# Matrix Decomposition-Based Approach to Estimate the STARTS Model

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**Abstract**

We propose a new estimation method for the Stable Trait, Auto Regressive Trait, and State (STARTS) model, which is well known for its frequent occurrence of improper solutions. The proposed approach is implemented through a two-stage estimation procedure that combines matrix decomposition factor analysis (MDFA) based on eigenvalue decomposition with conventional SEM estimation principles. By reformulating the STARTS model within a factor-analytic framework, this study presents a novel way of applying MDFA in the context of structural equation modeling (SEM). Through a simulation study and an empirical application to ToKyo Teen Cohort data, the proposed method was shown to entail a substantially lower risk of improper solutions than commonly used maximum likelihood, conditional ML, and (unweighted) least squares estimators, while tending to yield solutions similar to those obtained by ML. Compared with Bayesian estimation, the proposed method does not require the specification of appropriate (weakly informative) prior distributions and may effectively mitigate bias issues that arise when the number of time points is small. Applying the proposed method, as well as conducting sensitivity analyses informed by it, will enable researchers to more effectively delineate the range of plausible conclusions from data in estimating the STARTS model and other SEMs.

*Keywords:* structural equation modeling, improper solution, matrix decomposition factor analysis, stable trait, measurement errors,

# 1 Introduction

It is estimated that more than 30,000 longitudinal studies are published annually worldwide, and this number is expected to continue increasing (Usami, 2026). Among this massive volume of research, a substantial proportion aims to examine longitudinal relations among variables—that is, the dynamics of change over time. Particularly in psychology, growing attention has been directed toward modeling within-person relations while simultaneously accounting for the influence of stable individual differences by modeling stable traits (or, unit effects) as latent variables. For example, in personality research, analysis models often assume the existence of stable traits to evaluate the long-term stability and short-term variability of personality characteristics such as extraversion and neuroticism using longitudinal data. The widespread adoption of the random intercept cross-lagged panel model (RI-CLPM; Hamaker, Kuiper, & Grasman, 2015), which aims to examine reciprocal within-person relations among variables, is emblematic of this trend.

On the other hand, psychology has long employed models that explicitly incorporate measurement error in addition to stable traits, such as the stable trait–autoregressive trait–state (STARTS) model (Kenny & Zautra, 1995, 2001). This model, which is more general and is expected to be more closely aligned with the realities of psychological measurement, was proposed earlier than the RI-CLPM and continues to be widely used across various domains of psychological research today. The STARTS model decomposes individual differences in measurements across time into three sources of variation: a time-invariant stable component (i.e., stable traits factor), a time-varying autoregressive component (i.e., within-person fluctuations), and an occasion-specific state component (i.e., measurement error). For example, Dicke et al. (2022) examined changes in Australian school principals' emotional exhaustion (i.e., burnout) using longitudinal data ($N$ = 5,509; $T$= 8) analyzed with the STARTS model. Their results demonstrated that the variance in principals' emotional exhaustion was distributed almost evenly between a persistent autoregressive component (reflecting within-person fluctuations) and a stable trait component (reflecting stable traits factor), with a somewhat smaller portion attributable to occasion-specific fluctuations (reflecting measurement error). Furthermore, variability in these structural profiles was found to be primarily linked to individual attributes of the principals—such as years of experience and gender—rather than work-related

contextual factors (e.g., school type or educational stage).

Models such as the RI-CLPM and the STARTS model are sometimes referred to collectively as residual-level models (e.g., Andersen, 2022), as they describe dynamic processes operating on latent deviations (rather than observed scores). All of these can be formulated within the structural equation modeling (SEM) framework, and maximum likelihood (ML) estimation is most commonly used especially for the RI-CLPM. However, there are cases in which models other than residual models provide a better fit to empirical data (e.g., Usami, 2022), and modeling latent interactions in residual models often introduces additional implementation challenges (e.g., Usami, 2023). Consequently, the selection of an appropriate longitudinal model remains an active area of methodological discussion (e.g., Hamaker, 2023; Lucas, 2023; Lüdtke & Robitzsch, 2022, 2025; Orth et al., 2021; Usami, 2021; Usami, Murayama, & Hamaker, 2019). Although it should be kept in mind that such more fundamental theoretical discussions are still ongoing, it is nevertheless important to note that the STARTS model, in particular, capitalizes on the advantages of residual models by separating residuals in the autoregressive component from measurement error, thereby allowing measurement error to be represented explicitly. In light of the recent proliferation of intensive longitudinal data (ILD; e.g., McNeish & Hamaker, 2020), further applications of the STARTS model—as well as its extended variants—are expected in the near future.

