Evaluation of Goodness-of-Fit Test in Random Intercept Cross-Lagged Panel Model: Implications for Small Samples

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Abstract

The development of the random intercept cross-lagged panel model (RI-CLPM) is an extension of the traditional cross-lagged panel model (CLPM), which aims to study between and within person variances in longitudinal data. Despite its growing popularity in behavioral and social sciences, our understanding of goodness-of-fit tests of RI-CLPMs is limited. Using Monte Carlo simulations across different sample sizes and model complexity, this study evaluates goodness-of-fit tests applied to RI-CLPMs by comparing the test statistics of the maximum likelihood (ML), generalized least squares (GLS), and reweighted least squares (RLS), as well as their corresponding NFI, CFI, and RMSEA. Our results showed that when N was significantly large; ML, GLS, and RLS tended to have similar performances. When N was small relative to the model complexity, RLS outperformed ML and GLS and produced consistent χ^2_{df} test statistics and fit indices. These results have implications for fitting RI-CLPM with finite data.

Keywords: Goodness-of-fit test, RI-CLPM, reweighted least squares, covariance structure analysis

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Introduction

The random intercept cross-lagged panel model (RI-CLPM) is an extension of the traditional cross-lagged panel model (CLPM) put forth recently by Hamaker et al. (2015) to study reciprocal influences of multiple variables over time. In general, CLPMs are used to study autoregressive effects of one variable on itself over time and cross-lagged effects of one variable on another variable over time (i.e., reciprocal effect). A critique of traditional CLPMs is that between-person differences and within-person change over time are conflated therefore resulting in autoregressive and cross-lagged effects that do not solely reflect within-person stability (i.e., autoregressive effects) or within-person dynamics (i.e., reciprocal effects). The RI-CLPM resolves this problem through the inclusion of random intercepts which serve to separate between-person differences (i.e., variance of the random intercept) from within-person processes (Hamaker et al., 2015; Mund et al., 2021). In other words, the random intercepts in the RI-CLPM capture the influence of stable trait factors or unobserved time-invariant confounding variables (Usami et al., 2019). The RI-CLPM has gained popularity with methodological and substantive researchers who conduct research using longitudinal data (Burns et al., 2020; Etherson et al., 2022; Hamaker et al., 2015; Kojima et al., 2021; Paul et al., 2019; Usami, 2021; Usami et al., 2016; Usami et al., 2019). Yet, small samples are prevalent in longitudinal analysis. In particular, the performance of statistical estimators of the RI-CLPM has not been investigated especially in small samples which are commonly used when estimating RI-CLPM (e.g. Burns et al., 2020; Etherson et al., 2022; Paul et al., 2019). In addition, the RI-CPLM model is a special SEM model. Previous SEM studies have addressed the topic of how small samples and model size impact the performance of test statistics and fit indices (Kenny et al., 2015; Shi et al., 2020; Shi et al., 2019), as well as compared different

estimators on SEM fit indices (Shi & Maydeu-Olivares, 2020). However, none of these studies examined the RI-CLPM using RLS.

Most statistical software which can be used to estimate RI-CLPMs uses maximum likelihood (ML) as a default estimator. The ML goodness-of-fit tests in covariance structure analysis assumes asymptotic behavior of test statistics. This requires the sample size to be sufficiently large and the data to be approximately normally distributed for the goodness-of-fit test statistics to follow a standard chi-square distribution. The ML test statistics will not efficiently approximate the chi-square distribution for a model with sample size N that is not sufficiently greater than the number of variables p . As a result, chi-square test statistics using ML often over-reject correct models (Arruda & Bentler, 2017; Chi & Lange, 2014; Hayakawa, 2019; Zheng & Bentler, 2022b). Another popular normal theory estimator, generalized least squares (GLS) (Browne, 1974) is an alternative to ML. GLS avoids the over-rejection problem, whereas it tends to under-reject the null hypothesis when sample sizes are small, even though the model under consideration is correct. Hayakawa (2019) reintroduced the reweighted least squares (RLS) and showed that RLS produced highly consistent and unbiased test statistics and empirical rejection rates across different sample sizes in conventional confirmatory factor models and traditional CLPMs under multivariate normality. Recently, Zheng & Bentler (2022b) showed that RLS performed similarly in mean and covariance structure models. Yet, none of existing studies have applied RLS to examine RI-CLPM along with the normed fit index (NFI), the comparative fit index (CFI), and the root mean square error approximation (RMSEA).

The rationale for the study is that many applied researchers have small samples that fit the RI-CLPM, so it is important to understand if there are alternative estimators that perform better in smaller samples than ML. Although the RI-CLPMs are a special kind of SEM, they often involve

large degrees of freedom, making them complicated and hard to fit. To date, it is still not clear whether the results from conventional CFA models would extend to RI-CLPMs. Based on this rationale, this study aims to examine the statistical performance of ML, GLS, and RLS on four RI-CLPM models across five waves of simulated and normally distributed data. Goodness-of-fit test statistics in SEM are based primarily on asymptotic properties of estimators, which mostly do not involve parameter estimates (Jalal & Bentler, 2018). These 5-wave RI-CLPMs vary from simple to moderate to complicated in terms of model specification and degrees of freedom. We find that when models are relatively simple; ML, GLS, and RLS provide relatively consistent goodness-of-fit test statistics across all sample sizes. However, when sample size was small relative to model complexity, that is, models have more indicators and latent variables, RLS outperforms ML and GLS in goodness-of-fit test by producing more consistent chi-square test statistics, p -values, acceptable empirical Type-I error rates, and good model fit as indicated by other fit indices (NFI, CFI and RMSEA). The results of the present study enable us to evaluate the statistical performances and offer informed suggestions to researchers who apply RI-CLPM in their research.

This paper is organized as follows. First, we review RI-CLPMs and their covariance structure. Second, we review the goodness-of-fit test statistics in covariance structure analysis regarding ML, GLS, and RLS, and their relationship. Third, we discuss data generation and simulation procedures, followed by evaluation criteria. Fourth, we discuss model specifications and simulation results. The fifth section is the power analysis of all estimators under investigation in all models. Finally, we provide a discussion and conclusion.

RI-CLPM in Covariance Structure Analysis

Figure 1. Path Diagram of RI-CLPM in $T = 3$

This section reviews the RI-CLPM in covariance structure analysis. The development of RI-CLPM is based on traditional CLPM to account for stable and trait-like differences between two variables in multiple-wave panel data (Mulder & Hamaker, 2021). For illustration, we consider only a bivariate model. Supposed that we are interested in studying temporal reciprocal relations between two random variables x_i and y_i . Also, we use x_{it} and y_{it} to denote the measurements at time point t for individual i ($i = 1, \dots, n$; $t = 1, \dots, T$). The RI-CLPM can be expressed as follows:

$$x_{it} = \delta_{xt} + \eta_{xi} + x_{it}^*, \quad (1)$$

$$y_{it} = \delta_{yt} + \eta_{yi} + y_{it}^*. \quad (2)$$

Here let δ_{xt} and δ_{yt} represent temporal group means at time point t , and η_{xi} and η_{yi} are individual-level time-invariant trait factors. In the RI-CLPM δ_{xt} and δ_{yt} aim to capture mean growth trajectories and x_{it}^* and y_{it}^* are temporal deviation terms, which capture the temporal

within-person deviations from the means of each person, i . As such, we need to partition the between-person level and within-person level to understand the dynamics between the effect of time-invariant trait-like factors and time-varying occasion-specific factors. In the context of equations 1 and 2, x_{it}^* and y_{it}^* capture the temporal deviations from the expected values of x_{it} and y_{it} , that is, $\delta_{xt} + \eta_{xi}$ and $\delta_{yt} + \eta_{yi}$. Thus, the within-person reciprocal relations are modeled using lagged effects and temporal trait factors (Hamaker et al., 2015; Mulder & Hamaker, 2021; Usami, 2021). Thus, the within-person reciprocal relations are defined as:

$$x_{it}^* = \beta_x x_{i(t-1)}^* + \gamma_x y_{i(t-1)}^* + v_{xit}, \quad (3)$$

$$y_{it}^* = \beta_y y_{i(t-1)}^* + \gamma_y x_{i(t-1)}^* + v_{yit}, \quad (4)$$

where β_x and β_y are autoregressive parameters that measure the within-person stability of x and y , respectively. It is important to note that β_x and β_y do not necessarily represent the stability of the rank order of individuals from one occasion to another; instead, they indicate the magnitude of within-person carry-over effect (Hamaker et al., 2015). γ_x and γ_y are cross-lagged parameters that capture reciprocal relations between x and y . v_{xit} and v_{yit} are the residuals, which are assumed to follow a normal distribution with an unknown variance $N(0, \sigma^2)$.

