

Evaluating Person-Oriented Methods for Mediation

by

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ABSTRACT

Statistical inference from mediation analysis applies to populations, however, researchers and clinicians may be interested in making inference to individual clients or small, localized groups of people. Person-oriented approaches focus on the differences between people, or latent groups of people, to ask how individuals differ across variables, and can help researchers avoid ecological fallacies when making inferences about individuals. Traditional variable-oriented mediation assumes the population undergoes a homogenous reaction to the mediating process. However, mediation is also described as an intra-individual process where each person passes from a predictor, through a mediator, to an outcome (Collins, Graham, & Flaherty, 1998). Configural frequency mediation is a person-oriented analysis of contingency tables that has not been well-studied or implemented since its introduction in the literature (von Eye, Mair, & Mun, 2010; von Eye, Mun, & Mair, 2009). The purpose of this study is to describe CFM and investigate its statistical properties while comparing it to traditional and casual inference mediation methods. The results of this study show that joint significance mediation tests results in better Type I error rates but limit the person-oriented interpretations of CFM. Although the estimator for logistic regression and causal mediation are different, they both perform well in terms of Type I error and power, although the causal estimator had higher bias than expected, which is discussed in the limitations section.

DEDICATION

Jesse, thank you for this opportunity. I love you always.

Professor Carr, thank you for showing me the Hopewell way.

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Introduction

Statistical mediation is a method useful for discovering the why or how treatment variables effect outcomes (MacKinnon, 2008). Statistical inferences from mediation analysis apply to populations, however, researchers and clinicians may be interested in making inferences to individual clients or small, localized groups of people. Person-oriented mediation methods can help researchers avoid ecological fallacies when making inferences about individuals, however there are few, well-studied methodologies in the literature. Configural frequency mediation is a person-oriented analysis of contingency tables that has not been well-studied or implemented since its introduction in the literature (von Eye et al., 2010; von Eye, Mun, & Mair, 2009). The aim of this study is to clarify the guidelines of CFM and investigate the method's statistical properties, comparing CFM to traditional mediation analysis and mediation from the potential outcomes framework.

First, I will introduce two competing research paradigms, which will be referred to as variable-oriented and person-oriented approaches. Next, I will give a historical overview of the person-oriented approach up to the present day. Limitations of the variable-oriented and person-oriented approaches will then be discussed. The next section will review mediation, including the case where X, M, and Y are binary, as well as an issue with dichotomization of variables. The binary X, M, and Y case is selected because it simplifies the application of person-oriented mediation methods. Mediation will also be discussed as both a variable-oriented and a person-oriented process. Several variable-oriented and person-oriented mediation techniques will be presented. Hypotheses

contrasting the performance of variable-oriented and person-oriented mediation will be proposed, and the simulations conducted to investigate these methods will be described. Finally, the results of the simulations will be presented along with a discussion of the study, including limitations and future directions.

Two Approaches to Psychology

There has been tension in how the study of human behavior is conceptualized. The prominent perspective reflects reductionist science, in which any system can be understood by first understanding its constituent parts. This intellectual paradigm has provided the framework for centuries of scientific breakthroughs, driving methodological and theoretical developments in nearly all scientific disciplines, including psychology. For psychologists, reductionism requires conceptualizing and measuring numerous constructs that are used to formulate theories and mathematical models of human behavior. This approach to psychology, from the perspective that behavior can be broken down and understood as the sum of its parts, has been referred to as the *variable-oriented approach* (Bergman, Eklund, & Magnusson, 1991; Block, 1971/2014; Bogat, von Eye, & Bergman, 2016; Magnusson & Bergman, 1988).

However, another approach to psychology accentuates a holistic view of human behavior. Within this approach, individuals are understood as complex, dynamic systems whose behaviors are the result of the interactions of a myriad of factors, including mental, physiological, and situational influences (Magnusson, 1988). Any particular behavior is not considered to be the sum of relevant, independent effects, but rather a manifestation

of complex interactions that may be particular to an individual, or group of individuals with similar patterns of scores on relevant measures (Bergman & Magnusson, 1997).

An important distinction for this holistic approach is that the similarity of individuals in a group is based on patterns of responses, and not on “natural” variable groupings such as gender, ethnicity, or treatment condition. An example of this kind of patterning is found in the diagnostic categories of the *Diagnostic and Statistical Manual of Mental Disorders (DSM)*. Each diagnostic category is characterized by an array of symptoms and patients may present these symptoms differentially. Heterogeneity in symptom patterns may be a factor in variability of treatment effectiveness (Bogat et al., 2016). This approach to psychology, from the perspective that behavior is the result of complex biopsychosocial interactions for individuals (Engel, 1977) is known by several comparable names, such as *person-oriented*, *person-centered*, or *interactional approach* (Bergman & Magnusson, 1997; Block, 1971/2014; von Eye & Bergman, 2003).

Variable-oriented and person-oriented approaches are distinguished by their primary units of analysis, which are the variables themselves in the variable-oriented approach, or patterns of variables in the person-oriented approach. Variable-oriented theories concentrate on *interindividual* variation that results from differences in variable or construct factors, such as personality traits, IQ, gender, etc. Person-oriented theories, on the other hand, focus on *intraindividual* variation that occurs within individuals across the spectrum of measured constructs.

History of Person-Oriented Methods in Psychology

The idea of a person-oriented system of study has been a recurring theme in psychology, proposed as an alternative research paradigm at various points in history. William Stern's work in differential psychology is an early influence for modern person-oriented psychology. His conceptualization of the individual as "unitas multiplex," or a single unit comprised of multiple parts, is a precursor to modern ideas of holistic, dynamic complexity in individual development (Bergman & Magnusson, 1997; Stern, 1923). In the 1930's, Kurt Lewin described individual behavior as an interaction between the person and the immediate environment, using the whole context of the environment as a "life space" within which behavior could be analyzed (Lewin, 1935/2013). Lewin's field theory emphasized the person by environment interaction, prevising the modern person-oriented focus on the myriad interconnections between biological, psychological, and social influences of human behavior. Jack Block, considered by some as the "father of the modern person-oriented approach" (Bogat et al., 2016), asserted that lawfulness and universality are separate attributes of human behavior, which is reflected in the modern principles of person-oriented psychology (Block, 1971/2014). As a prominent critic of the five-factor model of personality, Block asserted that because personality structures are inherently individualistic, a variable-centered method, such as factor analysis, is insufficient to describe personality (Block, 1995). More recently, David Magnusson and Lars Bergman have defined the person-oriented approach in terms of a "holistic, interactionist view, in which the individual is seen as an organized whole...formed by interactions among the elements involved..." (Bergman & Magnusson, 1997). Bergman and Magnusson's definition reflects the influences of early

proponents of the person-oriented approach, but also reveals the ambiguity and lack of precision that is still inherent in this approach to psychology. For instance, the lack of specificity of putative effects makes it difficult to define specific theories, testable hypotheses, or to make model comparisons (Bergman & Andersson, 2010; Sterba & Bauer, 2010). It could also be argued that a paradigm in which “everything interacts with everything” (Magnusson & Törestad, 1993, p. 447) and patterns are “not meaningfully reducible to their component parts” (Sterba & Bauer, 2010, p. 240) yields limited scientific usefulness. However, as specific methodological shortcomings are identified, such as underdeveloped pattern analysis methods, work can be done to refine theories and methods that are appropriate for the person-oriented approach (Bogat et al., 2016; Sterba & Bauer, 2010). Finally, building on the work of Gustav Lienert, Alexander von Eye has proposed Configural Frequency Analysis to methodologically define the person-oriented approach (Lienert & Krauth, 1975; von Eye, 2002). This method is discussed in detail below.

Related to the development of the person-oriented approach is the idiographic approach to psychology. The idiographic approach emphasizes the analysis of the individual, as compared to analysis of the aggregate, as in nomothetic psychology. Proponents of the idiographic approach include David Barlow and Peter Molenaar (Barlow & Nock, 2009; Molenaar, 2004). Molenaar points out that violations of ergodicity in psychological processes mean that results estimated from aggregated data will differ from results estimated within subjects (Molenaar & Campbell, 2009). This reduces generalizability from the aggregate to the individual and calls into question

psychological theories that are posited in terms of within-subject processes, but are tested using between-subject methods. Barlow emphasizes the importance of individual subject studies for improving evidence-based therapeutic practices (Barlow, Nock, & Hersen, 2009). Echoing Gordon Allport's call to return to the individual (Allport, 1962), Barlow et al. (2009) detail experimental strategies designed to maximize the scientific yield from single-subject studies.

While the contrasts between nomothetic and idiographic psychology and between variable-oriented and person-oriented approaches are related, the theories and methods of each contrasting pair are not necessarily exchangeable. That is to say, although variable-oriented approaches are related to nomothetic approaches, they are not necessarily synonymous. Likewise, person-oriented approaches and idiographic approaches have similar concerns about individual change, yet are distinct. Standard, variable-oriented methods and nomothetic approaches are easily categorized together because both focus on interindividual or between-subject variation; however, the relation between person-oriented methods and the idiographic approach is not as well defined. Idiographic and person-oriented approaches are both concerned with intraindividual, or within-subject, variation (Bergman & Magnusson, 1997; Molenaar, 2004), however, idiographic science focuses on intensive, single-subject analyses, like time-series or single-case experimental designs, to study individual differences and to inform evidence-based therapeutic practices (Barlow et al., 2009; Gast, 2010; Molenaar, 2004). In contrast, the person-oriented approach is more akin to nomothetic science because it is concerned with identifying general laws of human behavior (Bergman & El-Khoury, 2003; Bergman &

Magnusson, 1997). In this regard, the person-oriented and variable-oriented approaches are similar. However, the person-oriented approach assumes that psychological processes are fundamentally emergent and self-organizing, similar to biological processes like motor coordination (Kelso, 1995; Thelen, 1989). This assumption means that the person-oriented approach takes into account within-subject variation, acknowledges that there is also structure underlying between-subject variation, and expects a small number of stable groups of people to emerge from a given sample (Bergman & Magnusson, 1997).

Current State of Person-Oriented Science

In recent work, researchers have recognized that the connection between person-oriented theories and methods is underdeveloped (Sterba & Bauer, 2010). Attempts have been made to codify a set of principles that formally define the person-oriented approach and guide researchers in the development of complementary methods (Bergman & Magnusson, 1997; Bogat, 2009; Sterba & Bauer, 2010; von Eye, 2010; von Eye & Bergman, 2003). These principles largely follow the assumptions described by Bergman & Magnusson (1997) and are outlined here.

1. Psychological processes are, at least in part, unique to the individual, and the individual's environment.
2. These processes are determined by complex interactions.
3. Despite complexity, the variability of these processes is coherent within the individual. Furthermore, there is structure in the ways in which processes differ between individuals. This lawfulness is mirrored in the variability within the environmental context and between environmental contexts.

4. The coherence of the processes occurs through the pattern of interacting factors.
5. The factors themselves have meaning only in relation to all other factors.
6. Globally, there will be “common” patterns that occur more or less frequently than expected.
7. Aggregation of patterns is justified if dimensional identity (invariance) exists.
8. Interpretations of processes are particular to the individual and environment.

Recent empirical studies using person-oriented methods are typically descriptive and exploratory. Examples using configural frequency analysis are in Table 1.

Developments have been made in configural frequency analysis to account for mediation processes (von Eye et al., 2010; von Eye, Mun, & Mair, 2009) however, to the best of my knowledge, no empirical examples using configural frequency mediation analysis are in the literature.

Insert Table 1 about here

Critiques of Variable-Oriented Theory/Methods

The primary criticism of the traditional, variable-oriented approach is its inadequacies in estimating individual level parameters given aggregated data, and in drawing inferences from the aggregate to the individual. According to Campbell, this is an issue of external validity, specifically, the generalization of results from a sample to an individual case (Shadish, Cook, & Campbell, 2002). Instances where aggregated, or

group level data, lead to incorrect inferences concerning individual cases is known as an ecological fallacy (Robinson, 1950). This is contrasted with the atomistic or individualistic fallacy, which occurs when individual data leads to incorrect inferences about the population (Diez Roux, 2002). Distinguishing between within-subject and between-subject differences and correctly inferring to individuals and populations is an important part of understanding the roles of both variable-oriented and person-oriented methods in research.

An implicit assumption of the variable-oriented approach is that human behavior is governed by universal laws that can be discovered and understood by examining the component parts of behavior, emotion, and cognition. These “component parts” are the variables or constructs that are measured and analyzed in psychological research. If human behavior can be described in terms of universals, then drawing conclusions about individuals from aggregated data is appropriate and a traditional variable-oriented approach would be sufficient on its own. However, the importance of analyzing potential interactions and moderators is a recognized aspect of data analysis within the variable-oriented paradigm. This concession to individual differences suggests that the assumed universality of human behavior may be an incomplete view, and that results based only on variable-oriented research do not always tell a complete story.

Critiques of Person-Oriented Theory/Methods

A principle limitation of the person-oriented approach is a misunderstanding of how its theories and methods are distinct from variable oriented theories and methods (Bogat et al., 2016). Proponents of the person-oriented approach suggest viewing

variables holistically, with individual patterns of variables, rather than the variables themselves, as the focus of analysis (Bogat et al., 2016). However, this perspective often relies on descriptive interpretations and post hoc comparisons rather than specific hypothesis testing or model comparison (Bergman & Magnusson, 1997; Sterba & Bauer, 2010). Many person-oriented techniques are not model based, but rather focus on all possible data patterns. As a result, hypothesis testing is generally limited to particular aspects of the expected data structure (Bergman, Magnusson, & El-Khoury, 2003). Rather than appealing to an empirical distinction between the person-oriented and variable-oriented paradigms, researchers must make potentially untestable, a priori assumptions about individual processes in human behavior, the nature of sample heterogeneity, and the role of psychological science as a method of understanding that nature (Barlow & Nock, 2009; von Eye & Bogat, 2006).

Statistical Mediation - The Single Mediator Model

Statistical mediation analysis is a method for determining the causal mechanisms between two variables through the effects of a third variable, known as a mediator (MacKinnon, 2008). The mediator variable (M) transmits the effect of the independent variable (X) to the outcome variable (Y) and thereby accounts for either all or part of the effect of X on Y. For theory development, the implications of a mediational model includes two components, action theory and conceptual theory (Chen, 1990). Action theory describes the effects of the independent variable on the mediator while conceptual theory describes the effects of the mediator on the outcome variable. Statistically, these two effects comprise the *indirect effect* of X on Y. It is also possible that the independent

variable has an effect on the outcome variable that is independent of the mediator, which is called the *direct effect*.

Mediation analysis is based on a series of three linear regression equations (MacKinnon, 2008). The total effect of the independent variable on the outcome, which implicitly includes the contribution of the mediator, is represented by the c -coefficient in Equation 1, where \hat{Y} is the estimate of the outcome, X is the predictor, i_1 is the intercept and e_1 is the residual. The effect of the independent variable on the mediator, which corresponds with action theory, is found in the a -coefficient of Equation 2, where \hat{M} is the estimate of the mediator, X is the predictor, i_2 is the intercept and e_2 is the residual. Finally, the effect of the independent variable on the outcome variable while adjusting for the mediator is represented by the c' -coefficient in Equation 3, and the effect of the mediator on the outcome, while adjusting for the independent variable, is represented by the b -coefficient in Equation 3 where \hat{Y} is the estimate of the outcome, X is the predictor, M is the mediator, i_3 is the intercept and e_3 is the residual. Tests of mediation are conducted using two of the three equations. Equations 2 and 3 are used to test the product of coefficients a and b (MacKinnon, Lockwood, Hoffman, West, & Sheets, 2002). Equations 1 and 3 are used to test the indirect effect as the difference of coefficients c and c' .

$$\hat{Y} = i_1 + cX + e_1 \quad (1)$$

$$\hat{M} = i_2 + aX + e_2 \quad (2)$$

$$\hat{Y} = i_3 + c'X + bM + e_3 \quad (3)$$

Single Mediator Model with Binary X, M, and Y

A basic case of mediation occurs when X, M, and Y are all binary variables. The binary X, M, and Y case is advantageous for investigating a person-oriented approach because there are only eight possible patterns for the three variables. Each pattern expresses either a ‘yes’ or ‘no’ value (represented by a 1 or 0, respectively) for each variable. For example, X=0, M=0, Y=0 codes the case where X, M, and Y are all ‘no’. Likewise, X=0, M=0, Y=1 codes the case where X and M are ‘no’ and Y is ‘yes.’ Table 2 enumerates the eight possible combinations.

 Insert Table 2 about here

Adjusting for Dichotomization of Continuous Variables

The dichotomization of continuous variables results in the loss of information. However, dichotomization also provides a way to explore person-oriented methods in the basic case of mediation described above. The variance accounted for when two variables are dichotomized is equal to .405 times the variance explained between two continuous variables (Cohen, 1983). The general formula for adjusting a correlation for dichotomization is shown in Equation 4. The equation for *e* is a function of *h*, the height of the standard unit normal curve at the point of dichotomization and *p*, the proportion of observations contained within either one of the intervals (Cohen, 1983).

$$e = \frac{h}{[p(1-p)]} \tag{4}$$

In the case of dichotomizing at the mean, $e = .798$. When both variables in a correlation are dichotomized in this way, the correction factor must be applied twice, resulting in $e = .798^2 = .636804$, meaning that the observed correlation between the dichotomized variables is approximately $.637r$, where r is the observed correlation between the continuous variables. Adjusting for r^2 means that $.637$ will also be squared, which is $.405$, as described above. In the case of simulated data generation, the population values of r can be divided by the value of e to correct for correlation attenuation.

Moving from Variable to Person-Oriented Mediation

Traditional mediation from a variable-oriented approach assumes a homogeneous mediating process within the population. Each person undergoing the mediation process will do so at the same rate and to the same degree. The focus of this type of mediation analysis is whether there is evidence that X causes M, and M causes Y. Variables are the focus of analysis, not individuals. A hypothetical example is an intervention designed to alter social norms associated with underage alcohol consumption. In this example, the independent variable (X) represents inclusion in either a treatment or control group, the mediator (M) is social norms about underage alcohol consumption, and the outcome variable (Y) is alcohol consumption. Variable-oriented mediation can answer whether the intervention influences social norms, and if social norms affect alcohol consumption. Analysis would focus on variables, specifically, variation between X, M and Y.

Mediation at the level of the person (or latent groups of people) is an intra-individual process that can occur differently within individuals (Collins et al., 1998). In

terms of the hypothetical alcohol example above, person-oriented mediation assumes that individuals react differently to the intervention as well as the social norms that are changed by the intervention. It is possible that some people may reduce alcohol consumption with norm change and others may increase alcohol consumption in response to the same norm change.

To move from variable to individual oriented mediation, it is useful to consider the eight patterns from Table 2. These patterns can represent eight groups of people who respond differentially to the X and M variables. The frequency with which these patterns occur, particularly those patterns that are deemed consistent with mediation, is a primary consideration in developing person-oriented methods for mediation because it can quantify heterogeneity in the mediation process.

Mediation Techniques

Four mediation techniques for the case of binary X, M and Y are described below. Logistic regression and causal mediation are both variable-oriented approaches that focus on variation at the level of the variable. The stage sequential method and configural frequency analysis are person-oriented approach in which mediation is considered an individual process and the focus of analysis is on variation among patterns of variables. Logistic regression is the conventional method used when Y is binary (MacKinnon, 2008). Causal estimators are non-parametric, allowing for both linear and non-linear estimation of mediation with causal interpretations (Pearl, 2012). The stage sequential method identifies patterns of mediation based on probabilities of an individual moving through stages of X, M, and Y (Collins et al., 1998). Configural frequency analysis,

determines mediation by comparing residuals in a series of log-linear models that collectively account for the relationships between X, M, and Y (von Eye et al., 2010).

Logistic regression. When analyzing data that includes a binary dependent variable, it is necessary to think in terms of the probability of an observation in a particular category of the dependent variable, rather than taking on a certain value of the variable. Modeling data with linear regression requires a transformation of the probability into a form suitable for the generalized linear model. This is accomplished by using the logit link function. The logit is the natural logarithm of the odds ratio and it is the outcome variable in a logistic regression of the form found in Equation 5, where \hat{p} is the observed probability of that the binary dependent variable takes on a value of 1, β_0 is the regression intercept, and β_1 is the regression coefficient relating X to Y.

$$\ln\left(\frac{\hat{p}}{1-\hat{p}}\right) = \beta_0 + \beta_1 X + e \quad (5)$$

Mediation analysis with binary X, M and Y variables can be accomplished using a system of logistic regression equations corresponding to Equations 1-3 (MacKinnon, 2008).

$$\ln\frac{\hat{p}(Y=1)}{(1-\hat{p}(Y=1))} = i_1 + cX + e_1 \quad (6)$$

$$\ln\frac{\hat{p}(M=1)}{(1-\hat{p}(M=1))} = i_2 + aX + e_2 \quad (7)$$

$$\ln\frac{\hat{p}(Y=1)}{(1-\hat{p}(Y=1))} = i_3 + c'X + bM + e_3 \quad (8)$$

The coefficients in Equations 6-8 are in the metric of the natural logarithm of the odds ratio. To aid researchers in interpretation, these values are converted to odds ratios by taking the antilogarithms of the coefficients.

The mediated effect can be estimated using either the product of coefficients (ab) or the difference of coefficients ($c-c'$) as in the standard single mediator model. However, in the case of logistic regression, these estimates are not equivalent (MacKinnon & Dwyer, 1993).

Causal estimators. The effects of the single mediator model can also be estimated based on the potential outcomes perspective (Pearl, 2012). In this case, frequencies are combined to make proportions that represent the total, direct, and indirect effects. Before calculating the total, direct, and indirect effects as summarized by Pearl (2012), six intermediate proportions are calculated based on the eight frequencies in Table 2. In the following equations, $g_{x,m}$ is expected values of Y given values of X and M, h_x is the expected value of M given X, and n_i is the frequency of observations for each of the eight possible combinations of X, M, and Y. Equation 9 represents the expected value of Y, given a “no” value on both X and M, or proportion of cases in the control condition that do not have the mediator, but do have the outcome ($g_{x,m} = g_{0,0}$). Similarly, Equation 10 represents the expected value of Y, given a “no” value on X and a “yes” value on M, or the proportion of cases in the control condition that have both the mediator and the outcome ($g_{0,1}$). Equations 11 and 12 mirror Equations 9 and 10 for the treatment group ($g_{1,0}$ and $g_{1,1}$, respectively). Equations 13 and 14 represent the expected value of M in the

control and treatment groups, respectively, or the proportion of cases in each condition that have the mediator, and any value of Y (h_0 and h_1).

$$g_{0,0} = \frac{n_2}{n_1 + n_2} \quad (9)$$

$$g_{0,1} = \frac{n_4}{n_3 + n_4} \quad (10)$$

$$g_{1,0} = \frac{n_6}{n_5 + n_6} \quad (11)$$

$$g_{1,1} = \frac{n_8}{n_7 + n_8} \quad (12)$$

$$h_0 = \frac{n_3 + n_4}{n_1 + n_2 + n_3 + n_4} \quad (13)$$

$$h_1 = \frac{n_7 + n_8}{n_5 + n_6 + n_7 + n_8} \quad (14)$$

From these intermediary proportions, the total effect (TE), direct effect (DE) and indirect effect (IE) are calculated, as in Equations 15, 16, and 17.

$$TE = g_{1,1}h_1 + g_{1,0}(1-h_1) - [g_{0,1}h_0 + g_{0,0}(1-h_0)] \quad (15)$$

$$DE = (g_{1,0} - g_{0,0})(1-h_0) + (g_{1,1} - g_{0,1})h_0 \quad (16)$$

$$IE = (h_1 - h_0)(g_{0,1} - g_{0,0}) \quad (17)$$

These equations and their standard errors can be estimated with several computer programs. The PROC CAUSALMED procedure in SAS will be used to estimate these direct and indirect effects in this study (SAS Institute Inc., 2017; VanderWeele, 2014).

