests leads to low power (D. MacKinnon & Lockwood, 2002). Thus, bootstrapping procedures should be used when testing the strength and significance of the indirect effect (Biesanz, Falk, & Savalei, 2010).

Other effects are also represented in this modeling framework. The direct effect, or how much X predicts Y not through M , is represented by c . The total effect, or how much X predicts Y , is then just $c + ab$. Although Baron and Kenny (1986) suggested that a statistically significant test of the total effect should be performed prior to testing the indirect effect, subsequent authors have refuted this claim (D. P. MacKinnon et al., 2002; Zhao et al., 2010). As c could be positive and ab negative, the sum of a large indirect effect a large direct effect would be close to zero. This possibility makes testing the total effect for significance before testing the others result in increased Type II error rates (D. MacKinnon & Lockwood, 2002).

The original mediation model described above is just-identified, and each model coefficient may be calculated as a straightforward function of the observed variances and correlations. Given the simplicity of the model, it is perhaps not surprising that the analysis of mediation in regression has achieved wide use (Hayes, 2009; Preacher, 2015).

Nevertheless, problems exist in both the model's use and the model itself. It is tempting to interpret a significant indirect effect as evidence of a causal pathway.

For example, Baron and Kenny (1986) called their stepwise mediation method the “Causal Steps Method.” Mediation¹ remains just a collection of predictions—which is useful in psychology. However, without random assignment, longitudinal design, or some other design or methodological approach, there is no reason why the covariance structure implies a causal relationship (Imai, Keele, & Yamamoto, 2010; D. P. MacKinnon et al., 2002; Shrout & Bolger, 2002; Spencer, Zanna, & Fong, 2005; Zhao et al., 2010). For example, suppose we model education mediating the effect of intelligence on fertility. Instead of that directional relationship, a common factor, genetic or otherwise, that causes all three could exist (Rodgers et al., 2008).

Beyond that misstep, the use of significance testing is problematic, especially without consensus on a good measure of effect size. Significance testing provides less information than often thought (Harlow, Mulaik, & Steiger, 1997). It only signals whether a parameter estimate differs from a null, often zero, by an unexpected amount—not whether this difference matters. Using confidence intervals or effect sizes allow practitioners to quantify that difference. One can construct confidence intervals for both methods that directly estimate the standard error of the product (Goodman, 1960; Sobel, 1982) and resampling methods

¹ Mediation now refers to a wide variety of models and techniques that describe how the effect of one construct can be transmitted through intermediate variables. These include the Bayesian net-based tradition and the propensity score approach (Preacher, 2015). For the purposes of this paper, mediation refers to the predictive model implemented in regression or SEM.

produce confidence intervals due to their nature (Preacher, Rucker, & Hayes, 2007). Nevertheless, no consensus on effect sizes in mediation exists (Preacher & Kelley, 2011).

There are other problems with mediation models beyond how they are currently used. Tests of mediation in regression models with manifest variables tend to have low power (D. MacKinnon, Lockwood, & Williams, 2004; D. P. MacKinnon et al., 2002). Moreover, regression models on manifest variables do not account for measurement error, which can lead to bias (Rigdon, 1994). The model also assumes that relationships between variables are linear and stable across the entire statistical population. As mediation is an intra-individual process (L. Collins, Graham, & Flaherty, 1998), it is perhaps surprising that the model relies entirely upon a random residual to account for individual differences, especially when methods exist that capture a wider array of individual differences in mediation and beyond (D. J. Bauer, 2011; Preacher, 2015). This assumption might well be incorrect — there could be two groups in the population, only one in which the indirect path is significant (Shrout & Bolger, 2002). If two or more groups do exist, some with significant effects, then regression coefficients estimated without considering possible subpopulations might produce biased estimates or fail to detect them altogether.

Although the notion of mediation analysis has elicited great enthusiasm from a wide range of researchers, it has become increasingly clear that this enthusiasm was premature. There is still much work to be done. Although mediation is well researched in the context of the simple regression model proposed by Baron and

Kenny (1986), researchers are still working on incorporating various conceptions of time and clustering into mediation (D. MacKinnon & Fairchild, 2009; Preacher, 2015). Nevertheless, social scientists will likely continue to employ mediation analyses, no matter how statisticians may decry this lack of a sophisticated understanding. Thus, if the methods can be improved, they should be.

The analysis of mediation through structural equation models can potentially alleviate a few of the problems that result from simple regression models on manifest variables. Structural equation modeling (SEM) describes relationships between unobserved, or *latent*, variables (Figure 2). To measure these latent variables, one uses multiple observations or measurements. These observed, or *manifest*, variables are called *indicators* if they are predicted by the latent variables. The model can then be represented as two equations. The latent variable model describes the relationships between latent variables, and the measurement model describes the relationships between the latent variables and the indicators they predict:

Latent Variable Model:

$$\boldsymbol{\eta} = \boldsymbol{\nu} + \boldsymbol{\beta}\boldsymbol{\eta} + \boldsymbol{\zeta} \quad (3)$$

where $\boldsymbol{\eta}$ is a $q \times 1$ random vector of latent variables with a multivariate normal distribution, q is the number of latent variables, $\boldsymbol{\nu}$ is a $q \times 1$ vector of means of the latent variables, $\boldsymbol{\beta}$ is a $q \times q$ matrix of weights from one latent variable to another, and $\boldsymbol{\zeta}$ is a $q \times 1$ random vector of residuals.

Measurement Model:

$$\boldsymbol{y} = \boldsymbol{\alpha} + \boldsymbol{\Lambda}\boldsymbol{\eta} + \boldsymbol{\delta} \quad (4)$$

where p is the number of manifest variables, y is a $p \times 1$ random vector of manifest variables, α is a $p \times 1$ vector of the means of the manifest variables, Λ is a $p \times q$ matrix of weights from the latent variables to the manifest variables, and δ is a $p \times 1$ random vector of manifest variables' residuals with a mean of 0. Using expected value and matrix algebra, we can derive the following mean and covariance structures:

$$\Sigma_{yy} = \Lambda(I - \beta)^{-1}\Phi(I - \beta')^{-1}\Lambda' + \theta \quad (5)$$

$$\mu = v + \Lambda(I - \beta)^{-1}\alpha \quad (6)$$

where Σ_{yy} is the $p \times p$ population covariance matrix of the manifest variables, Φ is a $q \times q$ covariance matrix of the latent variables, θ is the covariance matrix² of the measurement model residuals, μ is a $q \times 1$ vector of the population means of manifest variables. Parameters are then estimated so as to most closely reproduce the population mean and covariance structures, given the sample means and covariances. Maximum likelihood estimates of the model parameters are obtained by minimizing a discrepancy function that compares the model-implied variance-covariance matrix $\Sigma_{yy}(\theta)$ from Equation 5 with the sample covariance matrix S_{yy} (Bollen, 1989).

Modeling mediation through structural equation models instead of regression offers many advantages. Several approaches to mediation in regression estimate the relationship between X and M (a and r_1) separately from the relationships between X and Y and M and Y (b , c , and r_2). By estimating all paths in

² Assumed to be diagonal

structural equation models simultaneously, each parameter is estimated with all relationships in the model, which is more parsimonious (Iacobucci, Saldanha, & Deng, 2007). Structural equation models also estimate measurement error, whereas regression models do not. If measurement error is not modeled and manifest variables are not perfectly reliable, then parameter estimates can be biased. This bias can exist even if one employs a path analysis approach, estimating all coefficients simultaneously (Cole & Preacher, 2013). Simulation studies have demonstrated that SEM has more power to detect indirect effects than a path analysis on manifest variables, even in small samples (Iacobucci et al., 2007). While the smallest sample size included in the study was 30, multivariate analyses should probably be done with least that number of participants, if not more.

Nevertheless, regression models and basic structural equation models remain sensitive to the existence of distinct, meaningful subgroups³ within the population. Both models assume a single population with multivariate-normally distributed predictors. If one believes that certain weights and means differ across groups, one could use a few different methods in regression (Cohen, Cohen, West, & Aiken, 2003). One could dummy code group membership and include it as a

³ These subgroups are often considered to be qualitatively different, like those modeled with fixed effects of group membership. Contrast these with the groups or clusters that are modeled with random effects through multilevel or hierarchical modeling. Much research on meditation in multilevel modeling has occurred since the millennium (Bauer, Preacher, & Gil, 2006).

covariate and as a moderator. One could also run each group's model separately. Both approaches can produce problems in terms of estimation and parsimony. If there are a large number of groups or group-specific effects, the number of parameters might make convergence difficult. If one estimates each group's model separately, one might drastically reduce the sample size. Moreover, separately estimating group models is not parsimonious. In structural equation models, one can use both of these solutions. One can also free certain parameters to be freely estimated between groups or constrain other parameter estimates to be the same across groups. In constraining parameter estimates, one assumes that the parameters are equal across groups. In that case, the measurement and latent variable model change:

Latent Variable Model:

$$\boldsymbol{\eta}_k = \boldsymbol{\nu}_k + \boldsymbol{\beta}_k \boldsymbol{\eta}_k + \boldsymbol{\zeta}_k \quad (7)$$

Measurement Model:

$$\boldsymbol{y}_k = \boldsymbol{\alpha}_k + \boldsymbol{\Lambda}_k \boldsymbol{\eta}_k + \boldsymbol{\delta}_k \quad (8)$$

where k is group membership. Multi-group SEM is ultimately more parsimonious and flexible. It is parsimonious because all parameters are still estimated at the same time, and only those that are thought to differ across classes are not constrained to be the same across classes. It is also more flexible because any and all parameters can theoretically be freed, including variances. This multiple-group approach allows us to model different indirect effects between observed groups if group membership is known.

This method cannot model mediation in populations where *unobserved* groups exist. Standard multi-group analyses require group membership to be known. The potential existence of unknown subgroups becomes especially relevant in psychological research. For a clinical example, suppose that only a small subgroup of individuals has a disorder, and mediation occurs only in subjects with that disorder. One requires a different model to describe group-specific indirect effects if the groups are unobserved.

Finite mixture models posit the existence of unobserved subgroups that combine to account for the population distribution. Thus, any distribution can be represented as the probabilistically weighted sum of multivariate normal distributions. Let $f_k(\mathbf{y}_k|\boldsymbol{\theta}_k)$ represent the density functions implied by the structural model of the k^{th} class. Then,

$$f(\mathbf{y}|\boldsymbol{\pi}, \boldsymbol{\Theta}) = \sum_{k=1}^k \pi_k f_k(\mathbf{y}_k|\boldsymbol{\theta}_k) \quad (9)$$

where π_k is the proportion of the k^{th} class in a population and $\boldsymbol{\theta}_k$ is a vector of parameters in the class. These unobserved subgroups, or latent classes, have multiple interpretations. The “strong” interpretation is that these groups actually exist (L. M. Collins & Lanza, 2010). The “weak” interpretation, and the more tenable one by far, is that these groups provide a flexible approach to modeling non-normality (Bauer & Curran, 2004; Bauer & Curran, 2003). One should note that, within each class, no more individual differences are accounted for than in the original one class model at this point (Vermunt & Magidson, 2005). Random slopes and intercepts could be added if observations within or even between classes were

somehow grouped together (D. J. Bauer, 2011). Contrast this approach with latent growth curve models and multilevel models, which allow for intercepts, slopes, and other parameters to randomly vary across people and groups according to specified distributions.

In freeing certain paths to differ across class, we must consider the requirements of measurement invariance. Measurement invariance is an assumption first developed in multi-group structural equation modeling (W Meredith, 1993; Meredith & Teresi, 2006). Generally measurement invariance means that all measurement models remain constant across groups. For example, many hypotheses in cross-cultural psychology require constructs to be comparable across cultures (Meade & Bauer, 2007). Otherwise, it makes little sense to go further in analyzing culture specific or invariant phenomena.

There are several types of measurement invariance discussed in the literature. *Strong measurement invariance* occurs when both the item intercepts and factor-indicator weights do not vary across groups (Meredith, 1993). If this assumption holds true, then we can be more confident that the factors remain qualitatively the same across groups. If the factors are qualitatively the same across classes and only the relationships vary, then we can attribute the difference of paths between classes to the paths themselves, including unobserved moderators.

Latent class moderated mediation (LCMM) models unobserved groups that differ in their indirect effects. Moderation occurs whenever the effect of one variable on another depends on a third variable (Baron & Kenny, 1986). Thus, whenever the indirect path differs between classes, latent class moderated mediation occurs.

Moderated mediation is not a new concept and has been developed for a number of different situations (Bauer, Preacher, & Gil, 2006; Edwards & Lambert, 2007; Muller, Judd, & Yzerbyt, 2005; Preacher et al., 2007; Wang & Preacher, 2013). However, latent class moderated mediation, especially in structural equation modeling, remains an unexplored method.

This modeling approach seems most intuitive when one constrains all measurement models to be equal across groups. Issues of estimation and interpretation motivate this recommendation. First, given the sheer number of parameters in structural equation mixture models, equality constraints can noticeably improve estimation. Second, measurement invariance makes it more tenable to compare the sizes of indirect paths across classes. If measurement invariance does not exist, then the constructs are not comparable across classes. In that case, then one does not know whether the operative difference lies in the construct or in the process. The assumption of strong measurement invariance once again implies that the difference lies in the process, not in the constructs themselves.

Latent class moderated mediation could be useful in modeling mediation when the paths of each group cancel out when aggregated. Consider a two-class structural equation mediation model where the classes only differ in their indirect paths, and each class is around the same size. If $a_1 = -a_2$ and $b_1 = -b_2$, then they will cancel out. Even if these magnitudes are not exactly the same or the classes are not exactly equal, the overall estimated indirect effect would be close to zero. Unless

one somehow detects latent classes during the analytic process, within-class mediation effects may also go undetected.

Latent class moderated mediation presents the possibility of disentangling these effects. In doing so, we can identify possible mechanisms where we could not before. Later, covariates, such as SES or trauma, could be added as predictors of class membership. These covariates would improve the model's utility to clinicians and policy makers, by connecting latent processes to observable traits. Unlike in multi-group SEM, here we first check for the existence of different regression coefficients and then check whether manifest groups predict them.