Although incorporating measurement error is conceptually natural for most psychological measurement contexts, the major obstacle to broader adoption of the STARTS models lies in the frequent occurrence of improper solutions (e.g., negative error variances, non-positive definite covariance matrices among trait factors), non-convergence, and unstable parameter estimates. For example, Usami, Todo, and Murayama (2019) reported that while improper solutions can also occur in the RI-CLPM, they are far more prevalent in the STARTS models—even when the true data-generating process corresponds exactly to the STARTS structure.

Building on Lüdtke et al. (2018), the causes of these frequent estimation problems can be summarized as four interrelated aspects: (i) Highly dependent parameter estimates and a nearly singular Hessian matrix, (ii) Sensitivity to small changes in the sample covariance matrix, (iii) Parameter regions close to non-identification, and (iv) Empirical under-identification and flat likelihoods. First, because the three kinds of variance components (stable trait, autoregressive trait, and state vari-

ance) and the autoregressive coefficient are highly interdependent, ML estimation often encounters a nearly singular Hessian matrix. Second, this strong interdependence leads to large standard errors and instability of estimates—very small sampling fluctuations in the covariance matrix can induce large changes in parameter estimates, making ML estimation numerically unstable (Kenny & Zautra, 2001). Third, the STARTS model becomes particularly unstable when population parameters approach boundary conditions, specifically when the autoregressive variance is small or when the standardized stable-trait variance is near 0 or 1. Fourth, even when the model is technically identified, the likelihood surface can be flat with respect to variance parameters, making it difficult for optimization algorithms to find a unique solution—a phenomenon empirically demonstrated by Lüdtke et al. (2018, Figure 5), who showed that a broad range of parameter values can yield nearly identical likelihoods.

These issues are mutually interrelated, and depending on conditions such as the number of time points and population parameter values, avoiding improper solutions can be extremely difficult. One possible countermeasure is constrained estimation like constrained ML (CML), in which the optimization space is restricted to admissible values (e.g., variances constrained to be positive). However, constrained estimation frequently produces boundary values (i.e., estimates at the lower or upper bound), leading to biased estimates (Searle, Casella, & McCulloch, 1992; cited from Lüdtke et al., 2018). Moreover, although not in the context of the STARTS model but rather within confirmatory factor analysis (CFA), the usefulness of (unweighted) least squares (LS) with non-iterative estimators has also been discussed (e.g., Dhaene & Rosseel, 2023).

When improper solutions occur in the estimation of the STARTS model, it is often the case that researchers alter model specifications (e.g., by imposing equality constraints on parameters) or modify the data being analyzed (e.g., by excluding specific waves or participants) in order to obtain admissible solutions. As an alternative to such partly conservative approaches, Bayesian estimation is also useful and has been employed as a procedure for addressing improper solutions. Lüdtke et al. (2018), demonstrated that when appropriate (weakly informative) priors are specified, a Bayesian approach can effectively prevent improper solutions and stabilize parameter estimation in the STARTS model. Bayesian estimation is also well known as an effective strategy for avoiding improper solutions in hierarchical linear models, particularly those including random coefficients.

However, Bayesian estimation is known to carry the risk of inducing parameter bias; for example, in the context of mediation models, it has been reported that under small sample sizes, Bayesian estimation tends to yield more stable results than CML, but often at the cost of increased bias (e.g., Smid et al., 2020; Ulitzsch et al., 2023). Moreover, under such small-sample conditions, estimation results can be highly sensitive to the choice of prior distributions (e.g., Miočević et al., 2021). Therefore, sensitivity analyses comparing results under different prior specifications are commonly recommended. Yet, because the Bayesian approach for the STARTS model typically relies on Markov chain Monte Carlo (MCMC) algorithms to approximate posterior distributions, computational costs are usually higher than for ML, and these costs increase further when sensitivity analyses are performed. Furthermore, even when plausible prior distributions are specified, particularly when the prior information is weak, the resulting estimates may still correspond to the zero boundary, yielding solutions similar to those obtained by CML.