Stage sequential method. Implicit in the definition of statistical mediation is the temporal precedence of X to M and of both X and M to Y. In order for there to be a causal sequence between the three variables, they must occur in three temporally distinct stages. This is a foundational premise of the Stage Sequential Method (Collins et al., 1998) and is explicit in the defining conditions. Within this framework, a *mediation pattern* is defined as a case wherein an individual moves from having the mediator (M=1) to having the outcome (Y=1). To assess whether mediation has occurred, three conditions must be met (Collins et al., 1998):

1. It is more probable for an individual in the treatment group (X=1) to move from not having either the mediator or outcome at stage 1 (M=0, Y=0) to having both the mediator and outcome in stages 2-3 (M=1, Y=1).
2. It is more probable for an individual in the treatment group (X=1) to move from not having the mediator at stage 1 (M=0) to having the mediator at stage 2 (M=1).
3. It is more probable to move from having the mediator (M=1) to having the outcome (Y=1) than it is to move from *not* having the mediator (M=0) to having the outcome (Y=1) in both the treatment and control groups.

These three conditions are analogous to the effects discussed in the traditional single mediator model. The first condition establishes the logical precedence for mediation because it is assumed that in a mediation process the independent variable affects the mediator, which in turn affects the outcome variable. For this to be the case, it is logical to assume that the mediation pattern is more likely to occur in a treatment

condition ($X=1$). The second condition is comparable to the a -coefficient in Equation 2, which quantifies the effect of the independent variable on the mediator. The last condition is comparable to the b -coefficient in Equation 3, which quantifies the effect of the mediator on the outcome variable, controlling for X .

Collins et al. (1998), presents the following formalization of the three conditions of stage sequential mediation, letting X , M , and Y be $X=1$, $M=1$, and $Y=1$, respectively. Let \check{X} , \check{M} , and \check{Y} be $X=0$, $M=0$ and $Y=0$, respectively. Finally, let S_1, S_2 , and S_3 stages 1, 2, and 3, respectively.

$$P(M_{S_2} \text{ and } Y_{S_3} | X, \check{M}_{S_1}, \check{Y}_{S_1}) > P(M_{S_2} \text{ and } Y_{S_3} | \check{X}, \check{M}_{S_1}, \check{Y}_{S_1}) \quad (18)$$

$$P(M_{S_2} | X, \check{M}_{S_1}) > P(M_{S_2} | \check{X}, \check{M}_{S_1}) \quad (19)$$

$$\begin{aligned} P(Y_{S_3} | X, M_{S_{1or2}}, \check{Y}_{S_1}) > P(Y_{S_3} | X, \check{M}_{S_{1or2}}, \check{Y}_{S_1}) \text{ and} \\ P(Y_{S_3} | \check{X}, M_{S_{1or2}}, \check{Y}_{S_1}) > P(Y_{S_3} | \check{X}, \check{M}_{S_{1or2}}, \check{Y}_{S_1}) \end{aligned} \quad (20)$$

The stage sequential method defines mediation as a chain reaction where X affects M and then M affects Y . This differs from the conventional definition because the stage sequential method does not require an overall effect to be present (Collins et al., 1998). The stage sequential method is conceptually significant to the question of person-oriented mediation; however, it requires at least three waves of longitudinal data to test all three defining conditions. Since this study is not explicitly concerned with longitudinal data, and to the best of my knowledge this method has not been used since the original publication, the stage sequential method will not be evaluated in this study.

Configural frequency analysis. When predictors and outcomes are all categorical, as in the case of binary X , M and Y , analysis of the resulting contingency table can provide

estimates of association between variables. Configural frequency analysis is a method of estimating associations between patterns of variables, rather than between the variables themselves, distinguishing it as a person-oriented method (Lienert & Krauth, 1975; von Eye, 1990). A benefit of configural frequency analysis is that it provides a method of hypothesis testing through the comparison of expected and observed cell frequencies. Cell frequencies are modeled with log-linear regressions, beginning with the estimation of a base model that includes all expected effects. The resulting cell frequencies are then compared with the observed data and differences are tested for significance. Cell frequencies that are significantly higher than expected are *types* and those that are significantly lower than expected are *antitypes* (von Eye, 1990). Any resulting types and antitypes can then be interpreted in light of substantive context. For example, a study of risk and resilience in women experiencing domestic violence found two types and one antitype in a contingency table that included a woman's current symptom status with both her symptom status and victim status from the previous year (Von Eye, Mun, & Bogat, 2009). Symptom status was designated as either having or not having clinical level anxiety and/or depression. Victim status was designated as either being or not being a victim of domestic violence. The first type was found among women who had previous clinical symptoms, current clinical symptoms, and no previous violence. The second type included women who had both previous and current clinical symptoms as well as previous violence. The antitype included women who had no clinical symptoms at either time point, and no violence. An interpretation of the types and antitypes suggest that women with previous clinical symptoms of depression and/or anxiety are more likely to

have those symptoms a year later, regardless of previous violent experience, while women without previous symptoms or violence are less likely to have symptoms a year later (Von Eye, Mun, & Bogat, 2009).

Conducting mediation analysis within the configural frequency framework involves the estimation and comparison of four base models, with each model incorporating different aspects of the possible X, M and Y associations. Each test of one of the base models with the observed data reveals partial information about the three-variable system, specifically concerning whether or not certain pathways among the variables exist. The results of these four significance tests are then compared to each other to provide a view of the complete three-variable system. Formally, configural mediation analysis consists of (1) associations between X, M, and Y, which are identified through the existence of types and antitypes; (2) rules that identify the existence of mediation; and (3) rules that identify whether mediation is partial or complete (von Eye et al., 2010; von Eye, Mun, & Mair, 2009).

The first base model, shown in Equation 21 accounts for the main effects of X, M, and Y. In these equations, o refers to the observed frequency, \hat{o} refers to predicted frequency, and λ^j refers to the relation between variable j and the predicted frequency. When observed frequencies significantly deviate from the frequencies expected under this model, then there are possible associations between X and M, X and Y, M and Y, or among all three. The existence of types or antitypes in this comparison is a logical prerequisite for mediation.

$$\log \hat{o} = \lambda + \lambda^X + \lambda^M + \lambda^Y \quad (21)$$

Equation 22 illustrates the second base model, which accounts for the main effects of X, M, and Y as well as an interaction between X and M. When types or antitypes emerge from this model, then there are potential associations between X and Y, or M and Y (or both).

$$\log \hat{\phi} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} \quad (22)$$

The third base model, Equation 23, accounts for the three main effects, and interactions between X and M, as well as X and Y. This model implies that significant frequency deviations are the result of an association between M and Y.

$$\log \hat{\phi} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{XY} \quad (23)$$

Finally, the fourth base model, Equation 24, accounts for the three main effects and interactions between X and M as well as M and Y. If types and antitypes emerge when testing this model, then there is an association between X and Y.

$$\log \hat{\phi} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{MY} \quad (24)$$

According to von Eye et al. (2010) there is evidence for mediation if types and antitypes emerge from the testing of the four base models. To identify whether full or partial mediation exists, they suggest three further comparisons. First, comparing the results from test two and test three can reveal whether or not a *b* pathway exists between M and Y. Next, the existence of the *a* path can be determined by comparing test one to all of the other three tests. Finally, the effects of the three-way interaction of X, M and Y should be considered as an alternative reason for types and antitypes to exist in the tests of the base models (von Eye et al., 2010).

Hypotheses

Study 1: It was expected that under variable-oriented data generation, logistic regression and the causal mediation model would outperform configural mediation analysis in terms of power and Type 1 error rates. It was expected that the causal mediation model will outperform logistic regression in terms of parameter bias since it accounts for any interaction between X and M. Parameter bias comparisons were not be made for configural mediation analysis because this method does not directly estimate values a , b , and c' .

Study 2: It was expected that under person-oriented data generation, configural mediation analysis would outperform logistic regression and the causal mediation model in both power Type 1 error rates. It was also expected that the causal mediation model will outperform logistic regression in terms of parameter bias.

Method

Simulation Description

The SAS RANNOR function was used to generate continuous variables for X, M, and Y from a normal distribution with a mean of zero and variance of one. The current computer time was used as the seed. The X variable was randomly generated and then dichotomized at zero to create a binary predictor variable. Continuous values for M were generated using Equation 2 and the binary value for X. Coefficient values were systematically varied and the error term was generated with the RANNOR function . The M variable was then dichotomized at zero to create a binary variable. Continuous values for Y were generated using Equation 3 and the binary X and continuous M values. Coefficient values were systematically varied and the error term generated with the

RANNOR function. The Y variable was then dichotomized at zero to create a binary variable. Finally, each observation was coded as one of eight categories based on the combination of binary X, M, and Y values in Table 2.

Initial parameter values for a , b , and c' were chosen to correspond to effect sizes of zero, small, medium, and large (Cohen, 1988). Since dichotomization results in a loss of information and a reduction in the r^2 values between each pair of variables (Cohen, 1983), the effect sizes were adjusted according to Cohen's formula as described in Equation 4. The coefficient effect size levels were 0, .35, .96, and 1.46. Samples sizes were 300 and 900 observations, which were chosen to facilitate estimation. Mediation analysis was conducted with logistic regression, configural frequency mediation, and a causal inference model. For each condition, there will be 1,000 replications.

A second dataset was generated in the same manner described above, with the exception that each condition was made up of three sub-groups of data. One sub-group was generated with parameter values of zero for a , b , and c' . The second sub-group was generated with parameter values of 1.46, 1.46, and 0, which corresponds to a large mediated effect. The third sub-group was generated with parameter values of 0, 0, 1.46, which corresponds to a large direct effect, but no mediated effect. The data files for each of these sub-groups were combined into a single dataset to create a single simulation condition. Sample sizes for the sub-groups were 100, 300, and 900 observations so the total sample sizes were 300, 900, and 2700, respectively. 1,000 replications were run for each sub-group.

To examine whether dichotomization of the raw data biased the results, a third dataset was generated from a binomial distribution using the SAS RANBIN function. A binary variable X was generated with a mean of .5 and variance .25. The probability for a binary variable, M, was defined by Equation 25, where $p(M)$ is the probability of the mediator, and the term $(i_2 + aX)$ is from Equation 2. The probability for a binary variable, Y was defined by Equation 26, where $p(Y)$ is the probability of the outcome, and the term $(i_3 + c'X + bM)$ is from Equation 3. These probabilities were used to generate binary values for M and Y.

$$p(M) = \frac{1}{1 + e^{-(i_2 + aX)}} \quad (25)$$

$$p(Y) = \frac{1}{1 + e^{-(i_3 + c'X + bM)}} \quad (26)$$

To create a binomial generated dataset that was similar to the original, dichotomized data, the average logistic regression estimates from the original data were used as model true values in the binomial generated data. Table 3 shows the true effect sizes used to generate the normal data and the corresponding average logistic regression effects that were used to generate binomial data.

 Insert Table 3 about here

Calculation of Type I Error Rate and Empirical Power

Type I error is the probability that a significant effect is detected when there is not a true effect in the population. Type I error was calculated as the proportion of

replications for each condition in which the parameter estimates are found to be statistically significant ($\alpha = .05$) when the true population value is known to be zero. Values between .025-.075 are considered acceptable for Type I error (Bradley, 1978).

Empirical power is the probability that a significant effect is detected when there is a true effect in the population. Power was calculated as the proportion of replications for each condition in which the parameter estimates are found to be statistically significant ($\alpha = .05$) when the true population value is known to be nonzero. The minimum acceptable rate of detection was .80, commensurate with current discipline standards (Cohen, 1988).

Logistic regression. Equations 7 and 8 were estimated using logistic regression and the mediated effect was calculated as the product of the a and b coefficients.

The Sobel standard error of the mediated effect was calculated using Equation 29 and a p-value calculated from the z-score from Equation 30. In these equations, SE_{ab} is the standard error of the product, ab , a and b are regression coefficients from Equations 7 and 8, SE_a is the standard error of the a coefficient, SE_b is the standard error of the b coefficient, and z_{ab} is the z-score for the product, ab .

$$SE_{ab} = \sqrt{a^2 SE_b^2 + b^2 SE_a^2} \quad (29)$$

$$z_{ab} = \frac{ab}{SE_{ab}} \quad (30)$$

The frequency of replications with p-values less than or equal to .05 was computed for each condition, which indicates a statistically significant estimate of the mediated effect. The number of replications with a significant mediated effect was

divided by the number of replications in each parameter combination conditions (1,000). For parameter combination conditions with no true mediated effect, this is the Type I error rate. For parameter combination conditions with a true mediated effect, this quotient is statistical power.

The conditions in the second study are made up of three subgroups representing three subpopulations. One third of each condition consists of simulated cases with no true effects. One third consists of cases that are simulated with a large mediated effect. The final third of each condition consists of cases with a large direct effect, but no mediated effect. Combining the three subgroups together and treating the data as coming from a single population means the mediated effect would be the average true mediated effect of the three subgroups. Since at least one of the subgroups in each condition has a true mediated effect, each condition has a mediated effect, and Type I error is not applicable. Therefore, only statistical power is reported for study two.

The mediated effect was estimated in the same manner as study one. Logistic regression was used to estimate Equations 7 and 8 and the product of coefficients a and b was computed as the mediated effect. The Sobel standard error was calculated and used to compute a z -score and p -value for the mediated effect. The frequency of replications with p -values less than or equal to .05 was computed for each condition and then divided by the total number of replications in each condition.

Configural Frequency Mediation. Equations 21 through 24 were estimated using log-linear regression as the four base models of configural frequency mediation.

For each of the eight cells in each of the four models, a z-score was computed using Equation 25.

$$z = \frac{\text{observed frequency} - \text{predicted frequency}}{\sqrt{\text{predicted frequency}}} \quad (25)$$

A two-tailed significance test with a Bonferroni adjustment was conducted to test for significant differences between the observed and predicted frequencies in each cell. Cells with a z-score greater than 2.7344 were coded 1 to distinguish them as types, or cells with a greater than expected frequency. Cells with a z-score less than -2.7344 were coded -1 to distinguish them as anti-types, or cells with a lower than expected frequency. Non-significant cells were coded 0.

The resulting dataset of types and antitypes were then analyzed using a set of decision rules based on the comparisons in von Eye, et al (2010). The exact procedures for CFM are unclear, so the most reasonable interpretations of the analysis were defined and are presented here.

Determining if Mediation is Possible

CFM begins by testing the feasibility of mediation. This is accomplished by estimating the main effects log-linear model in Model 1. A chi-square test is conducted to determine the goodness of fit of this model. If it fits well, then it is not possible that any of the mediation pathways exist, and the mediation analysis stops. If Model 1 does not fit, then mediation is a possible explanation and further examination of the data is warranted. Misfit in Model 1 does not guarantee that a mediation process is at work in the data, but

merely fails to rule mediation out as a possibility. Therefore a series of models are estimated and logical comparisons are necessary to determine why the data do not conform to a main effects only model. All of the steps described below assume that Model 1 does not fit.

Evidence for the *b*-Path

An association between M and Y indicates that the *b*-path in the single mediator model exists. This is a necessary component in assessing statistical mediation and represents the conceptual theory, or how a mediator effects an outcome. In CFM, this association is inferred by estimating Model 3 and examining any residuals. Since Model 3 includes both the *a*-path and the *c'*- path but excludes the *b*-path, any residuals in Model 3 may be attributed to the existence of the *b*-path. If there are no residuals in Model 3, then there is no evidence that the *b*-path exists, and mediation is not possible.

Evidence for the *a*-Path

An association between X and M indicates that the *a*-path of the single mediator model exists. This path represents the action theory of mediation, or how a predictor effects a mediator. This is a necessary component in assessing mediation. In CFM, this association is inferred by comparing the pattern of residuals from Model 1 against the patterns of residuals in Models 2 through 4. If Model 1 has residuals, then one possible explanation is that the *a*-path exists. In order to rule out competing possibilities, the pattern of residuals in Model 1 is compared to the other models. When considered as a set, the other three models account for all other possible effects from the single mediator model. Therefore, if the pattern of residuals in Model 1 is different from the patterns in

any of the other models, it is inferred that the residuals are a result of the X-M association. That is to say, the only difference between Model 1 and the other three models is that Model 1 excludes the *a*-path and the other models include the *a*-path.

Evidence for the *c*-Path

An association between X and Y indicates that the *c*-path in the single mediator model exists. This association is not necessary for a mediation process to be detected, however, it can be used to distinguish between full or partial mediation. In CFM, the association between X and Y is inferred by estimating Model 4. Since Model 4 includes both the *a*-path and the *b*-path, any residuals from this model could be attributable to the *c*-path. In contrast, if there are no residuals from Model 4, it can be concluded that the *c*-path does not exist.

Full Mediation, Partial Mediation, and Direct Effects Models

According to von Eye et al. (2010), it is also necessary to estimate Model 2 and compare the residuals from Model 2 with Model 3. Testing Model 2 provides information about whether X and/or M are predictors of Y, but it does not provide specific information about those associations. This is because Model 2 includes only the *a*-path, and excludes both the *b* and *c*' paths. Therefore residuals in Model 2 indicate that either the *b*-path, the *c*'-path or both paths may exist. When Model 2 is considered in conjunction with Model 3, then distinctions can be made between full mediation, partial mediation, or a direct effects only model.

Based on these decision rules, the frequency of replications that were determined to have either full or partial mediation was calculated and divided by the total number of

replications in each condition (1,000). For conditions with no true mediated effect, this is the Type I error rate. For conditions with a true mediated effect, this is statistical power.

In the second study, the existence of a mediated effect was determined in the same manner as study one. Four log-linear base models were estimated from the frequency of cases that fell into one of eight combinations of binary X, M, and Y. The observed frequencies were compared to the predicted frequencies in each cell to determine significant differences, which were coded as either types and antitypes. The pattern of types and antitypes were then analyzed using a set of decision rules based upon the comparisons in von Eye, et al (2010). The frequency of replications that were determined to have either full or partial mediation was calculated and divided by the total number of replications in each condition.

Joint Significance Test with CFM.

The configural frequency mediation approach specified in von Eye, et al (2010) is based on the causal steps method (Baron & Kenny, 1986). This method is inferior to the joint significance test in regards to Type I error and power (MacKinnon et al, 2002). Given the pattern of results using the original CFM decision rules, further analyses were conducted to determine the significance of the *a* and *b* paths separately, as in a joint significance test. The logic of configural frequency mediation was used to determine which log-linear base models should be compared to determine the existence of the *a* and *b* paths.

The following process was used to conduct a series of significance tests between competing log-linear models. The logic of configural frequency mediation implies that

significant differences between two models suggests the plausible existence of any effects that are in the more complex model but not in the simpler one. The *a*-path and *b*-path were tested separately by computing a chi-square difference test between two models in which the path in question was the only specified difference. For each path, Type 1 error and power were calculated by dividing the number of significant replications by the total number of replications. If the *a* and *b* paths were both significant, the conclusion was that a mediated effect was present. Type 1 error and power for the mediated effect was determined by dividing the number of replications with a mediated effect by the total number of replications. A full list log-linear models used is in Appendix A.

Causal Inference Mediation

Causal estimates for both studies were obtained by modeling Equations 1 and 2 in PROC CAUSALMED. The true natural indirect effect (TNIE) was used as a comparison to the traditional product of coefficients mediated effect. A significance test was conducted for the TNIE using Wald confidence intervals. The frequency of replications with confidence intervals that did not include zero was calculated. This frequency was then divided by the total number of replications (1000). For conditions without a true mediated effect, this is the Type I error rate. For conditions with a true mediated effect, this is statistical power.

Accuracy of Point Estimates

Analysis of logistic regression and causal mediation included calculations of bias. An unbiased parameter estimate means that, on average, the estimates will match the true

population value (Cohen, Cohen, West, & Aiken, 2003). Therefore, bias was calculated as the difference of the average parameter estimates for each of the 1,000 replications and the known true population value designated in the simulation. Equation 26 shows this calculation, where $\hat{\theta}$ is the parameter estimate and θ is the true value of the parameter. Relative bias was calculated by dividing the bias found in Equation 26 by the true value of the parameter estimate, as in Equation 27. Standardized bias was calculated as the difference between the parameter estimate and the true population value, divided by the standard deviation of the parameter estimate, as in Equation 28.

$$\text{bias } (\hat{\Theta}) = E(\hat{\Theta}) - \Theta \quad (26)$$

$$\text{relative bias } (\hat{\Theta}) = \frac{E(\hat{\Theta}) - \Theta}{\Theta} \quad (27)$$

$$\text{standardized bias } (\hat{\Theta}) = \frac{E(\hat{\Theta}) - \Theta}{SD_{\hat{\Theta}}} \quad (28)$$

Results

Study 1

Convergence

The models in study 1 across all methods converged, with a software warning in a very small percentage of cases. For logistic regression, 99.9% of the models from Equations 1 and 2 converged, while 100.0% of the models from Equations 3 converged. Less than 1.0% of the models from both Equations 1 and 2 had possible quasi-complete data separation. The four CFM base models and the models used in the joint significance tests all had at least 99.9% convergence. In each model, less than 1.0% did not converge when the likelihood did not improve after 10 halvings. For causal mediation, both the mediator and outcome models had at least 99.9% convergence. Less than 1.0% of the models, resulted in warnings for ridging of the Hessian matrix.