No rigorous literature currently exists on using latent class moderated mediation. Although work has been done on structural equation mixture models (Tueller & Lubke, 2010; Vermunt & Magidson, 2005), it provides no evidence as to whether this modeling approach will detect these equal but opposite classes. Given the practical importance of measurement invariance, it also behooves us to examine the impact of violations of that assumption. Thus, I will investigate three questions. First, will a traditional one-class structural equation model not fit when there are two equally sized classes with indirect effects of the same magnitude but opposite signs? Second, how is model selection impacted by the size of the sample and the indirect effect while strong measurement invariance holds across classes? Finally, how is model selection affected by wrongfully imposing equality constraints on measurement models when strict measurement invariance does not hold in the population? I predict that a one-class structural equation model will fit for models with smaller indirect effects but not larger ones. I also predict that information

criteria will tend to select a two-class model when measurement invariance holds, but when measurement invariance does not hold in the population, information criteria will select the three-class model more often when equality constraints are wrongfully imposed on measurement models.

Methods

To answer these questions, I simulated data from two-class models with mediation between three latent factors. I generated the data and fit the models in *Mplus* through the R package *MplusAutomation*. Models are included in Appendix A, and selected code from post-processing is included in Appendix B.

Conditions of the Generating Models

The generating models varied based on three factors: sample size, indirect effect size, and extent of violations of measurement invariance (Figures 3, 4, and 5). Models had a sample size of either 300 or 800 subjects. These are reasonable sample sizes for substantive researchers who already use SEM or mixture models. The weights of the indirect paths had magnitudes of either 0.30 or 0.80. For each model, $a_1 = -a_2$, $b_1 = -b_2$, and $\pi_1 = \pi_2 = 0.50$.

Extent of violations of measurement invariance had three levels: none, mediating factor only, or all factors. I chose to examine the mediating factor for two reasons. First, it is between the two paths that vary across classes. A violation of measurement invariance in this location might have a larger effect. Second, if the a and b paths have weights of different signs, then the mediating process could be qualitatively different. The mediator itself might then be qualitatively different in that class.

In this simulation, a violation of measurement invariance meant that the measurement model differed between classes by the regression weights between the factor and the indicators. Each factor had three indicators, and the model was identified via a unit loading constraint on one of those indicators for each factor. If the assumption of strong measurement invariance was upheld, then the other two indicators for each factor had loadings of 0.60 across both classes. If the assumption of strong measurement was violated, loadings for the two remaining indicators were equal to 0.60 for one class and 0.80 and 0.30 for the other. These loadings were chosen so that each set of weights had approximately the same average squared loading. This equivalence prevents confounding between differences in factor communality and violations of strong measurement invariance.

For each of the twelve conditions, 1000 data sets were generated. Multiple samples were generated for each condition so as to obtain reliable results and estimate the variability of this approach.

Question 1: Detecting the Need for LCMM

All data sets were then fit with a one-class structural equation model. Afterwards, I examined whether the Chi-Square test and the Root Mean Square Error Approximation (RMSEA) could detect that a one-class model does not fit data generated from a two-class model.

The Chi-Square test ⁴ is a NHST performed by calculating the statistic

$$X^2 = -2(L_1 - L_0) \quad (10)$$

⁴ The Chi-Square test is also referred to as the likelihood ratio test (LRT).

which has degrees of freedom equal to

$$\nu = \frac{p(p+1)}{2} - m \quad (11)$$

where $L_1 - L_0$ is the in difference log likelihoods between the chosen model and the null model, q is the number of observed variables in the model, and m is the number of free parameters (Steiger, Shapiro, & Browne, 1985). In this case, the null model is simply a positive definite covariance matrix. Thus, the test's degrees of freedom is equal to the difference between the number of parameters estimated in covariance matrix (the "saturated" model) and the model under examination. For this study, I used alphas of .01 and .05 to test the rejection rate of the Chi-Square test. In practice, the chi-square statistic is computed as $(n-1)F_{ML}$, with n the sample size and F_{ML} the maximum likelihood discrepancy function minimized during the maximum likelihood estimation.

The RMSEA is calculated according to equation 12:

$$RMSEA = \sqrt{\frac{F^*}{\nu}} \quad (12)$$

where F^* is the value of the maximum likelihood discrepancy function that would be obtained if the model were fit to the population covariance matrix. ν is the degrees of freedom (Steiger & Lind, 1980). As one might notice, the RMSEA and the Chi-Square test are very similar. By constructing a certain confidence interval around the RMSEA, one can exactly reproduces the result of a Chi-Square test. Moreover, the RMSEA offers several advantages over the Chi-Square test. Specifically, it improves upon the NHST approach of the test by providing more graded measure of model fit.

The RMSEA results will be analyzed in accordance to recommended cut points (Browne and Cudeck, 1993). Under their approach, an RMSEA of 0 signals “perfect” fit, an RMSEA less than .01 signals “excellent” fit, less than .05 signals “good”, less than .08 signals “mediocre”, and a model with an RMSEA greater than .10 should not be used. While these cut-offs provide more information than Accept—Support testing, they still remain cut-offs.

It is clearly flawed to use a point estimate from a single index to determine model fit. Multiple sources of fit information should be considered when selecting a model. Additionally, many believe that point estimates of indices should not be preferred to interval estimates (Steiger, 2000). Although the use of fixed cutoff points is problematic, I include it because it is still employed widely throughout the field.

As I only fit data from a population with two classes to one-class models, these indices should reject the one-class model as poorly fitting. I recorded the proportion of times a one-class model is rejected by each method. I then compared these results across conditions and indices. While the Chi-Square test and the RMSEA are very similar, the RMSEA might provide a more nuanced picture.

Finally, having fit the data to a two-class model, I checked whether the indirect effect was estimated to be zero. To do so, I used the bootstrap method of testing the indirect effect (D. P. MacKinnon et al., 2004; Selig & Preacher, 2008). I then recorded how often an indirect effect would be detected.

Question 2: Understanding the Effectiveness of LCMM

Next, I examined whether the two-class model was selected from a choice of one-, two-, and three-class models fit to the data from a population with two classes. All data sets without violations of measurement invariance were then fit with one-, two- and three-class models. I then measured correct model selection rates with the Akaike Information Criteria (AIC), Schwarz's Bayesian Information Criteria (BIC), and sample-size adjusted BIC⁵ (aBIC) (Akaike, 1974; Boekee & Buss, 1981; Schwarz, 1978). These three statistics, or information criteria, integrate a model's log-likelihood with information about a model's complexity and sample size. A researcher can then use information criteria to compare models. The model with the lowest information criteria is considered the best fitting. The (AIC) can be calculated as follows:

$$AIC = -2L + 2m \quad (13)$$

where L is the log-likelihood of the model, and m is the number of unconstrained parameters in the model. While the AIC does not include information about sample

⁵ In looking for the first development of the aBIC, I found that Rissanen (1978) originally designed a similar information criteria for signal processing with an additional term. That additional term was dropped in a conference presentation given by Boekee and Buss (1981) in German—producing the aBIC. The first work in English discussing the new information criteria was published in *Psychometrika* by Sclove in 1987, which explains why he is sometimes cited for the aBIC (Sclove, 1987).

size, Schwarz's Bayesian Information Criteria (BIC) does. The BIC can be calculated according to Equation 14:

$$BIC = -2L + \log(n) m \quad (14)$$

where n is the number of subjects in the sample. So, as the sample size increases, the cost of adding a parameter also increases. As a result, the BIC chooses less complex models more often than the AIC. The AIC often selects models with more parameters, which possibly leads to fitting noise. The adjusted BIC (aBIC) still includes sample size but reduces its effect:

$$aBIC = -2L + \log\left(\frac{n+2}{24}\right)m \quad (15)$$

I tested the effectiveness of these three different information criteria in identifying the two-class model across various conditions by calculating rates of correct model selection. I compared how often the fit indices select a one- or three-class model to how often it selected a two-class model.

Question 3: Testing the Robustness of LCMM

Once I establish the model selection rates in ideal cases, I examined how robust information criteria are to violations of measurement invariance. Data from all generating models with all levels of measurement invariance were then fit with models that assumed strict metric invariance. Afterwards, I compared correct model selection rates across conditions.

Results

Detecting the Need for LCMM

The efficacy of the Chi Square test and the RMSEA were examined. The Chi-Square test identified misfit at rates less than the specified alpha (Table 1).

Moreover, examining a beeswarm plot displays a lack of an effect of sample size or indirect path size (Figure 6). I reran this analysis several times with the same result.

Issues with point estimates for the RMSEA were also evident in this simulation. Given the cut offs specified by Browne and Cudeck (1993), the vast majority of models with indirect path loadings of 0.30 were classified as having either “good” or “perfect” fit (Figure 7, Table 2). Ultimately, sample size had a more noticeable effect on fit, but all models demonstrated at least “mediocre” fit.

Using the bootstrapping method, it is clear that the indirect effects do cancel out. An increase in the sample size or strength of the indirect effect does seem to increase the rate of detecting an indirect effect (Table 3). However, that increase is from .4% at least to 1.3%. These rates are noticeably lower than the specified alpha of .05.

Understanding the Effectiveness of LCMM

I next examined whether information criteria would select the correct number of classes given measurement invariance between classes. The BIC invariably selected the one-class model in all but the models with loadings of 0.80 and sample sizes of 800. Under those conditions, the two-class model was selected 93% of the time. The BIC never selected a three-class model (Table 4, Figure 8).

For models with loadings of 0.30 in the indirect path, the AIC did better than the BIC at identifying the need for multiple classes (Table 5, Figure 9). However, the AIC selected the three-class model more than the two-class model for loadings of 0.80, across both sample sizes. This result represents the tendency of the AIC to select more complex models than might be necessary.

We also examined model selection using the aBIC. Like the BIC for conditions with indirect path loadings of 0.30, it rarely selected a mixture model (Table 6, Figure 10). Specifically, for sample sizes of 300, the aBIC selected the two-class model only 7% of the time, and the three-class model 2% of the time. When the sample size increased, it only selected the two-class model .4% of the time and never selected the three-class model. For larger indirect effect sizes, the aBIC performed better than the BIC, correctly identifying the need for a two-class model 77% of the time with 300 subjects and 99% of the time with 800 subjects. Although the aBIC does not often detect classes with small indirect effects, it does so more than the BIC.

Testing the Robustness of LCMM

Violations of measurement invariance drastically impacted class selection rates for all three indices tested. Even when only the measurement model of the mediator varied across classes, the misspecification affected class selection across most indices. With one incorrectly constrained measurement model, the AIC increasingly selected a three-class model. This effect grew as the size of the indirect effect and the sample increased. The AIC always supported the selection of a three-class model in 800 subject samples with indirect paths of 0.80 when the mediator was not invariant across classes. The aBIC was not much better. Model selection among models with smaller indirect effect sizes did not change much—the aBIC still overwhelmingly supported selecting the one-class model. In models with large indirect effects, however, a violation of measurement invariance drastically increased the rate of selecting the three-class model.

The information criteria least affected by violations of measurement invariance was the BIC. Even when the mediator's measurement model varied across classes, the behavior of the BIC remained relatively constant. It still supported the selection of the one-class model except when there were large indirect paths and sample sizes. Only then did it select the two-class model 91% of the time, a rate comparable to the measurement invariant condition. Thus, the BIC seems somewhat robust to certain violations of measurement invariance, even though it does not detect latent class moderated mediation with smaller indirect effects or with smaller sample sizes.

When all constructs violated the assumption of measurement invariance, all information criteria chose a three-class model the majority of the time they selected a mixture model. The rate of selecting a three-class model generally increased with the indirect effect size and sample size. There were a few exceptions. The BIC continued to select the one class model almost exclusively, besides when a population had large indirect effects and sample sizes. The aBIC continued to also overwhelmingly favor one-class models when populations had smaller indirect effects. Nevertheless, with widespread violations of measurement invariance, information criteria rarely supported the selection of the correct number of classes.

Discussion

In this study, I simulated data from various populations to test the utility of using latent class moderated mediation in SEM. I first predicted that the RMSEA and Chi-Square Test would detect the need for mixture modeling. The RMSEA did detect some misfit when one-class models were fit to a population with two classes with

larger indirect effects. Yet the RMSEA often did not detect misfit for models of populations with smaller indirect effects. The Chi Square test did terribly, but its perplexing results imply that its performance was affected by some other factor. More work is needed to determine what exactly caused the seemingly random noise. Thus, traditional fit indices may not reliably identify misfit in one-class models fit to populations with latent class moderated mediation models. These findings hold across the levels of sample size and indirect effect size tested. The inability to identify the need for a two-class model given strong measurement invariance is troubling.

The results also demonstrate that failing to identify the need for a different model results in a failure to detect significant indirect effects. Evidence of a significant indirect effect is exciting. Detecting it would provide not only theoretical advances, but also a publication. Although using latent class moderated mediation might increase model complexity, it could prevent missing substantively important relationships.

I also hypothesized that information criteria would be sufficient to select the correct number of classes. The aBIC did the best out of all three information criteria tested. However, the aBIC only reliably selected the two-class model given strong indirect effects in the population. The BIC would select the two-class model only with large samples of populations that had strong indirect effects. The AIC seemed ineffective in all conditions studied. With a smaller indirect effect, the AIC would often select the one-class model over the two-class model. With a larger indirect effect, the AIC would select the three-class model over the two-class model. Overall,

the aBIC selects the correct two-class LCMM model more often under ideal circumstances, but the three information criteria tested leave much to be desired in terms of sensitivity.

Finally, I predicted that violations of measurement invariance would lead to selecting more classes than in the generating model. This effect was evident—violations of measurement invariance severely reduced correct model selection. Only the BIC was robust to a violation of measurement invariance, and only for large samples of populations with sizeable indirect effects. The AIC and aBIC both selected the three-class models more often, given that they selected a model with multiple classes at all. Except in cases where one-class models were selected, if every measurement model differed across class, all information criteria overwhelmingly selected three-class models.

Applications to Latent Class Moderated Mediation Models

At first glance, it seems like using latent class moderated mediation in structural equation models is impractical. Using two common methods, it is unlikely that a one-class model does not completely represent data from a two-class model. Information criteria only reliably select the correct model when the indirect effect is large. Moreover, failing to account for different measurement models across classes results in selecting models with more classes than necessary.