In the present study, we propose a new estimation method to address the problem of improper solutions in the STARTS model. The proposed approach is implemented through a two-stage estimation procedure that combines matrix decomposition factor analysis (MDFA; Adachi & Trendafilov, 2018) based on eigenvalue decomposition with conventional SEM estimation principles. MDFA is an approach based on matrix algebra, and estimate parameters by iterative estimation using a LS criterion based on data space rather than covariance space as SEM. MDFA was originally proposed in the context of factor analysis, and recent developments include its extensions to SEMs involving structural relations among latent variables (Yamashita, 2024) and theoretical examinations of its estimator properties (Terada, 2025). One of the key features in MDFA is that negative variance estimates do not occur in principle during iterative updates. In the present study, by reformulating the STARTS model within a factor-analytic framework, we presents a novel way of applying MDFA in the context of SEM.

To date, the application of MDFA to longitudinal models—including the STARTS model—has not been reported, and its estimation performance and effectiveness in addressing the problem of improper solutions remain unexplored. Through a simulation study and an empirical application to ToKyo Teen Cohort (TTC) data, we will show that the proposed method entails a substantially lower risk of improper solutions than ML, CML and ULS estimators, and that it may effectively

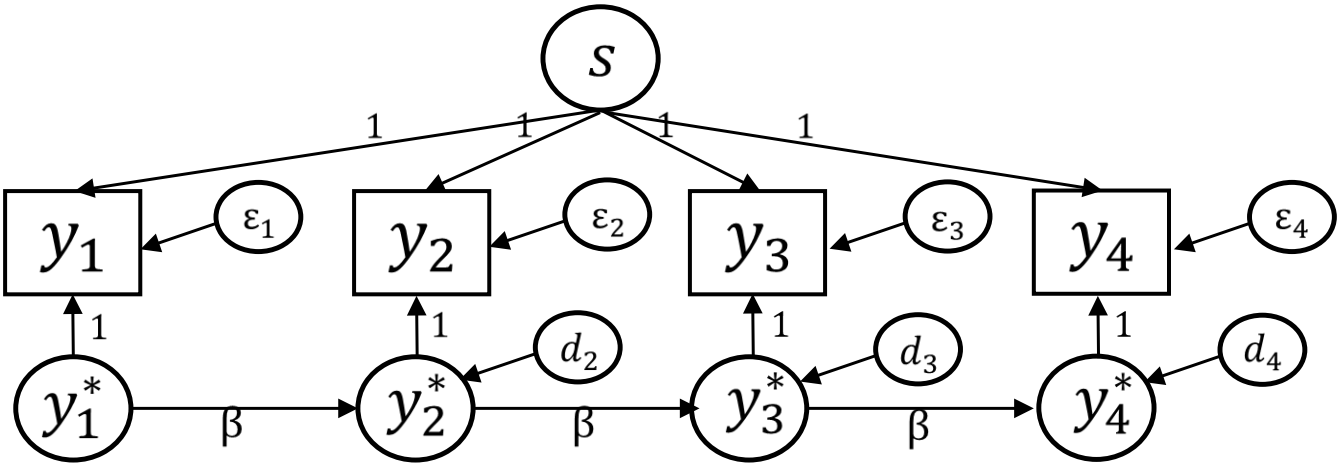


Figure 1: Path diagram of the STARTS model ($T = 4$)

mitigate bias issues that can arise especially in Bayesian estimation when the number of time points is small.

The structure of this paper is as follows. Section 2 provides an overview of the STARTS model and describes ML, CML, and ULS estimators. Section 3 introduces MDFA and shows how it can be applied to estimate parameters in the STARTS model. Section 4 presents a simulation study for evaluating the frequency of improper solutions, bias and RMSE of estimates, and computational cost across different estimation methods. Section 5 applies the proposed method to the TTC data. Section 6 concludes with a summary and directions for future research.

# 2 STARTS Model and Estimation

## 2.1 STARTS model

Suppose that data are generated at fixed and equally spaced time points, and let $y_{it}$ denote a continuous observed variable at time point $t$ ($t = 1, \ldots, T$) for person $i$ ($i = 1, \ldots, N$). For expository purposes, here we consider the case in which there is a single focal variable ($y$).

