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Ridge Structural Equation Modeling with Correlation Matrices for Ordinal and Continuous Data*

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Abstract

This paper develops a ridge procedure for structural equation modeling (SEM) with ordinal and continuous data by modeling polychoric/polyserial/product-moment correlation matrix **R**. Rather than directly fitting **R**, the procedure fits a structural model to $\mathbf{R}_a = \mathbf{R} + a\mathbf{I}$ by minimizing the normal-distribution-based discrepancy function, where $a > 0$. Statistical properties of the parameter estimates are obtained. Four statistics for overall model evaluation are proposed. Empirical results indicate that the ridge procedure for SEM with ordinal data has better convergence rate, smaller bias, smaller mean square error and better overall model evaluation than the widely used maximum likelihood procedure.

Keywords

Polychoric correlation; bias; efficiency; convergence; mean square error; overall model evaluation

1. Introduction

In social science research data are typically obtained by questionnaires in which respondents are asked to choose one of a few categories on each of many items. Measurements are obtained by coding the categories using 0 and 1 for dichotomized items or 1 to m for items with *m* categories. Because the difference between 1 and 2 cannot be regarded as equivalent to the difference between $m - 1$ and m, such obtained measurements only possess ordinal properties. Pearson product-moment correlations cannot reflect the proper association for items with ordinal data. Polychoric correlations are more appropriate if the ordinal variables can be regarded as categorization from an underlying continuous normal distribution. Under such an assumption, each observed ordinal random variable x is related to an underlying continuous random variable z according to

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$$
x = \begin{cases} 1 & \text{when } z \in (-\infty, \tau_1] \\ 2 & \text{when } z \in (\tau_1, \tau_2] \\ \vdots & \vdots \\ m & \text{when } z \in (\tau_{m-1}, \infty), \end{cases}
$$

where $0 = - \leq 1 \leq \ldots \leq m-1 \leq m =$ are thresholds. All the continuous variables together form a vector $\mathbf{z} = (z_1, z_2, ..., z_p)$ that follows a multivariate normal distribution $N_p(\mu)$, where $\mu = 0$ and $=$ (\hat{i}) is a correlation matrix due to identification considerations. When such an assumption holds, polychoric correlations are consistent, asymptotically normally distributed and their standard errors (SE) can also be consistently estimated (Olsson, 1979; Poon & Lee, 1987). On the other hand, the Pearson productmoment correlation is generally biased, especially when the number of categories is small and the observed frequencies of the marginal distributions are skewed. Simulation studies imply that polychoric correlations also possess certain robust properties when the underlying continuous distribution departs from normality (see e.g., Quiroga, 1992).

Because item level data in social sciences are typically ordinal, structural equation modeling (SEM) for such data has long been developed. Bock and Lieberman (1970) developed a maximum likelihood (ML) approach to factor analysis with dichotomous data and a single factor. Lee, Poon and Bentler (1990) extended this approach to general SEM with polytomous variables. Because the ML approach involves the evaluation of multiple integrals, it is computationally intensive. Instead of ML, Christoffersson (1975) and Muthén (1978) proposed procedures of fitting a multiple-factor model using pairwise frequencies for dichotomous data by generalized least squares with an asymptotically correct weight matrix (AGLS). Muthén (1984) further formulated a general procedure for SEM with ordinal and continuous data using AGLS, which forms the basis of LISCOMP (an early version of Mplus, Muthén & Muthén, 2007). An AGLS approach for SEM with ordinal and continuous data was developed in Lee, Poon and Bentler (1992), where thresholds, polychoric, polyserial and product-moment correlations were estimated by ML. Lee, Poon and Bentler (1995) further formulated another AGLS approach in which thresholds, polychoric, polyserial and product-moment correlations are estimated by ML using different subsets of variables; they named the procedure partition ML (see also Poon & Lee, 1987). The approach of Lee et al. (1995) has been implemented in EQS (Bentler, 1995) with various extensions for better statistical inference. Jöreskog (1994) also gave the technical details to SEM with ordinal variables, where thresholds are estimated using marginal frequencies and followed by the estimation of polychoric correlations using pairwise frequencies and holding the estimated thresholds constant. Jöreskog's development formed the basis for ordinal data in LISREL¹ (see e.g., Jöreskog 1990; Jöreskog & Sörbom, 1996). Technical details of the development in Muthén (1984) were provided by Muthén and Satorra (1995). Recently, Bollen and Maydeu-Olivares (2007) proposed a procedure using polychoric instrumental variables. In summary, various technical developments have been made for SEM with ordinal data, emphasizing AGLS.

Methods currently available in software are two-stage procedures where polychoric, polyserial and product-moment correlations are obtained first. This correlation matrix is then modeled with SEM using ML, AGLS, the normal-distribution-based GLS (NGLS), least

¹In LISREL, the AGLS procedure is called weighted least squares (WLS) while GLS is reserved for the GLS procedure when the weight matrix is obtained using the normal distribution assumption as in covariance structure analysis (Browne, 1974). We will further discuss the normal-distribution-based GLS in the concluding section.

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squares (LS), and diagonally-weighted least squares (DWLS), as implemented in EQS, LISREL and Mplus. We need to note that the ML procedure in software fits a structural model to a polychoric/polyserial/product-moment correlation matrix by minimizing the normal distribution based discrepancy function, treating the correlation matrix as a sample covariance matrix from a normally distributed sample, which is totally different from the ML procedure considered by Lee et al. (1990). We will refer to this ML method in SEM software as the ML method from now on. The main purpose of this paper is to develop a ridge procedure for SEM with ordinal and continuous data that has a better convergence rate, smaller bias, smaller mean square error (MSE) and better overall model evaluation than ML. We next briefly review studies on the empirical behavior of several procedures to identify the limitation and strength of each method and to motivate our study and development.

Babakus, Ferguson and Jöreskog (1987) studied the procedure of ML with modeling four different kinds of correlations (product-moment, polychoric, Spearman's rho, and Kendall's tau-b) and found that ML with polychoric correlations provides the most accurate estimates of parameters with respect to bias and MSE, but it is also associated with most nonconvergences. Rigdon and Ferguson (1991) studied modeling polychoric correlation matrices with several discrepancy functions and found that distribution shape of the ordinal data, sample size and fitting function all affect convergence rate. In particular, AGLS has the most serious problem of convergence and improper solutions, especially when the sample size is small. ML generates the most accurate estimates at sample size $n = 500$; ML almost generates the most accurate parameter estimates at $n = 300$, as reported in Table 2 of the paper. Potthast (1993) only studied AGLS estimators and found that the resulting SEs are substantially underestimated while the associated chi-square statistic is substantially inflated. Potthast also found that AGLS estimators contain positive biases. Dolan (1994) studied ML and AGLS with polychoric correlations and found that ML with polychoric correlations produces the least biased parameter estimates while AGLS estimators contain substantial biases. DiStefano (2002) studied the performance of AGLS and also found that the resulting SEs are substantially underestimated while the associated chi-square statistic is substantially inflated. There also exist many nonconvergence problems and improper solutions. The literature also shows that, for ML with polychoric correlations, the resulting SEs and test statistic behave badly, because without correction the formula for SEs and test statistics are not correct. Currently, when modeling polychoric/polyserial correlation matrices, software has the option of calculating SEs based on a sandwich-type covariance matrix and using rescaled or adjusted statistics for overall model evaluation (e.g., EQS, LISREL, Mplus). These corrected versions are often called robust procedures in the literature. A recent study by Lei (2009) on ML in EQS and DWLS in Mplus found that DWLS has a better convergence rate than ML. She also found that relative biases of ML and DWLS parameter estimates were similar conditioned on the study factors. She concluded (p. 505)

ML performed slightly better in standard error estimation (at smaller sample sizes before it started to over-correct) while robust WLS provided slightly better overall Type I error control and higher power in detecting omitted paths. In cases when sample size is adequately large for the model size, especially when the model is also correctly specified, it would matter little whether ML of EQS6 or robust WLS of Mplus3.1 is chosen. However, when sample sizes are very small for the model and the ordinal variables are moderately skewed, ML with Satorra-Bentler scaled statistics may be recommended if proper solutions are obtainable.

In summary, ML and AGLS are the most widely studied procedures, and the latter cannot be trusted with not large enough sample sizes although conditional on the correlation matrix it is asymptotically the best procedure. These studies indicate that robust ML and robust

DWLS are promising procedures for SEM with ordinal data. Comparing robust ML and robust DWLS, the former uses a weight matrix that is determined by the normal distribution assumption while the latter uses a diagonal weight matrix that treats all the correlations as independent. The ridge procedure to be studied can be regarded as a combination of ML and LS.