$$\begin{bmatrix} x_{it} \\ y_{it} \end{bmatrix} = \begin{bmatrix} \delta_{xt} \\ \delta_{yt} \end{bmatrix} + \begin{bmatrix} \eta_{xi} \\ \eta_{yi} \end{bmatrix} + \begin{bmatrix} \beta_x & \gamma_x \\ \beta_y & \gamma_y \end{bmatrix} \begin{bmatrix} x_{i(t-1)}^* \\ y_{i(t-1)}^* \end{bmatrix} + \begin{bmatrix} v_{xit} \\ v_{yit} \end{bmatrix} \quad (5)$$

Scholars pointed out that the initial observation, when $t = 1$, usually cannot be the beginning of the process because the initial within-person centered scores x_{it}^* and y_{it}^* are not correlated with the time-invariant trait factors η_x and η_y (Bollen & Curran, 2004; Jongerling & Hamaker, 2011; Usami, 2021; Usami et al., 2019). Therefore, in the initial condition, x_{i1} and y_{i1} are

$$\begin{bmatrix} x_{i1} \\ y_{i1} \end{bmatrix} = \begin{bmatrix} \delta_{x1} \\ \delta_{y1} \end{bmatrix} + \begin{bmatrix} \psi_{11} & \psi_{12} \\ \psi_{21} & \psi_{22} \end{bmatrix} \begin{bmatrix} \eta_{xi} \\ \eta_{yi} \end{bmatrix} + \begin{bmatrix} \varepsilon_{i1}^x \\ \varepsilon_{i1}^y \end{bmatrix}, \quad (6)$$

where ψ_i are the initial parameter values for autoregressive and cross-lagged effects (See Appendix for the corresponding covariance matrix of the RI-CLPM).

Goodness-of-Fit Test in Covariance Structures

In this section, we first review the classical covariance structure and the existing methods to derive parameter estimates and model fit statistics in Structural Equation Models (SEMs). In SEM a random sample $x_i \in \{x_1, \dots, x_n\}$ is assumed to be identically and independently distributed according to a multivariate normal distribution $N[\mathbf{0}, \mathbf{\Sigma}_0]$. We assume that $\mathbf{\Sigma}_0$ is a matrix function of an unknown population parameters $\boldsymbol{\theta}_0$ ($q \times 1$), and $\mathbf{\Sigma}_0 = \mathbf{\Sigma}(\boldsymbol{\theta}_0)$. Therefore, the sample covariance matrix is

$$\mathbf{S} = \frac{1}{N-1} \sum_{i=1}^N (x_i - \bar{x})(x_i - \bar{x})' \quad (7)$$

where the sample mean $\bar{x} = \frac{1}{N} \sum_{i=1}^N (x_1, \dots, x_N)$. The sample covariance matrix $\mathbf{S}$ is positive definite, and $\mathbf{S}$ is an unbiased estimator of population covariance structure $\mathbf{\Sigma}_0$.

Moreover, in a confirmatory factor analysis (CFA) model

$$x_i = \boldsymbol{\mu} + \mathbf{\Lambda} \boldsymbol{\xi}_i + \boldsymbol{\epsilon}_i, \quad i = 1, \dots, n \quad (8)$$

where x_i is a random sample, $\boldsymbol{\mu}$ is a $p \times 1$ sample mean vector, $\mathbf{\Lambda}$ ($p \times q$) is a matrix of factor loadings, $\boldsymbol{\xi}_i$ ($p \times 1$) is a vector of latent factors, and $\boldsymbol{\epsilon}_i$ ($p \times 1$) is a vector of residuals. In SEM, $\mathbf{\Sigma}$ is the population covariance matrix and $\mathbf{\Sigma} = \mathbf{\Lambda} \mathbf{\Phi} \mathbf{\Lambda}' + \mathbf{\Psi}$, where $\mathbf{\Phi}$ is a $q \times q$ covariance matrix of the factors, and $\mathbf{\Psi}$ is a $q \times q$ covariance matrix of unique scores. $\mathbf{\Sigma}$ is assumed to fit a model implied covariance structure $\mathbf{\Sigma}(\boldsymbol{\theta})$, in which $\boldsymbol{\theta}$ contains a vector of free parameters. We rely on

sample covariance matrix $\mathbf{S}$ as an unbiased estimator of the population covariance matrix. $\mathbf{\Sigma}(\boldsymbol{\theta})$ fit into a covariance structure framework through an objective function $F[\mathbf{\Sigma}(\boldsymbol{\theta}), \mathbf{S}]$, which measures the discrepancy between $\mathbf{\Sigma}(\boldsymbol{\theta})$ and $\mathbf{S}$. The test statistic T reflects the closeness of $\hat{\mathbf{\Sigma}} = \mathbf{\Sigma}(\hat{\boldsymbol{\theta}})$.

Maximum Likelihood

ML and GLS are the most common methods to obtain the test statistics for evaluating the goodness-of-fit in SEM. The ML method relies on the following discrepancy function T_{ML} (Jöreskog, 1969) to derive the goodness-of-fit test statistic:

$$F_{ML}(\boldsymbol{\theta}) = \log|\mathbf{\Sigma}(\boldsymbol{\theta})| - \log|\mathbf{S}| + \text{tr}(\mathbf{S}\mathbf{\Sigma}(\boldsymbol{\theta})^{-1}) - p, \quad (9)$$

$$\hat{\boldsymbol{\theta}}_{ML} = \text{argmin}_{\boldsymbol{\theta}} F_{ML}(\boldsymbol{\theta}). \quad (10)$$

As equations 9 and 10 show, at the minimum of the fit function $F_{ML}(\boldsymbol{\theta})$, $\hat{\boldsymbol{\theta}}_{ML}$ contains parameter estimates $\hat{\mathbf{\Lambda}}$, $\hat{\mathbf{\Phi}}$, and $\hat{\mathbf{\Psi}}$, where $\hat{\mathbf{\Lambda}}$ is a matrix of estimated factor loadings, $\hat{\mathbf{\Phi}}$ is an estimated factor covariance, and $\hat{\mathbf{\Psi}}$ is the covariance matrix of error variables. Through these parameter estimates, we can reconstruct the sample covariance matrix following the model implied covariance matrix $\mathbf{\Sigma}(\hat{\boldsymbol{\theta}}) = \hat{\mathbf{\Lambda}}\hat{\mathbf{\Phi}}\hat{\mathbf{\Lambda}}' + \hat{\mathbf{\Psi}}$, if the sample-implied covariance matrix matches the population matrix.

Moreover, the goodness-of-fit test statistic is defined as

$$T_{ML} = (N - 1)F_{ML}(\hat{\boldsymbol{\theta}}), \quad (11)$$

where T_{ML} is a ML test statistic, which is the product of $F_{ML}(\hat{\boldsymbol{\theta}})$ and $(N - 1)$. When sample size N is sufficiently large under normality and the correct model specification, T_{ML} should asymptotically follow a standard chi-square distribution. That is, $T_{ML} \xrightarrow{d} \chi^2_{p^* - q}$ in which $p^* - q$ degrees of freedom, and $p^* = p(p + 1)/2$ and q is the number of free parameters.