Type I Error

Logistic regression. Table 2.A shows average Type I error rates for combinations of the a and b parameters marginalized over values of c' . The overall Type I error for logistic regression was .034 for $N = 300$ and .039 for $N = 900$. For both $N = 300$ and $N = 900$, Type I error rates were below .075 in all parameter combinations but fell below .025 when both a and b were zero. Type I error rates fell below .025 for $N=300$ when a was small, and b was zero. Table 2.B shows Type I error rates for the binomial generated data, which show the same pattern of results as data generated from the normal distribution, within rounding error.

Configural frequency mediation. Table 2.A shows Type I error rates for combinations of the a and b parameters. For all parameter conditions and sample sizes, Type I error fell outside the nominal range of .025-.075, with some parameter combinations being too high and others being too low. The overall Type I error rates for configural frequency mediation were high at .283 for $N = 300$ and .349 for $N = 900$. However, conditions where the b effect was nonzero had considerable influence on the error rate. When a was zero and b was medium or large in the small sample, Type I error rates were high. In the large sample, Type I error rates were high in all conditions where a was zero and b was nonzero. In contrast, when b was zero, Type I error rates were below .025 for both $N = 300$ and $N = 900$. Table 2.B shows Type I error rates for the binomial generated data, which show the same pattern of results as data generated from the normal distribution, within rounding error.

Causal inference mediation. Table 4.A shows Type I error rates for combinations of the a and b parameters. For all conditions across both sample sizes, Type I error was below .075. For $N = 300$, overall Type I error was .015. For $N = 900$, the overall Type I error was .030. For $N = 300$, all but one parameter combination had Type I error below .025. Only when a was large and b was zero did the Type I error fall within the nominal range. For $N = 900$, only two parameter combinations were below .025, when both paths were zero, and when a was small and b was zero. Table 4.B shows Type I error rates for the binomial generated data, which show the same pattern of results as data generated from the normal distribution, within rounding error.

Insert Tables 4.A-4.B about here

Power

Logistic regression. Table 5.A shows statistical power as the magnitude of mediated effect increases. The magnitude of mediated effect is a function of both the a and b coefficients. The parameter combinations are listed with the smaller a coefficient listed first. As expected, power increased with sample size in each parameter combination. For $N = 900$, power was close to one in all parameter combinations. For $N = 300$, power was below .80 in three parameter combinations that had a small a effect. These included two with the smallest mediated effects. In these conditions, power tended to increase as the b coefficient increased. When both a and b were small, power was only .62. When a was small and b was medium or large, power was .77.

There was an unexpected pattern in two parameter combination, where the smaller effect had greater power. When a was medium and b was small, the product of coefficients was 1.51 and power was .93. However, when a was small and b was large, the product of coefficients was 1.69, and power was .77. Table 5.B shows power for the binomial generated data, which show the same pattern of results as data generated from the normal distribution, within rounding error.

Configural frequency mediation. Table 5.A shows that statistical power increased as the mediated effect increased. Power increased with sample size across all combinations of a and b . For both $N = 300$ and $N = 900$, power was above .80 whenever

b was medium or large. However, when the *b* effect was small, power was very low, ranging from .05-.13 for $N = 300$, and ranging from .58-.64 for $N = 900$. Given these results, it appears the magnitude of the *b*-path is more important than the *a*-path for the power of CFM to detect mediation. Table 5.B shows power for the binomial generated data, which show the same pattern of results as data generated from the normal distribution, within rounding error.

Causal inference mediation. Table 5.A shows that statistical power increased as the mediated effect increased. For $N = 300$, power exceeded .80 in two parameter combinations, when *a* was medium and *b* was medium (0.842) and when *a* was medium and *b* was large (0.817). However, power did not increase monotonically as the mediated effect increased. Power was .25 when *a* was small and *b* was large, even though the magnitude of the effect was similar to the conditions when *a* was medium and *b* was small, which had a power of .71. In addition, the two parameter combinations with the largest mediated effect showed a substantial drop in power compared to combinations with smaller effects. For $N = 900$, power was above .80 at all levels of mediated effect and parameter combinations. Table 5.B shows power for the binomial generated data, which show the same pattern of results as data generated from the normal distribution, within rounding error.

Insert Tables 5.A-5.B about here

Accuracy of Estimates

Logistic regression. Bias, relative bias, and standardized bias were calculated using the true values and results from the binomial generated data. Logistic regression showed minimal bias across all conditions and sample sizes. Bias decreased with sample size, but increased as the magnitude of the mediated effect increased. Relative bias did not exceed .05 in any condition. For most conditions, standardized bias decreased as sample size increased. Standardized bias also increased as the size of the mediated effect increased, although this trend was more pronounced for $N = 300$. Tables 6.A and 6.B summarize bias values.

Causal inference mediation. Bias, relative bias, and standardized bias were calculated using the true values and results from the binomial generated data. The true values for the TNIE were computed using Equation 29, where i_1 is the intercept from Equation 1, h is the coefficient for the XM interaction which in this case is zero, $x = 0$, $x^* = 1$, and a and b are the logistic regression coefficients from Equations 2 and 3.

$$TNIE = \frac{(1+e^{(i_1+ax^*)})(1+e^{(b+hx+i_1+ax)})}{(1+e^{(i_1+ax)})(1+e^{(b+hx+i_1+ax^*)})} \quad (29)$$

For all conditions in both sample sizes, relative bias exceeded 0.10, suggesting that either the estimator in Equation 29 needs improvement, or that clarification is needed concerning the estimation procedures that are implemented in PROC CAUSALMED. This is evidenced by the role that the c' coefficient seems to have in the bias values. For both $N = 300$ and $N = 900$, all three measures of bias increased as the magnitude of c' increased and the values of a and b were held constant, although the c' coefficient is not included in the calculation of the true TNIE values.

For N=300 there were eight conditions with unusually high bias and relative bias. Three way frequency tables of X, M, and Y suggest that sparse cells led to division by very small numbers, which can account for the unusual estimates. This issue was resolved when the sample increased to N=900, supporting the conclusion that the astronomical bias occurred as a result of data sparsity in some cells.

Insert Tables 6A-6D about here

Joint Significance Tests with Configural Frequency Models

Configural frequency mediation joint significance tests. Tables 7A and 7B compare the Type I error results from three joint significance tests and the original CFM analysis. The first joint significance test compared the models in Equations 21 and 22 to test the *a*-path and Equations 22 and 24 to test the *b*-path. This test included three of the base models used in configural frequency analysis. Overall Type I error for the mediated effect was .16 in the smaller sample and .23 in the larger sample. Both values are lower than the Type I error from the causal steps version of CFM. In addition, a comparison of Type I error rates by parameter combination shows that error rates are higher when the *a*-path is non-zero and the *b*-path is zero.

Tables 8A and 8B compares the power results from the three joint significance tests and the original CFM analysis. In the smaller sample, power was below .80 in three parameter combinations, all of which had a small effect for the *a*-path. Power was above .80 for all parameter combinations in the larger sample.

The second joint significance test compared the model in Equations 40 and 41 to test the *a*-path and Equations 42 and 41 to test the *b*-path. The saturated model in Equation 41 was chosen for these comparisons to account for the effects of any higher order interactions.

$$\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{MY} + \lambda^{XY} + \lambda^{XMY} \quad (40)$$

$$\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{XY} + \lambda^{MY} + \lambda^{XMY} \quad (41)$$

$$\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{XY} + \lambda^{XMY} \quad (42)$$

The overall Type I error rate was lower than the causal steps version of CFM, and the highest error rates occurred when the *a*-path was zero and the *b*-path was nonzero. This occurred for both N = 300 and N = 900. Power was generally lower in this test compared to the causal steps version of CFM. There were no parameter combinations that reached .80 power in the smaller sample. In the larger sample, power was above .80 in only three parameter combinations.

The third joint significance test compared the models in Equations 43 and 44 to test the *a*-path and Equations 42 and 41 again to test the *b*-path. These comparisons were chosen because they were the best performing for each path. Tables 9 – 12 summarize results for the separates tests of the *a* and *b* paths that make up the joint significance tests described above.

$$\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XY} \quad (43)$$

$$\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{XY} \quad (44)$$

This combination of models had Type I errors within the nominal range for most parameter combination for both N = 300 and N = 900. The exception was when both *a*

and b were zero, which had a Type I error rate of .01 in the small sample and .00 (with rounding error) in the large sample. In the smaller sample conditions, power was above .80 only when a and b both had at least a medium effect. All parameter combinations had power above .80 for $N = 900$.

Insert Tables 7A-12 about here

Study 2

Convergence

The models in study 2 converged adequately, with a software warning in a very small percentage of cases. For logistic regression, 99.8% of the models from Equation 3 converged, while 100.0% of the models from Equations 1 and 2 converged. Less than 1.0% of the models from Equations 3 had possible quasi-complete data separation. All of the models estimated for CFM, the joint significance test, and causal mediation converged.

Power

Logistic regression. Table 13 shows power results for data that were generated to have heterogenous subgroups. As expected, power increased as sample size increased. The average mediated effect in each condition may be most similar to conditions where a is large and b is small, or when a and b are both medium in the homogeneous conditions. For $N = 300$ and $N = 900$, power was much lower in the heterogeneous data than

comparable conditions in the homogeneous data. However, for $N = 2700$, power reached .99.

Configural frequency mediation. Table 13 shows power results for data that were generated to have heterogeneous subgroups. Power increased with sample size, but at a much smaller rate compared to logistic regression and causal mediation. For $N = 2700$, power was only .39. Because CFM was developed as a person-oriented method, it was expected to be better than traditional methods at detecting subgroups within a dataset. This does not appear to be the case.

Causal inference mediation. Table 13 shows power results for data that were generated to have heterogeneous subgroups. Causal mediation performed similarly to logistic regression, and as expected, power increased as sample size increased. However, causal mediation had more power than logistic regression for $N = 900$.

Joint Significance Tests with Configural Frequency Models

Configural frequency mediation joint significance tests. Table 14 compares the power results from three joint significance tests and the original CFM analysis. Tables 15 and 16 summarize results for the separate tests of the a and b paths that make up the joint significance tests described above.

Insert Tables 13-16 about here

The types and antitypes from the independence model for the three conditions in study 2 are shown in Tables 17-19. When there is evidence for mediation in CFM, these

are the subgroups that are used for a person-oriented interpretation of the mediation process. In all three conditions, there are types found for the configurations that have the same values for X, M, and Y (i.e. 000 or 111), as expected. For N=900 all other configurations are antitypes, when N=300, five of the six remaining configurations were antitypes, and when N=100, four of the six remaining configurations were antitypes.

Insert Tables 17-19 about here

The joint significance test has been shown to be a better choice than the causal steps method, both in the literature and in this study (MacKinnon et al., 2002). However, conducting a joint significance test with the CFM models can only answer the question of whether mediation is present. The next stage of analysis is to interpret which subgroups carry the mediation process. In the original CFM, this is done by looking at the types and antitypes from the independence model. Study 2 presented an opportunity to see if these interpretations would hold when mediation was determined through a joint significance test rather than the CFM decision rules. However, the types and antitypes from the independence model were inconclusive. The conditions in study 2 were generated such that one third of the sample had a large mediated effect. This resulted in types and antitypes for the variable configurations 000 and 111, which is what would be expected. However, it was not possible to determine which subgroup the observed frequencies came from.

The types and antitypes from study 2 were compared with four conditions in study 1 with $N=900$. These four conditions corresponded as closely as possible to the effects in the three subgroups and the average effects when the subgroups were combined into a single population. The pattern of types and antitypes from study 2 matched the pattern of types and antitypes for the study 1 condition that corresponded with the subgroup with mediation and the study 1 condition that corresponded to the average effects of the subgroup. Therefore, although a joint significance test can improve the statistical performance of the CFM models, nothing is gained in person-oriented interpretation.

Summary of Simulation Results

In both simulations, logistic regression performed as expected. Specifically, Type I error rates were below the nominal rate of .075 in all conditions. In addition, power increased as both effect size and sample size increased. However, in the smaller sample size of study 1, the a -path had a greater influence on power than the b -path, that is, when the product of the coefficients was the same, power was higher when the size of a was greater than b than when b was greater than a . A similar pattern of results for the a -path has been found in previous simulations (Fritz, Taylor, & MacKinnon, 2012). Relative bias was below 10% across all conditions and sample sizes.

Configural frequency analysis did not perform well in either simulation. Overall Type I error rates were high, and in a pattern that suggested the b -path had a greater influence than the a -path on Type I errors. This pattern was also reflected in power, which was lowest when the b -path was small. Joint significance tests were conducted to find a method of using configural frequency analysis to investigate mediation that had

better statistical properties. Type I error rates were below the nominal .075 level when the *a*-path was tested by comparing Equations 43 and 44, and the *b*-path was tested by comparing Equations 41 and 42.

Mediation from the potential outcomes framework uses the true natural indirect effect (TNIE) rather than the product of coefficients that is used in traditional regression-based mediation. In both simulations, causal mediation performed similarly to logistic regression in regard to Type I error rates, which were below the nominal .075 level in all conditions. In study 1, power increased with sample size, however, in the smaller sample, power did not increase monotonically with effect size. Bias for the TNIE was generally higher than expected, and cell sparsity led to unusually high values for several conditions when $N = 300$.

Discussion

The aim of this project was to investigate a method for mediation from a person-oriented perspective and compare it to a conventional mediation analysis and a modern causal inference approach. Two simulations were conducted, the first assuming a homogenous mediated effect in the population, and the second assuming a heterogenous mediated effect in the population. Both studies found that configural frequency mediation does not perform well in its current form, specifically with high Type I error rates. Performance may be improved using joint significance tests, however this strategy limits the interpretability of results from a person-oriented perspective.

Adapting mediation to configural frequency analysis was a step forward in finding statistical methods for person-oriented mediation (von Eye et al., 2010; von Eye,

Mun, & Mair, 2009). However, implementation of the published method is not straightforward, and may be a contributing factor to the lack of substantive examples of CFM in the literature. The currently published treatments of CFM provide descriptions of the process, which include estimating a series of log-linear models, evaluating the existence of mediation through a set of model comparison and decision rules, and determining the type of mediation effects that are present in the dataset. What remains unclear is the guiding principle that was used to develop the decision rules in the second stage of the process. In addition, there is no software in place to automate the decision rules.

Contributions

One contribution of this project was to provide an interpretation of the decision rules that were originally presented for CFM (von Eye et al., 2010). The guiding principle of this interpretation was to translate the decision rules into a set of “if, then, else” statements that captured the relevant bivariate relations among X, M, and Y that were deduced from each model comparison. A second contribution was the translation of decision rules into a program that would automate the decision rule process for any data set. Both of these contributions were necessary components that had to be developed in order to conduct a simulation study to evaluate CFM. A third contribution of this project was to contrast the person-oriented approach with variable-oriented approaches, and describe person-oriented research as a hybrid of nomothetic and idiographic methods.

Limitations

This study represents some beginning steps in understanding CFM, its statistical performance and usefulness as a research tool, and its comparability to traditional and causal methods. There are several limitations to discuss, including CFM model specifications, mixture modeling as an alternative, ambiguity in subgroup identification, significance testing in the context of the person-oriented approach, incongruities with CFM joint significance testing, and differences between the logistic and causal estimators.

First, the CFM log-linear models used in this study intentionally ignored the role of the three-way interaction between X, M, and Y. This choice was made in order to conduct a simplified evaluation of CFM within a simulation where the three-way interaction was not modeled. However, it should be noted that this interaction could possibly be responsible for any types and antitypes that are revealed in the independence model. Inclusion of the three-way interaction in future research would be necessary to fully evaluate this method.

Second, mixture modeling may be a more reasonable alternative for studying person-oriented mediation. There is currently little research on using mixture models explicitly in a mediation context, however there may be several advantages to preferring this framework over CFM for person-oriented mediation. First is that CFM is restricted to categorical variables, and the contingency tables can become unwieldy as the number of variables and the number of categories increases. In contrast, mixture models can be estimated for both discrete and continuous variables. In addition, the depth of

methodological research that exists for mixture models makes this method more accessible for researchers, both theoretically and in software packages.

Third, interpreting subgroups from the independence model is ambiguous. The first step in a CFM analysis is essentially a “gatekeeper” where the fit of the independence model is tested to ascertain the viability of a mediated relation in the data. In this step, a well fitting model precludes the possibility of mediation, while model misfit suggests that mediation could be one of several possible explanations for the misfit. It is only after the independence model is rejected that mediation can be ascertained through a series of model comparisons and inferences made about mediational process occurring in particular subgroups. There is an unstated assumption that if there is evidence for mediation when the data is treated as a single group, then the discrepancies between expected and observed cell frequencies in the independence model can be interpreted as subgroups for whom the mediation effect exists. However, this assumption may not be tenable because mediation is not the only possible way for the independence model to not fit the data. Types and antitypes could possibly result from any relation between the variables.

In addition, mediation is not explicitly tested in each subgroup, but rather, CFM subgroups are identified in an omnibus manner, showing up as types and antitypes in the independence model. It is assumed that each subgroup that has types or antitypes carries the mediation process, however, the actual effects of each subgroup are not distinguished. To illustrate, consider a population with three subgroups, much like the conditions in study 2. If one-third of the population has no effect, this subgroup will contribute

observations equally to each of the eight configuration cells (see Table 2). If one-third of the population has mediation, this subgroup will contribute more observations to cells where the values of X, M, and Y are equal, and fewer observations to the other cells. If one-third of the population has a direct effect only, then this subgroup will contribute more observations to cells where the values of X and Y are the same, and fewer observations to the other cells. When inspecting the types and antitypes from the independence model, it is ambiguous how each of the three subgroups are influencing the observed cell frequencies.

Fourth, it is unclear what the role of traditional significance testing is within a person-oriented framework. The results of this project show that inflated Type I error rates are a major flaw of CFM. However, it could be argued that making inferences from the traditional $p=.05$ significance cutoff is incompatible with the person-oriented approach. The reason is that inferences from traditional significance tests are inferences about the population given information in the sample. If the researcher is actually interested in the truth about an individual, then population statistics are irrelevant. However, evaluating Type I error rates is still a useful exercise in the person-oriented approach. One assumption of the person-oriented approach is that in a given population, a small number of stable subgroups will emerge because psychological processes are fundamentally self-organizing (Bergman & Magnusson, 1997; Sterba & Bauer, 2010). This means that although the researcher is interested in individual differences, inferences about individual effects are made from subgroup data. In this sense, inferences about statistical significance relate to subgroups in a population and are still relevant in the

person-oriented approach. In idiographic research, where there is only the individual participant, Type I errors can also be relevant when the single-n designs have quantitative components. An example would be within-subject variation in longitudinal designs, or dynamical models of a single time series. In idiographic research, instead of making inferences about a population made up of many individuals, the population in question would be values of a psychological construct at different points in time for a single person. In the context of this study, Type 1 error is relevant because the strategy in CFM is to first accumulate evidence for mediation in the whole sample, and then make interpretations about subgroups.

Fifth, the joint significance tests of the CFM models also has a problematic feature. The tests for each separate path (the *a*-path and *b*-path) are not symmetric in regards to the terms that are included in each log-linear model comparison. Remember that in CFM, evidence for the existence of a bivariate relation is found by comparing the fit of two models, one that contains the interaction between two variables, and one that is exactly the same, except that it excludes the interaction. If the model without the interaction has types or antitypes, and the model with the interaction does not have the types or antitypes (or has a different pattern of types and antitypes) then the bivariate relation is said to exist. In the case of the joint significance test, the best performing model comparison for the *a*-path involved the main effects and the XY interaction. In contrast, the best performing model comparison for the *b*-path involved the saturated model. It was expected that including the saturated model for both paths would be the

most complete and therefore more accurate comparison, however, for the *a*-path, using the saturated model resulted in Type I errors that were too high.

Finally, a fundamental limitation of this study is the three methods that were investigated are very different from each other. For example, CFM does not have parameter estimates that are part of the final tests of mediation, while logistic regression and causal mediation use different quantities to measure the mediated effect, *ab* for logistic regression and TNIE for causal mediation.

The product of coefficients and the natural indirect effect are both estimators of the effect of X on Y through the mediator, M. The product of coefficients is estimated using two simultaneous regression equations that include X, M, and Y. In the traditional regression framework, the coefficients reflect differences between the treatment and control groups in a randomized experiment. However, since M cannot be randomized, causal interpretation of the mediated effect is limited unless further design considerations are made (Pirlott & MacKinnon, 2016). The TNIE differs because it is estimated within the potential outcomes framework and represents the indirect effect assuming that all participants are placed in the treatment group. When both the mediator and outcome are continuous, and the interaction between XM is zero, then the estimates for the product of coefficients and the TNIE will be equivalent (MacKinnon, Valente, & Gonzales, 2018).

However, this study shows that when the mediator and outcome are both binary, the relation between *ab* and TNIE is not as clear. For example, power for TNIE did not increase monotonically with effect size, as it does with the traditional estimator. In addition, the true values for TNIE decreased as the true values for *ab* increased. It is

unclear at this time why these patterns occurred, and follow-up studies are needed to investigate these relations.

The results from the causal mediation analysis showed unexpectedly high bias at the N=300 sample size. In some of these conditions, this was likely because of very small frequencies in some data cells. However, this does not account for the high bias across all conditions and sample sizes. There are several possible explanations for these results, including an unknown discrepancy between the formulas used within PROC CAUSALMED and Equation 29, which was used to calculate true values for TNIE based on empirical true values of logistic regression coefficients. In addition, the interaction between the exposure and the mediator (XM) is an important aspect of estimating causal effects, but was not explicitly included in this project (VanderWeele, 2014). The context of this study was a simple, single mediator model that did not include this XM interaction. The interaction effect was not modeled in the data simulation, and therefore is implicitly zero. The interaction effect was also not modeled in the estimation of the causal effects, including the TNIE.

Future Directions

To address the limitations in the current study and expand the investigation of person-oriented mediation, future simulation research can focus on several things. First, mixture model simulations can be conducted to better understand how mediational processes may differ across subgroups in a sample. Second, simulations that generate data from the potential outcomes framework that include the XM interaction may clarify any links between traditional and potential outcome effects. As a first step in evaluating and comparing these methods, data was generated according to the traditional single

mediator model with parameters from both the normal distribution and from the binomial distribution. Since the traditional model was used for data generation, it is not surprising that the mediated effect estimated from logistic regression performed better than the TNIE which was estimated from the potential outcomes framework.

There are currently several variable-oriented methods that can provide information at the individual level, including intensive longitudinal models, growth mixture models, and latent class analysis. Idiographic, single-n designs and qualitative analyses could also be added to programs of research that wish to identify heterogeneous mediation effects at the individual level. A useful addition to the literature would be a comprehensive taxonomy that attempts to match data types (e.g. categorical or continuous, longitudinal or cross-sectional, group or single-n) with quantitative models and qualitative techniques, and the types of research questions that can be asked and types of inferences that can be made (e.g. inferences about a population or about individuals). A taxonomy of this kind could organize person-oriented mediation into more manageable parts.