One problem with ML is its convergence rate. This is partially because the polychoric/ polyserial correlations are obtained from different marginals, and the resulting correlation matrix may not be positive definite, especially when the sample size is not large enough and there are many items. As a matter of fact, the normal-distribution-based discrepancy function cannot take a correlation matrix that is not positive definite because the involved logarithm function cannot take non-positive values. When the correlation matrix is near singular and is still positive definite, the model implied matrix will need to mimic the near singular correlation (data) matrix so that the estimation problem becomes ill-conditioned (see e.g., Kelley, 1995), which results not only in slower or nonconvergence but also unstable parameter estimates and unstable test statistics (Yuan & Chan, 2008). Such a phenomenon can also happen to the sample covariance matrix when the sample size is small or when the elements of the covariance matrix are obtained by ad-hoc procedures (see e.g., Wothke, 1993). Although smoothing the eigenvalues and imposing a constraint of positive definitiveness is possible (e.g., Knol $\&$ ten Berge, 1989), the statistical consequences have not been worked out and remain unknown.

When a covariance matrix **S** is near singular, the matrix $S_a = S + aI$ with a positive scalar a will be positive definite and well-conditioned. Yuan and Chan (2008) proposed to model **S**^a rather than **S**, using the normal distribution based discrepancy function. They showed that the procedure results in consistent parameter estimates. Empirical results indicate that the procedure not only converges better, at small sample sizes the resulting parameter estimates are more accurate than the ML estimator (MLE) even when data are normally distributed. Compared to modeling sample covariance matrices, modeling correlations typically encounters more problems of convergence with smaller sample sizes, especially for ordinal data that are skew distributed. Actually, both EQS and LISREL contain warnings about proper application of modeling polychoric correlations when sample size is small. Thus, the methodology in Yuan and Chan (2008) may be even more relevant to the analysis of polychoric/polyserial correlation matrices than to sample covariance matrices. The aim of this paper is to extend the procedure in Yuan and Chan (2008) to SEM with ordinal and continuous data by modeling polychoric/polyserial/product-moment correlation matrices.

When a $p \times p$ sample covariance matrix $S = (s_{ij})$ is singular, the program LISREL provides an option of modeling $S + a \text{ diag}(s_{11}, \dots, s_{pp})$, which is called the ridge option (Jöreskog & Sörbom, 1996, p. 24). With a correlation matrix **R**, the ridge option in LISREL fits the structural model to $\mathbf{R} + a\mathbf{I}$, which is the same as extending the procedure in Yuan and Chan (2008) to correlation matrices. Thus, ridge SEM with ordinal data has already been implemented in LISREL. However, it is not clear how to properly apply this procedure in practice, due to lack of studies of its properties. Actually, McQuitty (1997) conducted empirical studies on the ridge option in LISREL 8 and concluded that (p. 251) "there appears to be ample evidence that structural equation models should not be estimated with LISREL's ridge option unless the estimation of unstandardized factor loadings is the only goal." One of the contributions of this paper is to obtain statistical properties of ridge SEM with ordinal data and to make it a statistically sound procedure. We will show that ridge SEM with ordinal data enjoys consistent parameter estimates and consistent SEs. We will also propose four statistics for overall model evaluation. Because ridge SEM is most useful when the polychoric/polyserial/product-moment correlation matrix is near singular, which tends to occur with smaller sample sizes, we will conduct Monte Carlo study to see how

ridge SEM performs with respect to bias and efficiency of parameter estimates. We will also empirically identify the most reliable statistics for overall model evaluation and evaluate the performance of formula-based SEs.

Section 2 provides the details of the development for model inference, including consistent parameter estimates and SEs as well as rescaled and adjusted statistic for overall model evaluation. Monte Carlo results are presented in section 3. Section 4 contains a real data example. Conclusion and discussion are offered at the end of the paper.

2. Model Inference

Let **R** be a $p \times p$ correlation matrix, including polychoric, polyserial and Pearson productmoment correlations for ordinal and continuous variables. Let **r** be the vector of all the correlations formed by the below-diagonal elements of **R** and be the population counterpart of **r**. Then it follows from Jöreskog (1994), Lee et al. (1995) or Muthén and Satorra (1995) that,

$$
\sqrt{n}(\mathbf{r} - \rho) \xrightarrow{\mathscr{L}} N(\mathbf{0}, \mathbf{\hat{T}}), \quad (1)
$$

where $\mathcal{L}_{\mathcal{A}}$ denotes convergence in distribution and **Y** is the asymptotic covariance matrix of \sqrt{n} that can be consistently estimated. For SEM with ordinal data, we will have a correlation structure (e). As mentioned in the introduction, popular SEM software has the option of modeling **R** by minimizing

$$
F_{ML}(\theta) = \text{tr}[\mathbf{R} \sum^{-1}(\theta)] - \log |\mathbf{R} \sum^{-1}(\theta)| - p \quad (2)
$$

for parameter estimates . Such a procedure is just to replace the sample covariance matrix **S** by the correlation matrix **R** in the most commonly used ML procedure for SEM. Equations (1) and (2) can be compared to covariance structure analysis when **S** is based on a sample from an unknown distribution. Actually, the same amount of information is provided in both cases, where ϒ's need to be estimated using fourth-order moments. Similar to modeling covariance matrices, (2) needs **R** to be positive definite. Otherwise, the term $\log |\mathbf{R}|^{-1}$ () is not defined.

For a positive a, let $\mathbf{R}_a = \mathbf{R} + a\mathbf{I}$. Instead of minimizing (2), ridge SEM minimizes

$$
F_{\mathit{MLa}}(\theta_a) = \text{tr}[\mathbf{R}_a \sum_a^{-1} (\theta_a)] - \log |\mathbf{R}_a \sum_a^{-1} (\theta_a)| - p \quad (3)
$$

for parameter estimates ∂_{α} , where $\partial_{\alpha}(\partial_{\alpha}) = (\partial_{\alpha} + aI)$. We will show that ∂_{α} is consistent and asymptotically normally distributed. Notice that corresponding to \mathbf{R}_a is a population covariance matrix $a = +aI$, which has identical off-diagonal elements with Δ . Although minimizing (2) for with $a = 0$ for categorical data is available in software, we cannot find any documentation of its statistical properties. Our development will be for an arbitrary positive a, including the ML procedure when $a = 0$. Parallel to Yuan and Chan (2008), the following technical development will be within the context of LISREL models.

2.1 Consistency

Let $z = (x^*, y^*)$ be the underlying standardized population. Using LISREL notation, the "measurement model 2 " is given by

$$
\mathbf{x}^* = \mu_x + \mathbf{\Lambda}_x \boldsymbol{\xi} + \delta, \ \mathbf{y}^* = \mu_y + \mathbf{\Lambda}_y \eta + \varepsilon,
$$

where $\mu_x = E(x^*)$, $\mu_y = E(y^*)$, \bar{x} and \bar{y} are factor loading matrices; and are vectors of latent constructs with $E(j) = 0$ and $E(j) = 0$; and and are vectors of measurement errors with $E(\) = 0, E(\) = 0, \quad = E(\)$, $E(\) = E(\)$. The structural model that describes interrelations of and is

$$
\eta{=}\mathbf{B}\eta{+}\mathbf{\Gamma}\boldsymbol{\xi}{+}\boldsymbol{\zeta},
$$

where is a vector of prediction errors with $E(z) = 0$ and $E(z) = E(z)$. Let $E(z) = E(z)$, the resulting covariance structure of **z** is (see Jöreskog & Sörbom, 1996, pp. 1–3)

$$
\sum(\theta) = \left(\begin{array}{cc} \boldsymbol{\Lambda}_x\boldsymbol{\Phi}\boldsymbol{\Lambda}_x^{'} + \boldsymbol{\Theta}_{\delta} & \boldsymbol{\Lambda}_x\boldsymbol{\Phi}\boldsymbol{\Gamma}^{'}(\mathbf{I}-\mathbf{B}')^{-1}\boldsymbol{\Lambda}_y^{'} \\ \boldsymbol{\Lambda}_y(\mathbf{I}-\mathbf{B})^{-1}\boldsymbol{\Gamma}\boldsymbol{\Phi}\boldsymbol{\Lambda}_x^{'} & \boldsymbol{\Lambda}_y(\mathbf{I}-\mathbf{B})^{-1}(\boldsymbol{\Gamma}\boldsymbol{\Phi}\boldsymbol{\Gamma}^{'}+\boldsymbol{\Psi})(\mathbf{I}-\mathbf{B}')^{-1}\boldsymbol{\Lambda}_y^{'}+\boldsymbol{\Theta}_{\varepsilon} \end{array}\right).
$$