One explanation for these results is that the classes were unrealistically similar. Indicators of each class were constrained to have the same mean, as well as factor means. The only parameters that differed across class when measurement invariance existed were the slopes of the indirect paths. The aforementioned

problems could have resulted from poor class separation. Researchers quantify class separation with entropy (Ramaswamy, Desarbo, Reibstein, & Robinson, 1993).

Entropy is calculated via Equation 16:

$$Entropy = 1 - \frac{\sum_{i=1}^N \sum_{k=1}^K (-\widehat{p}_{ik} \ln \widehat{p}_{ik})}{N \ln K} \quad (16)$$

where K is the number of classes, \widehat{p}_{ik} is the estimated posterior probability that person i will be in the k^{th} class. Entropy is bounded between 1 and 0 with 1 representing perfect class separation. Although class separation seems like an excellent way to select a model, simulation studies have demonstrated that entropy does not work well (L. M. Collins & Lanza, 2010; Henson, Reise, & Kim, 2007). Entropy does provide information as to how different the classes are, which can be useful in interpretation.

Another possible explanation is that, because of the constraints, the classes may not have been different in the ways that matter. Perhaps class-varying indicator means would support estimation. Covariates for class membership might also improve estimation. Future simulation studies are needed to determine whether this explanation even makes sense.

Even if measurement invariance does not hold across classes, all is not lost. Interpreting latent class moderated mediation in models that do not abide by measurement invariance is challenging. However, violations of measurement invariance in structural equation mixture models can provide valuable information about the psychological process under study. Just like in cross-cultural psychology (Byrne & Watkins, 2003; Byrne, Shavelson, & Muthen, 1989), if measurement

models differ across groups, then the constructs could differ qualitatively. It seems less tenable to directly compare the strengths of indirect effects across classes with qualitative differences in a factor between classes. However, these differences can provide information as to why the indirect effect varies across classes in the first place. To return to the clinical example, perhaps the measurement models of the construct of “stress” vary across the clinical and nonclinical subpopulations. Researchers could then investigate how between-group heterogeneity in perceived stress might contribute to unique processes or outcomes. Violations of measurement invariance cause problems only when one fails to model them. When modeled, they can describe complexity and direct further research.

Applications to Structural Equation Mixture Models

Beyond the latent class moderated mediation models tested, these findings can inform the use of structural equation mixture models. This study has demonstrated the need to develop model selection procedures that account for violations of measurement invariance for structural equation mixture models. If someone were to select the number of classes using information criteria first, they would select the wrong number of classes. If the incorrect number of classes is chosen⁶, then testing

⁶ This problem comes from the strong interpretation of classes. Under a weak interpretation of classes, then it might not be too problematic to select a model with more groups than necessary (Bauer & Curran, 2003). Future work needs to be done to see if wrongfully constrained measurement models also disrupt the use of mixtures to semi-parametrically fit nonlinear relationships.

for measurement invariance does not matter. Thus, the model selection procedure for structural equation mixture models must incorporate testing for measurement invariance.

There are a few possible model selection approaches that could incorporate testing the assumption of measurement invariance. One option would be to fit all models under consideration, with all possible numbers of classes and most levels of measurement invariance, and then use information criteria to sort through them. This approach sounds very time consuming. Another option would be to test for measurement invariance within class and then select the ideal number of classes. After selecting the best model for each number of classes, the models could be compared using information criteria. Finally, one could perform the second method, except testing only sequential models. For example, one would fit a one-class model. Then they would fit a two-class model and test for measurement invariance in that two-class model. Then the one-class model and best two-class model would be compared. The process would continue until the fit indices began to increase again. These three approaches are both atheoretical and untested. Work needs to be done to examine how well these methods select the correct number of classes given class-varying measurement models.

Limitations

The design of this study limits inferences in a number of ways. As a simulation study, it generates data based on a single “true” model, but true models do not exist (Box & Draper, 1987). Successfully fitting a model to data generated by that same model does not prove its utility. Moreover, there are countless models

with latent class-moderated mediation—I only simulated twelve of them. Some then might see the small number of models as a limitation. Yet the failure of information criteria to select the correct model suggests something else. These models were not terribly complex and had sizeable samples and reasonably large indirect effects. If selecting a model fit to data generated by that same model is unlikely, then there is a problem.

Nevertheless, I only examined one type of model, one with two equally sized classes with indirect paths of equal magnitude but opposite direction. Thus, it is impossible to determine whether this approach does not work well over all cases, or that this case is simply very hard to estimate. I can only infer that using latent class moderated mediation to model this type of population does not provide ideal results.

The number of conditions I used also reduced the inferences possible from this study. I only simulated two levels of sample size and effect size and three levels of measurement invariance to keep the simulation's runtime reasonable. The small number of conditions leaves many opportunities for future work. Two conditions can demonstrate the direction and magnitude of an effect. However, two conditions cannot provide any information as to the shape of the relationship. For example, additional levels of sample size and indirect effect size would better describe the stark differences observed in the BIC results. Simulating violations of measurement invariance for different constructs (X or Y), as well as different combinations (e.g. X and M but not Y) would also provide more information as to how the location of the violation(s) might impact model selection. All these possible, but unexamined,

conditions prevent a more nuanced comment on the effect of violations of measurement invariance on model selection in latent class moderated mediation in structural equation models.

Another limitation of this study is that I did not examine whether the Lo-Mendell-Rubin likelihood ratio test (LRT) (Lo, Mendell, & Rubin, 2001) or the Bootstrapped likelihood ratio test (BLRT) could identify the need for different measurement models under these conditions (McLachlan, 1987). Although the traditional LRT requires nested models, the Lo-Mendell-Rubin LRT can be used to compare models that are not nested. BLRT simply bootstraps the estimates of this ratio and then constructs confidence intervals around it. These tests can definitely be used to check for measurement invariance as well. The LMR-LRT, or the BLRT were not examined in this study, and the LRT was not used to test for measurement invariance. Previous work has demonstrated that the LMR-LRT and especially the BLRT perform well in model selection for structural equation mixture modeling (Henson et al., 2007; Nylund, Asparouhov, & Muthén, 2007). Future research should examine how these fit indices perform specifically with latent class moderated mediation and generally with structural equation mixture models with varying levels of measurement invariance.

Finally, even if improvements make latent class moderated mediation more usable in structural equation modeling, it does not eliminate all issues with causal inference in mediation. Latent class moderated mediation only offers a potential solution to the problem of latent groups with different indirect effects in the population. If possible, design-based approaches, such as random assignment and

manipulation, as well as longitudinal data collection, should still be applied. Moreover, integrating latent class moderated mediation into the causal model-based approaches remains an open field of research.

Conclusions:

In this study, I examined whether one can identify the need for latent class moderated mediation in structural equation models, how information criteria perform at selecting the correct number of classes, and the impact of violations of measurement invariance on latent class moderated mediation model selection. I then demonstrated that both the RMSEA and Chi-Square test have trouble with rejecting the null that a one-class model fits well to data generated from a two-class latent class moderated mediation model. The aBIC reliably selects the two-class model when fit to data generated from a two-class model with large indirect effects. Only the BIC is moderately robust to violations of measurement invariance. Model selection procedures for structural equation mixture models need to consider violations of measurement invariance before the number of classes is selected. However, these exact methods still require further study before any strong recommendation can be made. At the moment, currently tested approaches to latent class moderated mediation in structural equation mixture models have not rendered them useful to practitioners.

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Figure Captions

Figure 1: Mediation in regression, with X as the predictor, Y as the outcome, M as the mediator, and a , b , and c are regression weights.

Figure 2: Mediation in structural equation modeling, with η_1 as the predictor, η_3 as the outcome, and η_2 as the mediator.

Figure 3: Structural Equation Mixture Model with Latent Class Moderated Mediation which upholds the assumption of strong measurement invariance.

Figure 4: Structural Equation Mixture Model with Latent Class Moderated Mediation with a mediator that violates the assumption of strong measurement invariance.

Figure 5: Structural Equation Mixture Model with Latent Class Moderated Mediation with all three factors that violate the assumption of strong measurement invariance.

Figure 6: Chi-Square Test p-values across sample sizes and indirect path loadings in models where the assumption of strong measurement invariance holds.

Figure 7: RMSEA values across sample sizes and indirect path loadings in models where the assumption of strong measurement invariance holds.

Figure 8: Model selection rates of the AIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

Figure 9: Model selection rates of the BIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

Figure 10: Model selection rates of the aBIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

Figure 1: Mediation in regression, with X as the predictor, Y as the outcome, M as the mediator, and a , b , and c are regression weights.

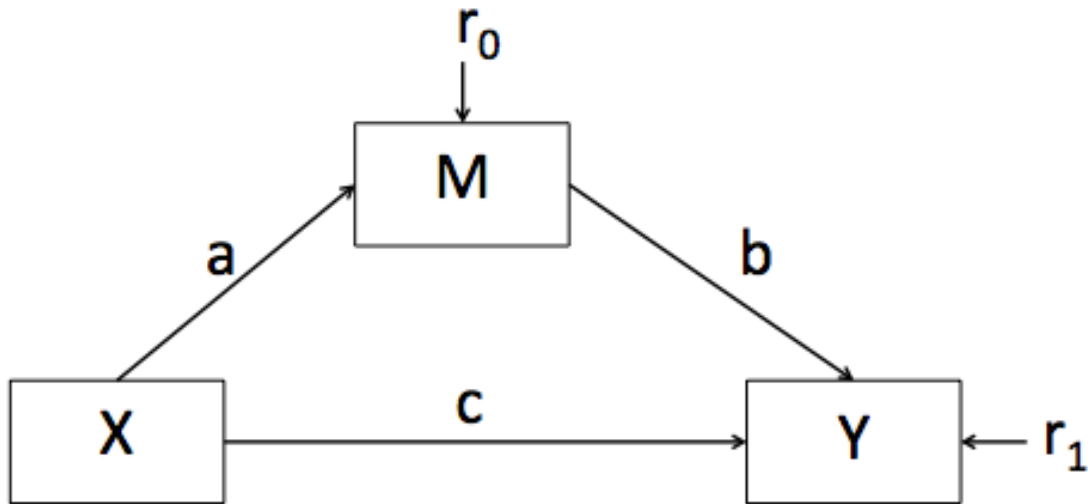


Figure 2: Mediation in structural equation modeling, with η_1 as the predictor, η_3 as the outcome, and η_2 as the mediator.

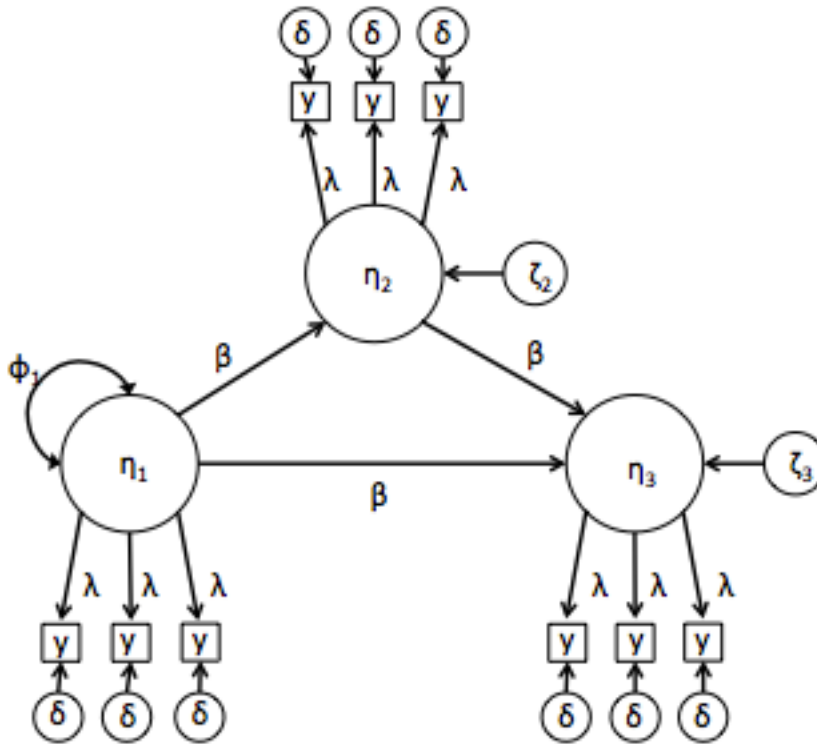


Figure 3: Structural Equation Mixture Model with Latent Class Moderated Mediation which upholds the assumption of strong measurement invariance.