Generalized Least Squares

GLS is another popular conventional estimator. Different from ML, the GLS function is minimized by

$$\mathbf{Q} = (\mathbf{s} - \boldsymbol{\sigma}(\boldsymbol{\theta}))' \mathbf{W} (\mathbf{s} - \boldsymbol{\sigma}(\boldsymbol{\theta})), \quad (12)$$

where $\mathbf{s} = \text{vech}(\mathbf{S})$ is a $p^* \times 1$ vector with p^* nonduplicated elements in $\mathbf{S}$, which is assumed to be asymptotically distributed. $\boldsymbol{\sigma}(\boldsymbol{\theta}) = \text{vech}[\boldsymbol{\Sigma}(\boldsymbol{\theta})]$ is a $p^* \times 1$ vector with the nonduplicated elements in $\boldsymbol{\Sigma}(\boldsymbol{\theta})$. $\mathbf{W}$ is a weight matrix. When $\boldsymbol{\theta}$ is a vector of parameter estimates, the optimal parameter estimates contained in $\hat{\boldsymbol{\theta}}$ are those that minimize the function $\mathbf{Q}$. We use T_{GLS} to denote the test statistic of GLS, which is usually computed as $(N - 1)\mathbf{Q}(\hat{\boldsymbol{\theta}}) \rightarrow \chi_{p^*-q}^2$, that is, when the sample size is large, the test statistic T_{GLS} will follow a chi-square distribution under normality and the correct specification.

Reweighted Least Squares

RLS method was built based on GLS fit function. As equation 13 shows, it is specialized to multivariate normal populations. This residual quadratic form is a function of $\boldsymbol{\Sigma}_0^{-1}$. As $\boldsymbol{\Sigma}_0$ is unknown, $\boldsymbol{\Sigma}_0^{-1}$ should be replaced by $\mathbf{V}$ ($p \times p$), which is a positive definite matrix. This GLS function was proposed by Browne (1974).

$$\begin{aligned} F_{GLS} &= 2^{-1} [\text{vec}(\mathbf{S} - \boldsymbol{\Sigma}(\boldsymbol{\theta}))' (\mathbf{V} \otimes \mathbf{V}) \text{vec}(\mathbf{S} - \boldsymbol{\Sigma}(\boldsymbol{\theta}))] \\ &= 2^{-1} \text{tr}[\{(\mathbf{S} - \boldsymbol{\Sigma}(\boldsymbol{\theta}))\mathbf{V}\}^2], \end{aligned} \quad (13)$$

where $\text{vec}()$ is a matrix operator that transforms a matrix into a vector by stacking rows of the matrix, and $\otimes$ is the Kronecker product. $\mathbf{V}$ can be constant definite matrix or a stochastic matrix that converges to a positive definite matrix (Lee, 2007), and $\mathbf{V}$ is a consistent estimator of $\boldsymbol{\Sigma}_0^{-1}$.

Following equation 13, at the minimum of $\hat{F}_{GLS}$, we will obtain parameter estimates $\hat{\boldsymbol{\theta}}_{GLS}$. The method of RLS is based on equation 13 with a modified weight matrix $\mathbf{V}$, which is assumed to be positive definite. Browne (1974) showed that when $\mathbf{V} = \boldsymbol{\Sigma}_0^{-1}$ the weighted least squares estimator shares most of the asymptotic properties of ML estimate such as consistency, asymptotic normality, and efficiency. As such, when sample sizes are sufficiently large, ML and RLS produce similar chi-square test statistics. However, when the sample size is small, or in high-dimensional framework, $\mathbf{V}$ will become a biased estimator for $\boldsymbol{\Sigma}_0^{-1}$ (Hayakawa, 2019; Kayakawa & Sun, 2022; Zheng & Bentler, 2022b). Also, Lee & Jennrich (1979) showed that the standard Gauss-Newton algorithm produces weighted least squares estimates that can produce maximum likelihood estimates in an iteratively reweighted form as well. Therefore, the test statistic of RLS T_{RLS} can be expressed as:

$$T_{RLS} = \frac{n}{2} \text{tr}\{(\mathbf{S} - \hat{\boldsymbol{\Sigma}}_{ML}) \hat{\boldsymbol{\Sigma}}_{ML}^{-1}\}^2, \quad (14)$$

where $\hat{\boldsymbol{\Sigma}}_{ML}^{-1}$ is a sample covariance matrix derived from the ML fit function (see eq. 18), and is updated iteratively to reflect the estimate of the model, while in GLS the weight matrix is fixed (Bentler, 2006). Technically, after we run the ML function in equation 9, we save the estimated covariance matrix $\hat{\boldsymbol{\Sigma}}_{ML}^{-1}$ and replace the biased weight matrix $\mathbf{V}$ in equation 13, which becomes equation 14. The key difference between GLS and RLS is that the new weight matrix $\hat{\boldsymbol{\Sigma}}_{ML}^{-1}$ is more consistent across different sample sizes. As a result, the test statistics of RLS are more consistent across all sample sizes, while the test statistics of GLS tend to under reject null hypothesis, and those of ML tend to over reject it when sample sizes are small. On the other side, RLS and ML share some common characteristics. Browne (1974) has shown that T_{ML} and T_{RLS} are related through the following equation:

$$T_{ML} = T_{RLS} + n \sum_{k=3}^{\infty} \frac{1}{k} \text{tr}\{I_p - S_N \hat{\Sigma}^{-1}\}^k. \quad (15)$$

As equation 15 shows, T_{ML} consists of two parts; the first part is T_{RLS} (same as equation 14), and second part. When $N \rightarrow \infty$ with p fixed and correction model specification, T_{ML} and T_{RLS} will converge to chi-square distribution, and $T_{ML} \approx T_{RLS}$. This is because the second half of equation 15 will asymptotically vanish as $N \rightarrow \infty$. Reversely, when N becomes small, the value of second half becomes larger. As such, when T_{ML} is inflated, T_{RLS} is about right (see Hayakawa, 2019). As a result, the most superior properties of T_{RLS} is that it can efficiently estimate the test statistic across various sample sizes, and also asymptotically follow a standard chi-square distribution (Hayakawa, 2019; Zheng & Bentler, 2022b). However, because of its complexity, when sample size is too small and the model is complicated (e.g., $N < 100$, $p > 20$), it is hard to obtain a positive-definite sample covariance matrix, resulting in non-convergence issues.

Monte Carlo simulation

In this section we propose to use Monte Carlo simulations to test goodness-of-fit on the RI-CLPMs, and compare the results of RLS to those produced by the normal theory—maximum likelihood ML and GLS. Data generation was accomplished with the “lavaan” package (Rosseel, 2012) in R. The generation scheme for the simulation follows the covariance matrix of RI-CLPM described earlier. In a normal distribution $\mathbf{z}_i = \mathbf{\Sigma}(\boldsymbol{\theta})^{1/2} \varepsilon_i$, and $\mathbf{\Sigma}(\boldsymbol{\theta})$ is drawn from a multivariate normal distribution with zero mean and unknown variance. ε_i follows a standard normal distribution $N(0, 1)$. For the parameter values, we set β_x autoregressive parameters $\beta_{xi} = .25$. For the parameters of β_y , we set $\beta_{y2} = .08$, $\beta_{y3} = .22$, $\beta_{y4} = .29$, $\beta_{y5} = .35$. For the cross lagged

parameters, we set the parameters of all $\gamma_{xi} = 0$ and $\gamma_{yi} = .17$ respectively. Note that we used the same parameter values and specification for the time-varying part in RI-CLPM to model within-person dynamics in all models, so that we can compare and validate the simulation results. We set the mean value of each $\bar{x}_i$: .24, .18, .18, .11, .11; the mean value of each $\bar{y}_i$: .34, .35, .32, .37, and .38. For Models 2, 3 and 4, because they have 20 and more indicators, we just repeated these mean values as needed. These models and parameter values have been used by Mulder & Hamaker (2021), which adopted from Narmandakh et al.'s (2020) five waves of panel data on sleep problems and anxiety. Using the same models and parameters can help validate the simulation and compare results to existing studies in literature. For the initial autoregressive and cross lagged parameters, we set $\Psi = (\mathbf{I} - \Phi)^{-1}$. It is important to note that, the choice of parameter values for simulations can be arbitrary, because they don't affect the test statistics and fit indices if the same models are specified correctly.

Following abovementioned data generating procedures, we compared four models with the same dimension. These models were introduced by Mulder & Hamaker (2021). Model 1 has 12 latent variables and 10 indicators. Model 2 has 10 latent variables and 20 indicators. Model 3 has 16 latent variables and 30 indicators. Model 4 has 22 latent variables and 30 indicators. We followed each of these population models' structure to generate one normal sample. This procedure was repeated 1,000 times. To examine the performance of the proposed methods, we estimated each model using ML, GLS and RLS. The simulation study included sample sizes ranging from 50 to 10,000. In each sample, the parameters were estimated, and various statistics related to T_{ML} , T_{GLS} , and T_{RLS} were computed. The ML and GLS can be run through 'lavaan', or other software, whereas existing R packages cannot compute RLS statistics. Thus, we programed specialized R code for the chi-square test and fit indices.