Recall that $\mu = E(z) = 0$ and that $\epsilon = Cov(z)$ is a correlation matrix when modeling polychoric/polyserial/product-moment correlations. We have $\mu_x = 0$, $\mu_y = 0$,

$$
\text{diag}(\mathbf{\Theta}_{\delta})\mathbf{=}\mathbf{I}_{\delta}-\text{diag}(\mathbf{\Lambda}_x\mathbf{\Phi}\mathbf{\Lambda}_x)
$$

and

$$
\mathrm{diag}(\mathbf{\Theta}_{\varepsilon})\mathbf{=}\mathbf{I}_{\varepsilon}-\mathrm{diag}[\mathbf{\Lambda}_y(\mathbf{I}-\mathbf{B})^{-1}(\mathbf{\Gamma}\mathbf{\Phi}\mathbf{\Gamma}'+\mathbf{\Psi})(\mathbf{I}-\mathbf{B}')^{-1}\mathbf{\Lambda}_y'],
$$

where $diag(A)$ means the diagonal matrix formed by the diagonal elements of A , and I and **I** are identity matrices with the same dimension as and , respectively. Thus, the diagonal elements of and are not part of the free parameters but part of the model of (b) through the functions of free parameters in $\mathbf{x}_1, \mathbf{y}_2, \mathbf{B}_2, \mathbf{y}_3, \mathbf{B}_3, \mathbf{y}_4$, offdiag(extending) and

offdiag(Θ), where offdiag(**A**) implies the off-diagonal elements of **A**.

When () is a correct model for , there exist matrices $\Lambda_x^{(0)}, \Lambda_y^{(0)}, \mathbf{B}^{(0)}, (0), (0), (0)$ and offdiag($\Theta_{\varepsilon}^{(0)}$) such that = (₀), where ₀ is the vector containing the population values of all the free parameters in Let $_{d0}$ be the corresponding vector of $_{d}$ at $\mathbf{B}^{(a)} = \mathbf{B}^{(0)}$, $(a) = (0)$, $(a) = (0)$, $(a) = (0)$, offdiag($\Theta_{\delta}^{(a)}$)=offdiag($\Theta_{\delta}^{(0)}$) and offdiag($\Theta_{\varepsilon}^{(a)}$)=offdiag($\Theta_{\varepsilon}^{(0)}$). In addition, let

 2 The model presented here is the standard LISREL model in which and are not correlated. Results in this paper still hold when and correlate.

$$
\text{diag}(\mathbf{\Theta}_{\delta}^{(a)}) = \text{diag}(\mathbf{\Theta}_{\delta}^{(0)}) + a\mathbf{I}_{\delta} \quad (4a)
$$

and

$$
\mathrm{diag}(\mathbf{\Theta}_{\varepsilon}^{(a)}) = \mathrm{diag}(\mathbf{\Theta}_{\varepsilon}^{(0)}) + a\mathbf{I}_{\varepsilon}.
$$
 (4b)

Thus, $a_0 = 0$ and $\Theta_{\delta}^{(a)}$ and $\Theta_{\epsilon}^{(a)}$ are functions of $a_0 = 0$ and a. Let the functions in (4a) and (4b) be part of the model of $\begin{bmatrix} a & a \end{bmatrix}$. Then we have $\begin{bmatrix} a = a & a \end{bmatrix}$ (a) = $\begin{bmatrix} a & a \end{bmatrix}$. Notice that $a(t)$ is uniquely determined by $($) and a. This implies that whenever $($) is a correct model for modeling θ , θ as a correct model for modeling θ . The above result also implies that for a correctly specified (), except for sampling errors, the parameter estimates for K , K , K , θ , θ , and the off-diagonal elements of and when modeling **R**^a will be the same as those when modeling **R**. The resulting estimates for the diagonals of and $\Theta_{\varepsilon}^{(a)}$ of modeling \mathbf{R}_a are different from those of modeling **R** by the constant a, which is up to our choice. Traditionally, the diagonal elements of and are estimates of the variances of measurement errors/uniquenesses. When modeling \mathbf{R}_{a} , these can be obtained by

$$
\text{diag}(\widehat{\boldsymbol{\Theta}}_{\delta}) \text{=} \text{diag}(\widehat{\boldsymbol{\Theta}}_{\delta}^{(a)}) - a \mathbf{I}_{\delta} \quad \text{(5a)}
$$

and

$$
\text{diag}(\widehat{\Theta}_{\varepsilon}) = \text{diag}(\widehat{\Theta}_{\varepsilon}^{(a)}) - a\mathbf{I}_{\varepsilon}.
$$
 (5b)

The above discussion implies that \mathbf{a} of modeling \mathbf{R}_a may be different from of modeling **R** due to sampling error, but their population counterparts are identical. We have the following formal result.

Theorem 1—Under the conditions (I) (b) is correctly specified and identified and (II) and is a compact subset of the Euclidean space \mathcal{R}^q , a is consistent for θ regardless of the value of a.

The proof of the theorem is essentially the same as that for Theorem 1 in Yuan and Chan (2008) when replacing the sample covariance matrix there by the correlation matrix **R**. Yuan and Chan (2008) also discussed the benefit of modeling $S_a = S + aI$ from a computational perspective using the concept of condition number; the same benefit holds for modeling \mathbf{R}_{a} . One advantage of estimation with a better condition number is that a small change in the sample will only cause a small change in α while a small change in the sample can cause a great change in if **is near singular. Readers who are interested in the details are referred** to Yuan and Chan (2008).

2.2 Asymptotic normality

We will obtain the asymptotic distribution of α , which allows us to obtain its consistent SEs. For such a purpose we need to introduce some notation first.

For a symmetric matrix **A**, let vech(**A**) be a vector by stacking the columns of **A** and leaving out the elements above the diagonal. We define $\mathbf{s}_a = \text{vech}(\mathbf{R}_a)$, \mathbf{s}_a = vech $\begin{bmatrix} a \\ a \end{bmatrix}$, $\mathbf{s} =$

vech(**R**), and () = vech[(b)]. Notice that s_a and **s** are vectors of length $p^* = p(p+1)/2$ while the **r** in (1) is a vector of length $p_* = p(p-1)/2$. The difference between **r** and \mathbf{s}_a is that \mathbf{s}_a also contains the p elements of $a + 1$ on the diagonal of \mathbf{R}_a , and $\mathbf{s}_a = \mathbf{s}$ when $a = 0$. Let **be the duplication matrix defined by Magnus and Neudecker (1999, p. 49), and**

$$
\mathbf{W}_a(\theta) = 2^{-1} \mathbf{D}_p' \left[\sum_a^{-1}(\theta) \otimes \sum_a^{-1}(\theta)\right] \mathbf{D}_p.
$$

We will use a dot on top of a function to denote the first derivative or the gradient. For example, if contains q unknown parameters, $\phi(z) = \phi(z) / \sin(z)$ is a $p^* \times q$ matrix. Under standard regularity conditions, including that θ_0 is an interior point of , θ_0 as at is fiest

$$
\mathbf{g}_{a}(\widehat{\theta}_{a}){=}0,\quad \ \ \textrm{(6)}
$$

where

$$
\mathbf{g}_a(\theta) = \sigma'_a(\theta) \mathbf{W}_a(\theta) [\mathbf{s}_a - \sigma_a(\theta)].
$$

In equation (6), because α and () only differ by a constant a, α () = () and s_a $a^{(n)} = s - (n)$. So the effect of a on $a^{(n)}$ in (6) is only through

$$
\mathbf{W}_{a}(\theta) = 2^{-1} \mathbf{D}_{p}^{\prime} \left\{ \left[\sum (\theta) + a \mathbf{I} \right]^{-1} \otimes \left[\sum (\theta) + a \mathbf{I} \right]^{-1} \right\} \mathbf{D}_{p} = \frac{1}{2(a+1)^{2}} \mathbf{U}_{a}, \quad (7)
$$

where

$$
\mathbf{U}_a = \mathbf{D}_p' \{ \left[\frac{1}{a+1} \sum_{n=1}^{a} (\theta) + \frac{a}{a+1} \mathbf{I} \right]^{-1} \otimes \left[\frac{1}{a+1} \sum_{n=1}^{a} (\theta) + \frac{a}{a+1} \mathbf{I} \right]^{-1} \} \mathbf{D}_p
$$

Notice that the constant coefficient $1/[2(a+1)^2]$ in (7) does not have any effect on e^a . It is U_a that makes a difference. When $a = 0$, $a =$ is the ML parameter estimate. When $a =$,

$$
\mathbf{U}_a{=}\mathbf{D}_p^{'}\mathbf{D}_p
$$

is the weight matrix corresponding to modeling **R** by least squares. Thus, ridge SEM can be regarded as a combination of ML and LS. We would expect that it has the merits of both procedures. That is, ridge SEM will have a better convergence rate and more accurate parameter estimates than ML and more efficient estimates than LS.