Bayesian inference and potential outcomes are two other areas that could be used to explore person-oriented mediation effects. One philosophical implication of Bayesian inference is that model parameters have estimated distributions, rather than point estimates. It is possible that the variance inherent in the posterior distribution of a mediated effect could account for heterogeneous effects between individuals while still incorporating a more global interpretation of the effect using summaries of the posterior distribution. Future studies can investigate the performance of Bayesian methods in

detecting heterogenous effects as a function of the standard deviation of the posterior distribution.

In the potential outcomes framework, the conditional average treatment effect (CATE) describes treatment effects at the subgroup level. Although the individual causal effects are impossible to estimate, the CATE can be an approximation of the effects for individuals within the group that has been conditioned on. From a person-oriented perspective, this would mean conditioning across a collection of relevant, interacting covariates. Future studies in this direction would include analyzing the variability in CATE mediation estimates to determine the degree to which inferences can be made from the CATE to individuals within the group, as well as testing the implications of assumptions regarding the equality of error terms across potential outcomes.

Conclusion

Detecting heterogenous mediation effects from a person-oriented perspective implies a holistic view of all possible influences on any given individual in any given situation. From a statistical perspective, this requires the measurement and analysis of every interaction among these influences. Configural frequency mediation studied in this research is an attempt to detect heterogenous effects among combinations of just three discrete variables, a treatment/predictor, a mediator, and an outcome. This study helps clarify the process of CFM and provides a program to automate the decisions rules for detecting mediation. In addition, it highlights the need for future research to revisit the principles used by CFM to detect both mediation effects and subgroups within a population.

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Table 1

Empirical Examples of Configural Frequency Analysis

Citation	Description
Müller, B., Gäbelein, W. D., & Schulz, H. (2006). A Taxonomic Analysis of Sleep Stages. <i>Sleep</i> , 29(7), 967-974.	categorizing patterns of physiological variables observed during sleep stages
Tuominen-Soini, H., Salmela-Aro, K., & Niemivirta, M. (2011). Stability and Change in achievement goal orientations: A person-centered approach. <i>Contemporary Educational Psychology</i> , 36(2), 82-100.	exploring temporal changes in group membership in groups identified through latent profile analysis
Napolitano, C. M., Bowers, E. P., Gestsdottir, S., Depping, M., von Eye, A., Chase, P., & Lerner, J. V. (2011). The role of parenting and goal selection in positive youth development: A person-centered approach. <i>Journal of Adolescence</i> , 34(6), 1137-1149.	exploring relations among goal setting, parenting styles, and positive youth development
Loeffert, S., Ommen, O., Kuch, C., Scheibler, F., Woehrmann, A., Baldamus, C., & Pfaff, H. (2010). Configural frequency analysis as a method of determining patients' preferred decision-making roles in dialysis. <i>BMC medical informatics and decision making</i> , 10:47.	predicting types of patients who prefer either active or passive participation in dialysis treatment decisions
von Eye, A., Bogat, G. A., & Rhodes, J. E. (2006). Variable-oriented and person-oriented perspectives of analysis: The example of alcohol consumption in adolescence. <i>Journal of Adolescence</i> , 29(6), 981-1004.	detecting differences in youth resilience to alcohol consumption
Martinez-Torteya, C., Bogat, G. A., von Eye, A., & Levendosky, A. A. (2009). Resilience among children exposed to domestic violence: The role of risk and protective factors. <i>Child Development</i> , 80(2), 562-577.	identifying factors of resilience in youth exposed to domestic violence
Stemmler, M., & Lösel, F. (2012). The stability of externalizing behavior in boys from preschool age to adolescence: A person-oriented analysis. <i>Psychological Test and Assessment Modeling</i> , 54(2), 195-207.	revealing stability in externalizing behaviors among young boys
Gradinger, P., Strohmeier, D., & Spiel, C. (2009). Traditional bullying and cyberbullying: Identification of risk groups for adjustment problems. <i>Journal of Psychology</i> , 217(4), 205-213.	identifying risks for traditional and cyberbullying
Stemmler, M., & Bäumlner, G. (2005). The detection of types among decathletes using configural frequency analysis (CFA). <i>Psychology Science</i> , 47(3/4), 447-466.	identifying athletic specializations among decathletes

Table 2

Patterns of Three Binary Variables

Pattern	X	M	Y
N1	0	0	0
N2	0	0	1
N3	0	1	0
N4	0	1	1
N5	1	0	0
N6	1	0	1
N7	1	1	0
N8	1	1	1

Table 3

Simulation Parameter Values

				N=300	N=900
Parameter	Normal	Average Logistic Regression Estimates ^a N=300	Average Logistic Regression Estimates ^a N=900	Binomial	Binomial
<i>a</i>					
<i>zero</i>	0.00	0.00	0.00	0.00	0.00
<i>small</i>	0.35	0.57	0.56	0.57	0.56
<i>medium</i>	0.96	1.61	1.60	1.61	1.60
<i>large</i>	1.46	2.60	2.57	2.60	2.57
<i>b</i>					
<i>zero</i>	0.00	0.00	0.00	0.00	0.00
<i>small</i>	0.35	0.92	0.91	0.92	0.91
<i>medium</i>	0.96	2.25	2.22	2.25	2.22
<i>large</i>	1.46	3.04	3.01	3.04	3.01
<i>c'</i>					
<i>zero</i>	0.00	0.25	0.24	0.25	0.24
<i>small</i>	0.35	0.79	0.79	0.79	0.79
<i>medium</i>	0.96	1.80	1.77	1.80	1.77
<i>large</i>	1.46	2.75	2.64	2.75	2.64

Note. Parameters used when generating data from a binomial distribution reflect the average empirical effects of the normal data obtained by logistic regression. Each binomial entry is collapsed over the other two parameters.

^a*These are the average logistic regression estimates for data generated from a normal distribution and then dichotomized.*

Table 4.A

Study 1 - Type 1 Error

ab Effect Size Combinations	N=300			N=900		
	Logistic Regression	Configural Frequency Mediation	Causal Mediation	Logistic Regression	Configural Frequency Mediation	Causal Mediation
Overall Type 1 Error	0.03	0.28	0.02	0.04	0.35	0.03
$a = 0, b = 0$	0.00	0.00	0.00	0.00	0.00	0.00
$a = 0, b = s$	0.03	0.02	0.01	0.04	0.44	0.03
$a = 0, b = m$	0.06	0.96	0.02	0.05	1.00	0.04
$a = 0, b = l$	0.05	1.00	0.01	0.05	1.00	0.04
$a = s, b = 0$	0.02	0.00	0.00	0.04	0.00	0.02
$a = m, b = 0$	0.05	0.00	0.03	0.04	0.00	0.04
$a = l, b = 0$	0.04	0.00	0.04	0.06	0.00	0.05

Note. Data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values above .075 are in bold; values below .025 are in bold and italics

Table 4.B
 Study 1 - Type 1 Error with Binomial Generated Data

ab Effect Size Combinations	N=300				N=900			
	Logistic Regression	Configural Frequency Mediation	Causal Mediation		Logistic Regression	Configural Frequency Mediation	Causal Mediation	
Overall Type 1 Error	0.03	0.28	0.01		0.04	0.35	0.03	
<i>a = 0, b = 0</i>	0.00	0.00	0.00		0.00	0.00	0.00	
<i>a = 0, b = .90</i>	0.03	0.02	0.01		0.04	0.44	0.03	
<i>a = 0, b = 2.20</i>	0.05	0.97	0.01		0.05	1.00	0.04	
<i>a = 0, b = 3.00</i>	0.05	1.00	0.01		0.05	1.00	0.04	
<i>a = .60, b = 0</i>	0.01	0.00	0.00		0.04	0.00	0.02	
<i>a = 1.60, b = 0</i>	0.05	0.00	0.02		0.04	0.00	0.04	
<i>a = 2.60, b = 0</i>	0.05	0.00	0.04		0.05	0.00	0.04	

Note. Data were generated from a binomial distribution; average effect size values are included because the general designations of *s, m, l* do not reflect consistent values across coefficients; values above .075 are in bold; values below .025 are in bold and italics

Table 5.A
Study 1 – Power

ab Effect Size Combinations	N=300			N=900		
	Logistic Regression	Configural Frequency Mediation	Causal Mediation	Logistic Regression	Configural Frequency Mediation	Causal Mediation
a = s, b = s	0.62	0.05	0.22	0.99	0.58	0.97
a = s, b = m	0.77	0.98	0.32	0.99	1.00	0.97
a = m, b = s	0.93	0.13	0.75	1.00	0.64	1.00
a = s, b = l	0.77	1.00	0.25	1.00	1.00	0.97
a = l, b = s	0.90	0.13	0.71	1.00	0.54	1.00
a = m, b = m	1.00	0.98	0.84	1.00	1.00	1.00
a = m, b = l	1.00	1.00	0.82	1.00	1.00	1.00
a = l, b = m	1.00	0.96	0.66	1.00	1.00	0.98
a = l, b = l	1.00	1.00	0.58	1.00	1.00	0.99

Note. Data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values below .80 are in bold

Table 5.B

Study 1 – Power with Binomial Generated Data

ab Effect Size Combinations	N=300				N=900			
	Logistic Regression	Configural Frequency Mediation	Causal Mediation	Logistic Regression	Configural Frequency Mediation	Causal Mediation	Logistic Regression	Configural Frequency Mediation
a = .57, b = .90	0.64	0.04	0.23	0.99	0.57	0.97	0.99	0.57
a = .57, b = 2.23	0.76	0.98	0.31	0.99	1.00	0.97	0.99	1.00
a = 1.62, b = .93	0.94	0.09	0.74	1.00	0.58	1.00	1.00	0.58
a = .56, b = 3.01	0.77	1.00	0.24	1.00	1.00	0.97	1.00	1.00
a = 2.60, b = .93	0.90	0.01	0.69	1.00	0.46	1.00	1.00	0.46
a = 1.61, b = 2.26	1.00	0.98	0.81	1.00	1.00	1.00	1.00	1.00
a = 1.61, b = 3.07	1.00	1.00	0.80	1.00	1.00	1.00	1.00	1.00
a = 2.61, b = 2.27	0.96	0.95	0.62	1.00	1.00	0.98	1.00	1.00
a = 2.60, b = 3.09	1.00	1.00	0.54	1.00	1.00	0.98	1.00	1.00

Note. Data were generated from a binomial distribution; average effect size values are included because the general designations of s , m , l do not reflect consistent values across coefficients; values below .80 are in bold

Table 6.A
Study 1 – Logistic Regression Bias of Mediated Effect for N = 300

\hat{a}	\hat{b}	c'	True Mediated Effect ab	Bias	Relative Bias	Standardized Bias
0.56	0.88	0.07	0.50	0.01	0.02	0.05
0.57	0.87	0.62	0.50	0.01	0.02	0.03
0.57	0.92	1.66	0.53	0.01	0.01	0.02
0.56	0.93	2.63	0.52	0.02	0.04	0.07
0.59	2.18	0.15	1.28	-0.01	-0.01	-0.02
0.57	2.19	0.69	1.24	0.04	0.03	0.07
0.57	2.26	1.67	1.29	0.00	0.00	-0.01
0.57	2.28	2.42	1.31	0.00	0.00	-0.01
0.57	2.94	0.18	1.69	0.05	0.03	0.07
0.56	2.97	0.72	1.66	0.03	0.02	0.03
0.57	3.04	1.60	1.75	0.04	0.03	0.06
0.55	3.10	2.29	1.71	0.07	0.04	0.09
1.62	0.92	0.22	1.50	0.04	0.03	0.08
1.61	0.92	0.78	1.49	0.03	0.02	0.06
1.62	0.94	1.87	1.52	0.02	0.01	0.04
1.62	0.93	2.90	1.51	0.04	0.03	0.07
1.60	2.23	0.48	3.57	0.09	0.03	0.11
1.61	2.25	1.02	3.62	0.11	0.03	0.14
1.61	2.28	2.01	3.68	0.12	0.03	0.13
1.60	2.28	2.92	3.66	0.10	0.03	0.12
1.60	3.02	0.59	4.85	0.13	0.03	0.12
1.62	3.06	1.06	4.97	0.10	0.02	0.10
1.61	3.10	2.00	4.97	0.16	0.03	0.15
1.61	3.09	2.77	4.97	0.19	0.04	0.17
2.60	0.92	0.40	2.40	0.12	0.05	0.14
2.61	0.94	0.98	2.45	0.09	0.04	0.10
2.60	0.95	2.07	2.46	0.07	0.03	0.08
2.60	0.91	3.26	2.35	0.05	0.02	0.05
2.59	2.28	0.84	5.93	0.16	0.03	0.12
2.61	2.28	1.37	5.95	0.07	0.01	0.05
2.60	2.29	2.48	5.97	0.28	0.05	0.21
2.61	2.23	3.96	5.82	0.24	0.04	0.18
2.62	3.10	1.02	8.11	0.35	0.04	0.22
2.59	3.08	1.51	7.97	0.27	0.03	0.17
2.61	3.10	2.46	8.09	0.21	0.03	0.13
2.59	3.08	3.61	7.98	0.24	0.03	0.15

Note. Data were generated from a binomial distribution; effect sizes for a, b, and c' are included because the general designations of s, m, l do not reflect consistent values across coefficients;

Table 6.B

Study 1 – Causal Mediation Bias of Mediated Effect for N = 300

\hat{a}	\hat{b}	c'	True TNIE	Bias	Relative Bias	Standardized Bias
0.56	0.88	0.07	0.90	-0.77	-0.86	-12.77
0.57	0.87	0.62	0.90	-0.68	-0.75	-6.69
0.57	0.92	1.66	0.89	-0.23	-0.26	-1.11
0.56	0.93	2.63	0.89	1.12	1.25	0.47
0.59	2.18	0.15	0.81	-0.54	-0.66	-4.54
0.57	2.19	0.69	0.82	-0.34	-0.42	-1.84
0.57	2.26	1.67	0.82	0.44	0.54	0.31
0.57	2.28	2.42	0.81	2.04	2.51	0.97
0.57	2.94	0.18	0.80	-0.47	-0.58	-3.30
0.56	2.97	0.72	0.80	-0.26	-0.32	-1.35
0.57	3.04	1.60	0.80	0.64	0.80	0.49
0.55	3.10	2.29	0.80	2.02	2.51	0.94
1.62	0.92	0.22	0.78	-0.42	-0.54	-3.71
1.61	0.92	0.78	0.78	-0.13	-0.16	-0.89
1.62	0.94	1.87	0.77	1.24	1.60	1.22
1.62	0.93	2.90	0.77	11352.62	14662.16	1.45
1.60	2.23	0.48	0.65	0.26	0.40	0.56
1.61	2.25	1.02	0.65	0.97	1.50	1.42
1.61	2.28	2.01	0.65	4.13	6.38	1.89
1.60	2.28	2.92	0.65	20917.87	32251.63	1.67
1.60	3.02	0.59	0.62	0.54	0.87	0.95
1.62	3.06	1.06	0.62	1.34	2.17	1.51
1.61	3.10	2.00	0.62	4.52	7.27	1.82
1.61	3.09	2.77	0.62	7282.72	11713.27	1.71
2.60	0.92	0.40	0.73	-0.18	-0.24	-1.23
2.61	0.94	0.98	0.73	0.30	0.41	0.60
2.60	0.95	2.07	0.72	2.58	3.56	1.65
2.60	0.91	3.26	0.73	141573.11	193295.78	1.35
2.59	2.28	0.84	0.59	1.13	1.92	1.70
2.61	2.28	1.37	0.59	2.42	4.13	1.97
2.60	2.29	2.48	0.59	19445.60	33132.64	1.76
2.61	2.23	3.96	0.59	1723814.29	2922418.30	0.88
2.62	3.10	1.02	0.56	1.87	3.34	1.72
2.59	3.08	1.51	0.56	3.59	6.41	1.82
2.61	3.10	2.46	0.56	26742.89	47829.19	1.65
2.59	3.08	3.61	0.56	1132824.34	2021949.84	1.07

Note. The TNIE was used to calculate bias for causal mediation. This is not the same estimator as the conventional product of coefficients reported in the logistic regression tables; data were generated from a binomial distribution; effect sizes for a , b , and c' are included because the general designations of s , m , l do not reflect consistent values across coefficients; inflated bias estimates are due to cell sparsity in at least one replication per condition; relative bias values with absolute values above .10 are in bold

Table 6.C
Study 1 – Logistic Regression Bias of Mediated Effect for N = 900

\hat{a}	\hat{b}	c'	True Mediated Effect ab	Bias	Relative Bias	Standardized Bias
0.56	0.89	0.07	0.50	0.00	0.01	0.02
0.56	0.89	0.64	0.50	0.00	0.00	0.01
0.57	0.91	1.65	0.52	0.01	0.01	0.04
0.56	0.92	2.61	0.52	0.00	0.00	-0.01
0.56	2.16	0.16	1.21	0.01	0.01	0.04
0.57	2.16	0.68	1.22	-0.02	-0.01	-0.05
0.56	2.23	1.64	1.25	0.01	0.01	0.04
0.56	2.25	2.41	1.25	0.01	0.01	0.03
0.57	2.92	0.19	1.66	0.03	0.02	0.08
0.56	2.93	0.70	1.63	0.02	0.01	0.04
0.57	3.03	1.59	1.72	0.00	0.00	0.00
0.56	3.06	2.26	1.73	0.01	0.01	0.02
1.60	0.91	0.22	1.47	0.01	0.01	0.05
1.60	0.92	0.79	1.47	0.00	0.00	0.01
1.60	0.92	1.84	1.48	0.02	0.01	0.07
1.59	0.92	2.85	1.47	0.01	0.01	0.04
1.60	2.22	0.47	3.55	0.04	0.01	0.10
1.60	2.23	0.99	3.56	0.01	0.00	0.02
1.60	2.27	1.97	3.62	0.02	0.01	0.05
1.60	2.24	2.83	3.60	0.04	0.01	0.08
1.61	3.00	0.56	4.83	0.00	0.00	0.00
1.60	3.02	1.08	4.83	0.04	0.01	0.06
1.60	3.05	1.98	4.90	0.05	0.01	0.08
1.59	3.06	2.69	4.87	0.03	0.01	0.05
2.57	0.93	0.39	2.39	0.06	0.02	0.12
2.57	0.92	0.95	2.38	0.01	0.00	0.01
2.57	0.92	2.05	2.38	0.03	0.01	0.06
2.56	0.92	3.11	2.34	0.02	0.01	0.04
2.57	2.27	0.82	5.82	0.08	0.01	0.12
2.56	2.27	1.37	5.81	0.02	0.00	0.03
2.57	2.26	2.37	5.82	0.05	0.01	0.07
2.57	2.22	3.30	5.71	0.04	0.01	0.05
2.58	3.06	1.01	7.89	0.12	0.02	0.13
2.57	3.06	1.51	7.86	0.11	0.01	0.13
2.57	3.07	2.40	7.87	0.07	0.01	0.09
2.56	3.02	3.18	7.74	0.10	0.01	0.11

Note. Data were generated from a binomial distribution; effect sizes for a, b, and c' are included because the general designations of s, m, l do not reflect consistent values across coefficients;

Table 6.D

Study 1 – Causal Mediation Bias of Mediated Effect for N = 900

\hat{a}	\hat{b}	c'	True TNIE	Bias	Relative Bias	Standardized Bias
0.56	0.88	0.07	0.90	-0.77	-0.86	-20.89
0.57	0.87	0.62	0.90	-0.68	-0.76	-10.24
0.57	0.92	1.66	0.89	-0.26	-0.29	-1.53
0.56	0.93	2.63	0.89	0.77	0.86	1.00
0.59	2.18	0.15	0.82	-0.56	-0.69	-7.52
0.57	2.19	0.69	0.82	-0.38	-0.46	-3.04
0.57	2.26	1.67	0.82	0.36	0.44	0.76
0.57	2.28	2.42	0.82	1.77	2.16	1.83
0.57	2.94	0.18	0.80	-0.49	-0.61	-5.37
0.56	2.97	0.72	0.80	-0.30	-0.37	-2.12
0.57	3.04	1.60	0.80	0.47	0.59	0.93
0.55	3.10	2.29	0.80	1.69	2.11	1.82
1.62	0.92	0.22	0.78	-0.42	-0.54	-6.12
1.61	0.92	0.78	0.78	-0.15	-0.19	-1.32
1.62	0.94	1.87	0.78	1.08	1.39	2.27
1.62	0.93	2.90	0.78	4.36	5.60	2.66
1.60	2.23	0.48	0.65	0.21	0.32	1.05
1.61	2.25	1.02	0.65	0.82	1.25	2.51
1.61	2.28	2.01	0.65	3.34	5.13	3.34
1.60	2.28	2.92	0.65	9.23	14.19	3.05
1.60	3.02	0.59	0.62	0.46	0.73	1.75
1.62	3.06	1.06	0.62	1.21	1.93	2.73
1.61	3.10	2.00	0.62	4.01	6.44	3.26
1.61	3.09	2.77	0.62	8.80	14.10	3.09
2.60	0.92	0.40	0.73	-0.18	-0.24	-1.87
2.61	0.94	0.98	0.73	0.23	0.32	1.08
2.60	0.95	2.07	0.73	2.26	3.10	3.03
2.60	0.91	3.26	0.73	7.97	10.89	2.72
2.59	2.28	0.84	0.59	1.02	1.74	3.03
2.61	2.28	1.37	0.59	2.22	3.77	3.51
2.60	2.29	2.48	0.59	7.25	12.29	3.24
2.61	2.23	3.96	0.59	21.89	37.00	2.44
2.62	3.10	1.02	0.56	1.63	2.90	3.09
2.59	3.08	1.51	0.56	3.14	5.60	3.28
2.61	3.10	2.46	0.56	8.94	15.92	2.99
2.59	3.08	3.61	0.56	21.51	38.22	2.46

Note. The TNIE was used to calculate bias for causal mediation. This is not the same estimator as the conventional product of coefficients reported in the logistic regression tables; data were generated from a binomial distribution; effect sizes for a , b , and c' are included because the general designations of s , m , l do not reflect consistent values across coefficients; relative bias values with absolute values above .10 are in bold

Table 7.A

Study 1 Joint Significance CFM - Type 1 Error for N=300

<i>ab</i> Effect Size Combinations	Standard CFM	Joint Significance Tests		
		Model 1-2 and Model 2-4	Model 8-Sat. and Model 7 - Sat.	Model 9-3 and Model 7-Sat.
Overall Type 1 Error	0.28	0.16	0.18	0.05
<i>a = 0, b = 0</i>	0.00	0.01	0.01	0.01
<i>a = 0, b = s</i>	0.02	0.04	0.16	0.05
<i>a = 0, b = m</i>	0.96	0.05	0.43	0.05
<i>a = 0, b = l</i>	1.00	0.06	0.48	0.06
<i>a = s, b = 0</i>	0.00	0.10	0.04	0.04
<i>a = m, b = 0</i>	0.00	0.39	0.06	0.06
<i>a = l, b = 0</i>	0.00	0.50	0.05	0.05