Evaluation criterion

We used a series of simulation results at different sample sizes to evaluate the statistical performances of ML, GLS, and RLS. The mean test statistics and empirical Type-I error rates (a.k.a. rejection rates) were based on $\alpha = 0.01$ and fit indices (NFI, CFI, and RMSEA). The chi-square test statistics of interest were T_{ML} , T_{GLS} , and T_{RLS} . Each of these mean test statistics was averaged over 1,000 replications. Due to the multivariate normal distribution and asymptotic behavior, the expected mean test statistics of each method should be approximately equal to their respective degrees of freedom. Likewise, the mean of expected standard deviation of each test statistic should approximately equal to $\sqrt{2df}$. Moreover, p -values are the criteria by which the null hypothesis was evaluated. Each replication generated a corresponding p -value for the fitted model, and the average p -values of all tests were calculated. Using the significance level $\alpha = 0.01$, we also calculated empirical rejection rates of all test statistics to examine whether they produced 0.01 empirical Type-I error rates.

If RI-CLPM test statistics follow a standard chi-square distribution with $p^* - q$ degrees of freedom, we expect all models will behave asymptotically when sample size becomes sufficiently large. Thus, when sample sizes are large, mean test statistics, mean standard deviations, and mean p -values ought to converge to theoretically expected values. Using the expected values as a reference, we can evaluate the performance of ML, GLS and RLS across different sample sizes. In other words, if the test statistics follow a central chi-square distribution, we expect the mean rejection rates to be approximately 0.01. When the test statistics are upwardly biased, we expect the mean rejection rates will exceed 0.01. Nevertheless, actual empirical rejection rates vary slightly around 0.01.

One of the important challenges in SEM is the evaluation of model fit. Rejection of a null hypothesis based on the chi-square metric may be inappropriate or incomplete, because chi-square test heavily depends on sample sizes (Bentler, 1990; Kenny et al., 2015). In SEM, the fit of the models should also examine a variety of model fit indices. Normed fit index (NFI), comparative fit index (CFI) and root mean square error of approximation (RMSEA) are popular adjuncts to traditional SEM test statistics. For NFI and CFI, their values are bounded within the range of 0-1, and values which are greater than .9 are considered as good fit. For RMSEA, values less than 0.05 are considered good fit. Although these fit indices evaluate the model fit based on their own metrics, small sample sizes affect NFI and RMSEA, but not CFI (Bentler, 1990). Scholars also found that the RMSEA tends to perform better in a model which contains more variables (Kenny et al., 2015).

Model Specifications and Test Results

Model 1

In Model 1, x_i and y_i are two observed variables measured over five waves. There were 10 indicators to measure two latent variables, RIX and RIY, which were the random intercepts. WX_t and WY_t represent the within components at each wave. Similar to Mulder & Hamaker (2021), we constrained the error variances of the latent variables of each measurement to be zero. As Mulder & Hamaker (2021) described, these random intercepts were designed to capture time-invariant deviation from the grand means and represent the stable differences between persons. It is assumed that the random intercepts have the exact same influence on the observed variables on each occasion. In this light, the random intercepts were specified by their latent variables with the repeated measures as their indicators with all factor loadings held constant. Moreover, within-person deviations over time were the differences between a unit's observed measurement and the

unit's expected score based on the grand means and random intercepts. Thus, WX_t and WY_t were two sets of latent variables indicating the within components of two latent traits. For each wave of measurement, the latent variables WX_t and WY_t were correlated, and the unique error variances were held constant. In addition, to highlight the presentation of the current models, as well as other models in this paper, error variances of the indicators and latent variables were omitted in the path diagrams.

Figure 2. Path diagram of Model 1

Figure 2 shows a path diagram of Model 1. There are 10 indicators to represent 12 latent variables. Hence, $p^* = p(p + 1)/2$ where p denotes the number of variables, and p^* denotes the number of data points. As $N \rightarrow \infty$, test statistics asymptotically follows a central chi-square distribution with $df = p^* - q$, where q denotes the number of free parameters. The standard deviation is $\sqrt{2df} = 6.48$. Moreover, the RI-CLPM was specified with the same residual correlations and metric measurement invariance constraints for both constructs across time. All autoregressive and cross-lagged coefficients were freely estimated.

Table 1. Mean test statistics, mean standard deviation, and mean p -values

N	Test Statistics			Standard Deviations			P-values			Rejection Rates < 0.01		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	23.580	18.463	22.338	7.479	4.608	6.832	0.403	0.612	0.433	0.026	0.000	0.008
70	23.176	19.136	21.808	7.109	4.884	6.500	0.408	0.577	0.430	0.022	0.000	0.014
100	22.355	19.678	21.566	6.918	5.511	6.300	0.442	0.554	0.472	0.010	0.002	0.008
200	21.870	19.897	21.523	6.776	5.966	6.635	0.462	0.550	0.480	0.016	0.004	0.010
300	21.220	20.375	21.165	6.290	5.940	6.277	0.488	0.525	0.513	0.012	0.004	0.009
400	21.363	20.705	21.717	6.462	6.398	6.629	0.484	0.515	0.468	0.014	0.008	0.012
500	21.833	20.869	21.038	6.560	6.497	6.364	0.461	0.506	0.514	0.014	0.008	0.008
800	20.814	20.938	21.440	6.806	6.671	6.716	0.512	0.506	0.484	0.012	0.012	0.012
1000	21.330	20.927	21.274	6.385	6.232	6.754	0.485	0.502	0.489	0.014	0.002	0.010
2000	21.285	20.886	21.239	6.442	6.449	6.922	0.497	0.503	0.492	0.012	0.004	0.012
5000	21.479	20.747	21.000	6.670	6.395	6.413	0.485	0.509	0.500	0.012	0.012	0.012
10000	21.015	21.013	21.003	6.439	6.218	6.471	0.499	0.499	0.500	0.011	0.016	0.010

Note: Expected mean test statistic is 21, and expected mean standard deviation is 6.48.

Table 1 shows the mean test statistics, standard deviations, p -values, and empirical rejection rates of ML, GLS, and RLS. Overall, these methods performed similarly. All estimators resulted in expected values of the test statistics that were close to the expected value of 21. However, when the sample sizes were smaller than 100, T_{ML} tended to positively deviate from 21, while T_{GLS} tended to negatively deviate from 21. The parallel changes also reflected in the mean standard deviations and average p -values of T_{ML} and T_{GLS} . In general, mean standard deviations and the mean p -values of all estimators were close to the expected values. The mean standard deviations of T_{ML} increased as sample size decreased, while the average p -values decreased. For T_{GLS} , its' standard deviations decreased as the sample size decreased. When $N \leq 200$, the empirical rejection rates of ML were elevated over 0.016, while those of GLS were less than 0.004. Therefore, we would expect based on prior work that when sample sizes were small, ML tended to over-reject the correct model, while GLS tended to over-accept the correct model.

In contrast, T_{RLS} produced the most consistent estimates across all sample sizes. Even when $N=50$, the mean test statistic and standard deviation were the closest to the expected true values compared to the other estimators. Moreover, the empirical rejection rates of RLS were largely within a range of between 0.008 and 0.014.

Table 2. Fit indices of Model 1

N	NFI			CFI			RMSEA		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	0.781	0.734	0.794	0.932	0.942	0.980	0.050	0.013	0.035
70	0.823	0.774	0.832	0.959	0.948	0.990	0.034	0.018	0.024
100	0.864	0.757	0.867	0.974	0.959	0.996	0.027	0.017	0.014
200	0.922	0.837	0.923	0.987	0.975	0.997	0.017	0.013	0.012
300	0.945	0.879	0.945	0.992	0.983	0.998	0.013	0.011	0.009
400	0.959	0.907	0.959	0.994	0.990	0.999	0.011	0.011	0.002
500	0.965	0.923	0.967	0.999	0.990	0.999	0.011	0.010	0.001
800	0.977	0.947	0.978	0.997	0.999	0.990	0.009	0.009	0.005
1000	0.982	0.958	0.982	0.998	0.998	0.999	0.007	0.005	0.006
2000	0.991	0.978	0.991	0.999	0.999	1.000	0.006	0.003	0.003
5000	0.996	0.991	0.996	0.999	0.999	1.000	0.004	0.003	0.004
10000	0.998	0.995	0.998	1.000	1.000	1.000	0.000	0.003	0.004

Table 2 reports NFI, CFI, and RMSEA. When sample sizes were greater than 400, the fit indices of all estimators indicated good model fit (e.g., NFI and CFI > 0.9). ML and RLS performed similarly on NFI when $N < 200$. For GLS, when $N < 400$ NFI became less than 0.9 indicating that the model no longer provided good fit. In contrast, the results for CFI indicated all models performed well across all sample sizes. In addition, RMSEA results indicated that ML, GLS and RLS performed similarly across all sample sizes, that is, RMSEA values were less than or equal to 0.05.