It follows from (6) and a Taylor expansion of $\mathbf{g}_d(\mathbf{a})$ at \mathbf{g}_0 that

$$
\sqrt{n}(\widehat{\theta}_a - \theta_0) = -[\dot{\mathbf{g}}_a(\overline{\theta})]^{-1} \mathbf{g}_a(\theta_0) = (\dot{\sigma}_a' \mathbf{W}_a \dot{\sigma}_a)^{-1} \dot{\sigma}_a' \mathbf{W}_a \sqrt{n}(\mathbf{s}_a - \sigma_a) + o_p(1), \quad (8)
$$

where $\dot{\mathbf{g}}_d$ $\overline{\mathbf{j}}$ is $q \times q$ matrix and each of its rows is evaluated at a vector that is between $\overline{\mathbf{g}}_0$ and $\partial_p(1)$ represents a quantity that converges to zero in probability as *n* increases. We also omitted the argument of the functions in (8) when evaluated at the population value $θ$. Notice that the rows of *a* corresponding to the diagonal elements of *a* are zeros and the vector $(s_a - a)$ constitutes of $(r - 1)$ plus p zeros. It follows from (1) that

$$
\sqrt{n}(\mathbf{s}_a - \sigma_a) \xrightarrow{\mathscr{L}} N(\mathbf{0}, \mathbf{\hat{T}}^*), \quad (9)
$$

where Y^* is a $p^* \times p^*$ matrix consisting of Y and p rows and p columns of zeros. Obviously, Y^* is singular. We may understand (9) by the general definition of a random variable, which is just a constant when its variance is zero. It follows from (8) and (9) that

$$
\sqrt{n}(\widehat{\theta}_a - \theta_0) \xrightarrow{\mathscr{L}} N(\mathbf{0}, \mathbf{\Omega}), \quad \text{(10a)}
$$

where

$$
\pmb{\Omega} {=} \big(\overset{\,\,{}_\circ}{\sigma}_{a}^{'}\mathbf{W}_{a} \overset{\,\,{}_\circ}{\sigma}_{a}\big)^{-1} \overset{\,\,{}_\circ}{\sigma}_{a}^{'}\mathbf{W}_{a} \pmb{\Upsilon}^{*}\mathbf{W}_{a} \overset{\,\,{}_\circ}{\sigma}_{a} \big(\overset{\,\,{}_\circ}{\sigma}_{a}^{'}\mathbf{W}_{a} \overset{\,\,{}_\circ}{\sigma}_{a}\big)^{-1}.\tag{10b}
$$

Let Y^* be a consistent estimator of Y^* , which can be obtained from a consistent Y plus p rows and p columns of zeros. A consistent estimate $=$ $\binom{j}{j}$ of can be obtained when replacing the unknown parameters in (10) by a and Y^* by Y^* . Notice that the in (10) is

the asymptotic covariance matrix. We will compare the formula-based SEs $\hat{\omega}_{jj}^{1/2}/\sqrt{n}$ against empirical SEs at smaller sample sizes using Monte Carlo.

A consistent Y can be obtained by the approach of estimating equations (see e.g., Yuan & Jennrich, 1998). Actually, the estimates of ϒ given in Lee et al. (1992, 1995), Jöreskog (1994) and Muthén and Satorra (1995) can all be regarded as using estimating equations.

2.3 Statistics for overall model evaluation

This subsection presents four statistics for overall model evaluation. When minimizing (3) for parameter estimates, we automatically get a measure of discrepancy between data and model, i.e., F_{MLa} (a). However, the popular statistic $T_{MLa} = nF_{MLa}$ (a) does not asymptotically follow a chi-square distribution even when $a = 0$. Let

$$
F_{_{RLSa}}(\widehat{\theta}_a) = [\mathbf{s}_a - \sigma_a(\widehat{\theta}_a)]^{'} \mathbf{W}_a(\widehat{\theta}_a) [\mathbf{s}_a - \sigma_a(\widehat{\theta}_a)] = \frac{1}{2} \text{tr} \{ [\mathbf{R}_a {\sum}_a^{-1} (\widehat{\theta}_a) - \mathbf{I}]^2 \}
$$

and

$$
T_{RLSa} = nF_{RLSa}(\theta_a) \quad (11)
$$

be the so-called reweighted LS statistic, which is in the default output of EQS when modeling the covariance matrix. Under the assumption of a correct model structure, there exists

$$
T_{\rm MLa} = T_{\rm RLSa} + o_p(1). \quad (12)
$$

Notice that $a = a(0)$. It follows from (8) that

 $\begin{aligned} \sqrt{n}[\,\mathbf{s}_a - \sigma_a(\widehat{\theta}_a)] &\hspace{-.05cm}=\hspace{-.05cm}\sqrt{n}\{(\mathbf{s}_a - \sigma_a) - [\,\sigma_a(\widehat{\theta}_a) - \sigma_a(\theta_0)]\} \\ &\hspace{-.05cm}=\hspace{-.05cm}\sqrt{n}\{(\mathbf{s}_a - \sigma_a) - \dot{\sigma}_a(\widehat{\theta}_a - \theta_0)\} {+} o_p(1) \\ &\hspace{-.05cm}=\hspace{-.05cm}\mathbf{P}_a\sqrt{n}(\mathbf{s}_a - \sigma_a) {+} o_p(1), \end{aligned}$ (13)

where

$$
\mathbf{P}_a = \mathbf{I} - \dot{\sigma}_a (\dot{\sigma}_a' \mathbf{W}_a \dot{\sigma}_a)^{-1} \dot{\sigma}_a' \mathbf{W}_a.
$$

Combining (12) and (13) leads to

$$
T_{_{MLa}} = n(\mathbf{s}_a - \sigma_a)' \mathbf{P}_a' \mathbf{W}_a \mathbf{P}_a (\mathbf{s}_a - \sigma_a) + o_p(1).
$$
 (14)

Notice that Y^* in (9) has a rank of p^* , there exists a $p^* \times p^*$ matrix **A** such that $AA = Y^*$. Let $\mathbf{u} \sim N_{\mathbf{p} *}(\mathbf{0}, \mathbf{I})$, then it follows from (9) that

$$
\sqrt{n}(\mathbf{s}_a - \sigma_a) = \mathbf{A}\mathbf{u} + o_p(1). \quad (15)
$$

Combining (14) and (15) yields

$$
T_{\text{MLa}} = \mathbf{u}'(\mathbf{P}_a\mathbf{A})'\mathbf{W}_a(\mathbf{P}_a\mathbf{A})\mathbf{u} + o_p(1).
$$
 (16)

Notice that ($\mathbf{P}_a \mathbf{A}$) $\mathbf{W}_a(\mathbf{P}_a \mathbf{A})$ is nonnegative definite and its rank is p_*-q . Let $0 < 1 \leq 2 \ldots$ p^* –q be the nonzero eigenvalues of $(\mathbf{P}_a\mathbf{A}) \mathbf{W}_a(\mathbf{P}_a\mathbf{A})$ or equivalently of $\mathbf{P}_a' \mathbf{W}_a \mathbf{P}_a \mathbf{\Upsilon}^*$. It follows from (16) that

$$
T_{\scriptscriptstyle MLa} = \sum_{j=1}^{p_*-q} \kappa_j u_j^2 + o_p(1). \quad (17)
$$

where u_j^2 are independent and each follows χ_1^2 . Unless all the j 's are 1.0, the distribution of T_{MLa} will not be $\chi^2_{p_*-q}$. However, the behavior of T_{MLa} might be approximately described by a chi-square distribution with the same mean. Let

$$
\widehat{m}\text{=} \text{tr}(\widehat{\textbf{T}}^*\widehat{\textbf{P}}_a'\widehat{\textbf{W}}_a\widehat{\textbf{P}}_a)/(p_*-q).
$$

Then, as n

$$
T_{\rm RMLa}\!\!=\!\!T_{\rm MLa}/\hat{m}
$$

approaches a distribution whose mean equals $p_* - q$. Thus, we may approximate the distribution of T_{MLa} by

 $T_{RMLa} \sim \chi^2_{p_*-q}$, (18)

parallel to the Satorra and Bentler (1988) rescaled statistic when modeling the sample covariance matrix. Again, the approximation in (18) is motivated by asymptotics, we will use Monte Carlo to study its performance with smaller sizes.