Note. The first column of each sample size reports the values from standard CFM as in Table 1.A; data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values above .075 are in bold; values below .025 are in bold and italics;

Table 7.B

Study 1 Joint Significance CFM - Type 1 Error for N=900

<i>ab</i> Effect Size Combinations	Standard CFM	Joint Significance Tests		
		Model 1-2 and Model 2-4	Model 8-Sat. and Model 7 - Sat.	Model 9-3 and Model 7-Sat.
Overall Type 1 Error	0.35	0.23	0.25	0.05
<i>a = 0, b = 0</i>	0.00	0.00	0.01	0.00
<i>a = 0, b = s</i>	0.44	0.05	0.34	0.05
<i>a = 0, b = m</i>	1.00	0.05	0.61	0.05
<i>a = 0, b = l</i>	1.00	0.05	0.62	0.05
<i>a = s, b = 0</i>	0.00	0.25	0.04	0.05
<i>a = m, b = 0</i>	0.00	0.58	0.05	0.05
<i>a = l, b = 0</i>	0.00	0.64	0.06	0.06

Note. The first column of each sample size reports the values from standard CFM as in Table 1.A; data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values above .075 are in bold; values below .025 are in bold and italics;

Table 8.A

Study 1 Joint Significance CFM – Power for N=300

<i>ab</i> Effect Size Combinations	Standard CFM	Joint Significance Tests		
		Model 1-2 and Model 2-4	Model 8-Sat. and Model 7 - Sat.	Model 9-3 and Model 7-Sat.
a = s, b = s	0.05	0.65	0.28	0.59
a = s, b = m	0.98	0.69	0.33	0.69
a = m, b = s	0.13	0.99	0.69	0.77
a = s, b = l	1.00	0.67	0.30	0.67
a = l, b = s	0.13	1.00	0.54	0.56
a = m, b = m	0.98	1.00	0.61	1.00
a = m, b = l	1.00	1.00	0.48	1.00
a = l, b = m	0.96	1.00	0.73	0.94
a = l, b = l	1.00	1.00	0.63	0.98

Note. The first column of each sample size reports the values from standard CFM as in Table 2.A; data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values below .80 are in bold

Table 8.B

Study 1 Joint Significance CFM – Power for N=900

<i>ab</i> Effect Size Combinations	Standard CFM	Joint Significance Tests		
		Model 1-2 and Model 2-4	Model 8-Sat. and Model 7 - Sat.	Model 9-3 and Model 7-Sat.
a = s, b = s	0.58	0.98	0.55	0.98
a = s, b = m	1.00	0.99	0.52	0.99
a = m, b = s	0.64	1.00	0.97	0.98
a = s, b = l	1.00	0.99	0.58	0.99
a = l, b = s	0.54	1.00	0.90	0.90
a = m, b = m	1.00	1.00	0.76	1.00
a = m, b = l	1.00	1.00	0.60	1.00
a = l, b = m	1.00	1.00	0.93	1.00
a = l, b = l	1.00	1.00	0.79	1.00

Note. The first column of each sample size reports the values from standard CFM as in Table 2.A; data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values below .80 are in bold

Table 9
Study 1 Joint Significance CFM - Type 1 Error for a-path

<i>ab</i> Effect Size Combinations	N=300				N=900			
	Standard CFM		Joint Significance Tests		Standard CFM		Joint Significance Tests	
	Model 1-2	Model 8-Sat.	Model 9-3	Model 6-5	Model 2	Model 8-Sat.	Model 9-3	Model 6-5
Overall Type 1 Error	0.78	0.05	0.29	0.05	0.88	0.05	0.41	0.41
<i>a</i> = 0, <i>b</i> = 0	0.47	0.06	0.06	0.06	0.56	0.05	0.05	0.05
<i>a</i> = 0, <i>b</i> = <i>s</i>	0.65	0.05	0.16	0.05	0.94	0.05	0.34	0.36
<i>a</i> = 0, <i>b</i> = <i>m</i>	1.00	0.05	0.43	0.05	1.00	0.05	0.61	0.61
<i>a</i> = 0, <i>b</i> = <i>l</i>	1.00	0.06	0.48	0.06	1.00	0.05	0.62	0.62

Note. The first column of each sample size reports the values from standard CFM; data were generated from a normal distribution and then dichotomized at zero; *s* = small effect, *m* = medium effect, *l* = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values above .075 are in bold; values below .025 are in bold and italics;

Table 10
 Study 1 Joint Significance CFM - Power for α -path

ab Effect Size Combinations	N=300					N=900				
	Standard CFM		Joint Significance Tests			Standard CFM		Joint Significance Tests		
	Model 1-2	Model 8-Sat.	Model 9-3	Model 6-5	Model 1-2	Model 8-Sat.	Model 9-3	Model 6-5		
a = s, b = s	0.55	0.67	0.55	0.67	0.63	0.77	0.99	0.92	0.99	0.98
a = s, b = m	0.93	1.00	0.99	1.00	1.00	1.00	1.00	1.00	1.00	1.00
a = m, b = s	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
a = s, b = l	0.86	0.67	0.32	0.67	0.34	1.00	0.98	0.55	0.98	0.61
a = l, b = s	1.00	0.69	0.25	0.69	0.22	1.00	0.99	0.52	0.99	0.48
a = m, b = m	1.00	1.00	0.90	1.00	0.99	1.00	1.00	0.99	1.00	1.00
a = m, b = l	1.00	0.67	0.30	0.67	0.27	1.00	0.99	0.58	0.99	0.56
a = l, b = m	1.00	1.00	0.98	1.00	1.00	1.00	1.00	1.00	1.00	1.00
a = l, b = l	1.00	1.00	0.61	1.00	0.77	1.00	1.00	0.76	1.00	0.98

Note. The first column of each sample size reports the values from standard CFM; data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values below .80 are in bold

Table 11
 Study 1 Joint Significance CFM - Type 1 Error for b-path

ab Effect Size Combinations	N=300			N=900		
	Standard CFM	Joint Significance Tests		Standard CFM	Joint Significance Tests	
		Model 2-4	Model 7 -Sat.		Model 2-4	Model 7 -Sat.
Overall Type 1 Error	0.00	0.27	0.06	0.00	0.38	0.05
<i>a = 0, b = 0</i>	0.00	0.05	0.06	0.00	0.05	0.05
<i>a = s, b = 0</i>	0.00	0.11	0.06	0.00	0.25	0.05
<i>a = m, b = 0</i>	0.00	0.39	0.06	0.00	0.58	0.05
<i>a = l, b = 0</i>	0.00	0.50	0.05	0.00	0.64	0.06

Note. The first column of each sample size reports the values from standard CFM; data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values above .075 are in bold; values below .025 are in bold and italics;

Table 12
Study 1 Joint Significance CFM - Power for b-path

<i>ab</i> Effect Size Combinations	N=300			N=900		
	Standard CFM	Joint Significance Tests		Standard CFM	Joint Significance Tests	
		Model 2-4	Model 7 -Sat.		Model 2-4	Model 7 -Sat.
a = s, b = s	0.02	0.91	0.92	0.44	1.00	1.00
a = s, b = m	0.96	1.00	1.00	1.00	1.00	1.00
a = m, b = s	1.00	1.00	1.00	1.00	1.00	1.00
a = s, b = l	0.05	0.97	0.89	0.58	1.00	1.00
a = l, b = s	0.98	0.99	1.00	1.00	1.00	1.00
a = m, b = m	0.13	1.00	0.77	0.64	1.00	0.98
a = m, b = l	1.00	1.00	1.00	1.00	1.00	1.00
a = l, b = m	0.13	1.00	0.56	0.54	1.00	0.90
a = l, b = l	0.98	1.00	0.99	1.00	1.00	1.00

Note. The first column of each sample size reports the values from standard CFM; data were generated from a normal distribution and then dichotomized at zero; s = small effect, m = medium effect, l = large effect; values for the effect sizes were .35, .96, and 1.46 prior to dichotomizing; values below .80 are in bold

Table 13
Study 2 - Power

Condition	Logistic Regression	Configural Frequency Mediation	Causal Mediation
N=300	0.06	0.00a	0.00
N=900	0.45	0.03	0.61
N=2700	0.99	0.39	0.98

Note. Data were generated from a normal distribution and then dichotomized at zero; each condition was comprised of three sub-groups of equal size; avalue was .004 rounded to third decimal

Table 14

Study 2 - Joint Significance CFM - Power

<i>Condition</i>	Standard CFM	<i>Joint Significance Tests</i>		
		Model 1-2 and Model 2-4	Model 8-Sat. and Model 7-Sat.	Model 9-3 and Model 7-Sat.
n=100	0.26	0.20	0.03	0.11
n=300	0.33	0.68	0.25	0.60
n=900	0.33	1.00	0.75	1.00

Table 15

Study 2 – Joint Significance CFM - Power for a-path

Joint Significance Tests				
<i>Condition</i>	Model 1-2	Model 8-Sat.	Model 9-3	Model 6-5
n=100	0.31	0.15	0.31	0.15
n=300	0.70	0.32	0.70	0.33
n=900	1.00	0.75	1.00	0.76

Table 16

Study 2 – Joint Significance CFM - Power for b-path

Joint Significance Tests

<i>Condition</i>	Model 2-4	Model 7-Sat.
n=100	0.57	0.41
n=300	0.96	0.86
n=900	1.00	1.00

Table 17

Study 2 - Types and Antitypes for Base Model N=100

Configuration XMY	Mean Observed Frequency	Mean Predicted Frequency	Base Model	Percentage
000	15.12	7.91	Type	41.80
001	9.97	13.63	Antitype	0.07
010	9.88	10.40		
011	15.04	18.06	Antitype	0.03
100	5.65	7.82	Antitype	0.07
101	12.27	13.64		
110	5.83	10.34	Antitype	0.87
111	26.25	18.19	Type	11.17

Table 18

Study 2 - Types and Antitypes for Base Model N=300

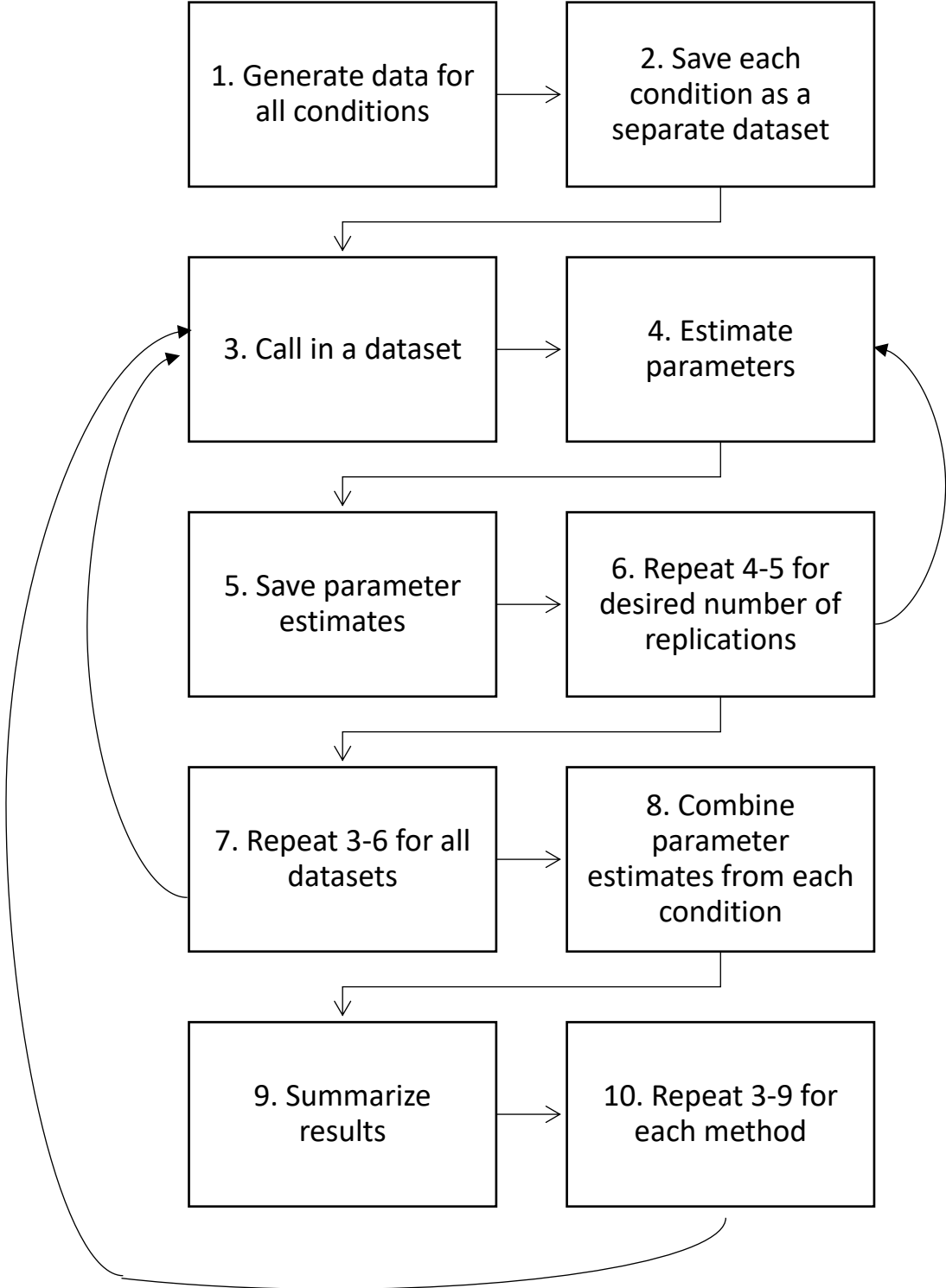
Configuration XMY	Mean Observed Frequency	Mean Predicted Frequency	Base Model	Percentage
000	45.24	23.64	Type	97.67
001	29.93	40.93	Antitype	4.73
010	29.94	31.32		
011	45.15	54.38	Antitype	0.70
100	17.01	23.47	Antitype	1.47
101	36.64	40.80	Antitype	0.03
110	17.39	31.16	Antitype	34.00
111	78.69	54.32	Type	81.30

Table 19

Study 2 - Types and Antitypes for Base Model N=900

Configuration XMY	Mean Observed Frequency	Mean Predicted Frequency	Base Model	Percentage
000	135.88	70.52	Type	100.00
001	89.39	122.65	Antitype	65.70
010	89.55	93.84	Antitype	0.03
011	135.55	163.36	Antitype	17.80
100	50.64	70.31	Antitype	29.23
101	110.03	122.47	Antitype	0.57
110	52.23	93.63	Antitype	99.47
111	236.73	163.22	Type	100.00

APPENDIX A
SIMULATION FLOWCHART



APPENDIX B
SAS DATA GENERATION MACRO

```

%MACRO SIMULATE (NSIM, NOBS, BMX, BYX, BYM, FILE, COND, TYPE, ERROR) ;

DATA SUMMARY; SET _NULL_ ;
  %DO I=1 %TO &NSIM;
    DATA SIM;
    DO n=1 TO &NOBS;
    XC=(&error)*RANNOR(0);
    IF XC>0 then X=1;
    IF XC<=0 then X=0;
    M=&BMX*X+(&error)*RANNOR(0);
    MeanM=&bmx*x;
    if M>0 then MC=1;
    if M<=0 then MC=0;
    Y=&BYX*X+&BYM*M+(&error)*RANNOR(0);
    MeanY=(&byx*x+&bym*m);
    if Y>0 then YC=1;
    if Y<=0 then YC=0;
    all3=X*100+MC*10+YC;
    X2=X*X;
    Prod=&BMX*&BYM;
    Cond=&COND;
    rep=&I;
    check=1;
    OUTPUT;
  END;
RUN;

/*Appending replications to a single dataset per condition*/
DATA New; SET Sim;
DATA Summary; SET Summary New;
%END;

/*Saving summary dataset as a new dataset in the Simdata library*/
data Simdata.&file; SET Summary;
;
RUN;
%MEND;

```

APPENDIX C
SAS BINOMIAL DATA GENERATION MACRO

```

%MACRO SIMULATE (NSIM, NOBS, MEANiM, MEANiY, MEANA, MEANB, MEANCP, FILE, COND) ;

DATA SUMMARY;
totaln=&NSIM*&NOBS;
  do n=1 to totaln;
    x=ranbin(0,1,.5);
    pm=1/(1+exp(-(&MEANiM+&MEANA*x)));
    m=ranbin(0,1,pm);
    py=1/(1+exp(-(&MEANiY+&MEANCP*x+&MEANB*m)));
    y=ranbin(0,1,py);
    Cond=&COND;
    /*
      rep=&nobs;*/
      file="&file";
      all3=X*100+M*10+Y;
      check=1;
    output;
  end;
run;

data data.&file; SET Summary;
;
RUN;

Proc datasets LIB=work KILL NOLIST; run; quit;
%MEND simulate;
run;

```

APPENDIX D
SAS LOGISTIC REGRESSION ANALYSIS MACRO

```

%MACRO ANALYZE1 (BMX,BYX,BYM,FILE,COND);

DATA SUMMARY2; SET _NULL_;

*Logistic regression model YC=X*
*Estimating and saving coefficients and standard errors*;
proc logistic data = Simdata.&FILE descending outest= FILE covout
noprnt;
    BY rep;
    model yc = x /clparm = both clodds=both;
DATA B; SET FILE;
    IF _TYPE_='PARMS'; C=X; LogL1C=_LNLIKE_;
    cond = &cond;
    StatusM1 = _STATUS_;
    KEEP cond rep C LogL1C StatusM1;
DATA C; SET FILE;
    IF _NAME_='X'; SEC=SQRT(X);
    cond = &cond;
    KEEP cond rep SEC;
DATA MODEL1; MERGE B C;
RUN;

*Logistic Regression: Model YC=X MC*
*Estimating and saving coefficients and standard errors*;
proc logistic data = Simdata.&FILE descending outest= FILE covout
noprnt;
    BY rep;
    model yc = x mc /clparm=both clodds = both covb;
DATA B; SET FILE;
    IF _TYPE_='PARMS'; Cprm=X; B=MC; LogL2BCprm=_LNLIKE_;
    cond = &cond;
    StatusM2 = _STATUS_;
    KEEP cond rep Cprm B LogL2BCprm StatusM2;
DATA C; SET FILE;
    IF _NAME_='X'; SECprm=SQRT(X);
    cond = &cond;
    KEEP cond rep SECprm;
DATA D; SET FILE;
    IF _NAME_='MC'; SEB=SQRT(MC);
    cond = &cond;
    KEEP cond rep SEB;
DATA MODEL2; MERGE B C D;
RUN;

*Logistic Regression: Model MC=X *
*Estimating and saving coefficients and standard errors*;
proc logistic data = Simdata.&FILE descending outest=FILE covout
noprnt;
    BY rep;
    model mc = x /clparm=both clodds = both covb;
DATA B; SET FILE;
    IF _TYPE_='PARMS'; A=X; LogL3A=_LNLIKE_;
    cond = &cond;
    StatusM3 = _STATUS_;

```

```

        KEEP cond rep A LogL3A StatusM3;
DATA C; SET FILE;
    IF _NAME_='X'; SEA=SQRT(X);
    cond = &cond;
    KEEP cond rep SEA;
DATA MODEL3; MERGE B C;
RUN;

*Combining models into single dataset;
DATA LogRegModels; MERGE MODEL1 MODEL2 MODEL3;

*Computing product of coefficients and true standard error of mediated
effect,
saving true values of path coefficients and product of coefficients;
DATA LogRegMedEff; SET LogRegModels;
    merge = 1;
    ProdMedEff = A*B;
    SobelAB = SQRT(A*A*SEB*SEB+B*B*SEA*SEA);
    ZSobel=ProdMedEff/SobelAB;
    PSobel=1-PROBNORM(ZSobel);
    BMX = &BMX;
    BYM = &BYM;
    BYX = &BYX;
    Prod=&BMX*&BYM;
RUN;

*Appending replications to a single dataset per condition*;
DATA Summary2; Set Summary2 LogRegMedEff;
DATA Dataout.LogRout&file; SET Summary2;

*Calculating and saving standard deviations of estimates across
replications;
proc means data = LogRegMedEff noprint;
    var rep C LogL1C cond SEC Cprm B LogL2BCprm SECprm SEB A LogL3A
SEA ProdMedEff SobelAB BMX BYM BYX;
    output out=lrmeans
        mean = rep C LogL1C cond SEC Cprm B LogL2BCprm SECprm SEB A
LogL3A SEA ProdMedEff SobelAB BMX BYM BYX
        STD = stdrep stdC stdLogL1C stdcond stdSEC stdCprm stdB
stdLogL2BCprm stdSECprm stdSEB stdA stdLogL3A stdSEA stdProdMedEff
stdSobelAB stdBMX stdBYM stdBYX;
RUN;

DATA lrmeans2; set lrmeans;
    merge = 1;
    keep merge cond stdC stdSEC stdCprm stdB stdSECprm stdSEB stdA
stdSEA stdProdMedEff;
run;

*Calculating bias, relative bias, and standardized bias;
DATA Logresults; merge LogRegMedEff lrmeans2; by merge;
    BiasCp = Cprm-BYX;
    RBCp = BiasCp/BYX;
    StBCp = BiasCp/stdCprm;

```

```
BiasB = B-BYM;
RBB = BiasB/BYM;
StBB = BiasB/stdB;
BiasA = A-BMX;
RBA = BiasA/BMX;
StBA = BiasA/stdA;
RUN;

*Saving results;
data Dataout.LogResultsout&file; SET Logresults;
;
run;
%MEND;
```


APPENDIX E
SAS CFM ANALYSIS MACRO

```

*Setting up dataset for frequencies;
data combbbb; input all3 COUNT;
cards;
0 0
1 0
10 0
11 0
100 0
101 0
110 0
111 0
;
run;

data MIDS;
input mergeid;
cards;
1
2
3
4
5
6
7
8
;
run;

%MACRO ANALYZE3 (NSIM, FILE, COND);

DATA SUMMARY4; SET _NULL_;
DATA output1a; SET _NULL_;
*Calculating frequencies;
proc freq data=Simdata.&FILE noprint;
    BY rep;
    tables all3/out=outputg;
run;

%DO I=1 %TO &NSIM;
    DATA interim; SET outputg;
    IF rep = &I;
    ;
    RUN;
proc sort data=interim; by all3; run;
data outputh; merge combbbb interim; by all3; run;

*Appending replications to a single dataset;
Data output1a; Set output1a outputh;run;
%END;

data output1; set output1a;
n=_n_;
if rep = '.' and all3=0 then do;