Model 2

Model 2 included indicator-specific random intercepts that captured trait-like differences between units, and occasion-specific factors that captured the within-person dynamics. In Model 2, each occasion-specific and within-person factor WX_t and WY_t was measured by two indicators, and the factor loadings were held constant. These indicators also measured the between-person factor RIX and RIY. Thus, compared to Model 1, Model 2 was more complicated in the sense that it had more indicators and more degrees of freedom. Moreover, Model 2 included a time-invariant outcome variable L_1 , that was regressed on the random intercepts RIX and RIY. Thus, L_1 was

explained by the variances of random intercepts. The time-varying part that was used to model within-person dynamics was the same as Model 1.

Figure 3. Path diagram of Model 2

Table 3. Mean test statistics of Model 2

N	Test Statistics			Standard Deviations			P-values			Rejection Rates < 0.01		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	202.214	137.071	176.195	20.121	15.021	20.621	0.115	0.924	0.380	0.300	0.000	0.000
70	191.911	141.484	175.766	19.492	16.172	18.630	0.206	0.882	0.399	0.116	0.000	0.022
100	186.285	150.190	172.401	19.659	16.711	18.621	0.269	0.786	0.437	0.049	0.000	0.000
200	178.237	160.824	171.213	19.583	16.961	19.913	0.380	0.642	0.493	0.038	0.000	0.028
300	174.933	165.199	171.498	19.015	17.401	18.840	0.423	0.572	0.478	0.022	0.004	0.014
400	173.609	166.021	171.621	18.388	19.428	18.041	0.445	0.568	0.463	0.018	0.014	0.018
500	173.113	166.710	170.193	19.213	17.065	19.081	0.451	0.558	0.501	0.020	0.070	0.006
800	171.810	168.633	170.015	18.559	17.907	18.607	0.471	0.523	0.496	0.012	0.080	0.009
1000	170.192	169.292	170.024	18.487	19.069	18.332	0.498	0.513	0.499	0.009	0.010	0.008
2000	172.043	169.348	170.477	18.176	18.188	18.785	0.543	0.507	0.494	0.011	0.011	0.017
5000	170.753	167.775	169.214	17.542	17.642	18.175	0.499	0.535	0.511	0.008	0.004	0.007
10000	170.356	169.001	170.417	18.110	17.881	18.077	0.506	0.510	0.492	0.010	0.007	0.008

Note: Expected mean test statistic is 170, and expected mean standard deviation is 18.44.

The mean test statistics of Model 2 showed that when sample size was large, ML, GLS and RLS produced similar test statistics that were close to the expected values of 170. What

differentiated Model 2 from Model 1 was the rate at which the different estimators deviated from the true value when sample sizes approached $N = 50$. When sample sizes were less than 800, both the means of T_{ML} and T_{GLS} started to deviate from the expected value of 170. Similar changes were observed for the mean standard deviations and p -values of T_{ML} and T_{GLS} . As a result, ML tended to over reject the null hypothesis when sample sizes approached $N = 50$, while GLS tended to under reject it. Relatively, RLS produced highly consistent test statistics; its rejection rates were within a range of between 0.000 and 0.028 across all sample sizes.

Table 4. Mean fit indices of Model 2

N	NFI			CFI			RMSEA		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	0.713	0.407	0.782	0.940	1.000	0.991	0.034	0.000	0.025
70	0.740	0.517	0.940	0.907	1.000	0.998	0.073	0.000	0.000
100	0.791	0.548	0.938	0.965	1.000	0.999	0.039	0.000	0.012
200	0.917	0.739	0.936	0.988	1.000	1.000	0.028	0.000	0.006
300	0.936	0.778	0.941	0.995	0.970	0.999	0.017	0.020	0.005
400	0.956	0.838	0.955	0.998	1.000	0.999	0.012	0.000	0.006
500	0.967	0.858	0.964	1.000	0.987	1.000	0.000	0.013	0.000
800	0.972	0.922	0.977	0.997	1.000	1.000	0.012	0.000	0.000
1000	0.979	0.936	0.982	1.000	1.000	1.000	0.003	0.000	0.000
2000	0.994	0.963	0.990	1.000	0.999	1.000	0.000	0.004	0.000
5000	0.995	0.985	0.996	1.000	0.999	1.000	0.005	0.003	0.000
10000	0.998	0.993	0.998	1.000	1.000	1.000	0.002	0.001	0.001

As Table 4 indicates, the model demonstrated poor fit according to NFI for ML and RLS when the sample sizes $N \leq 100$. For GLS when $N \leq 500$, NFI indicated poor fit. CFI indicated that all estimators had good model fit across all samples. When $N < 100$, the ML estimator resulted in poor fit according to the RMSEA while both GLS and RLS resulted in good fit according to the RMSEA.

Model 3

Model 3 contained six latent factors to account for the random intercepts, between-person factors: RIX_i and RIY_i ($i = 1, 2, 3$). Also, these random intercepts were allowed to freely correlate

with each other. Moreover, each within-person factor, WX_t and WY_t , was measured by 3 indicators and was included per occasion to capture the common within-person variability over time. RIX_i and RIY_i shared indicators with WX_t and WY_t respectively. Nevertheless, the factor loadings of RIX_i and RIY_i were fixed at 1, while the factor loadings of WX_t and WY_t were free to be estimated. As such, the within-person factor for each construct on each occasion was further decomposed into a time-invariant part, which was captured by the random intercept, and a time-varying part which was used to model the within-person dynamics.

Overall, Model 3 was relatively more complicated than Model 2 in that it had more indicators, more latent variables, and inter-correlations between latent variables. There were 30 indicators to measure 16 latent variables in Model 3. Hence $p^* = \frac{p(p+1)}{2} = 435$ data points, which yielded 364 degrees of freedom. We expected the test statistic to equal 364 with expected standard deviation 26.98.

Figure 4. Path diagram of Model 3

Table 5. Mean test statistics of Model 3

N	Test Statistics			Standard Deviations			P-values			Rejection Rates < 0.01		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	491.567	nc	nc	35.570	nc	nc	0.000	nc	0.402	1.000	nc	nc
70	445.973	nc	nc	32.493	nc	nc	0.014	nc	0.433	0.750	nc	nc
100	416.883	335.947	371.753	30.905	20.783	26.072	0.095	0.843	0.396	0.349	0.000	0.006
200	390.147	343.187	364.674	28.115	24.987	25.106	0.241	0.711	0.480	0.085	0.000	0.004
300	376.348	348.062	364.108	27.308	25.102	25.673	0.364	0.656	0.486	0.038	0.000	0.008
400	376.340	353.224	367.440	27.972	27.350	26.897	0.366	0.619	0.451	0.040	0.004	0.014
500	371.365	355.694	363.338	28.844	26.454	25.339	0.417	0.583	0.495	0.030	0.000	0.002
800	369.615	357.455	363.067	28.650	26.898	26.636	0.430	0.558	0.498	0.024	0.002	0.007
1000	369.513	357.626	359.417	27.579	26.998	26.945	0.432	0.557	0.538	0.018	0.006	0.008
2000	364.675	360.251	363.723	26.237	27.900	26.586	0.486	0.531	0.494	0.014	0.021	0.010
5000	362.541	362.144	362.355	26.327	26.983	26.407	0.507	0.691	0.505	0.006	0.005	0.004
10000	364.004	362.979	362.401	26.605	26.662	27.391	0.487	0.675	0.502	0.012	0.009	0.004

Note: Expected mean test statistic is 364 and expected mean standard deviation is 26.98.