Notice that the systematic part of T_{RMLa} is the quadratic form

$$
Q_{\rm {\rm \scriptscriptstyle RMLa}}{=}(p_{\ast}{-}q)\sum_{j=1}^{p_{\ast}{-}q}\kappa_{i}u_{j}^{2}/(\sum_{j=1}^{p_{\ast}-q}\kappa_{j}),
$$

which agrees with $\chi^2_{p_*-q}$ in the first moment. Allowing the degrees of freedom to be estimated rather than $p^* - q$, a statistic that agrees with the chi-square distribution in both the first and second moments was studied by Satterthwaite (1941) and Box (1954), and applied to covariance structure models by Satorra and Bentler (1988). It can also be applied to approximate the distribution of T_{MLa} . Let

$$
m_1 = \sum_{j=1}^{p_*-q} \kappa_j^2 / \sum_{j=1}^{p_*-q} \kappa_j, \quad m_2 = \left(\sum_{j=1}^{p_*-q} \kappa_j\right) / \sum_{j=1}^{p_*-q} \kappa_j^2.
$$

Then T_{MLa}/m_1 asymptotically agrees with $\chi^2_{m_2}$ in the first two moments. Consistent estimates of m_1 and m_2 are given by

$$
\widehat{m}_1 = \text{tr}[(\widehat{\mathbf{T}}^* \widehat{\mathbf{P}}_a' \widehat{\mathbf{W}}_a \widehat{\mathbf{P}}_a)^2] / \text{tr}(\widehat{\mathbf{T}}^* \widehat{\mathbf{P}}_a' \widehat{\mathbf{W}}_a \widehat{\mathbf{P}}_a), \quad \widehat{m}_2 = [\text{tr}(\widehat{\mathbf{T}}^* \widehat{\mathbf{P}}_a' \widehat{\mathbf{W}}_a \widehat{\mathbf{P}}_a)]^2 / \text{tr}[(\widehat{\mathbf{T}}^* \widehat{\mathbf{P}}_a' \widehat{\mathbf{W}}_a \widehat{\mathbf{P}}_a)^2].
$$
 (19)

Thus, using the approximation

$$
T_{\text{AMLa}} = T_{\text{MLa}} / \hat{m}_1 \sim \chi^2_{\hat{m}_2} \quad (20)
$$

might lead to a better description of T_{MLa} than (18). We will also study the performance of (20) using Monte Carlo in the next section.

In addition to T_{MLa} , T_{RLSa} can also be used to construct statistics for overall model evaluation, as printed in EQS output when modeling the sample covariance matrix. Like T_{MLa} , when modeling \mathbf{R}_a , T_{RLSa} does not asymptotically follow a chi-square distribution even when $a = 0$. It follows from (12) that the distribution of T_{RLSa} can be approximated using

$$
T_{RRLSa} = T_{RLSa} / \hat{m} \sim \chi^2_{p_*-q} \quad (21)
$$

or

$$
T_{ARLSa} = T_{RLSa} / \hat{m}_1 \sim \chi^2_{\hat{m}_2}.
$$
 (22)

The rationales for the approximations in (21) and (22) are the same as those for (18) and (20), respectively. Again, we will study the performance of T_{RRLSa} and T_{ARLSa} using Monte Carlo in the next section.

We would like to note that the $o_p(1)$ in equation (12) goes to zero as n . But statistical theory does not tell how close T_{MLa} and T_{RLSa} are at a finite *n*. The Monte Carlo study in the next section will allow us to compare their performances and to identify the best statistic for overall model evaluation at smaller sample sizes.

We also would like to note that the ridge procedure developed here is different from the ridge procedure for modeling covariance matrices developed in Yuan and Chan (2008). When treating \mathbf{R}_a as a covariance matrix in the analysis, we will get identical T_{MLa} and T_{RLSa} as defined here if all the diagonal elements of α β a) happen to be $a + 1$, which is true for many commonly used SEM models. However, the rescaled or adjusted statistics will be different. Similarly, we may also get identical estimates for factor loadings, but their SEs will be different when based on either the commonly used information matrix or the sandwich-type covariance matrix constructed using Y^* .

3. Monte Carlo Results

The population **z** contains 15 normally distributed random variables with mean zero and covariance matrix

$$
\sum{=}\Lambda \Phi \Lambda^{'}{+}\Psi,
$$

where

$$
\Lambda = \left(\begin{array}{ccc} \lambda & 0 & 0 \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{array}\right)
$$

with $= (.60, .70, 0.75, .80, .90)$ and **0** being a vector of five zeros;

$$
\mathbf{\Phi} = \left(\begin{array}{ccc} 1.0 & .30 & .40 \\ .30 & 1.0 & .50 \\ .40 & .50 & 1.0 \end{array} \right);
$$

and is a diagonal matrix such that all the diagonal elements of are 1.0. Thus, **z** can be regarded as generated by a 3-factor model, and each factor has 5 unidimensional indicators.

Three sets of conditions are used to obtain the observed variables. In condition 1, all the 15 variables in **x** are dichotomous and are obtained using thresholds

$$
\tau = (-0.52, -0.25, 0, 0.25, 0.52, -0.39, -0.25, -0.13, 0, 0.13, 0, 0.13, 0.25, 0.39, 0.52)
$$

which corresponds to 30%, 40%, 50%, 60%, 70%, 35%, 40%, 45%, 50%, 55%, 50%, 55%, 60%, 65%, and 70% of zeros at the population level for the 15 variables, respectively. In condition 2, for each factor the first two variables have five categories and the last three variables are dichotomous. The thresholds for the 6 five-category variables are respectively $t_1 = (-0.52, -0.25, 0.25, 0.52)$, corresponding to proportions (30%, 10%, 20%, 10%, 30%) for the five categories of x_1 ; $_2 = (-0.84, -0.25, 0.25, 0.84)$, corresponding to proportions $(20\%, 20\%, 20\%, 20\%, 20\%)$ for the five categories of x_2 ; $6 = (-0.84, -0.25, 0.25, 0.84)$, corresponding to proportions (20%, 20%, 20%, 20%, 20%) for the five categories of x_6 ; $\tau =$ (−0.84, −0.52, −0.25, 0.25), corresponding to proportions (20%, 10%, 10%, 20%, 40%) for the five categories of x_7 ; $_{11} = (-0.52, -0.25, 0.25, 0.52)$, corresponding to proportions (30%, 10%, 20%, 10%, 30%) for the five categories of x_{11} ; $12 = (-0.25, 0.25, 0.52, 0.84)$, corresponding to proportions $(40\%, 20\%, 10\%, 10\%, 20\%)$ for the five categories of x_{12} . The thresholds for the 9 dichotomous variables are $= (0, 0.25, 0.52, -0.25, 0, 0.13, 0.25,$ 0.39, 0.52), which correspond to 50%, 60%, 70%, 40%, 50%, 55%, 60%, 65%, 70% of zeros at the population level of x_3 , x_4 , x_5 , x_8 , x_9 , x_{10} , x_{13} , x_{14} and x_{15} , respectively. In condition 3, the first two variables for each factor are continuously observed and the last three variables are dichotomous using thresholds

$$
\tau = (0, 0.25, 0.52, -0.25, 0, 0.13, 0.25, 0.39, 0.52)
$$

which correspond to 50%, 60%, 70%, 40%, 50%, 55%, 60%, 65%, and 70% of zeros at the population level of variables x_3 , x_4 , x_5 , x_8 , x_9 , x_{10} , x_{13} , x_{14} and x_{15} , respectively.

Because it is with smaller sample sizes that ML encounter problems, we choose sample sizes³ $n = 100$, 200, 300 and 400. One thousand replications are used at each sample size. For each sample, we model \mathbf{R}_a with $a = 0$, .1 and .2, which are denoted by ML, ML.₁ and ML.2, respectively. Our evaluation includes the number of convergence or converging rate, the speed of convergence, biases and SEs as well as mean square errors (MSE) of the parameter estimates; and the performance of the four statistics given in the previous section. We also compare SEs based on the covariance matrix \quad in (10) against empirical SEs.

All the thresholds are estimated using the default probit function in SAS. Pearson productmoment correlations are obtained for continuously observed variables. Fisher scoring algorithms are used to obtain polychoric/polyserial correlations (Olsson, 1979; Olsson, Drasgow & Dorans, 1982) and to solve equation (6) for structural model parameters α (Lee & Jennrich, 1979; Olsson, 1979). The convergence criterion in estimating the polychoric/ polyserial correlations is set as $|r^{(k+1)} - r^{(k)}| < 10^{-4}$, where $r^{(k)}$ is the value of r after the kth iteration; the convergence criterion for obtaining θ is set as

, where θ_i^{\wedge} is the *j*th parameter after the *k*th iteration. True population values are set as the initial value in both estimation processes. We record the

³Actually, at sample size 400, we found that all replications converged with ML.