```

```

        n=n+1;
        end;
        set output1a(keep=rep) point=n;
if rep = '.' and all3 >0 then do;
        n=n-1;
        end;
        set output1a(keep=rep) point=n;
run;

%DO I=1 %TO &NSIM;
    DATA Rep; SET output1;
        IF rep = &I;
    ;
    RUN;

data n1; set Rep; if all3=0;
    If all3=0 then n1=COUNT; keep n1;
data n2; set Rep; if all3=1;
    If all3=1 then n2=COUNT; keep n2;
data n3; set Rep; if all3=10;
    If all3=10 then n3=COUNT; keep n3;
data n4; set Rep; if all3=11;
    If all3=11 then n4=COUNT; keep n4;
data n5; set Rep; if all3=100;
    If all3=100 then n5=COUNT; keep n5;
data n6; set Rep; if all3=101;
    If all3=101 then n6=COUNT; keep n6;
data n7; set Rep; if all3=110;
    If all3=110 then n7=COUNT; keep n7;
data n8; set Rep; n8=0; if all3=111;
    If all3=111 then n8=COUNT; keep n8;
data freqs; merge n1 n2 n3 n4 n5 n6 n7 n8;

proc transpose data=freqs out=newfreq; var n1 n2 n3 n4 n5 n6 n7 n8;
RUN;

data new; set newfreq;
    x=0; m=0; y=0;
    if _n_=2 then y=1;
    if _n_=3 then m=1;
    if _n_=4 then m=1; if _n_=4 then y=1;
    if _n_=5 then x=1;
    if _n_=6 then x=1; if _n_=6 then y=1;
    if _n_=7 then x=1; if _n_=7 then m=1;
    if _n_=8 then x=1; if _n_=8 then m=1; if _n_=8 then y=1;
    freq=coll;
    keep x m y freq;
run;

*CFA Base Model 1 First Order CFA Main Effects of XMY
Estimating and saving frequencies;
ods results off;
ods listing close;
ods html close;

```

```

ods output PredictedFreqs=outputm1 anova=outputm1a
convergencestatus=cs1 Estimates=outputm1e;
proc catmod data=new;
    weight freq;
    model X*M*Y=_response_ / pred=freq zero=samp ML;
    loglin X M Y;
    title2 'MODEL 1: Main Effects only';
quit;
ods output close;
ods listing;
ods html;
run;

*Adding convergence status to predicted frequencies;
data outputm1; merge outputm1 cs1; run;

*Testing frequencies for types and antitypes;
data typeres1; set outputm1
    (rename=(obsstderr=obsse_1 predfunction=predfreq_1
predstderr=predse_1 residual=residual_1 reason=reason_1
status=status_1));
    pearson_z1=(obsfunction-predfreq_1)/sqrt(predfreq_1);
    neyman_1=(obsfunction-predfreq_1)/sqrt(obsfunction);
    if pearson_z1 > 2.7344 then types_1 = 1;
    if pearson_z1 < -2.7344 then types_1 = -1;
    if pearson_z1 >= -2.7344 & pearson_z1 <= 2.7344 then types_1 = 0;
run;

*CFA Base Model 2 Main Effects and XM Interaction
Estimating and saving frequencies;
ods listing close;
ods html close;
ods output PredictedFreqs=outputm2 anova=outputm2a
convergencestatus=cs2 Estimates=outputm2e;
proc catmod data=new;
    weight freq;
    model X*M*Y=_response_ / pred=freq zero=samp ML;
    loglin X M Y x*M;
    title2 'MODEL 2: XM Interaction and Main Effects';
quit;
ods output close;
ods listing;
ods html;
run;

*Adding convergence status to predicted frequencies;
data outputm2; merge outputm2 cs2; run;

*Testing frequencies for types and antitypes;
data typeres2; set outputm2
    (rename=(obsstderr=obsse_2 predfunction=predfreq_2
predstderr=predse_2 residual=residual_2 reason=reason_2
status=status_2));
    pearson_z2=(obsfunction- predfreq_2)/sqrt(predfreq_2);

```

```

neyman_2=(obsfunction- predfreq_2)/sqrt(obsfunction);
if pearson_z2 > 2.7344 then types_2 = 1;
if pearson_z2 < -2.7344 then types_2 = -1;
if pearson_z2 >= -2.7344 & pearson_z2 <= 2.7344 then types_2 = 0;
run;

*CFA Base Model 3 Main Effects and XM XY Interactions
Estimating and saving frequencies;
ods listing close;
ods html close;
ods output PredictedFreqs=outputm3 anova=outputm3a
convergencestatus=cs3 Estimates=outputm3e;
proc catmod data=new;
    weight freq;
    model X*M*Y=_response_ / pred=freq zero=samp ML;
    loglin X M Y x*M x*Y;
    title2 'MODEL 3: XM XY Interactions and Main Effects';
quit;
ods output close;
ods listing;
ods html;
run;

*Adding convergence status to predicted frequencies;
data outputm3; merge outputm3 cs3; run;

*Testing frequencies for types and antitypes;
data typeres3; set outputm3
    (rename=(obsstderr=obsse_3 predfunction=predfreq_3
predstderr=predse_3 residual=residual_3 reason=reason_3
status=status_3));
    pearson_z3=(obsfunction- predfreq_3)/sqrt(predfreq_3);
    neyman_3=(obsfunction- predfreq_3)/sqrt(obsfunction);
    if pearson_z3 > 2.7344 then types_3 = 1;
    if pearson_z3 < -2.7344 then types_3 = -1;
    if pearson_z3 >= -2.7344 & pearson_z3 <= 2.7344 then types_3 = 0;
run;

*CFA Base Model 4 Main Effects and XM MY Interactions
Estimating and saving frequencies;
ods listing close;
ods html close;
ods output PredictedFreqs=outputm4 anova=outputm4a
convergencestatus=cs4 Estimates=outputm4e;
proc catmod data=new ;
    weight freq;
    model X*M*Y=_response_ / pred=freq zero=samp ML;
    loglin X M Y x*M m*Y;
    title2 'MODEL 4: XM MY Interactions and Main Effects';
quit;
ods output close;
ods listing;
ods html;

```

```

run;

*Adding convergence status to predicted frequencies;
data outputm4; merge outputm4 cs4; run;

*Testing frequencies for types and antitypes;
data typeres4; set outputm4
    (rename=(obsstderr=obsse_4 predfunction=predfreq_4
predstderr=predse_4 residual=residual_4 reason=reason_4
status=status_4));
    pearson_z4=(obsfunction- predfreq_4)/sqrt(predfreq_4);
    neyman_4=(obsfunction- predfreq_4)/sqrt(obsfunction);
    if pearson_z4 > 2.7344 then types_4 = 1;
    if pearson_z4 < -2.7344 then types_4 = -1;
    if pearson_z4 >= -2.7344 & pearson_z4 <= 2.7344 then types_4 = 0;
run;

*Second Order CFA Main Effects and XM MY XY Interactions
Estimating and saving frequencies;
ods listing close;
ods html close;
ods output PredictedFreqs=outputm5 anova=outputm5a
convergencestatus=cs5 Estimates=outputm5e;
proc catmod data=new;
    weight freq;
    model X*M*Y=_response_ / pred=freq zero=samp ML;
    loglin X|M|Y @2;
    title2 'Second Order CFA Main and all 2-way effects';
quit;
ods output close;
ods listing;
ods html;
run;

*Adding convergence status to predicted frequencies;
data outputm5; merge outputm5 cs5; run;

*Testing frequencies for types and antitypes;
data typeres5; set outputm5
    (rename=(obsstderr=obsse_5 predfunction=predfreq_5
predstderr=predse_5 residual=residual_5 reason=reason_5
status=status_5));
    pearson_z5=(obsfunction-predfreq_5)/sqrt(predfreq_5);
    neyman_5=(obsfunction-predfreq_5)/sqrt(obsfunction);
    if pearson_z5 > 2.7344 then types_5 = 1;
    if pearson_z5 < -2.7344 then types_5 = -1;
    if pearson_z5 >= -2.7344 & pearson_z5 <= 2.7344 then types_5 = 0;
run;

*Sorting and merging model results into a single file;
proc sort data=typeres1; by fonctionnum; run;
proc sort data=typeres2; by fonctionnum; run;
proc sort data=typeres3; by fonctionnum; run;
proc sort data=typeres4; by fonctionnum; run;

```

```

proc sort data=typeres5; by fonctionnum; run;

data allmodels;
  merge typeres1 typeres2 typeres3 typeres4 typeres5;
  by fonctionnum;
  drop model sample control;
run;
quit;

proc sort data=outputm1a; by source; run;
proc sort data=outputm2a; by source; run;
proc sort data=outputm3a; by source; run;
proc sort data=outputm4a; by source; run;
proc sort data=outputm5a; by source; run;
data like1; set outputm1a (obs=1); run;
data like2; set outputm2a (obs=1); run;
data like3; set outputm3a (obs=1); run;
data like4; set outputm4a (obs=1); run;
data like5; set outputm5a (obs=1); run;

data b; set allmodels;
  keep obsfunction;
run;
data b1; Merge MIDS b;
run;

data c; set like1;
  rename df=df1;
  rename chisq=chisq1;
  rename probchisq=probchisq1;
  drop model dfkey control;
  output; output; output; output; output; output; output; output;
run;

data d; set like2;
  rename df=df2;
  rename chisq=chisq2;
  rename probchisq=probchisq2;
  drop model dfkey control;
  output; output; output; output; output; output; output; output;
run;

data e; set like3;
  rename df=df3;
  rename chisq=chisq3;
  rename probchisq=probchisq3;
  drop model dfkey control;
  output; output; output; output; output; output; output; output;
run;

data f; set like4;
  rename df=df4;
  rename chisq=chisq4;
  rename probchisq=probchisq4;

```

```

        drop model dfkey control;
        output; output; output; output; output; output; output; output; output;
run;

data g; set like5;
        rename df=df5;
        rename chisq=chisq5;
        rename probchisq=probchisq5;
        drop model dfkey control;
        output; output; output; output; output; output; output; output;
run;

data c1; Merge MIDS c;
run;
data d1; Merge MIDS d;
run;
data e1; Merge MIDS e;
run;
data f1; Merge MIDS f;
run;
data g1; Merge MIDS g;
run;

data allchisq;
        merge b1 c1 d1 e1 f1 g1;
        by mergeid;
        drop Source;
run;

data allmodmerg; Merge MIDS allmodels;
run;

proc sort data=outputm1e; by parameter; run;
proc sort data=outputm2e; by parameter; run;
proc sort data=outputm3e; by parameter; run;
proc sort data=outputm4e; by parameter; run;
proc sort data=outputm5e; by parameter; run;

/*model 1 estimates*/
data m1estrow1; set outputm1e;
if Parameter = "x" THEN DO; xest_m1=estimate; xse_m1=stderr;
xchisq_m1=chisq; xpval_m1=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m1estrow2; set outputm1e;
if Parameter = "m" THEN DO; mest_m1=estimate; mse_m1=stderr;
mchisq_m1=chisq; mpval_m1=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

```



```

data mlestrow3; set outputm1e;
if Parameter = "y" THEN DO; yest_m1=estimate; yse_m1=stderr;
ychisq_m1=chisq; ypval_m1=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data mlest; merge mlestrow1 mlestrow2 mlestrow3; run;

/*model 2 estimates*/
data m2estrow1; set outputm2e;
if Parameter = "x" THEN DO; xest_m2=estimate; xse_m2=stderr;
xchisq_m2=chisq; xpval_m2=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m2estrow2; set outputm2e;
if Parameter = "m" THEN DO; mest_m2=estimate; mse_m2=stderr;
mchisq_m2=chisq; mpval_m2=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m2estrow3; set outputm2e;
if Parameter = "y" THEN DO; yest_m2=estimate; yse_m2=stderr;
ychisq_m2=chisq; ypval_m2=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m2est; merge m2estrow1 m2estrow2 m2estrow3; run;

/*model 3 estimates*/
data m3estrow1; set outputm3e;
if Parameter = "x" THEN DO; xest_m3=estimate; xse_m3=stderr;
xchisq_m3=chisq; xpval_m3=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m3estrow2; set outputm3e;
if Parameter = "m" THEN DO; mest_m3=estimate; mse_m3=stderr;
mchisq_m3=chisq; mpval_m3=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

```

```

data m3estrow3; set outputm3e;
if Parameter = "y" THEN DO; yest_m3=estimate; yse_m3=stderr;
ychisq_m3=chisq; ypval_m3=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m3est; merge m3estrow1 m3estrow2 m3estrow3; run;

/*model 4 estimates*/
data m4estrow1; set outputm4e;
if Parameter = "x" THEN DO; xest_m4=estimate; xse_m4=stderr;
xchisq_m4=chisq; xpval_m4=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m4estrow2; set outputm4e;
if Parameter = "m" THEN DO; mest_m4=estimate; mse_m4=stderr;
mchisq_m4=chisq; mpval_m4=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m4estrow3; set outputm4e;
if Parameter = "y" THEN DO; yest_m4=estimate; yse_m4=stderr;
ychisq_m4=chisq; ypval_m4=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m4est; merge m4estrow1 m4estrow2 m4estrow3; run;

/*model 5 estimates*/
data m5estrow1; set outputm5e;
if Parameter = "x" THEN DO; xest_m5=estimate; xse_m5=stderr;
xchisq_m5=chisq; xpval_m5=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m5estrow2; set outputm5e;
if Parameter = "m" THEN DO; mest_m5=estimate; mse_m5=stderr;
mchisq_m5=chisq; mpval_m5=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

```

```

data m5estrow3; set outputm5e;
if Parameter = "y" THEN DO; yest_m5=estimate; yse_m5=stderr;
ychisq_m5=chisq; ypval_m5=probchisq; end;
else do; delete; end;
cond=&cond;
drop model parameter classvalue estimate note stderr chisq probchisq;
run;

data m5est; merge m5estrow1 m5estrow2 m5estrow3; run;

data allest; merge m1est m2est m3est m4est m5est; run;

data newallmod;
    merge allmodmerg allchisq;
    by mergeid;
    rep = &I;
run;

*Arranging data into single row per replication;
data namrow1; set newallmod; if mergeid=1;
    x_n1 = x; m_n1 = m; y_n1 = y; FunctionNum_n1 = FunctionNum;
ObsFunction_n1 = ObsFunction; obsse_m1_n1 = obsse_1; predfreq_m1_n1 =
predfreq_1; predse_m1_n1 = predse_1; residual_m1_n1 = residual_1;
pearson_zm1_n1 = pearson_z1; neyman_m1_n1 = neyman_1; types_m1_n1 =
types_1; obsse_m2_n1 = obsse_2; predfreq_m2_n1 = predfreq_2;
predse_m2_n1 = predse_2; residual_m2_n1 = residual_2; pearson_zm2_n1 =
pearson_z2; neyman_m2_n1 = neyman_2; types_m2_n1 = types_2; obsse_m3_n1
= obsse_3; predfreq_m3_n1 = predfreq_3; predse_m3_n1 = predse_3;
residual_m3_n1 = residual_3; pearson_zm3_n1 = pearson_z3; neyman_m3_n1
= neyman_3; types_m3_n1 = types_3; obsse_m4_n1 = obsse_4;
predfreq_m4_n1 = predfreq_4; predse_m4_n1 = predse_4; residual_m4_n1 =
residual_4; pearson_zm4_n1 = pearson_z4; neyman_m4_n1 = neyman_4;
types_m4_n1 = types_4; obsse_m5_n1 = obsse_5; predfreq_m5_n1 =
predfreq_5; predse_m5_n1 = predse_5; residual_m5_n1 = residual_5;
pearson_zm5_n1 = pearson_z5; neyman_m5_n1 = neyman_5; types_m5_n1 =
types_5; df_m1_n1 = df1; chisq_m1_n1 = chisq1; p_m1_n1 = probchisq1;
df_m2_n1 = df2; chisq_m2_n1 = chisq2; p_m2_n1 = probchisq2; df_m3_n1 =
df3; chisq_m3_n1 = chisq3; p_m3_n1 = probchisq3; df_m4_n1 = df4;
chisq_m4_n1 = chisq4; p_m4_n1 = probchisq4; df_m5_n1 = df5; chisq_m5_n1
= chisq5; p_m5_n1 = probchisq5;
    cond = &cond;
    drop mergeid x m y FunctionNum ObsFunction
    obsse_1 predfreq_1 predse_1 residual_1 pearson_z1 neyman_1
types_1
    obsse_2 predfreq_2 predse_2 residual_2 pearson_z2 neyman_2
types_2
    obsse_3 predfreq_3 predse_3 residual_3 pearson_z3 neyman_3
types_3
    obsse_4 predfreq_4 predse_4 residual_4 pearson_z4 neyman_4
types_4
    obsse_5 predfreq_5 predse_5 residual_5 pearson_z5 neyman_5
types_5