Table 5 shows that when the sample sizes were greater than 2000 all test statistics were close to the expected value 364. However, like Models 1 and 2, the mean test statistics of ML and GLS started to deviate from 364 when the sample sizes were less than 500. From $N=200$ to 10,000, the mean test statistics for RLS should approximately equal to the expected value of 364. Moreover, when $N<800$, the mean rejection rates of ML were larger than 0.030, when $N=50$ the mean rejection rate was 1.0. On the contrary, the mean rejection rates of GLS became close to zero when $N<1000$. In contrast, the mean rejection rates of RLS were within a range of between 0.004 and 0.014, which was reasonably close to the expected rejection rate of 0.01. In addition, we also found that when $N<100$, GLS and RLS started to encounter non-convergence issues. The non-convergence rates increased as N became smaller.

Table 6. Mean fit indices of Model 3

N	NFI			CFI			RMSEA		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	0.544	nc	nc	0.783	nc	nc	0.091	nc	nc
70	0.691	nc	nc	0.928	nc	nc	0.052	nc	nc
100	0.754	0.461	0.875	0.972	1.000	0.997	0.030	0.000	0.016
200	0.837	0.660	0.877	0.974	1.000	0.997	0.028	0.000	0.008
300	0.881	0.743	0.903	0.977	0.990	0.999	0.026	0.010	0.003
400	0.923	0.833	0.926	0.997	1.000	1.000	0.009	0.000	0.002
500	0.945	0.844	0.941	1.000	1.000	0.999	0.000	0.000	0.006
800	0.959	0.899	0.961	0.997	1.000	1.000	0.009	0.000	0.001
1000	0.968	0.915	0.969	0.999	0.997	1.000	0.007	0.006	0.003
2000	0.983	0.962	0.984	0.999	1.000	1.000	0.005	0.000	0.001
5000	0.993	0.983	0.994	0.999	1.000	1.000	0.005	0.000	0.000
10000	0.997	0.992	0.997	1.000	1.000	1.000	0.000	0.000	0.000

Quite consistent with Models 1 and 2, NFI indicated poor model fit for ML and RLS when sample sizes were less than 400 and 300 respectively, and when sample sizes were less than 800 for GLS. Both CFI and RMSEA indicated good model fit for all estimators across all sample sizes.

Model 4

Figure 5. Path diagram of Model 4

Model 4 was the most complicated model in terms of the numbers of indicators, latent variables, and degrees of freedom. In this model there were latent variables FX_t and FY_t , and $t = 1, \dots, 5$ per measurement occasion, their factor loadings with WX_t and WY_t were held constant at 1. Each latent construct FX_t and FY_t was measured by three indicators, x_i and y_i , and $i = 1, \dots, 15$. WX_t and WY_t aimed to capture the common within-person dynamics over time. RIX and RIY were the second-order latent factors that aimed to capture the trait-like dynamics, and they were allowed to freely correlate with one another. We assumed that the random intercepts had equal influence on

the indicators at each measurement occasion; hence, the factor loadings between RIX and FX_t , as well as between RIY and FY_t were fixed at 1.

Table 7. Mean test statistics of Model 4

N	Test Statistics			Standard Deviations			P-values			Rejection Rates < 0.01		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	549.412	324.938	413.900	39.941	16.359	27.949	0.001	0.993	0.339	0.986	0.000	0.040
70	491.535	342.667	408.615	35.400	17.294	28.074	0.021	0.959	0.383	0.765	0.000	0.022
100	457.335	362.434	406.329	32.129	20.561	28.304	0.079	0.840	0.408	0.384	0.000	0.022
200	425.086	383.347	403.511	29.772	24.168	27.896	0.249	0.640	0.429	0.086	0.000	0.008
300	415.130	391.804	401.829	29.275	26.610	26.528	0.330	0.552	0.478	0.050	0.004	0.008
400	409.621	393.362	401.520	28.602	26.638	27.273	0.373	0.535	0.479	0.034	0.019	0.010
500	408.433	394.082	400.674	27.331	27.350	26.729	0.382	0.531	0.513	0.016	0.022	0.010
800	405.709	394.617	400.399	27.764	27.617	28.602	0.406	0.536	0.468	0.020	0.028	0.012
1000	400.684	394.844	400.444	27.755	28.052	29.442	0.459	0.533	0.466	0.018	0.029	0.016
2000	399.658	395.024	398.778	27.726	28.938	28.957	0.476	0.531	0.480	0.012	0.038	0.008
5000	397.022	397.177	397.488	27.840	28.028	28.228	0.505	0.521	0.495	0.014	0.044	0.012

Note: Expected chi-square test statistic is 397, and expected standard deviation is 28.18

Table 7 shows a similar pattern as was observed for the previous models. All test statistics followed a chi-square distribution and when sample sizes were large enough (e.g., $N > 1000$), their test statistics roughly met the expected value of 397 and the expected standard deviation of 28.18. Nonetheless, due to the model complexity, T_{ML} started to deviate from the expected value quite noticeably when $N < 1000$, and when $N < 200$, the mean T_{ML} was substantially inflated, the mean p -value became close to zero, making the rejection rates almost 100 percent. On the other hand, despite the mean test statistics of GLS across different sample sizes didn't deviate far from 397, their mean p -values were increasingly inflated as N became smaller, resulting in under-rejection the null hypothesis. Unavoidably, T_{RLS} was also affected by the small sample size and model complexity but compared to ML and GLS, RLS produced relatively stable test statistics across most sample sizes except when N became very small (e.g., $N \leq 70$). From $N = 200$ to 5000, RLS produced stable mean p -values around 0.5, and its average rejection rates were around 0.01. Due to the complexity of the model, convergence issues became a challenge for all estimators when sample sizes $N < 300$, resulting in large variation of mean standard deviations of T_{ML} , T_{GLS} , and T_{RLS} .

Table 8. Fit indices of Model 4

N	NFI			CFI			RMSEA		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	0.725	0.221	0.780	0.929	1.000	0.988	0.069	0.000	0.029
70	0.784	0.294	0.810	0.950	1.000	0.993	0.057	0.000	0.021
100	0.840	0.390	0.872	0.964	1.000	0.997	0.049	0.000	0.015
200	0.927	0.622	0.930	0.995	1.000	0.999	0.002	0.000	0.009
300	0.947	0.699	0.949	1.000	1.000	1.000	0.005	0.000	0.004
400	0.946	0.758	0.964	0.996	0.984	1.000	0.016	0.011	0.004
500	0.972	0.816	0.971	0.999	0.983	1.000	0.009	0.000	0.012
800	0.979	0.870	0.981	0.999	1.000	1.000	0.009	0.000	0.003
1000	0.983	0.883	0.985	0.999	0.986	0.998	0.009	0.011	0.003
2000	0.993	0.953	0.992	1.000	1.000	1.000	0.001	0.000	0.000
5000	0.997	0.979	0.997	1.000	0.998	1.000	0.003	0.004	0.001

Table 8 summarizes the fit indices of NFI, CFI and RMSEA. For Model 4, when $N < 200$ ML and RLS' NFI values started to demonstrate poor model fit. GLS required $N > 1000$ to result in good model fit. For CFI, all estimators showed good fit across all sample sizes. For RMSEA, when $N < 100$ ML demonstrated poor fit; whereas, GLS and RLS demonstrated good fit across all sample sizes.

Statistical Power

In addition, we evaluated the statistical power of ML, RLS and GLS to reject false models which requires that $\Sigma \neq \Sigma(\theta)$. This is done by modifying the population models as illustrated in Figure 6, while the original analysis model remains the same. Because the modified population model is no longer the same as the original one, the analysis model becomes misspecified. This model misspecification will lead to poor model fit. The higher power of the estimator is, the smaller the sample size is needed to reject the false model. For all modified population models, we added six additional lag-2 parameters to account for within-person delayed effects. That is, we created lag-2 effect paths as indicated by unidirectional arrows in Figure 6 by connecting WX_1 with WX_3 , WX_2 with WX_4 , WX_3 with WX_5 , WY_1 with WY_3 , WY_2 with WY_4 , WY_3 with WY_5 . All lag-2

coefficients of these paths were set at the value of 0.45 for all models. The degrees of misspecification varied with the nature of model and lag-2 effect sizes. To ensure the lag-2 effect sizes were comparable across all models, we standardized the lag-2 effects according to method mentioned in Hamaker et al. (2015). However, the magnitudes of lag-2 effects changed slightly across all models. That is, the standardized coefficients range from 0.405 to 0.45 in these models, which were very similar to those of the population coefficients.