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estimation as unable to reach a convergence if the convergence criterion cannot be reached after 100 iterations. For each **R**, the ϒ in (1) is estimated using estimating equations.

Note that not all of the $N = 1000$ replications converge in all the conditions, all the empirical results are based on N_c converged replications for each estimation method. Let $_{ij}$ be the estimate of j in the *i*th converged replication. For each estimation method at a given sample size we obtained

Bias_j =
$$
\frac{1}{N_c} \sum_{i=1}^{N_c} \hat{\theta}_{ij} - \theta_{j0}
$$
, Var_j = $\frac{1}{N_c - 1} \sum_{i=1}^{N_c} (\hat{\theta}_{ij} - \overline{\theta}_{j})^2$,

with $\overline{\theta}_{j} = \sum_{i=1}^{N_c} \widehat{\theta}_{ij} / N_c$, and

$$
\text{MSE}_{j} = \frac{1}{N_c} \sum_{i=1}^{N_c} (\hat{\theta}_{ij} - \theta_{j0})^2.
$$

For the performance of the formula-based SE, we also obtained

$$
\text{SE}_{Fj} = \frac{1}{N_c} \sum_{i=1}^{N_c} \text{SE}_{ij},
$$

where SE_{ij} is the square root of the *j*th diagonal element of π in the *i*th converged replication. In contrast, the empirical SE, SE_{Ej} is just the square root of Var_j . Notice that there are 18 free model parameters: 15 factor loadings and 3 factor correlations. With 3 data conditions, 3 estimation methods and 4 sample sizes, there will be too many tables to include in the paper if we report bias, MSE and SEs for each individual parameter. Instead, these are put on the web at "www.anonymous.edu/ridge-item-SEM/". In the paper, for each sample size and each estimation method, we report the averaged bias, variance and MSE given by

Bias=
$$
\frac{1}{18}\sum_{j=1}^{18}|\text{Bias}_j|
$$
, Var= $\frac{1}{18}\sum_{j=1}^{18}\text{Var}_j$, MSE= $\frac{1}{18}\sum_{j=1}^{18}\text{MSE}_j$,
SE_F= $\frac{1}{18}\sum_{j=1}^{18}\text{SE}_{F_j}$, SE_E= $\frac{1}{18}\sum_{j=1}^{18}\text{SE}_{E_j}$,

and the averaged difference

$$
AD = \frac{1}{18} \sum_{j=1}^{18} |SE_{Fj} - SE_{Ej}|.
$$

which will give us the information of the formula-based SEs when predicting empirical SEs.

Results for data condition 1 with 15 dichotomous indicators are in Tables 1 to 5. All replications reached convergence when estimating **R**. But more than half replications cannot converge when solving (6) with $a = 0$ and .1 at $n = 100$, as reported in the upper panel of Table 1. When $a = 0.2$, the number of convergence doubles that when $a = 0$ at $n = 100$. When $n = 200$, there are still about one third of the replications cannot reach convergence at $a = 0$ while all reach convergence at $a = 0.2$. Ridge SEM not only results in more convergences but also converges faster, as reported in the lower panel of Table 1, where each entry is the average of the number of iterations for N_c converged replications.

Tables 2 contains the averaged bias, variance and MSE for the four sample sizes and three estimation methods. Clearly, all the averaged biases are at the 3rd decimal place. Except for $n = 100$, all the other variances and MSEs are also at the 3rd decimal place. Because the N_c 's for the three different a's for $n = 100$ and 200 are so different, it is had to compare the results between different estimation methods. When $n = 400$, all the three methods converged for all the replications, the averaged bias, variance, and MSE all become smaller as a changes from 0 to .2. At $n = 300$, both ML.₁ and ML.₂ converged for all the replications, the averaged bias, variance, and MSE corresponding to ML_2 are also smaller. These indicate that the ridge procedure with a proper a leads to less biased, more efficient and more accurate parameter estimates than ML. The corresponding biases, variances and MSEs for individual parameters are in Tables A1 to A4 at "www.nd.edu~kyuan/ridge-item-SEM/". From these tables we may notice that most individual biases are also at the 3rd decimal place although they tend to be negative. We may also notice that estimates for smaller loadings tend to have greater variances and MSEs.

Table 3 contains the empirical mean, standard deviation (SD), the number of rejection and the rejection ratio of the statistics T_{RMLa} and T_{AMLa} , based on the converged replications. Each rejection is compared to the 95th percentiles of the reference distribution in (18) or (20). For reference, the mean and SD of T_{MLa} are also reported. Both T_{RMLa} and T_{AMLa} over-reject the correct model although they tend to improve as $n \text{ or } a$ increases. Because the three N_c 's at $n = 100$ are very different, the rejection rates, means or SDs of the three estimation methods are not comparable for this sample size. Table 3 also suggests that T_{MLa} cannot be used for model inference because its empirical means and SDs are far away from those of the nominal χ^2_{87} .

Table 4 contains the results of T_{RRLSa} and T_{ARLSa} parallel to those in Table 3. For $n = 200$, 300 and 400, the statistic T_{RRLSa} performed very well in mean, SD and rejection rate although there is a slight over-rejection at smaller n . While T_{RLSa} monotonically decreases with a, T_{RRLSa} is very stable when a changes. The statistic T_{ARLSa} also performed well with a little bit of under-rejection.

Table 5 compares the averages of the formula-based SEs against the empirical ones. We use 4 decimals to inform the fine differences among the three estimation methods. As expected, within each estimation method, both the averaged SE_E and SE_F become smaller as n increases, as reflected by Table 5(a). They are also smaller at a given n when a changes from 0 to .2, although at $n = 100$ and 200 they are based on different number of replications. Table 5(a) also implies that formula-based SEs tend to slightly under-predict empirical SEs. The results in Table 5(b) indicate that SE_F predicts SE_E better when either a or n increases. At $n = 400$, the under-prediction is between 1% and 2% with ML.₂. It is interesting to note that the averaged difference between SE_F and SE_E is smaller at $n = 300$ and $a = .2$ than that at $n = 400$ and $a = 0$ or .1. The corresponding SEs for individual parameters are in Tables A5 to A8 on the web, where almost all individual SE_{FS} are slightly under-predicted by the corresponding SE_F s, with only a few exceptions mostly for factor correlations.

Results for data condition 2 with 6 five-category and 9 dichotomous indicators are in Tables 6 to 10. All replications converged when estimating **R**. But only 294 out of 1000 replications converged when solving (6) with $a = 0$ at $n = 100$, as reported in the upper panel of Table 6. At $n = 100$, the number of convergences almost tripled when $a = 0.1$, and only 3 replications could not reach convergence with ML.₂. Nonconvergences still exist for ML at $n = 200$ and 300 while all replications converged for ML_1 and ML_2 . The lower panel of Table 6 implies that ridge SEM also converges faster. It is interesting to see that ML at $n = 100$ in Table 6 enjoys fewer convergences than that in Table 1. Further examination indicates that almost all the nonconvergences are due to nonpositive definite or near singular **R**. This is because positive definiteness is a function of all the elements in **R**. One element in **R** can change the smallest eigenvalue from positive to negative.

Tables 7 contains the averaged bias, variance and MSE for data condition 2. At $n = 400$ when all the three estimation methods converged on all replications, bias, variance and MSE all become smaller when a changes from 0 to .2. These quantities also become smaller as a increases at $n = 100$, 200 and 300. These indicate that the ridge procedure with a proper a leads to less biased, more efficient and more accurate parameter estimates than ML. Compared to the results in Table 2, we notice that, except for the averaged bias of ML at $n =$ 100, all the other numbers in Table 7 are smaller. This indicates that having indicators with more categories leads to less biased and more efficient parameter estimates for all the three estimation methods. The exception for the averaged bias with ML at $n = 100$ is due to the very different convergence rates. The corresponding biases, variances and MSEs for individual parameters are in Tables A9 to A12 on the web. From these tables we may notice that most individual biases are negative. We may also notice that estimates for smaller loadings do not tend to have greater variances or MSEs anymore, due to their corresponding indicators having more categories.