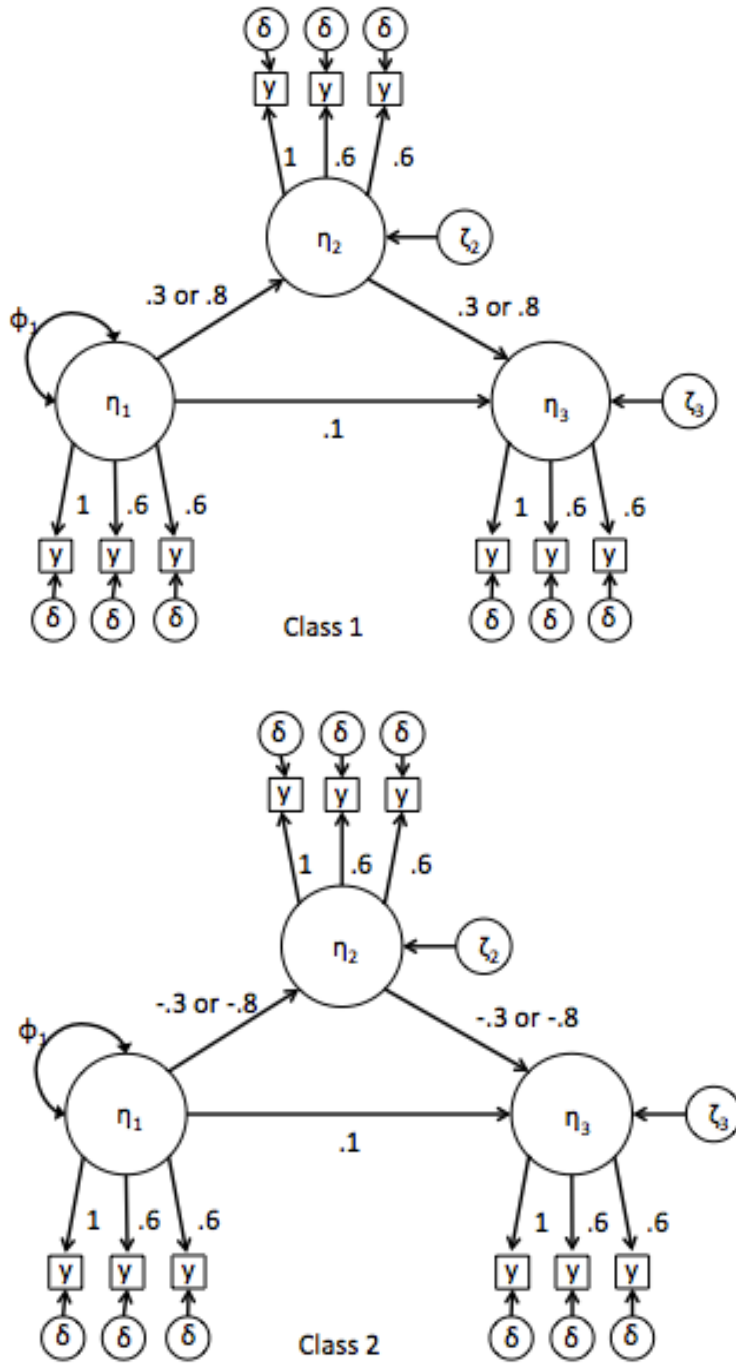


Figure 4: Structural Equation Mixture Model with Latent Class Moderated Mediation with a mediator that violates the assumption of strong measurement invariance.

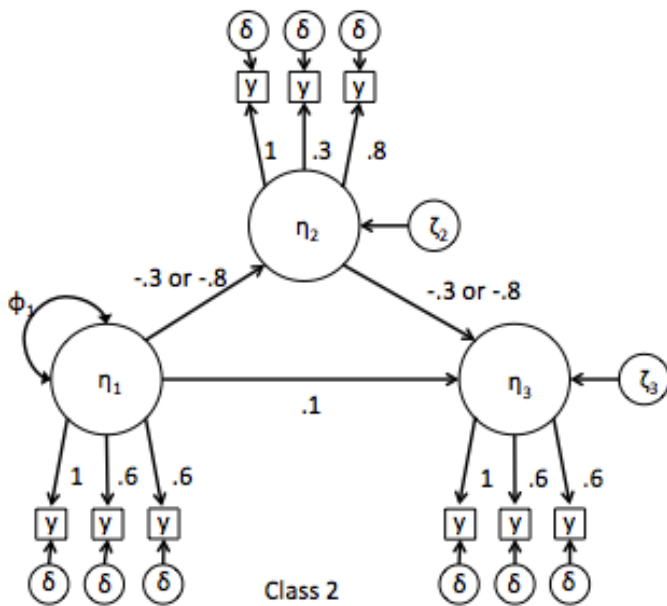
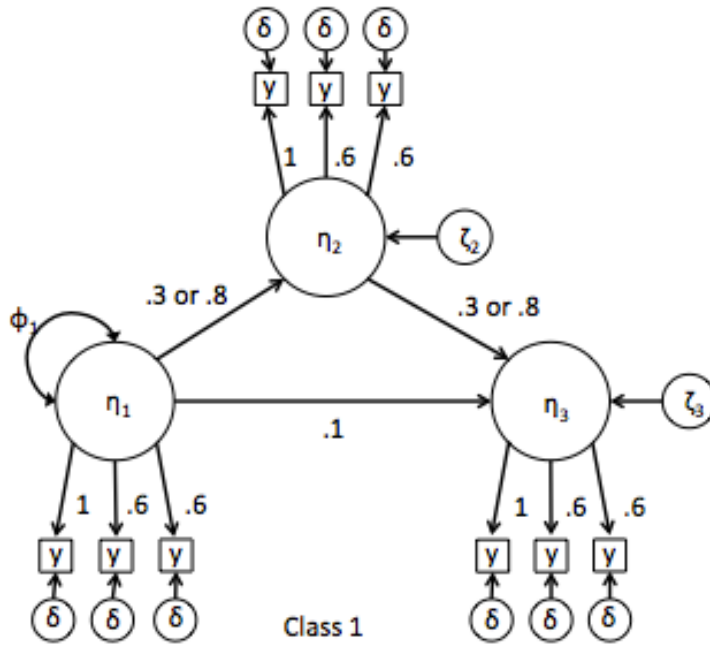


Figure 5: Structural Equation Mixture Model with Latent Class Moderated Mediation with all three factors that violate the assumption of strong measurement invariance.

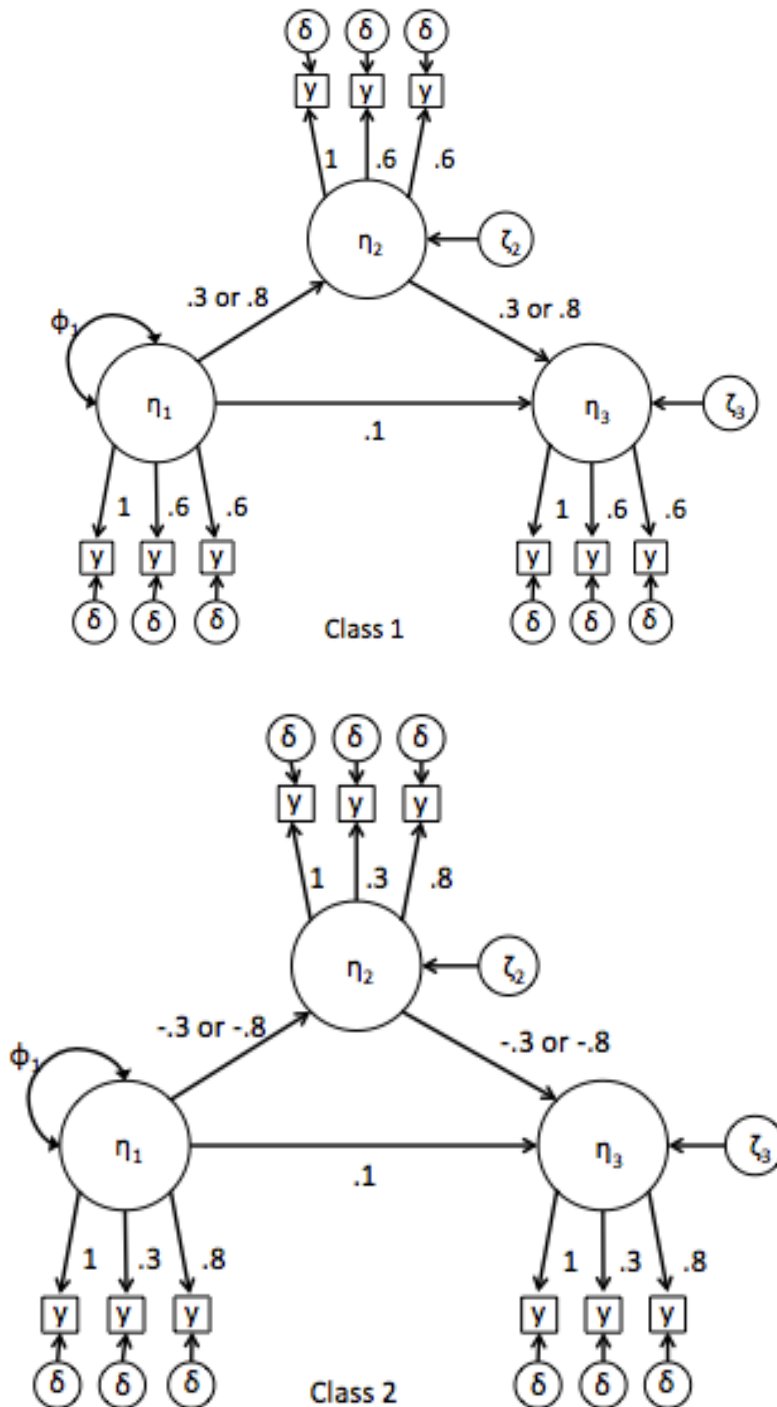


Figure 6: Chi-Square Test p-values across sample sizes and indirect path loadings in models where the assumption of strong measurement invariance holds.

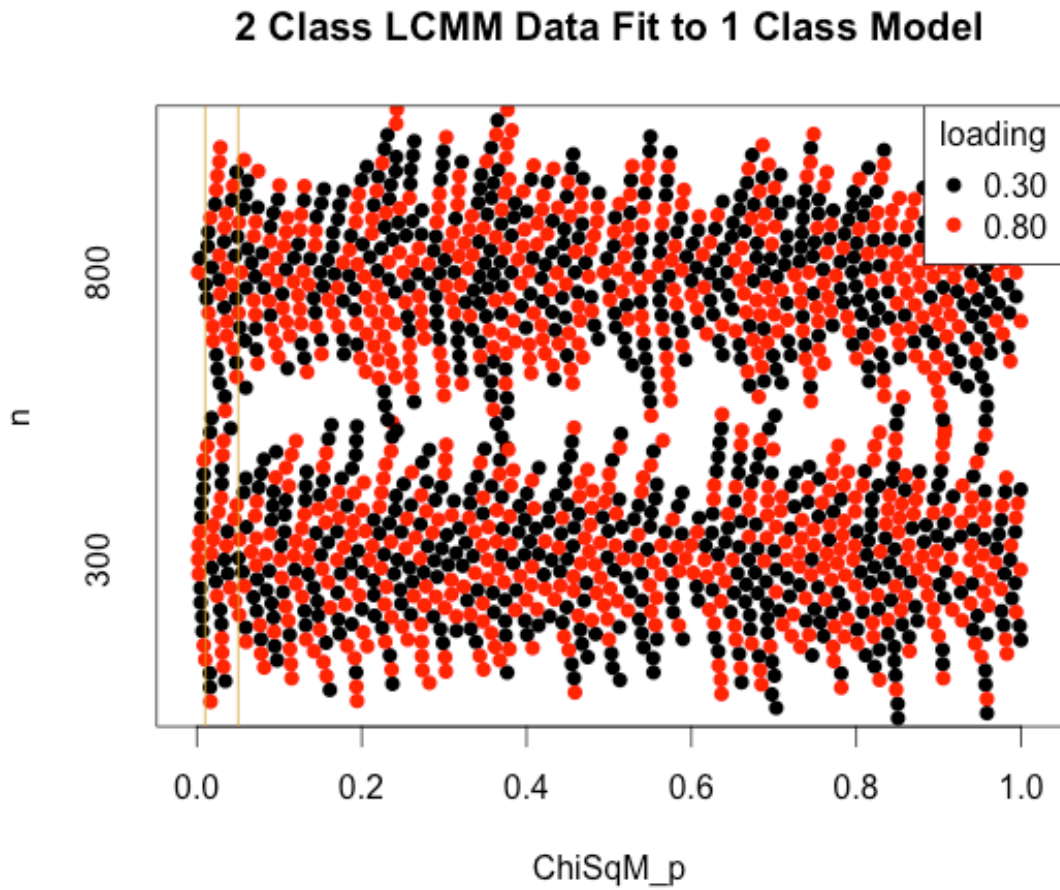


Figure 7: RMSEA values across sample sizes and indirect path loadings in models where the assumption of strong measurement invariance holds.

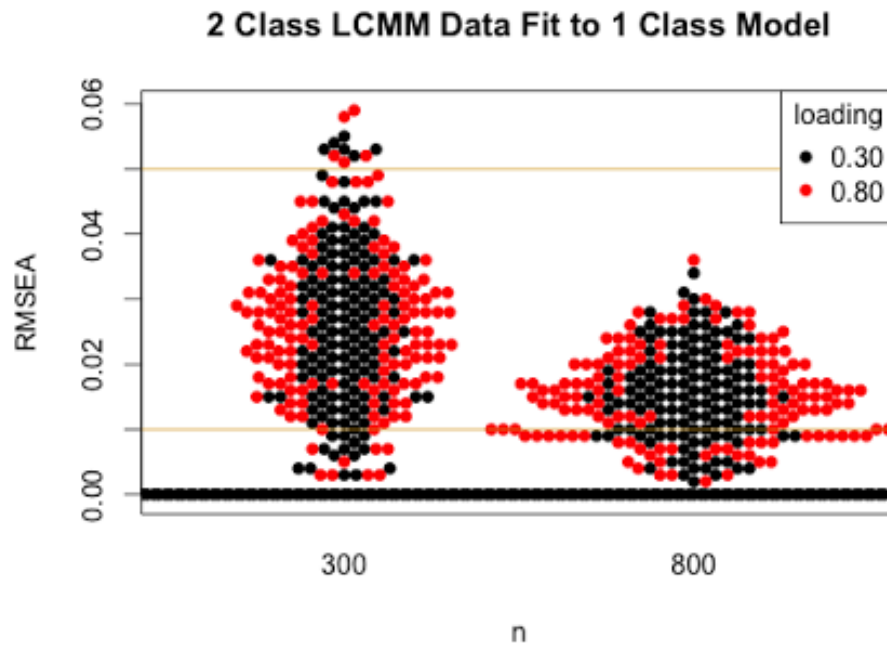


Figure 8: Model selection rates of the AIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