Because the analysis models do not fit the modified population model, we expect the p -values of the chi-square test statistics < 0.05 . The rejection rates, thus, indicate an estimate of the empirical power of the estimators. For each of the following models in this study, we drew 1,000 replicated samples from each modified population model and fitted with its corresponding original analysis model. The mean chi-square test statistic, its standard deviation, mean p -value and rejection rate based on $\alpha = 0.01$ and 0.05 for each replicated sample were computed.

Figure 6. A modified population model

Table 9. Power analysis results

Model 1

N	P-values			Rejection Rates < 0.01			Rejection Rates < 0.05		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	0.089	0.284	0.128	0.386	0.009	0.182	0.645	0.140	0.491
70	0.050	0.134	0.066	0.576	0.128	0.432	0.776	0.402	0.682
80	0.033	0.089	0.040	0.670	0.233	0.536	0.844	0.529	0.786
90	0.020	0.060	0.028	0.764	0.386	0.648	0.892	0.681	0.856
100	0.014	0.041	0.019	0.836	0.530	0.746	0.926	0.798	0.900
200	0.000	0.001	0.000	0.998	0.982	0.994	1.000	0.998	0.998
300	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
500	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
700	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
1000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
2000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
5000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
10000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000

Model 2

N	P-values			Rejection Rates < 0.01			Rejection Rates < 0.05		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	nc	nc	nc	nc	nc	nc	nc	nc	nc
70	nc	nc	nc	nc	nc	nc	nc	nc	nc
80	nc	nc	nc	nc	nc	nc	nc	nc	nc
90	0.357	nc	nc	0.033	nc	nc	0.098	nc	nc
100	0.314	0.897	0.528	0.043	0.000	0.000	0.133	0.000	0.000
200	0.230	0.438	0.326	0.103	0.000	0.036	0.276	0.095	0.144
300	0.200	0.315	0.235	0.137	0.063	0.094	0.352	0.188	0.250
500	0.090	0.126	0.118	0.349	0.200	0.279	0.591	0.508	0.526
700	0.043	0.060	0.046	0.566	0.424	0.554	0.782	0.709	0.784
1000	0.013	0.012	0.010	0.842	0.822	0.856	0.942	0.930	0.960
2000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
5000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
10000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000

Model 3

N	P-values			Rejection Rates < 0.01			Rejection Rates < 0.05		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	nc	nc	nc	nc	nc	nc	nc	nc	nc
70	nc	nc	nc	nc	nc	nc	nc	nc	nc
80	nc	nc	nc	nc	nc	nc	nc	nc	nc
90	0.160	nc	nc	0.133	nc	nc	0.367	nc	nc
100	0.131	nc	nc	0.330	nc	nc	0.435	nc	nc
200	0.069	0.407	0.169	0.428	0.000	0.168	0.682	0.114	0.392
300	0.046	0.217	0.091	0.500	0.062	0.338	0.750	0.259	0.580
500	0.009	0.053	0.019	0.856	0.474	0.724	0.946	0.740	0.898
700	0.001	0.007	0.002	0.980	0.862	0.978	0.998	0.963	0.996
1000	0.000	0.001	0.000	1.000	0.992	0.998	1.000	0.996	1.000
2000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
5000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
10000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000

Model 4

N	P-values			Rejection Rates < 0.01			Rejection Rates < 0.05		
	ML	GLS	RLS	ML	GLS	RLS	ML	GLS	RLS
50	nc	nc	nc	nc	nc	nc	nc	nc	nc
70	nc	nc	nc	nc	nc	nc	nc	nc	nc
80	nc	nc	nc	nc	nc	nc	nc	nc	nc
90	0.071	0.964	0.398	0.413	0.000	0.000	0.641	0.000	0.000
100	0.039	0.702	0.369	0.592	0.000	0.034	0.813	0.000	0.118
200	0.029	0.145	0.183	0.680	0.191	0.136	0.870	0.383	0.336
300	0.017	0.130	0.083	0.758	0.204	0.389	0.914	0.462	0.651
400	0.006	0.049	0.032	0.896	0.453	0.638	0.978	0.723	0.831
500	0.001	0.008	0.012	0.962	0.875	0.846	0.996	0.975	0.944
700	0.000	0.000	0.001	1.000	0.965	0.984	1.000	1.000	1.000
1000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
2000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
5000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000
10000	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000	1.000

Table 9 shows the results of the power analysis of all estimators under investigation, and reports the mean p -values, rejection rates at $\alpha = 0.01$ and 0.05 . The power analysis of Model 1 showed that the empirical power of ML, GLS, and RLS increased with larger sample sizes; when $N > 200$ they had identical power to reject the null hypothesis at $\alpha = 0.01$ and 0.05 . Whereas when $N < 200$ ML tended to have smaller mean p -values, thus ML had higher statistical power than GLS and RLS. In contrast, GLS tended to consistently produce the lowest statistical power. These patterns were consistent with both rejection rates.

The results in Model 2 were similar to those in Model 1, in that both ML and RLS tended to have similar statistical power. However, when $N < 500$, ML had smaller p -values and had higher statistical power to reject the incorrect models. When $N > 500$, all estimators had similar statistical power in both rejection rates. The results reported in Model 3 showed that ML had higher statistical power to reject the null hypothesis than both RLS and GLS when $N < 1000$. When $N = 200$, GLS rejection rate at $\alpha = 0.01$ was 0, RLS was 0.010, while ML was 0.428. Likewise, GLS rejection rate at $\alpha = 0.05$ was 0.392, RLS was 0.114, and ML was 0.682. Model 4 affirmed the findings in previous models that ML had higher statistical power to reject incorrect models when sample sizes were small in both rejection rates.

Discussion

The RI-CLPM is an extension of the traditional cross-lagged panel model (CLPM) put forth recently by Hamaker et al. (2015) to study reciprocal influences of multiple variables over time. The RI-CLPM includes random intercepts which serve to separate between-person differences (i.e., variance of the random intercept) from within-person processes (Hamaker et al., 2015; Mund et al., 2021). Little research has been done to evaluate the performance of estimators and model fit indices in these novel longitudinal models. In this paper we have evaluated several estimators and

model fit statistics in hope of providing social and behavior science researchers with clear guidance on which estimators and model fit statistics perform well as a function of model complexity and sample size. This is important because applied researchers do not always have sample sizes large enough to take advantage of the asymptotic properties of normal theory estimators (e.g., Burns et al., 2020; Etherson et al., 2022; Paul et al., 2019).

In this study, we tried to reconcile the studies on goodness-of-fit test statistics in covariance structure with the RI-CLPM. We chose four typical RI-CLPM models which were introduced by Mulder & Hamaker (2021). We have examined the performances of ML, GLS and RLS test statistics and fit indices across different sample sizes and levels of complexity using Monte Carlo simulations. Theoretically, the test results were mostly consistent with what the existing literature on ML, GLS, and RLS in confirmatory factor analysis (Arruda & Bentler, 2017; Hayakawa, 2019; Jalal & Bentler, 2018; Zheng & Bentler, 2022a, 2022b). Surprisingly, the complicated nature of RI-CLPM poses computing and model specification challenges to ML, GLS and RLS. Unlike conventional confirmatory factory analysis models, RI-CLPMs have more latent variables, which is inherently more difficult to specify a model and compute. Hence, when the sample sizes were small relative to model complexity, we encountered serious non-convergence issues. This issue was due to a covariance matrix that was not invertible, in large part, because the matrix was not full rank.

By and large, the tests of all models coherently suggested that the performances of ML and GLS were impacted by both sample size and model complexity. When sample sizes were sufficiently larger than the number of variables, their test statistics followed the chi-square distribution with $p^* - q$ degrees of freedom. Nonetheless, when sample sizes were smaller, both T_{ML} and T_{GLS} became increasingly upward or downward biased, respectively. This is because

when the ratio of N to p are not substantially greater than 1, it is insufficient to estimate higher order moments precisely in the covariance matrix. In this study, we provided empirical evidence that the RLS estimator outperformed ML and GLS in various RI-CLPMs. When models were complicated with large degrees of freedom, the test statistics of RLS negligibly deviate from the theoretically expected values across all sample sizes. These findings offer a new alternative for applied researchers when dealing with these kinds of data.