Parallel to Table 3, Table 8 contains the results for the statistics T_{RMLa} and T_{AMLa} , based on the converged replications. Similar to those in Table 3, both T_{RMLa} and T_{AMLa} over-reject the correct model although they tend to improve as n or a increases. Among the statistics, T_{AMLa} performed the best at $a = .2$. Table 8 also suggests that T_{MLa} cannot be used for model inference. Table 9 contains the results of T_{RRLSa} and T_{ARLSa} parallel to those in Table 4. Both T_{RRLSa} and T_{ARLSa} continue to be stable when *n* or *a* changes. But T_{RRLSa} tends to reject the correct model more than in Table 4 while T_{ARLSa} slightly under-rejects the correct model. Tables 8 and 9 also suggest that T_{MLa} and T_{RLSa} tend to be smaller with indicators having more categories, but they are still too far away from the expected χ^2_{87} .

Table 10 contains the averages of empirical and the formula-based SEs. Similar to those in Table 5, the SE becomes smaller as either *n* or *a* increases. Table 10(a) also implies that formula-based SEs tend to slightly under-predict empirical SEs. The results in Table 10(b) indicate that SE_F predicts SE_E better when either a or n increases. SE_F also predicts SE_E better under ML.₂ at $n = 300$ than under ML at $n = 400$. Comparing the results in Table 10 to those in Table 5, we notice that the formula-based SEs predict the empirical ones better when indicators have more categories. The corresponding SEs for individual parameters are in Tables A13 to A16 on the web, where almost all individual SE_{E} s are slightly underpredicted by the corresponding SE_F s, with only a few exceptions.

Results for data condition 3 with 6 continuous and 9 dichotomous indicators are in Tables 11 to 15. Similar to data conditions 1 and 2, all nonconvergences occurred when solving (6) with $a = 0$ at $n = 100$, 200, 300 and with $a = 0.1$ at $n = 100$, as reported in the upper panel of Table 11. Obviously, ridge SEM not only results in more convergences but also converges faster, as reported in the lower panel of Table 1. Similar to being observed previously, the condition with 6 continuous and 9 dichotomous indicators does not necessarily correspond

to more positive definite \bf{R} than the condition with 15 dichotomous indicators when n is small. It is expected that both ML_{1} and ML_{2} perform well.

Tables 12 contains the averaged bias, variance and MSE. Similar to the two previous conditions, bias, variance and MSE all become smaller from $a = 0$ to $a = .2$. Compared to the results in Tables 2 and 7, we notice that, except for the averaged bias of ML at $n = 100$, all the other numbers in Table 12 are smaller. This is expected because more continuous indicators should correspond to less biased and more efficient parameter estimates. The exception for the averaged bias with ML at $n = 100$ is due to the very different convergence rates. The corresponding biases, variances and MSEs for individual parameters are in Tables A17 to A20 on the web.

Table 13 gives the results of T_{RMLa} and T_{AMLa} , parallel to those in Tables 3 and 8. Similar to being observed earlier, both T_{RMLa} and T_{AMLa} over-reject the correct model although they tend to improve as *n* or *a* increases. Table 14 contains the results of T_{RRLSa} and T_{ARLSa} parallel to those in Tables 4 and 9. Both T_{RRLSa} and T_{ARLSa} continue to be stable to the changes of *n* and *a*. But T_{RRLSa} tends to reject the correct model more often than in previous tables. T_{ARLSa} performed quite well, only slightly under-rejecting the correct model. Tables 13 and 14 suggest that T_{MLa} and T_{RLSa} tend to be smaller with more continuous indicators, but they are still too far away from the expected χ^2_{87} .

Table 15 compares SE_F against SE_E for data condition 3, parallel to Tables 5 and 10. Both the averaged SE_F and SE_F become smaller as *n* increases or *a* changes from 0 to .2. Formula-based SEs still tend to slightly under-predict empirical SEs. The results in Table 15(b) indicate that SE_F predicts SE_E better when either a or n increases. Again, the averaged difference between SE_F and SE_E under ML.₂ at $n = 300$ is smaller than those under ML and ML.₁ at $n = 400$. Comparing the numbers in Table 15 with those in Tables 5 and 10 we found that more continuous indicators not only lead to more efficient parameter estimates but also more accurate prediction of empirical SEs by formula-based SEs. The corresponding SEs for individual parameters are in Tables A21 to A24 on the web, where most individual SE_{E} s are still slightly under-predicted by the corresponding SE_{F} s.

In summary, for the three data conditions and four sample sizes, ML.₂ performed better than ML.1, which was a lot better than ML with respect to convergence rate, convergence speed, bias, efficiency, as well as the accuracy of formula-based SEs.

4. An Empirical Example

The empirical results in the previous section indicate that, with a proper a , ML_a performed much better than ML. This section further illustrates the effect of a on individual parameter estimates and test statistics using a real data example, where ML fails.

Eysenck and Eysenck (1975) developed a Personality Questionnaire. The Chinese version of it was available through Gong (1983). This questionnaire was administered to 117 first year graduate students in a Chinese university. There are four subscales in this questionnaire (Extraversion/Introversion, Neuroticism/Stability, Psychoticism/Socialisation, Lie), and each subscale consists of 20 to 24 items with two categories. We have access to the dichotomized data of the Extraversion/Introversion subscale, which has 21 items. According to the manual of the questionnaire, answers to the 21 items reflect a respondent's latent trait of Extraversion/Introversion. Thus, we may want to fit the dichotomized data by a one-factor model. The tetrachoric correlation matrix⁴ **R** was first obtained together with **Y**. However, **R** is not positive definite. Its smallest eigenvalue is −.473. Thus, the ML procedure cannot be used to analyze **R**.

Table 16(a) contains the parameter estimates and their SEs when modeling $\mathbf{R}_a = \mathbf{R} + a\mathbf{I}$ with $a = .5$, 6 and .7. To be more informative, estimates of error variances ($_{11}$ to $_{21,21}$) are also reported. The results imply that both parameter estimates and their SEs change little when ^a changes from .5 to .7. Table 16(b) contains the statistics T_{RMLa} , T_{AMLa} , T_{RRLSa} and T_{ARLSa} as well as the associated p -values. The estimated degrees of freedom m_2 for the adjusted statistics are also reported. All statistics indicate that the model does not fit the data well, which is common when fitting practical data with a substantive model. The statistics $T_{RMI,a}$ and T_{AMLa} decrease as a increases, while T_{RRLSa} and T_{ARLSa} as well as m_2 are barely affected by a. Comparing the statistics implies that statistics derived from T_{MLa} may not be as reliable as those derived from T_{RLSa} . The p-values associated with T_{RRLSa} are smaller than those associated with T_{ARLSa} , which agrees with the results in the previous section where T_{ARLSa} tends to slightly under-reject the correct model.

5. Conclusion and Discussion

Procedures for SEM with ordinal data have been implemented in major software. However, there exist problems of convergence in parameter estimation and lack of reliable statistics for overall model evaluation, especially when the sample size is small and the observed frequencies are skewed in distribution. In this paper we studied a ridge procedure paired with the ML estimation method. We have shown that parameter estimates are consistent, asymptotically normally distributed and their SEs can be consistently estimated. We also proposed four statistics for overall model evaluation. Empirical results imply that the ridge procedure performs better than ML in convergence rate, convergence speed, accuracy and efficiency of parameter estimates, and accuracy of formula-based SEs. Empirical results also imply that the rescaled statistic T_{RRLSa} performed best at smaller sample sizes and T_{ARLSa} also performed well for $n = 300$ and 400, especially when **R** contains product-moment correlations.

For SEM with covariance matrices, Yuan and Chan (2008) suggested choosing $a = p/n$. Because p/n 0 as n , the resulting estimator is asymptotically equivalent to the ML estimator. Unlike a covariance matrix that is always nonnegative definite, the polychoric/ polyserial/product-moment correlation matrix may have negative eigenvalues that are greater than p/n in absolute value, hence choosing $a = p/n$ may not lead to a positive definite \mathbf{R}_a , as is the case with the example in the previous section. In practice, one should choose an a that makes the smallest eigenvalue of \mathbf{R}_a greater than 0 for a proper convergence when estimating σ . Once converged, a greater a makes little difference on parameter estimates and test statistics T_{RRLSa} and T_{ARLSa} as illustrated by the example in the previous section and the Monte Carlo results in section 3. If the estimation cannot converge for an a that makes the smallest eigenvalue of \mathbf{R}_a greater than, say, 1.0, then one needs to choose either a different set of starting values or to reformulate the model. A good set of starting values can be obtained from submodels where analytical solutions exist. For example, when z_i , z_j and z_k are unidimensional indicators for a factor, with loading i , j and k , respectively; then $ij = i j$ and $i = (i j i k / j k)^{1/2}$. Thus, $(r_{ij} r_{ik}/r_{jk})^{1/2}$ gives a good starting value for i . When all the correlations are positive, we may choose .5 for all the free parameters. Actually, all the starting values of factor loadings for the example in the previous section are set at .5 without any convergence problem with $a = .5$, .6 and .7 even when three of the 21 estimates are negative. The product-moment correlations of the ordinal and continuous data can be used as the starting values when estimating the polychoric and polyserial correlations.