In the STARTS model (Figure 1 for the case of $T = 4$), $y_{it}$ is considered to consist of latent true scores ($f_{it}$) and measurement errors ($\epsilon_{it}$), that is,

$$y_{it} = f_{it} + \epsilon_{it}, \tag{1}$$

for all time points. These measurement errors are usually assumed to be normally distributed (with zero mean and variance of $\psi^2$) and mutually uncorrelated.

The latent true scores $f_{it}$ are then modeled as

$$f_{it} = \mu_t + s_i + y^*_{it} \tag{2}$$

for all time points. This equation is used to decompose latent true scores $f_{it}$ into a temporal group mean at $t$ ($\mu_t$), a stable trait factor of person $i$ ($s_i$), and a temporal deviation ($y^*_{it}$). Since $\mu_t$ is not of substantive interest here (i.e., mean structure is irrelevant to the current discussion), and in the subsequent section for the proposed method, we assume $y_{it}$ is centered by group mean (i.e., $\mu_t = 0$). Also, we assume both the trait factor and temporal deviation have zero mean, and they are uncorrelated with measurement errors. The variance of $s_i$ is expressed here by $\phi^2$.

The stable trait factor ($s_i$) exhibits the between-person or stable individual differences, and the temporal deviation ($y^*_{it}$) represents the within-person variability from an expected value for person $i$ at $t$ (i.e., $\mu_t + s_i$). The initial within-person variability ($y^*_{i1}$) is modeled as an exogeneous variable, and its variance ($Var(y^*_{i1}) = \sigma^2_1$) is estimated.

Importantly, the stable trait factor is assumed to be uncorrelated with the within-person variability:

$$Cov(s_i, y^*_{it}) = 0 \tag{3}$$

for each $i$ and $t$. Consequently, as with the RI-CLPM, the stable trait factor $s$ has only direct effects on outcomes, and each latent true score can be decomposed into a (linear) sum of time-invariant ($s_i$) and time-varying ($y^*_{it}$) factors that are mutually uncorrelated.

Within-person variability $y^*_{it}$ is further modeled as

$$y^*_{it} = \beta y^*_{i(t-1)} + d_{it} \tag{4}$$

for $t \geq 2$. In Equation (4), the (first-order) autoregressive process is assumed to represent the within-person relation. $\beta$ is an (time-invariant) autoregressive coefficient, and $d_{it}$ denotes a residual that is uncorrelated with $y^*_{it'}$ ($t' \leq t-1$) and $s_i$. Here, (time-invariant) residual variance is assumed as $Var(d_{it}) = \omega^2$.[1]

[1]In the STARTS model, it is common to impose appropriate nonlinear constraints on the parameters so that

From Equation (4), $y^*_{it}$ can be expanded as

$$\begin{aligned} y^*_{it} &= \beta y^*_{i(t-1)} + d_{it} \\ &= \beta(\beta y^*_{i(t-2)} + d_{i(t-1)}) + d_{it} \\ &= \beta(\beta(\beta y^*_{i(t-3)} + d_{i(t-2)}) + d_{i(t-1)}) + d_{it} \\ &\quad \vdots \\ &= \beta^{t-1} y^*_{i1} + d_{it} + \beta d_{i(t-1)} + \beta^2 d_{i(t-2)} + \cdots + \beta^{t-2} d_{i2}. \end{aligned} \tag{5}$$

Therefore, $y^*_{it}$ can be expressed by a function of initial within-person variability $y^*_{i1}$ and a total of $t-1$ residuals, $d_{i2}, d_{i3}, \ldots, d_{it}$. From this result, the variance of $y^*_{it}$ and covariance between $y^*_{it}$ and $y^*_{it'}$ $(t' < t)$ can be expressed as

$$\begin{aligned} Var(y^*_{it}) &= \beta^{2(t-1)} Var(y^*_{i1}) + (1 + \beta^2 + \beta^4 + \cdots + \beta^{2(t-2)})\omega^2 \\ &= \beta^{2(t-1)}\sigma_1^2 + \frac{1-\beta^{2(t-1)}}{1-\beta^2}\omega^2, \end{aligned} \tag{6}$$

$$Cov(y^*_{it}, y^*_{it'}) = \beta^{t-t'} Var(y^*_{i1}) = \beta^{t-t'}\sigma_1^2 \tag{7}$$

for $t \geq 2$.

