

Can We Include Dichotomous Variables in Meta-Analytic Structural Equation Modeling? Mind the Prevalence

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Meta-analytic structural equation modeling (MASEM) is a method to systematically synthesize results from primary studies, allowing the researchers to simultaneously examine multiple relations among variables by fitting a structural equation model to the pooled correlations. Incorporating dichotomous variables (e.g., having a specific disease or not) into MASEM poses challenges. While primary studies that investigate the relation between a dichotomous and continuous variable typically report standardized mean differences (e.g., Cohen's d), in the specialized MASEM software it is not possible to directly include standardized mean differences. Instead, MASEM typically uses correlation matrices as input. A proposed solution is to convert the standardized mean differences to point-biserial correlations. Here lies a complication because, in contrast to a standardized mean difference, the point-biserial correlation depends on the distribution of group membership. Through three Monte Carlo simulation studies, we investigated which conversion formula is suitable when one wants to include a dichotomous variable in MASEM. We varied the prevalence, sampling plan, and within-study sample sizes, and the distribution of participants over two groups. Our results show that which conversion is suitable, and which is not depends on the aim of the meta-analyst. We have extended our freely available web application to fill the existing gap and to assist the meta-analyst with their conversions.

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