⁴Four of the 21 \times 20/2 = 210 contingency tables contain a cell with zero observations, which was replaced by .1 to facilitate the estimation of **R**.

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We have only studied ridge ML in this paper, mainly because ML is the most popular and most widely used procedure in SEM. In addition to ML, the normal-distribution-based NGLS procedure has also been implemented in essentially all SEM software. The ridge procedure developed in section 2 can be easily extended to NGLS. Actually, the asymptotic distribution in (10) also holds for the NGLS estimator after changing $\left(\right)$ in the definition of W_a to S_a ; the rescaled and adjusted statistics parallel to those in (21) and (22) for the NGLS procedure can be similarly obtained. Further Monte Carlo study on such an extension is valuable.

Another issue with modeling polychoric/polyserial/product-moment correlation matrix is the occurrence of negative estimates of error variances. Such a problem can be caused by model misspecification and/or small sample together with true error variances being small (see e.g, Kano, 1998; van Driel, 1978). Negative estimates of error variances can also occur with the ridge estimate although it is more efficient than the ML estimator. This is because δ () will be also misspecified if (e) is misspecified, and true error variances corresponding to the estimator in (5) continue to be small when modeling \mathbf{R}_a . For correctly specified models, negative estimates of error variances is purely due to sampling error, which should be counted when evaluating empirical efficiency and bias, as is done in this paper.

We have only considered the situation when $\mathbf{z} \sim N(\boldsymbol{\mu})$ and when (e) is correctly specified. Monte Carlo results in Lee et al. (1995), Flora and Curran (2004), and Maydeu-Olivares (2006) imply that SEM by analyzing the polychoric correlation matrix with ordinal data has certain robust properties when $\mathbf{z} \sim N(\boldsymbol{\mu})$ is violated, which is a direct consequence of the robust properties possessed by **R**, as reported in Quiroga (1992). These robust properties should equally hold for ridge SEM because θ is a continuous function of **R**. When both () is misspecified and $\mathbf{z} \sim N(\boldsymbol{\mu})$ does not hold, the two misspecifications might be confounded. Test procedures for checking $\mathbf{z} \sim N(\boldsymbol{\mu})$ under ordinal data exist (see e.g., Maydeu-Olivares, 2006). Further study is needed for their practical use in SEM with a polychoric/polyserial/product-moment correlation matrix.

As a final note, the developed procedure can be easily implemented in a software that already has the option of modeling polychoric/polyserial/product-moment correlation matrix **R** by robust ML. With **R** being replaced by \mathbf{R}_{a} , one only needs to set the diagonal of the fitted model to $a + 1$ instead of 1.0 in the iteration process. The resulting statistics T_{MI} , T_{RML} , T_{AML} and T_{RLS} will automatically become T_{MLa} , T_{RMLa} , T_{AMLa} and T_{RLSa} , respectively. To our knowledge, no software currently generates T_{RRLSa} and T_{ARLSa} . However, with T_{RLSa} , m_1 and m_2 , these two statistics can be easily calculated. Although \mathbf{R}_a is literally a covariance matrix, except unstandardized ∂_a when diag(\mathbf{R}_a) = (∂_a) happen to hold, treating \mathbf{R}_a as a covariance matrix will not generate correct analysis (see e.g., McQuitty, 1997).

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Number of convergences and average number of iterations with 15 dichotomized indicators, 1000 replications.

Averaged bias×10 , variance×10 and MSE×10 with 15 dichotomized indicators, based on converged replications.

 $q = 87$, RN=reject number, p* − T_{AMLa} with 15 dichotomized indicators, based on converged replications ($df =$ T_{RMLa} and Performance of the statistics RR=reject ratio). RR=reject ratio).

Performance of the statistics T_{RRLSa} and T_{ARLSa} with 15 dichotomized indicators, based on converged replications ($df =$ Performance of the statistics T_{RRLSa} and T_{ARLSa} with 15 dichotomized indicators, based on converged replications ($dt = p_* - q = 87$, RN=reject number, RR=reject ratio). $q = 87$, RN=reject number, RR=reject ratio).

Performance of standard errors with 15 dichotomized indicators, based on converged replications. Performance of standard errors with 15 dichotomized indicators, based on converged replications.

(a) Averaged empirical standard errors and formula-based standard errors **(a) Averaged empirical standard errors and formula-based standard errors**

Number of convergence and average number of iterations with 6 five-category and 9 dichotomous indicators, 1000 replications.

Averaged bias×10 , variance×10 and MSE×10 , with 6 five-category and 9 dichotomous indicators, based on converged replications.

 $q = 87,$ p* − T_{AMLa} with 6 five-category and 9 dichotomous indicators, based on converged replications ($df =$ T_{RMLa} and RN=reject number, RR=reject ratio). RN=reject number, RR=reject ratio). Performance of the statistics

 $q = 87,$ p* − T_{ARLSa} with 6 five-category and 9 dichotomous indicators, based on converged replications ($df =$ T_{RRLSa} and RN=reject number, RR=reject ratio). RN=reject number, RR=reject ratio). Performance of the statistics

Performance of standard errors with 6 five-category and 9 dichotomous indicators, based on converged replications. Performance of standard errors with 6 five-category and 9 dichotomous indicators, based on converged replications.

(a) Averaged empirical standard errors and formula-based standard errors **(a) Averaged empirical standard errors and formula-based standard errors**

Number of convergences and average number of iterations with 6 continuous and 9 dichotomized indicators, 1000 replications.

Averaged bias×10 , variance×10 and MSE×10 , with 6 continuous and 9 dichotomized indicators, based on converged replications.

 $q = 87,$ p* − T_{AMLa} with 6 continuous and 9 dichotomized indicators, based on converged replications ($df =$ T_{RMLa} and RN=reject number, RR=reject ratio). RN=reject number, RR=reject ratio). Performance of the statistics

 $q = 87,$ p* − T_{ARLSa} with 6 continuous and 9 dichotomized indicators, based on converged replications ($df =$ T_{RRLSa} and RN=reject number, RR=reject ratio). RN=reject number, RR=reject ratio). Performance of the statistics

Performance of standard errors with 6 continuous and 9 dichotomized indicators, based on converged replications. Performance of standard errors with 6 continuous and 9 dichotomized indicators, based on converged replications.

(a) Averaged empirical standard errors and formula-based standard errors **(a) Averaged empirical standard errors and formula-based standard errors**

Table 16(a)

Parameter estimates Parameter estimates _a and their standard errors for Example 1. a and their standard errors for Example 1.

a

55 \mathcal{C} $\overline{\tau}$

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 67 **0.5 0.6 0.7 0.5 0.6 0.7** 0.6 SE *a* **SE** 0.5 0.7 0.698 0.569 0.348 0.805 0.490 0.694 0.572 0.517 0.585 0.298 0.644 0.581 0.894 55 0.494 0.492 0.490 66 0.697 0.695 0.694 77 0.574 0.573 0.572 88 0.518 0.518 0.517 99 0.589 0.587 0.585 10,10 0.302 0.300 0.298 $11,11$ 0.699 0.698 0.698 12,12 0.646 0.645 0.644 13,13 0.567 0.568 0.569 14,14 0.343 0.346 0.348 15,15 0.576 0.579 0.581 16,16 0.895 0.895 0.894 $17,17$ 0.803 0.804 0.805 0.492 0.573 0.518 0.587 0.300 0.698 0.645 0.568 0.346 0.579 0.895 0.804 $\ddot{\boldsymbol{\theta}}$ 0.695 0.5 0.574 0.518 0.589 0.302 0.699 0.646 0.567 0.343 0.576 0.895 0.803 0.494 0.697

 $10,10$ $\rm mH$ $12,12$ $13,13$ $14, 14$ $15,15$ 16,16 $17.17\,$ $18,18$ 19,19 $20,\!20$ $21,21$

 $88\,$ 99

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18,18 0.945 0.945 0.944 19,19 0.346 0.348 0.350 20,20 0.893 0.892 0.891 21,21 0.340 0.342 0.343

0.945 0.348 0.892 0.342

0.945 0.346 0.893 0.340

0.944

0.350

0.343

0.891

Table 16(b)