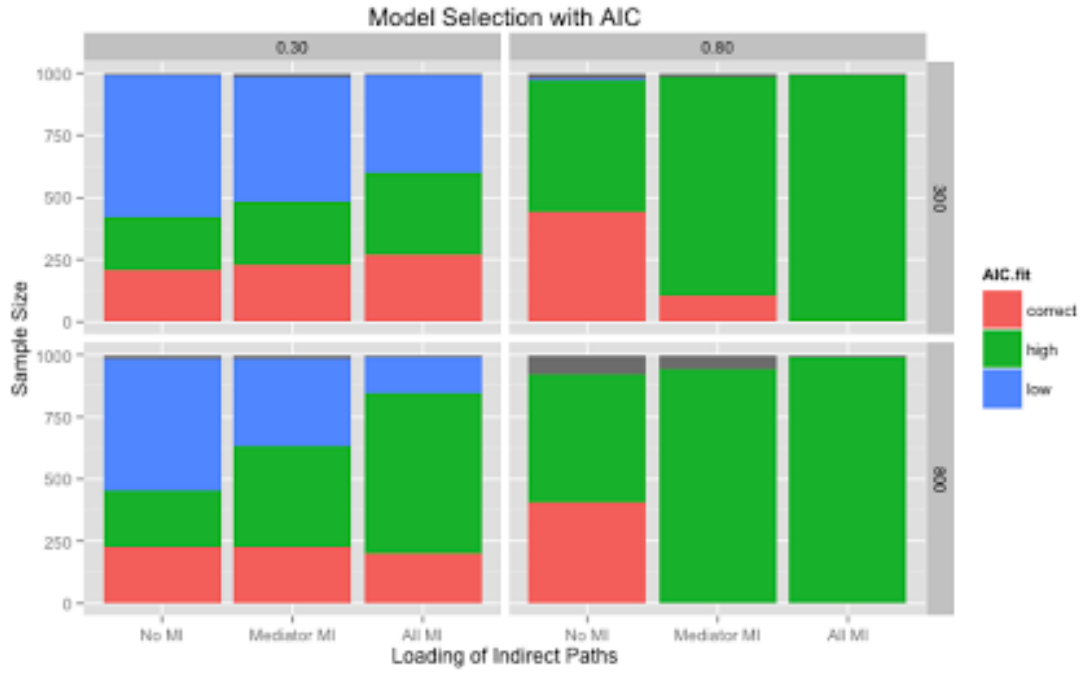


Figure 9: Model selection rates of the BIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

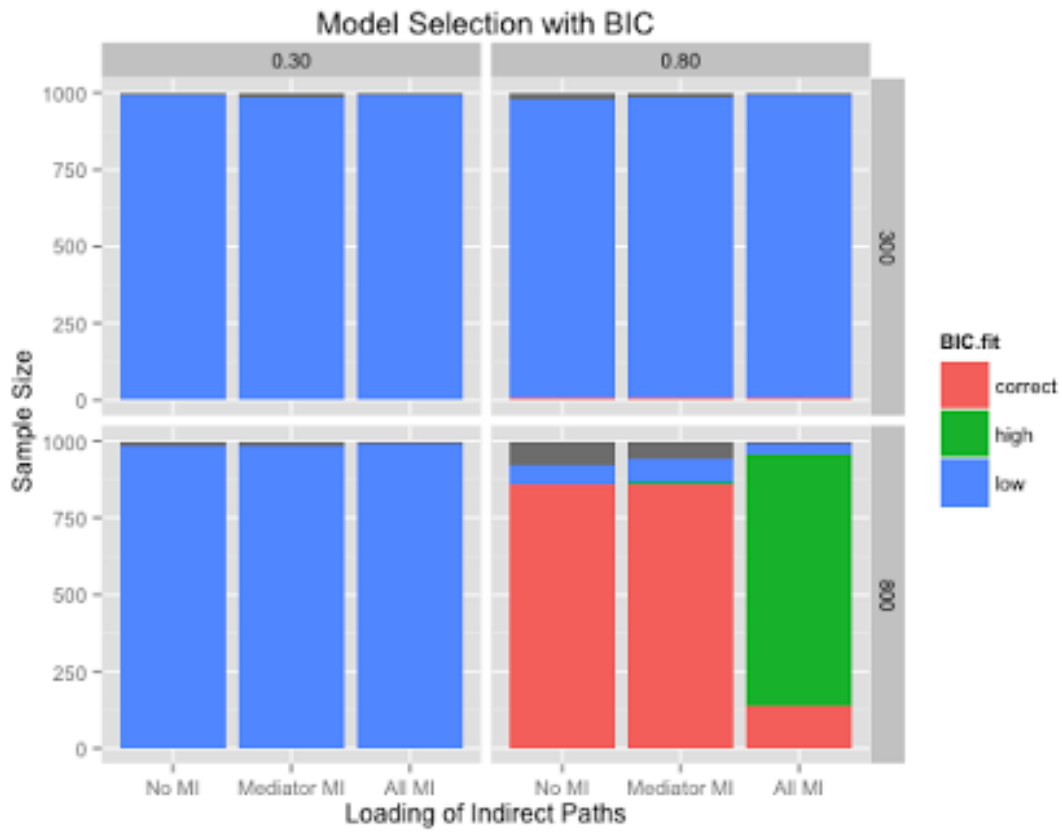


Figure 10: Model selection rates of the aBIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

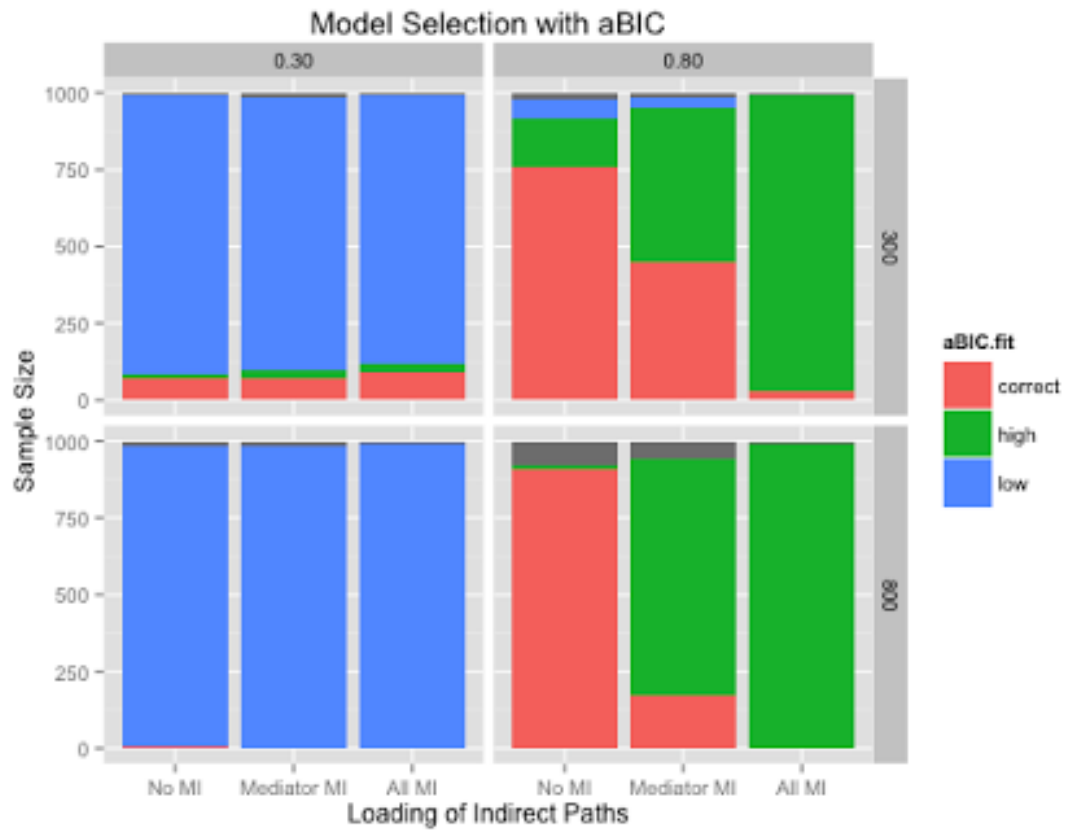


Table Captions

Table 1: Misfit of 1-class model fit to 2-class data as measured by the Chi-Square test.

Table 2: Misfit of 1-class model fit to 2-class data as measured by the RMSEA.

Table 3: Rate of detecting an indirect effect via bootstrap in misfitted 1-class model.

Figure 4: Model selection rates of the AIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

Figure 5: Model selection rates of the BIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

Figure 6: Model selection rates of the aBIC between 1-, 2-, and 3- class models across levels of sample size, indirect path loadings, and measurement invariance.

Table 1: Percent Rejection by Chi-Square Test of Incorrect 1-Class Model

Loading	N	Reject at .01	Reject at .05
0.30	300	1.4%	3.8%
	800	.6%	4.1%
0.80	300	1%	4.3%
	800	.4%	4.4%

Table 2: Misfit by RMSEA of Incorrect 1-Class Model

Loading	N	Perfect Fit	Excellent Fit	Good Fit	Mediocre Fit	Poor Fit	Bad Fit
0.30	300	52.94%	4.13%	40.80%	1.75%	0%	0%
	800	52.75%	10.25%	33.88%	0%	0%	0%
0.80	300	53.25%	3.00%	41.12%	1.50%	0%	0%
	800	52.62%	10.75%	34.75%	0%	0%	0%

Table 3: Detecting an Indirect Effect in 1-Class Model

Loading	N	ab Significant
0.30	300	.1%
	800	.4%
0.80	300	.9%
	800	1.3%

Table 4: BIC Model Selection by Indirect Path Loading, MI, and N

Loading	MI	N	Incorrect 1-Class	Correct 2-Class	Incorrect 3-Class
0.30	No MI	300	100%	0%	0%
		800	100%	0%	0%
	Mediator MI	300	100%	0%	0%
		800	100%	0%	0%
	All MI	300	100%	0%	0%
		800	100%	0%	0%
0.80	No MI	300	99.28%	0.72%	0%
		800	7.04%	92.96%	0%
	Mediator MI	300	99.29%	0.71%	0.00%
		800	8.36%	91.22%	0.42%
	All MI	300	99.09%	0.91%	0%
		800	2.94%	13.68%	83.38%

Table 5: AIC Model Selection by Indirect Path Loading, MI, and N

Loading	MI	N	Incorrect	Correct	Incorrect
			1-Class	2-Class	3-Class
0.30	No MI	300	57%	21%	22%
		800	54%	23%	23%
	Mediator MI	300	51%	23%	26%
		800	36%	23%	42%
	All MI	300	39%	27%	33%
		800	15%	20%	65%
0.80	No MI	300	00%	45%	54%
		800	00%	44%	56%
	Mediator MI	300	00%	10%	89%
		800	00%	00%	100%
	All MI	300	00%	00%	100%
		800	00%	00%	100%

Table 6: aBIC Model Selection by Indirect Path Loading, MI, and N

Loading	MI	N	Incorrect 1-Class	Correct 2-Class	Incorrect 3-Class
0.30	No MI	300	91.62%	6.87%	1.52%
		800	99.59%	0.41%	0.00%
	Mediator MI	300	90.36%	7.31%	2.34%
		800	100%	0%	0%
	All MI	300	87.77%	9.10%	3.13%
		800	99.70%	0.30%	0%
0.80	No MI	300	6.25%	77.46%	16.29%
		800	0%	98.59%	1.41%
	Mediator MI	300	3.55%	45.28%	51.17%
		800	0%	18.20%	81.80%
	All MI	300	0.40%	3.22%	96.38%
		800	0%	0%	100%

Appendices

Appendix A: Model Code for *MplusAutomation*

Appendix B: Code From Postprocessing

Appendix A: Code From Models**Data Generation File:**

```

[[init]]
iterators = ns loading mi;
ns = 1:2;
loading = 1:2;
mi = 1:3; ! 1 is no 2 is factor and 3 is total
n#ns = 300 800;
c2#loading = 0.30 0.80;
c1#loading = -0.30 -0.80;
factorh#mi = 0.60 0.80 0.80; !for the factor with measurement invariance
factorl#mi = 0.60 0.30 0.30;
filename = "[[n#ns]]_[[c2#loading]].inp";
outputDirectory = "C:\Users\markiend\Desktop\First_Run"; !change based on
computer
[[/init]]

TITLE:2class_[[n#ns]]_[[c2#loading]]
MONTECARLO:
NAMES ARE y1-y9;
NOBSERVATIONS = [[n#ns]];
NREPS = 500;
SEED = 45236;
GENCLASSES = class(2);
CLASSES = class(2);
REPSAVE = ALL; !Save data from ALL replications
SAVE =
C:\Users\markiend\Desktop\First_Run\data\[ [n#ns] ]_[ [c2#loading] ]_[ [mi] ]_*.DAT;
MODEL POPULATION:
%overall%
[class#1*0];

[[mi<3]] !when there's no and factor measurement invariance
fx BY y1*1 y2*.6 y3*.6;
fy BY y7*1 y8*.6 y9*.6;
[[/mi<3]]

[[mi=1]] !for when there's no measurement invariance
fm BY y4*1 y5*.6 y6*.6;
[[/mi=1]]

!factor variances
fx@1; fm*1; fy*1;

!residual variances
y1*1; y2*0.36; y3*0.36; y4*1; y5*0.36; y6*0.36; y7*1; y8*0.36; y9*0.36;

```

```

!item intercepts
[y1*0 y2*0 y3*0
y4*0 y5*0 y6*0
y7*0 y8*0 y9*0];

fm WITH fy@0;

%class#1%

[[mi>1]] !
fm BY y4*1 y5*[[factorh#mi]] y6*[[factorl#mi]];
[[/mi>1]]

[[mi>2]] !when there's no and factor measurement invariance
fx BY y1*1 y2*[[factorh#mi]] y3*[[factorl#mi]];
fy BY y7*1 y8*[[factorh#mi]] y9*[[factorl#mi]];
[[/mi>2]]

fy ON fm*[[c1#loading]];
fy ON fx*0.10;
fm ON fx*[[c1#loading]];

!factor means
[fx*0 fm*0 fy*0];

%class#2%

[[mi>2]] !when there's no and factor measurement invariance
fx BY y1*1 y2*.6 y3*.6;
fy BY y7*1 y8*.6 y9*.6;
[[/mi>2]]

[[mi>1]] !for when there's no measurement invariance
fm BY y4*1 y5*.6 y6*.6;
[[/mi>1]]

fy ON fm*[[c2#loading]];
fy ON fx*.10;
fm ON fx*[[c2#loading]];

!factor means
[fx*0 fm*0 fy*0];

ANALYSIS: TYPE = MIXTURE;