```

```

df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5
obsse_m2_n1 obsse_m3_n1 obsse_m4_n1 obsse_m5_n1;

data namrow2; set newallmod; if mergeid=2;
x_n2 = x; m_n2 = m; y_n2 = y; FunctionNum_n2 = FunctionNum;
ObsFunction_n2 = ObsFunction; obsse_m1_n2 = obsse_1; predfreq_m1_n2 =
predfreq_1; predse_m1_n2 = predse_1; residual_m1_n2 = residual_1;
pearson_zm1_n2 = pearson_z1; neyman_m1_n2 = neyman_1; types_m1_n2 =
types_1; obsse_m2_n2 = obsse_2; predfreq_m2_n2 = predfreq_2;
predse_m2_n2 = predse_2; residual_m2_n2 = residual_2; pearson_zm2_n2 =
pearson_z2; neyman_m2_n2 = neyman_2; types_m2_n2 = types_2; obsse_m3_n2
= obsse_3; predfreq_m3_n2 = predfreq_3; predse_m3_n2 = predse_3;
residual_m3_n2 = residual_3; pearson_zm3_n2 = pearson_z3; neyman_m3_n2
= neyman_3; types_m3_n2 = types_3; obsse_m4_n2 = obsse_4;
predfreq_m4_n2 = predfreq_4; predse_m4_n2 = predse_4; residual_m4_n2 =
residual_4; pearson_zm4_n2 = pearson_z4; neyman_m4_n2 = neyman_4;
types_m4_n2 = types_4; obsse_m5_n2 = obsse_5; predfreq_m5_n2 =
predfreq_5; predse_m5_n2 = predse_5; residual_m5_n2 = residual_5;
pearson_zm5_n2 = pearson_z5; neyman_m5_n2 = neyman_5; types_m5_n2 =
types_5; df_m1_n2 = df1; chisq_m1_n2 = chisq1; p_m1_n2 = probchisq1;
df_m2_n2 = df2; chisq_m2_n2 = chisq2; p_m2_n2 = probchisq2; df_m3_n2 =
df3; chisq_m3_n2 = chisq3; p_m3_n2 = probchisq3; df_m4_n2 = df4;
chisq_m4_n2 = chisq4; p_m4_n2 = probchisq4; df_m5_n2 = df5; chisq_m5_n2
= chisq5; p_m5_n2 = probchisq5;
cond = &cond;
drop mergeid x m y FunctionNum ObsFunction
obsse_1 predfreq_1 predse_1 residual_1 reason_1 status_1
pearson_z1 neyman_1 types_1
obsse_2 predfreq_2 predse_2 residual_2 reason_2 status_2
pearson_z2 neyman_2 types_2
obsse_3 predfreq_3 predse_3 residual_3 reason_3 status_3
pearson_z3 neyman_3 types_3
obsse_4 predfreq_4 predse_4 residual_4 reason_4 status_4
pearson_z4 neyman_4 types_4
obsse_5 predfreq_5 predse_5 residual_5 reason_5 status_5
pearson_z5 neyman_5 types_5
df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5
obsse_m2_n2 obsse_m3_n2 obsse_m4_n2 obsse_m5_n2
df_m1_n2 chisq_m1_n2 p_m1_n2 df_m2_n2 chisq_m2_n2 p_m2_n2
df_m3_n2
chisq_m3_n2 p_m3_n2 df_m4_n2 chisq_m4_n2 p_m4_n2 df_m5_n2
chisq_m5_n2 p_m5_n2;

data namrow3; set newallmod; if mergeid=3;
x_n3 = x; m_n3 = m; y_n3 = y; FunctionNum_n3 = FunctionNum;
ObsFunction_n3 = ObsFunction; obsse_m1_n3 = obsse_1; predfreq_m1_n3 =
predfreq_1; predse_m1_n3 = predse_1; residual_m1_n3 = residual_1;
pearson_zm1_n3 = pearson_z1; neyman_m1_n3 = neyman_1; types_m1_n3 =
types_1; obsse_m2_n3 = obsse_2; predfreq_m2_n3 = predfreq_2;
predse_m2_n3 = predse_2; residual_m2_n3 = residual_2; pearson_zm2_n3 =
pearson_z2; neyman_m2_n3 = neyman_2; types_m2_n3 = types_2; obsse_m3_n3
= obsse_3; predfreq_m3_n3 = predfreq_3; predse_m3_n3 = predse_3;

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residual_m3_n3 = residual_3; pearson_zm3_n3 = pearson_z3; neyman_m3_n3
= neyman_3; types_m3_n3 = types_3; obsse_m4_n3 = obsse_4;
predfreq_m4_n3 = predfreq_4; predse_m4_n3 = predse_4; residual_m4_n3 =
residual_4; pearson_zm4_n3 = pearson_z4; neyman_m4_n3 = neyman_4;
types_m4_n3 = types_4; obsse_m5_n3 = obsse_5; predfreq_m5_n3 =
predfreq_5; predse_m5_n3 = predse_5; residual_m5_n3 = residual_5;
pearson_zm5_n3 = pearson_z5; neyman_m5_n3 = neyman_5; types_m5_n3 =
types_5; df_m1_n3 = df1; chisq_m1_n3 = chisq1; p_m1_n3 = probchisq1;
df_m2_n3 = df2; chisq_m2_n3 = chisq2; p_m2_n3 = probchisq2; df_m3_n3 =
df3; chisq_m3_n3 = chisq3; p_m3_n3 = probchisq3; df_m4_n3 = df4;
chisq_m4_n3 = chisq4; p_m4_n3 = probchisq4; df_m5_n3 = df5; chisq_m5_n3
= chisq5; p_m5_n3 = probchisq5;
    cond = &cond;
    drop mergeid x m y FunctionNum ObsFunction
    obsse_1 predfreq_1 predse_1 residual_1 reason_1 status_1
pearson_z1 neyman_1 types_1
    obsse_2 predfreq_2 predse_2 residual_2 reason_2 status_2
pearson_z2 neyman_2 types_2
    obsse_3 predfreq_3 predse_3 residual_3 reason_3 status_3
pearson_z3 neyman_3 types_3
    obsse_4 predfreq_4 predse_4 residual_4 reason_4 status_4
pearson_z4 neyman_4 types_4
    obsse_5 predfreq_5 predse_5 residual_5 reason_5 status_5
pearson_z5 neyman_5 types_5
    df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5
    obsse_m2_n3 obsse_m3_n3 obsse_m4_n3 obsse_m5_n3
    df_m1_n3 chisq_m1_n3 p_m1_n3 df_m2_n3 chisq_m2_n3 p_m2_n3
df_m3_n3
    chisq_m3_n3 p_m3_n3 df_m4_n3 chisq_m4_n3 p_m4_n3 df_m5_n3
chisq_m5_n3 p_m5_n3;

data namrow4; set newallmod; if mergeid=4;
    x_n4 = x; m_n4 = m; y_n4 = y; FunctionNum_n4 = FunctionNum;
ObsFunction_n4 = ObsFunction; obsse_m1_n4 = obsse_1; predfreq_m1_n4 =
predfreq_1; predse_m1_n4 = predse_1; residual_m1_n4 = residual_1;
pearson_zm1_n4 = pearson_z1; neyman_m1_n4 = neyman_1; types_m1_n4 =
types_1; obsse_m2_n4 = obsse_2; predfreq_m2_n4 = predfreq_2;
predse_m2_n4 = predse_2; residual_m2_n4 = residual_2; pearson_zm2_n4 =
pearson_z2; neyman_m2_n4 = neyman_2; types_m2_n4 = types_2; obsse_m3_n4
= obsse_3; predfreq_m3_n4 = predfreq_3; predse_m3_n4 = predse_3;
residual_m3_n4 = residual_3; pearson_zm3_n4 = pearson_z3; neyman_m3_n4
= neyman_3; types_m3_n4 = types_3; obsse_m4_n4 = obsse_4;
predfreq_m4_n4 = predfreq_4; predse_m4_n4 = predse_4; residual_m4_n4 =
residual_4; pearson_zm4_n4 = pearson_z4; neyman_m4_n4 = neyman_4;
types_m4_n4 = types_4; obsse_m5_n4 = obsse_5; predfreq_m5_n4 =
predfreq_5; predse_m5_n4 = predse_5; residual_m5_n4 = residual_5;
pearson_zm5_n4 = pearson_z5; neyman_m5_n4 = neyman_5; types_m5_n4 =
types_5; df_m1_n4 = df1; chisq_m1_n4 = chisq1; p_m1_n4 = probchisq1;
df_m2_n4 = df2; chisq_m2_n4 = chisq2; p_m2_n4 = probchisq2; df_m3_n4 =
df3; chisq_m3_n4 = chisq3; p_m3_n4 = probchisq3; df_m4_n4 = df4;
chisq_m4_n4 = chisq4; p_m4_n4 = probchisq4; df_m5_n4 = df5; chisq_m5_n4
= chisq5; p_m5_n4 = probchisq5;
    cond = &cond;

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```

    drop mergeid x m y FunctionNum ObsFunction
    obsse_1 predfreq_1 predse_1 residual_1 reason_1 status_1
pearson_z1 neyman_1 types_1
    obsse_2 predfreq_2 predse_2 residual_2 reason_2 status_2
pearson_z2 neyman_2 types_2
    obsse_3 predfreq_3 predse_3 residual_3 reason_3 status_3
pearson_z3 neyman_3 types_3
    obsse_4 predfreq_4 predse_4 residual_4 reason_4 status_4
pearson_z4 neyman_4 types_4
    obsse_5 predfreq_5 predse_5 residual_5 reason_5 status_5
pearson_z5 neyman_5 types_5
    df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5
    obsse_m2_n4 obsse_m3_n4 obsse_m4_n4 obsse_m5_n4
    df_m1_n4 chisq_m1_n4 p_m1_n4 df_m2_n4 chisq_m2_n4 p_m2_n4
df_m3_n4
    chisq_m3_n4 p_m3_n4 df_m4_n4 chisq_m4_n4 p_m4_n4 df_m5_n4
chisq_m5_n4 p_m5_n4;

data namrow5; set newallmod; if mergeid=5;
    x_n5 = x; m_n5 = m; y_n5 = y; FunctionNum_n5 = FunctionNum;
ObsFunction_n5 = ObsFunction; obsse_m1_n5 = obsse_1; predfreq_m1_n5 =
predfreq_1; predse_m1_n5 = predse_1; residual_m1_n5 = residual_1;
pearson_zm1_n5 = pearson_z1; neyman_m1_n5 = neyman_1; types_m1_n5 =
types_1; obsse_m2_n5 = obsse_2; predfreq_m2_n5 = predfreq_2;
predse_m2_n5 = predse_2; residual_m2_n5 = residual_2; pearson_zm2_n5 =
pearson_z2; neyman_m2_n5 = neyman_2; types_m2_n5 = types_2; obsse_m3_n5
= obsse_3; predfreq_m3_n5 = predfreq_3; predse_m3_n5 = predse_3;
residual_m3_n5 = residual_3; pearson_zm3_n5 = pearson_z3; neyman_m3_n5
= neyman_3; types_m3_n5 = types_3; obsse_m4_n5 = obsse_4;
predfreq_m4_n5 = predfreq_4; predse_m4_n5 = predse_4; residual_m4_n5 =
residual_4; pearson_zm4_n5 = pearson_z4; neyman_m4_n5 = neyman_4;
types_m4_n5 = types_4; obsse_m5_n5 = obsse_5; predfreq_m5_n5 =
predfreq_5; predse_m5_n5 = predse_5; residual_m5_n5 = residual_5;
pearson_zm5_n5 = pearson_z5; neyman_m5_n5 = neyman_5; types_m5_n5 =
types_5; df_m1_n5 = df1; chisq_m1_n5 = chisq1; p_m1_n5 = probchisq1;
df_m2_n5 = df2; chisq_m2_n5 = chisq2; p_m2_n5 = probchisq2; df_m3_n5 =
df3; chisq_m3_n5 = chisq3; p_m3_n5 = probchisq3; df_m4_n5 = df4;
chisq_m4_n5 = chisq4; p_m4_n5 = probchisq4; df_m5_n5 = df5; chisq_m5_n5
= chisq5; p_m5_n5 = probchisq5;
    cond = &cond;
    drop mergeid x m y FunctionNum ObsFunction
    obsse_1 predfreq_1 predse_1 residual_1 reason_1 status_1
pearson_z1 neyman_1 types_1
    obsse_2 predfreq_2 predse_2 residual_2 reason_2 status_2
pearson_z2 neyman_2 types_2
    obsse_3 predfreq_3 predse_3 residual_3 reason_3 status_3
pearson_z3 neyman_3 types_3
    obsse_4 predfreq_4 predse_4 residual_4 reason_4 status_4
pearson_z4 neyman_4 types_4
    obsse_5 predfreq_5 predse_5 residual_5 reason_5 status_5
pearson_z5 neyman_5 types_5
    df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5

```

```

obsse_m2_n5 obsse_m3_n5 obsse_m4_n5 obsse_m5_n5
df_m1_n5 chisq_m1_n5 p_m1_n5 df_m2_n5 chisq_m2_n5 p_m2_n5
df_m3_n5
chisq_m3_n5 p_m3_n5 df_m4_n5 chisq_m4_n5 p_m4_n5 df_m5_n5
chisq_m5_n5 p_m5_n5;

data namrow6; set newallmod; if mergeid=6;
x_n6 = x; m_n6 = m; y_n6 = y; FunctionNum_n6 = FunctionNum;
ObsFunction_n6 = ObsFunction; obsse_m1_n6 = obsse_1; predfreq_m1_n6 =
predfreq_1; predse_m1_n6 = predse_1; residual_m1_n6 = residual_1;
pearson_zm1_n6 = pearson_z1; neyman_m1_n6 = neyman_1; types_m1_n6 =
types_1; obsse_m2_n6 = obsse_2; predfreq_m2_n6 = predfreq_2;
predse_m2_n6 = predse_2; residual_m2_n6 = residual_2; pearson_zm2_n6 =
pearson_z2; neyman_m2_n6 = neyman_2; types_m2_n6 = types_2; obsse_m3_n6
= obsse_3; predfreq_m3_n6 = predfreq_3; predse_m3_n6 = predse_3;
residual_m3_n6 = residual_3; pearson_zm3_n6 = pearson_z3; neyman_m3_n6
= neyman_3; types_m3_n6 = types_3; obsse_m4_n6 = obsse_4;
predfreq_m4_n6 = predfreq_4; predse_m4_n6 = predse_4; residual_m4_n6 =
residual_4; pearson_zm4_n6 = pearson_z4; neyman_m4_n6 = neyman_4;
types_m4_n6 = types_4; obsse_m5_n6 = obsse_5; predfreq_m5_n6 =
predfreq_5; predse_m5_n6 = predse_5; residual_m5_n6 = residual_5;
pearson_zm5_n6 = pearson_z5; neyman_m5_n6 = neyman_5; types_m5_n6 =
types_5; df_m1_n6 = df1; chisq_m1_n6 = chisq1; p_m1_n6 = probchisq1;
df_m2_n6 = df2; chisq_m2_n6 = chisq2; p_m2_n6 = probchisq2; df_m3_n6 =
df3; chisq_m3_n6 = chisq3; p_m3_n6 = probchisq3; df_m4_n6 = df4;
chisq_m4_n6 = chisq4; p_m4_n6 = probchisq4; df_m5_n6 = df5; chisq_m5_n6
= chisq5; p_m5_n6 = probchisq5;
cond = &cond;
drop mergeid x m y FunctionNum ObsFunction
obsse_1 predfreq_1 predse_1 residual_1 reason_1 status_1
pearson_z1 neyman_1 types_1
obsse_2 predfreq_2 predse_2 residual_2 reason_2 status_2
pearson_z2 neyman_2 types_2
obsse_3 predfreq_3 predse_3 residual_3 reason_3 status_3
pearson_z3 neyman_3 types_3
obsse_4 predfreq_4 predse_4 residual_4 reason_4 status_4
pearson_z4 neyman_4 types_4
obsse_5 predfreq_5 predse_5 residual_5 reason_5 status_5
pearson_z5 neyman_5 types_5
df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5
obsse_m2_n6 obsse_m3_n6 obsse_m4_n6 obsse_m5_n6
df_m1_n6 chisq_m1_n6 p_m1_n6 df_m2_n6 chisq_m2_n6 p_m2_n6
df_m3_n6
chisq_m3_n6 p_m3_n6 df_m4_n6 chisq_m4_n6 p_m4_n6 df_m5_n6
chisq_m5_n6 p_m5_n6;

data namrow7; set newallmod; if mergeid=7;
x_n7 = x; m_n7 = m; y_n7 = y; FunctionNum_n7 = FunctionNum;
ObsFunction_n7 = ObsFunction; obsse_m1_n7 = obsse_1; predfreq_m1_n7 =
predfreq_1; predse_m1_n7 = predse_1; residual_m1_n7 = residual_1;
pearson_zm1_n7 = pearson_z1; neyman_m1_n7 = neyman_1; types_m1_n7 =
types_1; obsse_m2_n7 = obsse_2; predfreq_m2_n7 = predfreq_2;

```

```

predse_m2_n7 = predse_2; residual_m2_n7 = residual_2; pearson_zm2_n7 =
pearson_z2; neyman_m2_n7 = neyman_2; types_m2_n7 = types_2; obsse_m3_n7
= obsse_3; predfreq_m3_n7 = predfreq_3; predse_m3_n7 = predse_3;
residual_m3_n7 = residual_3; pearson_zm3_n7 = pearson_z3; neyman_m3_n7
= neyman_3; types_m3_n7 = types_3; obsse_m4_n7 = obsse_4;
predfreq_m4_n7 = predfreq_4; predse_m4_n7 = predse_4; residual_m4_n7 =
residual_4; pearson_zm4_n7 = pearson_z4; neyman_m4_n7 = neyman_4;
types_m4_n7 = types_4; obsse_m5_n7 = obsse_5; predfreq_m5_n7 =
predfreq_5; predse_m5_n7 = predse_5; residual_m5_n7 = residual_5;
pearson_zm5_n7 = pearson_z5; neyman_m5_n7 = neyman_5; types_m5_n7 =
types_5; df_m1_n7 = df1; chisq_m1_n7 = chisq1; p_m1_n7 = probchisq1;
df_m2_n7 = df2; chisq_m2_n7 = chisq2; p_m2_n7 = probchisq2; df_m3_n7 =
df3; chisq_m3_n7 = chisq3; p_m3_n7 = probchisq3; df_m4_n7 = df4;
chisq_m4_n7 = chisq4; p_m4_n7 = probchisq4; df_m5_n7 = df5; chisq_m5_n7
= chisq5; p_m5_n7 = probchisq5;
    cond = &cond;
    drop mergeid x m y FunctionNum ObsFunction
    obsse_1 predfreq_1 predse_1 residual_1 reason_1 status_1
pearson_z1 neyman_1 types_1
    obsse_2 predfreq_2 predse_2 residual_2 reason_2 status_2
pearson_z2 neyman_2 types_2
    obsse_3 predfreq_3 predse_3 residual_3 reason_3 status_3
pearson_z3 neyman_3 types_3
    obsse_4 predfreq_4 predse_4 residual_4 reason_4 status_4
pearson_z4 neyman_4 types_4
    obsse_5 predfreq_5 predse_5 residual_5 reason_5 status_5
pearson_z5 neyman_5 types_5
    df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5
    obsse_m2_n7 obsse_m3_n7 obsse_m4_n7 obsse_m5_n7
    df_m1_n7 chisq_m1_n7 p_m1_n7 df_m2_n7 chisq_m2_n7 p_m2_n7
df_m3_n7
    chisq_m3_n7 p_m3_n7 df_m4_n7 chisq_m4_n7 p_m4_n7 df_m5_n7
chisq_m5_n7 p_m5_n7;

data namrow8; set newallmod; if mergeid=8;
    x_n8 = x; m_n8 = m; y_n8 = y; FunctionNum_n8 = FunctionNum;
ObsFunction_n8 = ObsFunction; obsse_m1_n8 = obsse_1; predfreq_m1_n8 =
predfreq_1; predse_m1_n8 = predse_1; residual_m1_n8 = residual_1;
pearson_zm1_n8 = pearson_z1; neyman_m1_n8 = neyman_1; types_m1_n8 =
types_1; obsse_m2_n8 = obsse_2; predfreq_m2_n8 = predfreq_2;
predse_m2_n8 = predse_2; residual_m2_n8 = residual_2; pearson_zm2_n8 =
pearson_z2; neyman_m2_n8 = neyman_2; types_m2_n8 = types_2; obsse_m3_n8
= obsse_3; predfreq_m3_n8 = predfreq_3; predse_m3_n8 = predse_3;
residual_m3_n8 = residual_3; pearson_zm3_n8 = pearson_z3; neyman_m3_n8
= neyman_3; types_m3_n8 = types_3; obsse_m4_n8 = obsse_4;
predfreq_m4_n8 = predfreq_4; predse_m4_n8 = predse_4; residual_m4_n8 =
residual_4; pearson_zm4_n8 = pearson_z4; neyman_m4_n8 = neyman_4;
types_m4_n8 = types_4; obsse_m5_n8 = obsse_5; predfreq_m5_n8 =
predfreq_5; predse_m5_n8 = predse_5; residual_m5_n8 = residual_5;
pearson_zm5_n8 = pearson_z5; neyman_m5_n8 = neyman_5; types_m5_n8 =
types_5; df_m1_n8 = df1; chisq_m1_n8 = chisq1; p_m1_n8 = probchisq1;
df_m2_n8 = df2; chisq_m2_n8 = chisq2; p_m2_n8 = probchisq2; df_m3_n8 =
df3; chisq_m3_n8 = chisq3; p_m3_n8 = probchisq3; df_m4_n8 = df4;

```



```

chisq_m4_n8 = chisq4; p_m4_n8 = probchisq4; df_m5_n8 = df5; chisq_m5_n8
= chisq5; p_m5_n8 = probchisq5;
    cond = &cond;
    drop mergeid x m y FunctionNum ObsFunction
    obsse_1 predfreq_1 predse_1 residual_1 reason_1 status_1
pearson_z1 neyman_1 types_1
    obsse_2 predfreq_2 predse_2 residual_2 reason_2 status_2
pearson_z2 neyman_2 types_2
    obsse_3 predfreq_3 predse_3 residual_3 reason_3 status_3
pearson_z3 neyman_3 types_3
    obsse_4 predfreq_4 predse_4 residual_4 reason_4 status_4
pearson_z4 neyman_4 types_4
    obsse_5 predfreq_5 predse_5 residual_5 reason_5 status_5
pearson_z5 neyman_5 types_5
    df1 chisq1 probchisq1 df2 chisq2 probchisq2 df3 chisq3 probchisq3
df4 chisq4 probchisq4 df5 chisq5 probchisq5
    obsse_m2_n8 obsse_m3_n8 obsse_m4_n8 obsse_m5_n8
    df_m1_n8 chisq_m1_n8 p_m1_n8 df_m2_n8 chisq_m2_n8 p_m2_n8
df_m3_n8
    chisq_m3_n8 p_m3_n8 df_m4_n8 chisq_m4_n8 p_m4_n8 df_m5_n8
chisq_m5_n8 p_m5_n8;

data NewAllMod2; merge namrow1 namrow2 namrow3 namrow4 namrow5 namrow6
namrow7 namrow8 allest; run;
run;

*Appending replications to a single dataset per condition*;
Data Summary4; Set Summary4 NewAllMod2;
%END;

*Saving results;
data Dataout.Cfigout&file; SET Summary4;
;
RUN;
%MEND;

```

APPENDIX F
SAS CFM DECISION RULES

*Comparing types and antitypes to determine whether X, M, and Y relationships exist and whether model is independent, direct effects only, full mediation, or partial mediation;

```
DATA Types;
  FORMAT cond newrep;
  SET data.allcmas2;
  Keep cond newrep types_m1_n1 types_m1_n2 types_m1_n3 types_m1_n4
types_m1_n5 types_m1_n6 types_m1_n7 types_m1_n8 types_m2_n1 types_m2_n2
types_m2_n3 types_m2_n4 types_m2_n5 types_m2_n6 types_m2_n7 types_m2_n8
types_m3_n1 types_m3_n2 types_m3_n3 types_m3_n4 types_m3_n5 types_m3_n6
types_m3_n7 types_m3_n8 types_m4_n1 types_m4_n2 types_m4_n3 types_m4_n4
types_m4_n5 types_m4_n6 types_m4_n7 types_m4_n8 types_m5_n1 types_m5_n2
types_m5_n3 types_m5_n4 types_m5_n5 types_m5_n6 types_m5_n7
types_m5_n8;
run;
```

```
DATA step1; SET Types;
  IF types_m1_n1 = 0 AND types_m1_n2 = 0 AND types_m1_n3 = 0 AND
types_m1_n4 = 0 AND types_m1_n5 = 0 AND types_m1_n6 = 0 AND types_m1_n7
= 0 AND types_m1_n8 = 0
  THEN M1TAs = 0; ELSE M1TAs = 1;
  IF M1TAs = 0
  THEN DO; XYrelated = 0; MYrelated = 0; XMrelated = 0; end;
Run;
```

```
DATA step2; SET step1;
  IF types_m2_n1 = 0 AND types_m2_n2 = 0 AND types_m2_n3 = 0 AND
types_m2_n4 = 0 AND types_m2_n5 = 0 AND types_m2_n6 = 0 AND types_m2_n7
= 0 AND types_m2_n8 = 0
  THEN M2TAs = 0; ELSE M2TAs = 1;
  IF M1TAs = 1 and M2TAs = 0
  THEN DO XYrelated = 0; MYrelated = 0; end;
Run;
```

```
DATA step3; SET step2;
  IF types_m3_n1 = 0 AND types_m3_n2 = 0 AND types_m3_n3 = 0 AND
types_m3_n4 = 0 AND types_m3_n5 = 0 AND types_m3_n6 = 0 AND types_m3_n7
= 0 AND types_m3_n8 = 0
  THEN M3TAs = 0; ELSE M3TAs = 1;
  IF M1TAs = 1 and M3TAs = 1
  THEN DO MYrelated = 1; end;
Run;
```

```
DATA step4; SET step3;
  IF types_m4_n1 = 0 AND types_m4_n2 = 0 AND types_m4_n3 = 0 AND
types_m4_n4 = 0 AND types_m4_n5 = 0 AND types_m4_n6 = 0 AND types_m4_n7
= 0 AND types_m4_n8 = 0
  THEN M4TAs = 0; ELSE M4TAs = 1;
  IF M1TAs = 1 and M4TAs = 1
  THEN XYrelated = 1;
Run;
```

```

DATA step5; SET step4;
    IF M1TAs = 1 and M2TAs = 1 and M3TAs = 1
    THEN Comp1 = 1; ELSE Comp1 = 0;
    IF M1TAs = 1 and M2TAs = 1 and M3TAs = 0
    THEN CompY = 1; ELSE CompY = 0;
Run;

DATA step6; SET step5;
    IF Comp1 = 1 and types_m2_n1 = types_m3_n1 AND types_m2_n2 =
types_m3_n2 AND types_m2_n3 = types_m3_n3 AND types_m2_n4 = types_m3_n4
AND types_m2_n5 = types_m3_n5 AND types_m2_n6 = types_m3_n6 AND
types_m2_n7 = types_m3_n7 AND types_m2_n8 = types_m3_n8
    THEN do; XYrelated = 0; end;
    IF Comp1 = 1 and types_m2_n1 ^= types_m3_n1 OR types_m2_n2 ^=
types_m3_n2 OR types_m2_n3 ^= types_m3_n3 OR types_m2_n4 ^= types_m3_n4
OR types_m2_n5 ^= types_m3_n5 OR types_m2_n6 ^= types_m3_n6 OR
types_m2_n7 ^= types_m3_n7 OR types_m2_n8 ^= types_m3_n8
    THEN do; XYrelated = 1; end;
    IF CompY = 1
    THEN DO XYrelated = 1; MYrelated = 0; end;
run;

DATA step7; SET step6;
    IF M1TAs = 1 AND types_m1_n1 ^= types_m2_n1 or types_m1_n1 ^=
types_m3_n1 or types_m1_n1 ^= types_m4_n1
or types_m1_n2 ^= types_m2_n2 or types_m1_n2 ^= types_m3_n2 or
types_m1_n2 ^= types_m4_n2
or types_m1_n3 ^= types_m2_n3 or types_m1_n3 ^= types_m3_n3 or
types_m1_n3 ^= types_m4_n3
or types_m1_n4 ^= types_m2_n4 or types_m1_n4 ^= types_m3_n4 or
types_m1_n4 ^= types_m4_n4
or types_m1_n5 ^= types_m2_n5 or types_m1_n5 ^= types_m3_n5 or
types_m1_n5 ^= types_m4_n5
or types_m1_n6 ^= types_m2_n6 or types_m1_n6 ^= types_m3_n6 or
types_m1_n6 ^= types_m4_n6
or types_m1_n7 ^= types_m2_n7 or types_m1_n7 ^= types_m3_n7 or
types_m1_n7 ^= types_m4_n7
or types_m1_n8 ^= types_m2_n8 or types_m1_n8 ^= types_m3_n8 or
types_m1_n8 ^= types_m4_n8
    THEN XMrelated = 1;

Run;

DATA step8; SET step7;
    IF M1TAs = 1 AND types_m1_n1 = types_m2_n1 = types_m3_n1 =
types_m4_n1
and types_m1_n2 = types_m2_n2 = types_m3_n2 = types_m4_n2
and types_m1_n3 = types_m2_n3 = types_m3_n3 = types_m4_n3
and types_m1_n4 = types_m2_n4 = types_m3_n4 = types_m4_n4
and types_m1_n5 = types_m2_n5 = types_m3_n5 = types_m4_n5
and types_m1_n6 = types_m2_n6 = types_m3_n6 = types_m4_n6