Other than chi-square test, NFI, CFI and RMSEA provided additional information for our goodness-of-fit evaluation. These fit indices have their own metrics for model fit evaluations. Across all models conducted in this research, NFI tended to be affected by small sample sizes. According to Bentler & Bonett (1980), NFI is defined as $NFI = \frac{T_i - T_k}{T_i}$, where T_i is a baseline chi-square value of an independent model, and T_k is a chi-square value of a specific model. Both T_i and T_k are obtained from a specific fitting function. When $T_i = T_k$, $NFI=1$, which indicates a perfect fit. Whereas when T_k deviates from the expected values, NFI will be less than 1. That is, when a T_k is problematic, NFI based on it could be problematic too (Bentler, 2006). Like NFI, RMSEA is also affected the model complexity and sample size. The higher the degrees of freedom, the smaller the sample size is, the higher RMSEA values (Bentler, 2006; Kenny et al., 2015). In contrast, CFI is based on a different metric, differential sample size would not affect CFI (Bentler & Bonett, 1980). Even though RLS didn't seem to perform better than ML in terms of Type I error rates in NFI, it performed consistently in CFI and RMSEA across all sample sizes. Concerning the power to reject misspecified models, ML tended to outperform RLS and GLS when sample sizes were small. On the other hand, ML also tended to over reject the correctly-specified models when sample sizes were small. In contrast, RLS still had higher statistical power than GLS and more accurate Type 1 error rates across all sample sizes. Therefore, we conclude that RLS performed

well in terms of statistical power and Type 1 error rates compared to the other estimators under investigation when sample size is small relative to model complexity.

The limitation of this study is that our data simulation is based on multivariate normal distribution. In real data analysis, non-normal data are ubiquitous. Future research should explore the performance of these methods in the context of nonnormal data and examine the performances of robust test statistics based on ML, GLS, and RLS. As Hayakawa (2019) introduced a new adjusted test with a correction based on RLS, which produced consistent p -values that are within the acceptable range and overcame the over-rejection problems in nonnormal data. In addition, it is Important and interesting to explore new estimators on RI-CLPM. For example, another new method, regularized GLS (RGLS) introduced by Arruda & Bentler (2017), is a good alternative to ML, GLS, and RLS. Recent study has shown that RGLS provides equivalent performance as RLS in both normal and non-normal data (Zheng & Bentler, 2022a).

In conclusion, we recommend applied researchers consider estimating RI-CLPMs using RLS when they have sample sizes are closer to the degrees of freedom of the analysis models and they are worried about spuriously rejecting the fitted model as it produces more accurate chi-square tests, empirical Type-I error rates, and model fit indices across a wide range of sample sizes. This is a particularly important finding for applied researchers that fit RI-CLPM but do not have sufficiently large sample sizes to take advantage of the normal theory properties of common statistical estimators such as ML and GLS.

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Appendix

The Covariance Matrix of the RI-CLPM

The RI-CLPM can be expressed as a covariance matrix. In the context of covariance structure analysis, we can rewrite equations 5 and 6 in matrix form as follows:

$$\mathbf{z}_{it} = \boldsymbol{\delta}_i + \boldsymbol{\Phi} \mathbf{z}_{i(t-1)}^* + \boldsymbol{\eta}_i + \mathbf{v}_{it}, \quad (i = 1, \dots, n, t = 1, \dots, T) \quad (\text{A1})$$

$$\mathbf{z}_{i1} = \boldsymbol{\delta}_i + \boldsymbol{\Psi} \boldsymbol{\eta}_i + \varepsilon_{i1}, \quad (i = 1, \dots, n) \quad (\text{A2})$$

where

$$\mathbf{z}_{it} = \begin{bmatrix} x_{it} \\ y_{it} \end{bmatrix}, \boldsymbol{\Phi} = \begin{bmatrix} \beta_x & \gamma_x \\ \beta_y & \gamma_y \end{bmatrix}, \boldsymbol{\eta}_i = \begin{bmatrix} \eta_{xi} \\ \eta_{yi} \end{bmatrix}, \mathbf{v}_i = \begin{bmatrix} v_{xit} \\ v_{yit} \end{bmatrix}, \boldsymbol{\delta}_i = \begin{bmatrix} \delta_{xi} \\ \delta_{yi} \end{bmatrix},$$

$$\boldsymbol{\Psi} = \begin{bmatrix} \psi_{11} & \psi_{12} \\ \psi_{21} & \psi_{22} \end{bmatrix}, \varepsilon_{i0} = \begin{bmatrix} \varepsilon_{i0}^y \\ \varepsilon_{i0}^x \end{bmatrix}. \quad (\text{A3})$$

Following the covariance matrix of the CLPM introduced by Hayakawa (2019), we assume that the maximum eigenvalue of $\boldsymbol{\Phi}$ is less than 1, so that $\mathbf{z}_{it}$ can maintain a stable process. Following these matrices, we combine equations 5 and 6, which becomes

$$\mathbf{B} \mathbf{z}_i = \boldsymbol{\delta}_i + \mathbf{J} \boldsymbol{\pi}_i + \mathbf{u}_i, \quad (\text{A4})$$

where

$$\mathbf{B} = \begin{bmatrix} \mathbf{I}_2 & \mathbf{0} & \cdots & \mathbf{0} \\ -\boldsymbol{\Phi} & \mathbf{I}_2 & \cdots & \vdots \\ \vdots & \ddots & \ddots & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & -\boldsymbol{\Phi} & \mathbf{I}_2 \end{bmatrix}, \quad (\text{A5})$$

$$\mathbf{\Gamma} = \mathbf{B}^{-1} = \begin{bmatrix} \mathbf{I}_2 & \mathbf{0} & \cdots & \mathbf{0} \\ \mathbf{\Phi} & \mathbf{I}_2 & \cdots & \vdots \\ \vdots & \ddots & \ddots & \mathbf{0} \\ \mathbf{\Phi}^{T-1} & \mathbf{0} & \mathbf{\Phi} & \mathbf{I}_2 \end{bmatrix}, \quad (\text{A6})$$

$$\mathbf{z}_{it} = \begin{bmatrix} z_{i1} \\ z_{i2} \\ \vdots \\ z_{iT} \end{bmatrix}, \quad \mathbf{u}_i = \begin{bmatrix} \varepsilon_{i1} \\ v_{i2} \\ \vdots \\ v_{iT} \end{bmatrix}, \quad (\text{A7})$$

$$\mathbf{J} = \begin{bmatrix} 1 & \mathbf{\Psi} \\ 0 & \mathbf{I}_2 \end{bmatrix}, \quad \boldsymbol{\pi}_i = \begin{bmatrix} \delta_i \\ \boldsymbol{\eta}_i \end{bmatrix}, \quad (\text{A8})$$

$$\mathbf{z}_i = \mathbf{\Gamma}(\mathbf{J}\boldsymbol{\pi}_i + \mathbf{u}_i). \quad (\text{A9})$$

Thus, we assume that $\boldsymbol{\pi}_i \sim (0, \Sigma_{\boldsymbol{\pi}})$, $v_{it} \sim (0, \Sigma_v)$, $\varepsilon_{i0} \sim (0, \Sigma_{\varepsilon})$, and δ_i , η_i , v_{it} , and ε_{i1} are uncorrelated, and each of them is independent and identically distributed. Therefore, the covariance matrix of $\mathbf{z}_i$ can be written as

$$\Sigma(\boldsymbol{\theta}) = \mathbf{\Gamma}(\mathbf{J}\Sigma_{\boldsymbol{\pi}}\mathbf{J}' + \Sigma_u)\mathbf{\Gamma}' \quad (\text{A10})$$

where $\boldsymbol{\theta} = (\mathbf{\Phi}, \mathbf{\Psi}, \sigma_{\pi}^2, \sigma_v^2, \sigma_{\varepsilon}^2)'$, and $\Sigma_u = \text{diag}(\sigma_{\varepsilon}^2, \sigma_v^2 \mathbf{I}_T)$.