```

Single Class Fit File:

```

[[init]] iterators = ns loading mi fitclasses rep;
rep = 1:500;
fitclasses = 1;
ns = 1:2;
loading = 1:2;
mi = 1:3;
n#ns = 300 800;
c2#loading = 0.30 0.80;
c1#loading = -0.30 -0.80;
filename= "ft_[[fitclasses]]_[[n#ns]]_[[c2#loading]]_[[mi]]_[[rep]].inp";
outputDirectory = "C:\Users\markiend\Desktop\First_Run\an";
[[/init]]

```

TITLE:

DATA: FILE =

C:\Users\markiend\Desktop\First_Run\data\[[n#ns]]_[[c2#loading]]_[[mi]]_[[rep]].DAT;

VARIABLE:

NAMES = y1-y9;

ANALYSIS: STARTS = 20;

MODEL:

fx BY y1*1 y2*.6 y3*.6;

fm BY y4*1 y5*.6 y6*.6;

fy BY y7*1 y8*.6 y9*.6;

!factor variance

fx@1;

!residual variances

y1*1; y2*0.36; y3*0.36; y4*1; y5*0.36; y6*0.36; y7*1; y8*0.36; y9*0.36;

!item intercepts [y1*0 y2*0 y3*0 y4*0 y5*0 y6*0 y7*0 y8*0 y9*0]; fy ON fm*0;

fy ON fx*0.10;

fm ON fx*0;

fm WITH fy@0;

!factor means

[fx@0 fm@0 fy@0]

Two and Three Class Fit Model:

```

[[init]]
iterators = ns loading rep fitclasses;
rep = 1:500;
fitclasses = 2:3;
ns = 1:2;
loading = 1:2;
mi = 1:3; ! 1 is no 2 is factor and 3 is total
n#ns = 300 800;
c2#loading = 0.30 0.80;
c1#loading = -0.30 -0.80;
factorh#mi = 0.60 0.80 0.80; !for the factor with measurement invariance
totalh#mi = 0.60 0.60 0.80;
factorl#mi = 0.60 0.30 0.30;
totall#mi = 0.60 0.60 0.30;
filename = "ft_[[fitclasses]]_[[n#ns]]_[[c2#loading]]_m[[i]]_[[rep]]_inp";
outputDirectory = "C:\Users\markiend\Desktop\First_Run\an";
[[/init]]

```

TITLE:

DATA: FILE =

C:\Users\markiend\Desktop\First_Run\data_[[n#ns]]_[[c2#loading]]_[[rep]].DAT;

VARIABLE: NAMES = y1-y9;

CLASSES = class([[fitclasses]]);

ANALYSIS: TYPE = MIXTURE;

STARTS = 200 20;

MODEL:

%overall%

[[fitclasses>1]]

[class#1*0];

[[/fitclasses>1]]

[[mi<3]] !when there's no and factor measurement invariance

fx BY y1*1 y2*.6 y3*.6;

fy BY y7*1 y8*.6 y9*.6;

[[/mi<3]]

[[mi=1]] !for when there's no measurement invariance

fm BY y4*1 y5*.6 y6*.6;

[[/mi=1]]

!factor variance

fx@1;

!residual variances

y1*1; y2*0.36; y3*0.36; y4*1; y5*0.36; y6*0.36; y7*1; y8*0.36; y9*0.36;

!item intercepts

[y1*0 y2*0 y3*0
y4*0 y5*0 y6*0
y7*0 y8*0 y9*0];

fm WITH fy@0;

[[fitclasses>1]]
%class#1%
[[/fitclasses>1]]

fy ON fm*[[c1#loading]];
fy ON fx*0.10;
fm ON fx*[[c1#loading]];

[[mi>1]] !
fm BY y4*1 y5*[[factorh#mi]] y6*[[factorl#mi]];
[[/mi>1]]

[[mi>2]] !when there's no and factor measurement invariance
fx BY y1*1 y2*[[factorh#mi]] y3*[[factorl#mi]];
fy BY y7*1 y8*[[factorh#mi]] y9*[[factorl#mi]];
[[/mi>2]]

!factor means
[fx*0 fm*0 fy*0];

[[fitclasses>1]]
%class#2%
fy ON fm*[[c2#loading]];
fy ON fx*.1;
fm ON fx*[[c2#loading]];

[[mi>2]] !when there's no and factor measurement invariance
fx BY y1*1 y2*.6 y3*.6;
fy BY y7*1 y8*.6 y9*.6;
[[/mi>2]]

[[mi>1]] !for when there's no measurement invariance
fm BY y4*1 y5*.6 y6*.6;
[[/mi>1]]

```
!factor means  
[fx*0 fm*0 fy*0];  
[[/fitclasses>1]]
```

```
[[fitclasses>2]]  
%class#3%  
fy ON fm*0;  
fy ON fx*.1;  
fm ON fx*0;
```

```
[[mi>2]] !when there's no and factor measurement invariance  
fx BY y1 y2 y3;  
fy BY y7 y8 y9;  
[[/mi>2]]
```

```
[[mi>1]] !for when there's no measurement invariance  
fm BY y4 y5 y6;  
[[/mi>1]]
```

```
!factor means  
[fx*0 fm*0 fy*0];  
[[/fitclasses>2]]
```

Appendix B: Selected Code From Post-Processing

```

loadings<-c("0.30","0.80") #these are strings not numbers because of the specific
titles give to the output files.
ns<-c(300,800)
class<-c(1,2,3)
mi<-c(1,2,3)

lists<-as.vector(NULL)
rowdata<-NULL
frame<-NULL
load(file.choose())
count=0
frame.2<-as.data.frame(frame.2)
frame.t<-rbind(frame.m, frame.2)
range(frame.t[, "rep"])
for (f in 1:2){
  loading<-loadings[f]
  for (g in 1:2){
    n <- ns[g]
    for (i in 1:3){
      mi <- i
      for (h in 1:800){
        rep <- h
        for (j in 1:3){
          class<-j
          if (class>1){case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_1_",
rep,".out"),collapse="")} #paste0 concatenates without spaces in between.
          else {case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_",
rep,".out"),collapse="")}
          case<-paste0("interlist<-second.results$",case) #concatenate that with first run
          eval(parse(text=case))
          AIC<-as.numeric(as.character(interlist$summaries$AIC))
          #AICC<-as.numeric(as.character(interlist$summaries$AICC))
          BIC<-as.numeric(as.character(interlist$summaries$BIC))
          aBIC<-as.numeric(as.character(interlist$summaries$aBIC))
          LL<-as.numeric(as.character(interlist$summaries$LL))
          # CAIC<-((-
2*interlist$summaries$LL)+(log(interlist$summaries$Observations)+1)*interlist$
summaries$Parameters)
          # ssBIC<-((-
2*interlist$summaries$LL)+log((interlist$summaries$Observations+2)/24)*interlis
t$summaries$Parameters)

          # if (class==1){
          # RMSEA<-as.numeric(as.character(interlist$summaries$RMSEA_Estimate))

```

```

# RMSEA.lb<-as.numeric(as.character(interlist$summaries$RMSEA_90CI_LB))
# RMSEA.ub<-as.numeric(as.character(interlist$summaries$RMSEA_90CI_UB))
# ChiSqM_val <- (as.character(interlist$summaries$ChiSqM_Value))
# ChiSqM_df <- (as.character(interlist$summaries$ChiSqM_DF))
# ChiSqM_p <- (as.character(interlist$summaries$ChiSqM_PValue))
# ChiSqBase_val <- (as.character(interlist$summaries$ChiSqBaseline_Value))
# ChiSqBase_df <- (as.character(interlist$summaries$ChiSqBaseline_DF))
# ChiSqBase_p <- (as.character(interlist$summaries$ChiSqBaseline_PValue))}
#else{
  # RMSEA<-NA
  # RMSEA.lb <- NA
  # RMSEA.ub <- NA
  # ChiSqM_val <- NA
  # ChiSqM_df <- NA
  # ChiSqM_p <- NA
  # ChiSqBase_val <- NA
  # ChiSqBase_df <- NA
  # ChiSqBase_p <- NA}

#put all of the fit indices in here
rowdata <- c(loading, n, mi, rep, class, AIC, BIC, aBIC, LL) #putting it together
frame.2<-rbind(frame.2, rowdata)#adding it to the data frame
}
}
}
}
}
}
}
frame.2<-NULL
, RMSEA, RMSEA.lb, RMSEA.ub, ChiSqM_val, ChiSqM_df, ChiSqM_p, ChiSqBase_val,
ChiSqBase_df, ChiSqBase_p

frame.m[,"rep"]<-as.numeric(as.character(frame.m[,"rep"]))

frame.2[,"rep"]<-as.numeric(as.character(frame.2[,"rep"]))+200
# changing the index for rep number so things dont get weird.

#####IS This Effect Evident?
frame.ie<-NULL

for (f in 1:2){
  loading<-loadings[f]
  for (g in 1:2){
    n <- ns[g]

```

```

for (i in 1){
  mi <- i
  for (h in 1:1000){
    rep <- h
    for (j in 1){
      class<-j
      if (class>1){case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_1_",
rep,".out"),collapse="")} #paste0 concatenates without spaces in between.
      else {case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_",
rep,".out"),collapse="")}
      case<-paste0("interlist<-results.t$",case) #concatenate that with first run
      eval(parse(text=case))
      a<-as.numeric(as.character(interlist$parameters$unstandardized$est[10]))
      b<-as.numeric(as.character(interlist$parameters$unstandardized$est[12]))
      a.se<-as.numeric(as.character(interlist$parameters$unstandardized$se[10]))
      b.se<-as.numeric(as.character(interlist$parameters$unstandardized$se[12]))
      a.p<-as.numeric(as.character(interlist$parameters$unstandardized$pval[10]))
      b.p<-as.numeric(as.character(interlist$parameters$unstandardized$pval[12]))

      RMSEA<-as.numeric(as.character(interlist$summaries$RMSEA_Estimate))
      RMSEA.lb<-as.numeric(as.character(interlist$summaries$RMSEA_90CI_LB))
      RMSEA.ub<-as.numeric(as.character(interlist$summaries$RMSEA_90CI_UB))

      ChiSqM_val <- (as.character(interlist$summaries$ChiSqM_Value))
      ChiSqM_df <- (as.character(interlist$summaries$ChiSqM_DF))
      ChiSqM_p <- (as.character(interlist$summaries$ChiSqM_PValue))
      ChiSqBase_val <- (as.character(interlist$summaries$ChiSqBaseline_Value))
      ChiSqBase_df <- (as.character(interlist$summaries$ChiSqBaseline_DF))
      ChiSqBase_p <- (as.character(interlist$summaries$ChiSqBaseline_PValue))

      #put all of the fit indices in here
      rowdata <- c(loading, n, mi, rep, class, a, b, a.se, b.se, a.p, b.p, RMSEA, RMSEA.lb,
RMSEA.ub, ChiSqM_val, ChiSqM_df, ChiSqM_p, ChiSqBase_val, ChiSqBase_df,
ChiSqBase_p) #putting it together
      frame.1t<-rbind(frame.1t, rowdata)#adding it to the data frame
    }
  }
}
}
}
}

##because I dropped the chi square p values:
for (f in 1:2){
  loading<-loadings[f]

```

```

for (g in 1:2){
  n <- ns[g]
  for (i in 1){
    mi <- i
    for (h in 1:1000){
      rep <- h
      for (j in 1){
        class<-j
        if (class>1){case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_1_",
rep,".out"),collapse="")} #paste0 concatenates without spaces in between.
        else {case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_",
rep,".out"),collapse="")}
        case<-paste0("interlist<-results.t$",case) #concatenate that with first run
        eval(parse(text=case))

        ChiSqM_p <- as.numeric(as.character(interlist$summaries$ChiSqM_PValue))
        rowdata <- c(loading, n, rep, ChiSqM_p )
        blank.cs<-rbind(blank.cs, rowdata)#adding it to the data frame
      }
    }
  }
}
blank.cs<-as.data.frame(blank.cs)
##

rowdata<-NULL
colnames(blank.cs)<-c("loading", "n", "rep", "ChiSqM_p")

frame.1t<-NULL

frame.1t<-as.data.frame(frame.1t)
colnames(frame.1t)<-c("loading", "n", "mi", "rep", "class", "a", "b", "a.se", "b.se", "a.p",
"b.p", "RMSEA", "RMSEA.lb", "RMSEA.ub", "ChiSqM_val", "ChiSqM_df", "ChiSqM_p",
"ChiSqBase_val", "ChiSqBase_df", "ChiSqBase_p")

library(beeswarm)
class(frame.ie[, "a.p"])
frame.1t[, "rep"]<-as.numeric(as.character(frame.1t[, "rep"]))
)library(beeswarm)
beeswarm(a ~ n, pwcol=loading, pch=16, data =
frame.1t[which(frame.1t[, "rep"]<400),])
abline(h=.05, col="goldenrod")
abline(h=.01, col="goldenrod")

colnames(frame.ie) <- c("Loading", "N", "MI", "Rep", "class", "a", "b", "a.p", "b.p")