```

```

and types_m1_n7 = types_m2_n7 = types_m3_n7 = types_m4_n7
and types_m1_n8 = types_m2_n8 = types_m3_n8 = types_m4_n8
    THEN Tway = 1; ELSE Tway = 0;

DATA step9; SET step8;
    IF M1TAs = 0 THEN Independent = 1; ELSE Independent = 0;
    IF M1TAs = 1 AND Tway = 0 and XMrelated = 1 and MYrelated = 1 and
XYrelated = 0
    THEN Fullmed = 1; ELSE Fullmed = 0;
    IF M1TAs = 1 AND Tway = 0 and XMrelated = 1 and MYrelated = 1 and
XYrelated = 1
    THEN Partmed = 1; ELSE Partmed = 0;
    IF M1TAs = 1 AND Tway = 0 and XMrelated = 1 and MYrelated = 0 and
XYrelated = 1
    THEN Direct = 1; ELSE Direct = 0;
Run;

DATA data.Allstepss2; SET step9;
    Keep Cond newrep Independent XMrelated XYrelated MYrelated
FullMed Direct PartMed;
Run;

```

APPENDIX G
SAS CAUSAL MEDIATION MACRO

```

%MACRO ANALYZE2 (BMX,BYX,BYM,FILE,COND);

DATA SUMMARY3; SET _NULL_;

*Estimating and saving estimates, standard errors, and significance
tests;
ods results = OFF;
ods listing close;
ods html close;
ods output EffectDecomp=outputD MediatorEstimates=outputM
OutcomeEstimates=outputO;
PROC CAUSALMED DATA=Simdata.&File pALL;
    BY rep;
    CLASS YC X MC/DESCENDING;
    MODEL YC = X MC;
    MEDIATOR MC = X;
quit;
ods output close;
ods listing;
ods html;
run;

*Arranging outputs into single row by replication;
DATA drow1; SET outputD;
    IF Decomp="NDE+NIE" and Effect="Natural Direct" THEN DO;
NDEEst=Estimate; NDEStdErr=StdErr; NDELWCL=LowerWaldCL;
NDEUPCL=UpperWaldCL; NDEZ=Z; NDEProbZ=ProbZ;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow2; SET outputD;
    IF Decomp="NDE+NIE" and Effect="Natural Indirect" THEN DO;
NIEEst=Estimate; NIEStdErr=StdErr; NIELWCL=LowerWaldCL;
NIEUPCL=UpperWaldCL; NIEZ=Z; NIEProbZ=ProbZ;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow3; SET outputD;
    IF Decomp="CDE+PE" and Effect="Controlled Direct" THEN DO;
CDEEst=Estimate; CDEStdErr=StdErr; CDELWCL=LowerWaldCL;
CDEUPCL=UpperWaldCL; CDEZ=Z; CDEProbZ=ProbZ;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow4; SET outputD;

```

```

        IF Decomp="CDE+PE" and Effect="Portion Eliminated" THEN DO;
PEEst=Estimate; PESTdErr=StdErr; PELWCL=LowerWaldCL;
PEUPCL=UpperWaldCL; PEZ=Z; PEProbZ=ProbZ;
        END; ELSE DO; DELETE; END;
        cond = &cond;
        DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow5; SET outputD;
        IF Decomp="TDE+PIE" and Effect="Total Direct" THEN DO;
TDEEst=Estimate; TDEStdErr=StdErr; TDELWCL=LowerWaldCL;
TDEUPCL=UpperWaldCL; TDEZ=Z; TDEProbZ=ProbZ;
        END; ELSE DO; DELETE; END;
        cond = &cond;
        DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow6; SET outputD;
        IF Decomp="TDE+PIE" and Effect="Pure Indirect" THEN DO;
PIEEst=Estimate; PIEStdErr=StdErr; PIELWCL=LowerWaldCL;
PIEUPCL=UpperWaldCL; PIEZ=Z; PIEProbZ=ProbZ;
        END; ELSE DO; DELETE; END;
        cond = &cond;
        DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow7; SET outputD;
        IF Decomp="NDE+PIE+IMD" and Effect="Mediated Interaction" THEN
DO; MedxEst=Estimate; MedxStdErr=StdErr; MedxLWCL=LowerWaldCL;
MedxUPCL=UpperWaldCL; MedxZ=Z; MedxProbZ=ProbZ;
        END; ELSE DO; DELETE; END;
        cond = &cond;
        DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow8; SET outputD;
        IF Decomp="CDE+PIE+PAI" and Effect="Portion Due to Interaction"
THEN DO; PAIEst=Estimate; PAIStdErr=StdErr; PAILWCL=LowerWaldCL;
PAIUPCL=UpperWaldCL; PAIZ=Z; PAIProbZ=ProbZ;
        END; ELSE DO; DELETE; END;
        cond = &cond;
        DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow9; SET outputD;
        IF Decomp="Four-Way" and Effect="Reference Interaction" THEN DO;
RefxEst=Estimate; RefxStdErr=StdErr; RefxLWCL=LowerWaldCL;
RefxUPCL=UpperWaldCL; RefxZ=Z; RefxProbZ=ProbZ;
        END; ELSE DO; DELETE; END;

```



```

        cond = &cond;
        DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA drow10; SET outputD;
    IF Decomp="Total" and Effect="Excess Relative Risk" THEN DO;
    ERREst=Estimate; ERRStdErr=StdErr; ERRLWCL=LowerWaldCL;
    ERRUPCL=UpperWaldCL; ERRZ=Z; ERRProbZ=ProbZ;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    DROP Decomp Effect Estimate StdErr LowerWaldCL UpperWaldCL Z
ProbZ;
RUN;

DATA alld; merge drow1 drow2 drow3 drow4 drow5 drow6 drow7 drow8 drow9
drow10;
run;

DATA mrow1; SET outputM;
    IF Parameter="Intercept" THEN DO; MIntEst=Estimate;
    MIntStdErr=StdErr; MIntLWCL=LowerWaldCL; MIntUPCL=UpperWaldCL;
    MIntChiSq=ChiSq; MIntProbChSq=ProbChiSq;
    END;
    ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA mrow2; SET outputM;
    IF Level1 = "0" THEN DO; MX0Est=Estimate; MX0StdErr=StdErr;
    MX0LWCL=LowerWaldCL; MX0UPCL=UpperWaldCL; MX0ChiSq=ChiSq;
    MX0ProbChSq=ProbChiSq;
    END;
    ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA mrow3; SET outputM;
    IF Level1 = "1" THEN DO; MX1Est=Estimate; MX1StdErr=StdErr;
    MX1LWCL=LowerWaldCL; MX1UPCL=UpperWaldCL; MX1ChiSq=ChiSq;
    MX1ProbChSq=ProbChiSq;
    END;
    ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA allm; merge mrow1 mrow2 mrow3;
run;

```

```

DATA orow1; SET outputo;
    IF Parameter="Intercept" THEN DO; OIntEst=Estimate;
OIntStdErr=StdErr; OIntLWCL=LowerWaldCL; OIntUPCL=UpperWaldCL;
OIntChiSq=ChiSq; OIntProbChSq=ProbChiSq;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA orow2; SET outputo;
    IF Parameter = "X" and Level1 = "0" THEN DO; OX0Est=Estimate;
OX0StdErr=StdErr; OX0LWCL=LowerWaldCL; OX0UPCL=UpperWaldCL;
OX0ChiSq=ChiSq; OX0ProbChSq=ProbChiSq;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA orow3; SET outputo;
    IF Parameter = "X" and Level1 = "1" THEN DO; OX1Est=Estimate;
OX1StdErr=StdErr; OX1LWCL=LowerWaldCL; OX1UPCL=UpperWaldCL;
OX1ChiSq=ChiSq; OX1ProbChSq=ProbChiSq;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA orow4; SET outputo;
    IF Parameter = "MC" and Level1 = "0" THEN DO; OMC0Est=Estimate;
OMC0StdErr=StdErr; OMC0LWCL=LowerWaldCL; OMC0UPCL=UpperWaldCL;
OMC0ChiSq=ChiSq; OMC0ProbChSq=ProbChiSq;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA orow5; SET outputo;
    IF Parameter = "MC" and Level1 = "1" THEN DO; OMC1Est=Estimate;
OMC1StdErr=StdErr; OMC1LWCL=LowerWaldCL; OMC1UPCL=UpperWaldCL;
OMC1ChiSq=ChiSq; OMC1ProbChSq=ProbChiSq;
    END; ELSE DO; DELETE; END;
    cond = &cond;
    Drop Parameter Level1 Estimate StdErr LowerWaldCL UpperWaldCL
ChiSq ProbChiSq;
RUN;

DATA allo; MERGE orow1 orow2 orow3 orow4 orow5;
RUN;

```

```

DATA CMOutput; MERGE allm alld allo;
RUN;

*Saving true values of a, b, and cprime to output;
DATA CausMedOutput; SET CMOutput;
merge=1;
BMX = &BMX;
BYM = &BYM;
BYX = &BYX;
Prod=&BMX*&BYM;
run;

*Appending replications to a single dataset per condition*;
DATA Summary3; SET Summary3 CausMedOutput;
data dataout.cmo&file; SET Summary3;

*Calculating and saving standard deviations of estimates across
replications;
proc means data = CausMedOutput noprint;
    var rep cond merge MIntEst MIntStdErr MIntLWCL MIntUPCL MIntChiSq
MIntProbChSq
    MX0Est MX0StdErr MX0LWCL MX0UPCL MX0ChiSq MX0ProbChSq
    MX1Est MX1StdErr MX1LWCL MX1UPCL MX1ChiSq MX1ProbChSq
    NDEEst NDEStdErr NDELWCL NDEUPCL NDEZ NDEProbZ
    NIEEst NIEStdErr NIELWCL NIEUPCL NIEZ NIEProbZ
    CDEEst CDEStdErr CDELWCL CDEUPCL CDEZ CDEProbZ
    PEEEst PEEStdErr PELWCL PEUPCL PEZ PEProbZ
    TDEEst TDEStdErr TDELWCL TDEUPCL TDEZ TDEProbZ
    PIEEst PIEStdErr PIELWCL PIEUPCL PIEZ PIEProbZ
    MedxEst MedxStdErr MedxLWCL MedxUPCL MedxZ MedxProbZ
    PAIEEst PAIStdErr PAILWCL PAIUPCL PAIZ PAIProbZ
    RefxEst RefxStdErr RefxLWCL RefxUPCL RefxZ RefxProbZ
    ERREEst ERRStdErr ERRLWCL ERRUPCL ERRZ ERRProbZ
    OIntEst OIntStdErr OIntLWCL OIntUPCL OIntChiSq OIntProbChSq
    OX0Est OX0StdErr OX0LWCL OX0UPCL OX0ChiSq OX0ProbChSq
    OX1Est OX1StdErr OX1LWCL OX1UPCL OX1ChiSq OX1ProbChSq
    OMC0Est OMC0StdErr OMC0LWCL OMC0UPCL OMC0ChiSq OMC0ProbChSq
    OMC1Est OMC1StdErr OMC1LWCL OMC1UPCL OMC1ChiSq OMC1ProbChSq;
    output out=causmeans
    mean = rep cond MIntEst MIntStdErr MIntLWCL MIntUPCL MIntChiSq
MIntProbChSq
    MX0Est MX0StdErr MX0LWCL MX0UPCL MX0ChiSq MX0ProbChSq
    MX1Est MX1StdErr MX1LWCL MX1UPCL MX1ChiSq MX1ProbChSq
    NDEEst NDEStdErr NDELWCL NDEUPCL NDEZ NDEProbZ
    NIEEst NIEStdErr NIELWCL NIEUPCL NIEZ NIEProbZ
    CDEEst CDEStdErr CDELWCL CDEUPCL CDEZ CDEProbZ
    PEEEst PEEStdErr PELWCL PEUPCL PEZ PEProbZ
    TDEEst TDEStdErr TDELWCL TDEUPCL TDEZ TDEProbZ
    PIEEst PIEStdErr PIELWCL PIEUPCL PIEZ PIEProbZ
    MedxEst MedxStdErr MedxLWCL MedxUPCL MedxZ MedxProbZ
    PAIEEst PAIStdErr PAILWCL PAIUPCL PAIZ PAIProbZ
    RefxEst RefxStdErr RefxLWCL RefxUPCL RefxZ RefxProbZ
    ERREEst ERRStdErr ERRLWCL ERRUPCL ERRZ ERRProbZ
    OIntEst OIntStdErr OIntLWCL OIntUPCL OIntChiSq OIntProbChSq

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```

OX0Est OX0StdErr OX0LWCL OX0UPCL OX0ChiSq OX0ProbChSq
OX1Est OX1StdErr OX1LWCL OX1UPCL OX1ChiSq OX1ProbChSq
OMC0Est OMC0StdErr OMC0LWCL OMC0UPCL OMC0ChiSq OMC0ProbChSq
OMC1Est OMC1StdErr OMC1LWCL OMC1UPCL OMC1ChiSq OMC1ProbChSq
STD = stdrep stdcond stdMIntEst stdMIntStdErr stdMIntLWCL
stdMIntUPCL stdMIntChiSq stdMIntProbChSq
stdMX0Est stdMX0StdErr stdMX0LWCL stdMX0UPCL stdMX0ChiSq
stdMX0ProbChSq
stdMX1Est stdMX1StdErr stdMX1LWCL stdMX1UPCL stdMX1ChiSq
stdMX1ProbChSq
stdNDEEst stdNDEStdErr stdNDELWCL stdNDEUPCL stdNDEZ stdNDEProbZ
stdNIEEst stdNIEStdErr stdNIELWCL stdNIEUPCL stdNIEZ stdNIEProbZ
stdCDEEst stdCDEStdErr stdCDELWCL stdCDEUPCL stdCDEZ stdCDEProbZ
stdPEEst stdPEStdErr stdPELWCL stdPEUPCL stdPEZ stdPEProbZ
stdTDEEst stdTDEStdErr stdTDELWCL stdTDEUPCL stdTDEZ stdTDEProbZ
stdPIEEst stdPIEStdErr stdPIELWCL stdPIEUPCL stdPIEZ stdPIEProbZ
stdMedxEst stdMedxStdErr stdMedxLWCL stdMedxUPCL stdMedxZ
stdMedxProbZ
stdPAIEst stdPAIStdErr stdPAILWCL stdPAIUPCL stdPAIZ stdPAIProbZ
stdRefxEst stdRefxStdErr stdRefxLWCL stdRefxUPCL stdRefxZ
stdRefxProbZ
stdERREst stdERRStdErr stdERRLWCL stdERRUPCL stdERRZ stdERRProbZ
stdOIntEst stdOIntStdErr stdOIntLWCL stdOIntUPCL stdOIntChiSq
stdOIntProbChSq
stdOX0Est stdOX0StdErr stdOX0LWCL stdOX0UPCL stdOX0ChiSq
stdOX0ProbChSq
stdOX1Est stdOX1StdErr stdOX1LWCL stdOX1UPCL stdOX1ChiSq
stdOX1ProbChSq
stdOMC0Est stdOMC0StdErr stdOMC0LWCL stdOMC0UPCL stdOMC0ChiSq
stdOMC0ProbChSq
stdOMC1Est stdOMC1StdErr stdOMC1LWCL stdOMC1UPCL stdOMC1ChiSq
stdOMC1ProbChSq;
run;

DATA causmeans2; set causmeans;
merge = 1;
keep merge stdMIntEst stdMIntStdErr stdMIntLWCL stdMIntUPCL
stdMIntChiSq stdMIntProbChSq
stdMX0Est stdMX0StdErr stdMX0LWCL stdMX0UPCL stdMX0ChiSq
stdMX0ProbChSq
stdMX1Est stdMX1StdErr stdMX1LWCL stdMX1UPCL stdMX1ChiSq
stdMX1ProbChSq
stdNDEEst stdNDEStdErr stdNDELWCL stdNDEUPCL stdNDEZ stdNDEProbZ
stdNIEEst stdNIEStdErr stdNIELWCL stdNIEUPCL stdNIEZ stdNIEProbZ
stdCDEEst stdCDEStdErr stdCDELWCL stdCDEUPCL stdCDEZ stdCDEProbZ
stdPEEst stdPEStdErr stdPELWCL stdPEUPCL stdPEZ stdPEProbZ
stdTDEEst stdTDEStdErr stdTDELWCL stdTDEUPCL stdTDEZ stdTDEProbZ
stdPIEEst stdPIEStdErr stdPIELWCL stdPIEUPCL stdPIEZ stdPIEProbZ
stdMedxEst stdMedxStdErr stdMedxLWCL stdMedxUPCL stdMedxZ
stdMedxProbZ
stdPAIEst stdPAIStdErr stdPAILWCL stdPAIUPCL stdPAIZ stdPAIProbZ
stdRefxEst stdRefxStdErr stdRefxLWCL stdRefxUPCL stdRefxZ
stdRefxProbZ
stdERREst stdERRStdErr stdERRLWCL stdERRUPCL stdERRZ stdERRProbZ

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```

        stdOIntEst stdOIntStdErr stdOIntLWCL stdOIntUPCL stdOIntChiSq
stdOIntProbChSq
        stdOX0Est stdOX0StdErr stdOX0LWCL stdOX0UPCL stdOX0ChiSq
stdOX0ProbChSq
        stdOX1Est stdOX1StdErr stdOX1LWCL stdOX1UPCL stdOX1ChiSq
stdOX1ProbChSq
        stdOMC0Est stdOMC0StdErr stdOMC0LWCL stdOMC0UPCL stdOMC0ChiSq
stdOMC0ProbChSq
        stdOMC1Est stdOMC1StdErr stdOMC1LWCL stdOMC1UPCL stdOMC1ChiSq
stdOMC1ProbChSq merge;
run;

*Calculating bias, relative bias, and standardized bias;
DATA Causresults; MERGE CausMedOutput causmeans2; by merge;
    BiasCDE = CDEEst-BYX;
    RBCDE = BiasCDE/BYX;
    StBCDE = BiasCDE/stdCDEEst;
    BiasPIE = PIEEst-Prod;
    RBPIE = BiasPIE/Prod;
    StBPIE = BiasPIE/stdPIEEst;
run;

*Saving results;
data Dataout.CRO&File; SET Causresults;
;
RUN;
%MEND;

```

APPENDIX H
DOCUMENT NOTATION

X	Independent variable, observed
M	Mediating variable, observed
\hat{M}	Estimated score on mediating variable
Y	Dependent variable, observed
\hat{Y}	Estimated score on dependent variable
a	Relation between independent and mediating variable
b	Relation between mediating variable and dependent variable while controlling for independent variable
c	Relation between independent variable and dependent variable
c'	Relation between independent variable and dependent variable while controlling for mediating variable
ab	Product of coefficient mediated effect
$c-c'$	Difference of coefficients mediated effect
i_k	Intercept for model k
e_k	Residual for model k
N1-N8	Designations for the eight possible combinations for binary X, M, and Y
n1-n8	Frequency of observations for the eight possible combinations for binary X, M, and Y
e	Correlation correction factor for dichotomization
h	Height of the standard unit normal curve at point of dichotomization
p	Proportion of observations
r	Correlation coefficient
r^2	Squared multiple correlation
\hat{p}	Observed probability of “success” on a binary dependent variable
β_0	Intercept in logistic regression model
β_1	Regression coefficient in logistic regression model
$g_{x,m}$	Expected value of dependent variable given values of X and M
h_x	Expected value of mediating variable given values of X

TE	Total Effect
DE	Direct Effect
IE	Indirect Effect
CDE	Controlled Direct Effect
PIE	Pure Indirect Effect
PDE	Pure Direct Effect
TIE	True Indirect Effect
TNIE	True Natural Indirect Effect
\check{X}	In the stage sequential method, $X=0$
M_{Si}	In the stage sequential method, $M=1$ at stage i
\check{M}_{Si}	In the stage sequential method, $M=0$ at stage i
Y_{Si}	In the stage sequential method, $Y=1$ at stage i
\check{Y}_{Si}	In the stage sequential method, $Y=0$ at stage i
\hat{o}	Expected cell frequency
λ	Intercept for log-linear model
λ^j	Relation of variable j on expected cell frequency in log-linear model
λ^{jk}	Relation of the interaction of variables j and k on expected cell frequency in log-linear model
Θ -hat	Parameter estimate
Θ	True population parameter value
SD_{Θ -hat	Standard deviation of parameter estimate
α	alpha, significance criterion
SE_{ab}	Standard error of ab
SE_a	Standard error of a
SE_b	Standard error of b
z_{ab}	z-score for ab
h	coefficient for XM interaction

APPENDIX I

LOG-LINEAR MODELS USED FOR CFM AND JOINT SIGNIFICANCE TESTS

Model 1 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y$

Model 2 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM}$

Model 3 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{XY}$

Model 4 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{MY}$

Model 5 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XY} + \lambda^{XM} + \lambda^{MY}$

Model 6 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XY} + \lambda^{MY}$

Model 7 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{XY} + \lambda^{XMY}$

Model 8 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{MY} + \lambda^{XY} + \lambda^{XMY}$

Model 9 - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XY}$

Saturated Model - $\log \hat{\delta} = \lambda + \lambda^X + \lambda^M + \lambda^Y + \lambda^{XM} + \lambda^{XY} + \lambda^{MY} + \lambda^{XMY}$