```

```
legend('topright', legend = levels(frame.ie$loading), title = 'loading', pch = 16, col = 1:2)
```

```
legend(title = 'AIC Selection')
```

```
qplot(b.p, method="hist",facets=N~Loading,
data=frame.ie[which(frame.ie$MI==1),])
qplot(a.p, method="hist",facets=N~Loading,
data=frame.ie[which(frame.ie$MI==1),])
```

```
abline(v=.05, col="goldenrod")
class(frame.ie[v,"a.p"])
v=1
while(v<2401){
if (frame.ie[v,"b.p"]<0.05){frame.ie.rb[v]<-1}
else {frame.ie.rb[v]<-0}
v=v+1
}
frame.ie.rb<-NULL
frame.ie.r<-as.data.frame(frame.ie.r)
frame.ie<-cbind(frame.ie[,1:5],frame.ie.r,frame.ie.r1,frame.ie.rb,frame.ie.rb1)
```

```
colnames(frame.ie)<-
c("Loading","N","MI","Rep","class","r.a.05","r.a.01","r.b.05","r.b.01")
frame.ie<-frame.ie[which(frame.ie["MI"]==1),]
aggregate(frame.ie[, "r.a.05"],by=list(frame.ie$Loading, frame.ie$N), Mean)
aggregate(frame.ie[, "r.a.01"],by=list(frame.ie$Loading, frame.ie$N), Mean)
aggregate(frame.ie[, "r.b.05"],by=list(frame.ie$Loading, frame.ie$N), Mean)
aggregate(frame.ie[, "r.b.01"],by=list(frame.ie$Loading, frame.ie$N), Mean)
```

```
###testing indirect effects via bootstrapping
```

```
frame.1t[,6]<-as.numeric(as.character(frame.1t[,6]))
frame.1t[,7]<-as.numeric(as.character(frame.1t[,7]))
frame.1t[,8]<-as.numeric(as.character(frame.1t[,8]))
frame.1t[,9]<-as.numeric(as.character(frame.1t[,9]))
```

```
for (i in 1:4000){
a <- frame.1t[i,6]
b <- frame.1t[i,7]
a.v <- frame.1t[i,8]^2
b.v <- frame.1t[i,9]^2
pest=c(a,b)
acov <- matrix(c(
```



```

a.v, 0,
0, b.v
),2,2)
mcmc <- mvrnorm(1000,pest,acov,empirical=FALSE)
ab <- mcmc[,1]*mcmc[,2]
low=(1-95/100)/2
upp=((1-95/100)/2)+(95/100)
LL=quantile(ab,low)
UL=quantile(ab,upp)
if(LL<0 & UL>0){
  ie.present[i] <- 0}
else{
  ie.present[i] <- 1
}
}
ie.present<-as.data.frame(ie.present)
frame.1t<-cbind(frame.1t,ie.present)
ie.present<-NULL

xtable(aggregate(frame.1t[, "ie.present"],by=list(frame.1t$loading, frame.1t$n),
Mean), digits=3)

qplot(ie.present, data=frame.1t, facets=n~loading, main = "Indirect Effect",
xlab="Loading of Indirect Paths", ylab="Sample Size")

####

frame<-as.data.frame(frame)
colnames(frame)<-c("loading", "N", "mi", "rep", "classfit", "AIC", "BIC", "aBIC", "LL",
"RMSEA", "RMSEA.lb", "RMSEA.ub", "ChiSqM_val", "ChiSqM_df", "ChiSqM_p",
"ChiSqBase_val", "ChiSqBase_df", "ChiSqBase_p")

colnames(frame.2)<-c("loading", "N", "mi", "rep", "classfit", "AIC", "BIC", "aBIC", "LL")

rownames( aBIC.selection ) <- seq_len( nrow( aBIC.selection ) )

frame.1t[, "RMSEA"]<-as.numeric(as.character(frame.1t[, "RMSEA"]))
## Beeswarm Plot for RMSEA
class(bframe[, "RMSEA"])
library(beeswarm)

```

```

beeswarm.rmsea <- beeswarm(RMSEA ~ n, data =
frame.1t[which(frame.1t[, "rep"]>800),], method = 'swarm', pwc = loading,
pch=16, spacing=1.2, main = "RMSEA 2 Class LCMM Data Fit to 1 Class Model")

colnames(beeswarm) <- c("x", "y", "N", "loading")
legend('topright', legend = levels(frame.1t$loading), title = 'loading', pch = 16, col =
1:2)

abline(h=.05, col="goldenrod")
abline(h=.01, col="goldenrod")
abline(h=.08, col="goldenrod")
##

## Table for RMSEA
RMSEA.summary <- aggregate(frame.1t[, "RMSEA"], by=list(frame.1t$loading,
frame.1t$n, frame.1t$mi), Mean)

a=1
while(a<4000){
  if(frame.1t[a, "RMSEA"]<1){
if(frame.1t[a, "RMSEA"]==0){frame.1t[a, "RMSEA.Perf"]=1}else{frame.1t[a, "RMSEA.P
erf"]=0}
if(frame.1t[a, "RMSEA"]<0.01 &
frame.1t[a, "RMSEA"]!=0){frame.1t[a, "RMSEA.Ex"]=1}else{frame.1t[a, "RMSEA.Ex"]=
0}
if(frame.1t[a, "RMSEA"]<0.05 & frame.1t[a, "RMSEA"]
>0.01){frame.1t[a, "RMSEA.Good"]=1}else{frame.1t[a, "RMSEA.Good"]=0}
if(frame.1t[a, "RMSEA"]<0.08 & frame.1t[a, "RMSEA"]
>0.05){frame.1t[a, "RMSEA.Medi"]=1}else{frame.1t[a, "RMSEA.Medi"]=0}
if(frame.1t[a, "RMSEA"]>0.08 & frame.1t[a, "RMSEA"]
<0.1){frame.1t[a, "RMSEA.Poor"]=1}else{frame.1t[a, "RMSEA.Poor"]=0}
if(frame.1t[a, "RMSEA"]>0.1){frame.1t[a, "RMSEA.Bad"]=1}else{frame.1t[a, "RMSEA.B
ad"]=0}
}
else{
  frame.1t[a, "RMSEA.Perf"] <- NA
  frame.1t[a, "RMSEA.Ex"] <- NA
  frame.1t[a, "RMSEA.Good"] <- NA
  frame.1t[a, "RMSEA.Medi"] <- NA
  frame.1t[a, "RMSEA.Poor"] <- NA
  frame.1t[a, "RMSEA.Bad"] <- NA
}
a=a+1
}

frame.1t[, "RMSEA.Perf"] <- NULL

```

```

frame.1t["RMSEA.Ex"] <- NULL
frame.1t["RMSEA.Good"] <- NULL
frame.1t["RMSEA.Medi"] <- NULL
frame.1t["RMSEA.Poor"] <- NULL
frame.1t["RMSEA.Bad"] <- NULL

RMSEA.perf <- aggregate(frame.1t["RMSEA.Perf"],by=list(frame.1t$loading,
frame.1t$n, frame.1t$mi), Mean)

RMSEA.ex <- aggregate(frame.1t["RMSEA.Ex"],by=list(frame.1t$loading,
frame.1t$n, frame.1t$mi), Mean)

RMSEA.good <- aggregate(frame.1t["RMSEA.Good"],by=list(frame.1t$loading,
frame.1t$n, frame.1t$mi), Mean)

RMSEA.medi <- aggregate(frame.1t["RMSEA.Medi"],by=list(frame.1t$loading,
frame.1t$n, frame.1t$mi), Mean)

RMSEA.poor <- aggregate(frame.1t["RMSEA.Poor"],by=list(frame.1t$loading,
frame.1t$n, frame.1t$mi), Mean)

RMSEA.bad <- aggregate(frame.1t["RMSEA.Bad"],by=list(frame.1t$loading,
frame.1t$n, frame.1t$mi), Mean)

RMSEA.summary <- cbind(RMSEA.summary[,1:4], RMSEA.perf[,4]*100,
RMSEA.ex[,4]*100, RMSEA.good[,4]*100, RMSEA.medi[,4]*100,
RMSEA.poor[,4]*100, RMSEA.bad[,4]*100)

colnames(RMSEA.summary)<-c("loading","n","mi","mean RMSEA", "Perfect Fit",
"Excellent Fit", "Good Fit", "Mediocre Fit", "Poor Fit", "Bad Fit")

RMSEA.summary.table<-RMSEA.summary[order(RMSEA.summary$loading,
RMSEA.summary$n) , ]

rownames( RMSEA.summary.table ) <- seq_len( nrow( RMSEA.summary.table ) )

RMSEA.summary.table<-
cbind(RMSEA.summary.table[,1],rmsea.mi.factor,RMSEA.summary.table[,2],RMSEA.
summary.table[,4:10])

colnames(RMSEA.summary.table)<-c("loading","mi","N","mean RMSEA")

RMSEA.summary.table[,"mi"] <- as.factor(RMSEA.summary.table[,"mi"])

```

```

is.factor(RMSEA.summary.table[, "mi"])

rmsea.mi.factor <- as.data.frame(factor(RMSEA.summary.table[, "mi"], levels=c("1",
"2", "3"), labels=c("No MI", "Mediator MI", "All MI")))

xtable(RMSEA.summary.table)

##

## Chi Square
frame.1t[, "ChiSqM_p"] <- as.numeric(as.character(blank.cs[, "ChiSqM_p"]))
a=1
while(a<4000){
  if(frame.1t[a, "ChiSqM_p"]<=1){

if(frame.1t[a, "ChiSqM_p"]<0.01){frame.1t[a, "R0.01"]=1}else{frame.1t[a, "R0.01"]=0}

if(frame.1t[a, "ChiSqM_p"]<0.05){frame.1t[a, "R0.05"]=1}else{frame.1t[a, "R0.05"]=0}
}
else{
  frame.1t[a, "R0.01"] <-NA
  frame.1t[a, "R0.05"] <-NA
}
  a=a+1
}

cq.01 <- aggregate(frame.1t[, "R0.01"], by=list(frame.1t$loading, frame.1t$n), Mean)

cq.05<- aggregate(frame.1t[, "R0.05"], by=list(frame.1t$loading, frame.1t$n), Mean)

cq.summary<-cbind(cq.01, cq.05[,3])

cq.summary.table<-cq.summary[order(cq.summary[,1], cq.summary[,2]), ]

rownames( cq.summary.table ) <- seq_len( nrow( cq.summary.table ) )
xtable(cq.summary.table, digits=3)
cq.summary.table<-cbind(cq.summary.table[,1],
cq.summary.table[,2],cq.summary.table[,3],cq.summary.table[,4:5]*100)
cq.summary.table[,3]<-as.integer(cq.summary.table[,3])
cq.mi.factor <- as.data.frame(factor(cq.summary.table[, "MI"], levels=c("1", "2", "3"),
labels=c("No MI", "Mediator MI", "All MI")))
cq.summary.table[,2]<-cq.mi.factor
colnames(cq.summary.table) <- c("Loading", "MI", "N", "0.01", "0.05")
xtable(cq.summary.table)
##

```

#####Is Entropy to blame?

```

rowdata<-NULL
count=0

for (f in 1:2){
  loading<-loadings[f]
  for (g in 1:2){
    n <- ns[g]
    for (i in 1:3){
      mi <- i
      for (h in 1:200){
        rep <- h
        for (j in 2:3){
          class<-j
          if (class>1){case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_1_",
rep,".out"),collapse="")} #paste0 concatenates without spaces in between.
          else {case<-paste0(c("ft","_", class,"_", n,"_", loading,"_", mi,"_",
rep,".out"),collapse="")}
          case<-paste0("interlist<-results$",case) #concatenate that with first run
          eval(parse(text=case))
          Entropy<-as.numeric(as.character(interlist$summaries$Entropy))
          rowdata <- c(loading, n, mi, rep, class, Entropy) #putting it together
          frame.ent<-rbind(frame.ent, rowdata)#adding it to the data frame
        }
      }
    }
  }
}

frame.ent<- as.data.frame(frame.ent)
colnames(frame.ent)<-c("loading","N", "MI","rep","class","Entropy")
frame.ent[,"Entropy"]<-as.numeric(as.character(frame.ent[,"Entropy"]))

frame.ent[,"MI"]<-as.numeric(as.character(frame.ent[,"MI"]))
frame.ent<-frame.ent[which(frame.ent[,"MI"]==1),]

aggregate(frame.ent[,"Entropy"],by=list(frame.ent[,"loading"], frame.ent[,"N"],
frame.ent[,"class"]), Mean)

#####

```

```

frame.1t
blank.cs[, "rep"] <- as.numeric(as.character(blank.cs[, "rep"]))
## Beeswarm Plot for Chi Square
class(blank.cs[, "ChiSqM_p"])
library(beeswarm)
beeswarm(ChiSqM_p ~ n, data = blank.cs[which(blank.cs[, "rep"] < 400), ], method =
'swarm', pwc = loading, pch = 16, spacing = 1.2, main = "2 Class LCMM Data Fit to 1
Class Model", vertical = F)

legend('topright', legend = levels(frame.1t$loading), title = 'loading', pch = 16, col =
1:2)

abline(v = .05, col = "goldenrod")
abline(v = .01, col = "goldenrod")

##

class(bframe[, "ChiSqM_p"])

frame[fitclasses]

bframe[, "ChiSqM_p"] <- as.numeric(as.character(bframe[, "ChiSqM_p"]))

bwplot(factor(N) ~ ChiSqM_p | loading, frame)

#looking at RMSEA
frame <- as.numeric(as.character(frame))
onlyone <- frame[ which(frame$classfit == 1), ]
hist(as.numeric(as.character(onlyone[, "RMSEA"])), breaks = 100)

quantile(as.numeric(as.character(onlyone[, "RMSEA"])), breaks = 100)

quantile(as.numeric(as.character(onlyone[, "RMSEA"])), c(.10, .20, .30, .50, .60, .70, .80, .85, .90, .95, .99))

#creating a better data frame
bframe = frame
bframe[, "RMSEA"] <- as.numeric(as.character(frame[, "RMSEA"]))
bframe[, "loading"] <- as.numeric(as.character(frame[, "loading"]))
bframe[, "N"] <- as.numeric(as.character(frame[, "N"]))
write.csv(bframe, file = "ft_1&2_RMSEA.csv")
plot(bframe[, "N"], bframe[, "RMSEA"])

fit <- lm(RMSEA ~ N + loading, data = bframe)
summary(fit)

```

```
plot(fit)
```

```
case<-paste0(c("ft", classes,n, loading, rep,".out"), collapse= "_") #paste0
concatenates without spaces in between.
  case<-paste0("interlist<-first.run$",case) #concatenate that with first run
  eval(parse(text=case)) #eval runs the code, parse turns the string into code
  #store it into a working list called interlist
```

```
#pull that data file
```

```
#parameters into one line
#fit indices into another
#append
```

```
> bwplot(factor(N) ~ RMSEA | loading, frame, layout = c(5, 1))
> frame[,"RMSEA.ub"]<-as.numeric(as.character(frame[,"RMSEA.ub"]))
> bwplot(factor(N) ~ RMSEA.ub | loading, frame, layout = c(5, 1))
```

```
#making headers for the data frame
```

```
first.run$ft_1_100_0.00_1_.out$parameters$unstandardized[,1]
est.1<-
paste(first.run$ft_1_100_0.00_1_.out$parameters$unstandardized[,1],first.run$ft_1_
100_0.00_1_.out$parameters$unstandardized[,2], "est")
se.1<-
paste(first.run$ft_1_100_0.00_1_.out$parameters$unstandardized[,1],first.run$ft_1_
100_0.00_1_.out$parameters$unstandardized[,2], "se")
pval.1<-
paste(first.run$ft_1_100_0.00_1_.out$parameters$unstandardized[,1],first.run$ft_1_
100_0.00_1_.out$parameters$unstandardized[,2], "pval")
```

```
RMSEA.length<-frame[which(frame[,"classfit"]==1), "RMSEA.ub"]-
frame[which(frame[,"classfit"]==1), "RMSEA.lb"]
```

```
frame.m[,"aBIC"]<-as.numeric(as.character(frame.m[,"aBIC"]))
```

```
#####
```

```
AIC BIC comparison
```

```
frame.t[,"aBIC"]<-as.numeric(as.character(frame.t[,"aBIC"]))
frame.t[,"AIC"]<-as.numeric(as.character(frame.t[,"AIC"]))
frame.t[,"BIC"]<-as.numeric(as.character(frame.t[,"BIC"]))
correct<-NULL
low<-NULL
```

```

high<-NULL
models<-NULL
AIC.fit<-NULL

a=1
b=0
c=0
d=1
while (a < 36000){
  b<-a+1
  c<-a+2
  if (is.na(frame.t[a,"AIC"])){
    correct[d]<-NA
    AIC.fit[d]<-NA
  }
  else{
    if(is.na(frame.t[b,"AIC"])){
      correct[d]<-NA
      AIC.fit[d]<-NA
    }
    else{
      if (is.na(frame.t[c,"AIC"])){
        correct[d]<-NA
        AIC.fit[d]<-NA
      }
      else{
        if (frame.t[a,"AIC"]<1000){
          correct[d]<-NA
          AIC.fit[d]<-NA
        }
        else{
          if (frame.t[b,"AIC"]<1000){
            correct[d]<-NA
            AIC.fit[d]<-NA
          }
          else{
            if (frame.t[c,"AIC"]<1000){
              correct[d]<-NA
              AIC.fit[d]<-NA
            }
            else{
              if (frame.t[a,"AIC"]>frame.t[b,"AIC"] && frame.t[c,"AIC"] > frame.t[b,"AIC"] ){
                correct[d]<-1
                AIC.fit[d]<-"correct"
              }
            }
          }
        }
      }
    }
  }
}
else{correct[d]<-0}

```



```

if (frame.t[b,"AIC"]>frame.t[c,"AIC"] && frame.t[a,"AIC"]>frame.t[c,"AIC"]){
  high[d]<-1
  AIC.fit[d]<-"high"
}
else{high[d]<-0}
if (frame.t[c,"AIC"]>frame.t[a,"AIC"] && frame.t[b,"AIC"]>frame.t[a,"AIC"] ){
  low[d]<-1
  AIC.fit[d]<-"low"
}
else{low[d]<-0}
}
}
models<-rbind(models,frame.t[a,1:4])
a<-a+3
d<-d+1
}
}
}
}
}
summary(frame.t[, "mi"])
AIC.selection<-cbind(frame.t[which(frame.t[, "classfit"]==1),1:4], low, correct, high,
AIC.fit)

AIC.selection$mi <- factor(AIC.selection$mi, levels=c("1", "2", "3"), labels=c("No MI",
"Mediator MI", "All MI"))

qplot(mi, data=AIC.selection, facets=N~loading, geom="bar", main = "Model
Selection with AIC", fill=AIC.fit, xlab="Loading of Indirect Paths", ylab="Sample
Size")

#####
##BIC Selection
low<-NULL
high<-NULL
models<-NULL
BIC.fit<-NULL

a=1
b=0
c=0
d=1
while (a < 36000){
  b<-a+1

```

```

c<-a+2
if (is.na(frame.t[a,"BIC"])){
  correct[d]<-NA
  BIC.fit[d]<-NA
}
else{
  if(is.na(frame.t[b,"BIC"])){
    correct[d]<-NA
    BIC.fit[d]<-NA
  }
  else{
    if (is.na(frame.t[c,"BIC"])){
      correct[d]<-NA
      BIC.fit[d]<-NA
    }
    else{
      if (frame.t[a,"BIC"]<1000){
        correct[d]<-NA
        BIC.fit[d]<-NA
      }
      else{
        if (frame.t[b,"BIC"]<1000){
          correct[d]<-NA
          BIC.fit[d]<-NA
        }
        else{
          if (frame.t[c,"BIC"]<1000){
            correct[d]<-NA
            BIC.fit[d]<-NA
          }
          else{
            if (frame.t[a,"BIC"]>frame.t[b,"BIC"] && frame.t[c,"BIC"] > frame.t[b,"BIC"] ){
              correct[d]<-1
              BIC.fit[d]<-"correct"
            }
            else{correct[d]<-0}
            if (frame.t[b,"BIC"]>frame.t[c,"BIC"] && frame.t[a,"BIC"]>frame.t[c,"BIC"] ){
              high[d]<-1
              BIC.fit[d]<-"high"
            }
            else{high[d]<-0}
            if (frame.t[c,"BIC"]>frame.t[a,"BIC"] && frame.t[b,"BIC"]>frame.t[a,"BIC"] ){
              low[d]<-1
              BIC.fit[d]<-"low"
            }
            else{low[d]<-0}
          }
        }
      }
    }
  }
}

```

```

    }
  }
  a<-a+3
  d<-d+1
}
}
}
}
}
}
}
}
}

```

```
summary(aBIC.selection)
```

```
BIC.selection<-cbind(frame.t[which(frame.t[, "classfit"]==1),1:4], low, correct, high, BIC.fit)
```

```
BIC.selection$mi <- factor(BIC.selection$mi, levels=c("1", "2", "3"), labels=c("No MI", "Mediator MI", "All MI"))
```

```
qplot(mi, data=BIC.selection, facets=N~loading, fill=BIC.fit, geom="bar", main = "Model Selection with BIC", ylab="Sample Size", xlab="Loading of Indirect Paths")
```

```
## End of BIC selection
```

```
##aBIC Selection
```

```
low<-NULL
```

```
high<-NULL
```

```
models<-NULL
```

```
aBIC.fit<-NULL
```

```
a=1
```

```
b=0
```

```
c=0
```

```
d=1
```

```
while (a < 36000){
```

```
  b<-a+1
```

```
  c<-a+2
```

```
  if (is.na(frame.t[a,"aBIC"])){
```

```
    correct[d]<-NA
```

```
    aBIC.fit[d]<-NA
```

```
  }
```

```
  else{
```

```
    if(is.na(frame.t[b,"aBIC"])){
```

```
      correct[d]<-NA
```

```
      aBIC.fit[d]<-NA
```

```
    }
```

```
  } else{
```

```
    if (is.na(frame.t[c,"aBIC"])){
```

```

correct[d]<-NA
aBIC.fit[d]<-NA
}
else{
  if (frame.t[a,"aBIC"]<1000){
    correct[d]<-NA
    aBIC.fit[d]<-NA
  }
  else{
    if (frame.t[b,"aBIC"]<1000){
      correct[d]<-NA
      aBIC.fit[d]<-NA
    }
    else{
      if (frame.t[c,"aBIC"]<1000){
        correct[d]<-NA
        aBIC.fit[d]<-NA
      }
      else{
        if (frame.t[a,"aBIC"]>frame.t[b,"aBIC"] && frame.t[c,"aBIC"] >
frame.t[b,"aBIC"] ){
          correct[d]<-1
          aBIC.fit[d]<- "correct"
        }
        else{correct[d]<-0}
        if (frame.t[b,"aBIC"]>frame.t[c,"aBIC"] &&
frame.t[a,"aBIC"]>frame.t[c,"aBIC"] ){
          high[d]<-1
          aBIC.fit[d]<- "high"
        }
        else{high[d]<-0}
        if (frame.t[c,"aBIC"]>frame.t[a,"aBIC"] &&
frame.t[b,"aBIC"]>frame.t[a,"aBIC"] ){
          low[d]<-1
          aBIC.fit[d]<- "low"
        }
        else{low[d]<-0}
      }
    }
  }
  models<-rbind(models,frame.t[a,1:4])
  a<-a+3
  d<-d+1
}
}
}
}

```

```

}

aBIC.selection<-cbind(frame.t[which(frame.t[,"classfit"]==1),1:4], low, correct, high,
aBIC.fit)

aBIC.selection$mi <- factor(aBIC.selection$mi, levels=c("1", "2", "3"), labels=c("No
MI", "Mediator MI", "All MI"))

qplot(mi, data=aBIC.selection, facets=N~loading, fill=aBIC.fit, geom="bar", main =
"Model Selection with aBIC",ylab="Sample Size", xlab="Loading of Indirect Paths")

## End of aBIC selection

##making tables
Mean <-function(x){
  mean(x, na.rm=T)
}

aBIC.correct <- aggregate(aBIC.selection[,"correct"],by=list(aBIC.selection$loading,
aBIC.selection$N, aBIC.selection$mi), Mean)

colnames(aBIC.correct)<-c("loading", "N", "mi", "correct")

aBIC.low <- aggregate(aBIC.selection[,"low"],by=list(aBIC.selection$loading,
aBIC.selection$N, aBIC.selection$mi), Mean)

colnames(aBIC.low)<-c("loading", "N", "mi", "low")

aBIC.high <- aggregate(aBIC.selection[,"high"],by=list(aBIC.selection$loading,
aBIC.selection$N, aBIC.selection$mi), Mean)

colnames(aBIC.high)<-c("loading", "N", "mi", "high")

aBIC.summary <-cbind( aBIC.low, aBIC.correct[,4], aBIC.high[,4])
colnames(aBIC.summary)<-c("loading", "N", "mi","low","correct", "high")
##

##BIC
BIC.correct <- aggregate(BIC.selection[,"correct"],by=list(BIC.selection$loading,
BIC.selection$N, BIC.selection$mi), Mean)

colnames(BIC.correct)<-c("loading", "N", "mi", "correct")

BIC.low <- aggregate(BIC.selection[,"low"],by=list(BIC.selection$loading,
BIC.selection$N, BIC.selection$mi), Mean)

```

```

colnames(BIC.low)<-c("loading", "N", "mi", "low")

BIC.high <- aggregate(BIC.selection[, "high"], by=list(BIC.selection$loading,
BIC.selection$N, BIC.selection$mi), Mean)

colnames(BIC.high)<-c("loading", "N", "mi", "high")

BIC.summary <- cbind( BIC.low, BIC.correct[,4], BIC.high[,4])
colnames(BIC.summary)<-c("loading", "N", "mi", "low", "correct", "high")
##

##AIC
AIC.correct <- aggregate(AIC.selection[, "correct"], by=list(AIC.selection$loading,
AIC.selection$N, AIC.selection$mi), Mean)

colnames(AIC.correct)<-c("loading", "N", "mi", "correct")

AIC.low <- aggregate(AIC.selection[, "low"], by=list(AIC.selection$loading,
AIC.selection$N, AIC.selection$mi), Mean)

colnames(AIC.low)<-c("loading", "N", "mi", "low")

AIC.high <- aggregate(AIC.selection[, "high"], by=list(AIC.selection$loading,
AIC.selection$N, AIC.selection$mi), Mean)

colnames(AIC.high)<-c("loading", "N", "mi", "high")

AIC.summary <- cbind( AIC.low, AIC.correct[,4], AIC.high[,4])
colnames(AIC.summary)<-c("loading", "N", "mi", "low", "correct", "high")

##Effectiveness of the Chi Square Cut off
prop.chisqtest<-bframe[ which(bframe[, "loading"]==0.30 &
bframe[, "N"]==300), "ChiSqM_p"]
list.results<-sapply(prop.chisqtest, function(x)if(x<.05){1}else{0})
mean(list.results) # 15%

prop.chisqtest<-bframe[ which(bframe[, "loading"]==0.30 &
bframe[, "N"]==800), "ChiSqM_p"]
list.results<-sapply(prop.chisqtest, function(x)if(x<.05){1}else{0})
mean(list.results) # 37%
##
results[1]

```

```
##Is a difference in Entropy corellated with correct model selection?
```

```
Ident.ent<-NULL
```

```
a=1
```

```
c=1
```

```
while (a<16001){
```

```
  b=a+1
```

```
  Ident.ent[c]<-frame.ent[b,"Entropy"]-frame.ent[a,"Entropy"]
```

```
  a=a+2
```

```
  c=c+1
```

```
}
```

```
  ##
```

```
  ##
```

```
##
```

```
AIC.summary <-cbind( AIC.low, AIC.correct[,4], AIC.high[,4])
```

```
colnames(AIC.summary)<-c("loading", "N", "mi", "low", "correct", "high")
```

```
##
```

```
##
```

```
library("eeptools",
```

```
lib.loc="/Library/Frameworks/R.framework/Versions/3.0/Resources/library")
```

```
AIC.summary<-AIC.summary[order(AIC.summary$loading, AIC.summary$mi,
```

```
AIC.summary$N) , ]
```

```
AIC.summary.table<-
```

```
cbind(AIC.summary[,1],AIC.summary[,3],AIC.summary[,2],AIC.summary[,4:6])
```

```
xtable(AIC.summary.table)
```

```
aBIC.summary<-aBIC.summary[order(aBIC.summary$loading, aBIC.summary$mi,
```

```
aBIC.summary$N) , ]
```

```
aBIC.summary.table<-
```

```
cbind(aBIC.summary[,1],aBIC.summary[,3],aBIC.summary[,2],aBIC.summary[,4:6]*1
```

```
00)
```

```
xtable(aBIC.summary.table)
```

```
BIC.summary<-BIC.summary[order(BIC.summary$loading, BIC.summary$mi,
```

```
BIC.summary$N) , ]
```

```
BIC.summary.table<-
```

```
cbind(BIC.summary[,1],BIC.summary[,3],BIC.summary[,2],BIC.summary[,4:6]*100)
```

```
xtable(BIC.summary.table)
```

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