Suppose $y_{it}$ is now mean-centered at each time point (i.e., $\mu_t = 0$), from Equations (1) and (2), $y_{it}$ can now be expressed as

$$y_{it} = s_i + y^*_{it} + \epsilon_{it}. \tag{8}$$

The variance of $y_{it}$ and covariance between $y_{it}$ and $y_{it'}$ $(t' < t)$ can be orthogonally decomposed as

$$\begin{aligned} Var(y_{it}) &= Var(s_i) + Var(y^*_{it}) + Var(\epsilon_{it}) \\ &= \phi^2 + Var(y^*_{it}) + \psi^2, \end{aligned} \tag{9}$$

$$\begin{aligned} Cov(y_{it}, y_{it'}) &= Var(s_i) + Cov(y^*_{it}, y^*_{it'}) + Cov(\epsilon_{it}, \epsilon_{it'}) \\ &= \phi^2 + Cov(y^*_{it}, y^*_{it'}), \end{aligned} \tag{10}$$

the variances of the trait factor, within-person variation (corresponding to the 'autoregressive trait' in the STARTS context), and measurement error (corresponding to the 'state' in the same context) remain time-invariant (Donnellan et al., 2012; Lüdtke et al., 2018). In contrast, such constraints are typically not imposed in the RI-CLPM. In this paper, we likewise discuss the model under the settings where no such constraints are supposed.

where $Var(y^*_{it})$ and $Cov(y^*_{it}, y^*_{it'})$ are expressed as in Equations (6)-(7). The parameters in the STARTS model can be identified from data with $T \geq 4$.

## 2.2 Several estimators in SEM and improper solutions

### 2.2.1 Maximum likelihood estimation

Suppose that outcomes are now mean-centered at each time point, and $\boldsymbol{y}_i = (y_{i1}, \ldots, y_{iT})^\top$ follow a multivariate normal distribution: $\boldsymbol{y}_i \sim i.i.d. MVN(\boldsymbol{0}, \boldsymbol{\Sigma}(\boldsymbol{\theta}))$, where $\boldsymbol{\Sigma}(\boldsymbol{\theta})$ is a $T \times T$ covariance structure expressed as in Equations (9)-(10), which is a function of unknown parameters $\boldsymbol{\theta} = (\psi^2, \phi^2, \beta, \omega^2, \sigma_1^2)^\top$.

The observed log-likelihood is given by $LL(\boldsymbol{\theta}|\boldsymbol{Y}) = \sum_{i=1}^{N} LL_i(\boldsymbol{\theta}|\boldsymbol{y}_i)$, where,

$$LL_i(\boldsymbol{\theta}|\boldsymbol{y}_i) = -\frac{T}{2}\log(2\pi) - \frac{1}{2}\log|\boldsymbol{\Sigma}(\boldsymbol{\theta})| - \frac{1}{2}\boldsymbol{y}_i^\top \boldsymbol{\Sigma}(\boldsymbol{\theta})^{-1}\boldsymbol{y}_i, \tag{11}$$

and $\boldsymbol{Y} = (\boldsymbol{y}_1^\top, \ldots, \boldsymbol{y}_N^\top)^\top$. Instead of maximizing $LL(\boldsymbol{\theta}|\boldsymbol{Y})$, it is common to estimate $\hat{\boldsymbol{\theta}}$ by minimizing the following loss function based on the likelihood ratio test statistic that is used for evaluating analysis models:

$$f_{ML}(\boldsymbol{\theta}) = \mathrm{tr}(\boldsymbol{S}\boldsymbol{\Sigma}(\boldsymbol{\theta})^{-1}) - \log|\boldsymbol{S}\boldsymbol{\Sigma}(\boldsymbol{\theta})^{-1}| - T, \tag{12}$$

where tr denotes the trace of a matrix and $\boldsymbol{S}$ is a $T \times T$ (unbiased) sample covariance matrix of outcomes. The ML estimator has been used most widely in SEM applications. Hayakawa & Sun (2022) showed that the ML estimator is consistent and more efficient than other estimators (e.g., generalized LS) when both $N$ and $P$ (the number of variables, which is equal to $T$ in the current setting) tend to infinity with $P/N \to c$ ($c$ is a finite constant with $0 < c < 1$).

It is common to perform iterative calculations using numerical methods like Newton–Raphson method to obtain parameter estimates $\hat{\boldsymbol{\theta}}$. Previous simulation studies and empirical applications of the STARTS model with ML estimation have indicated that estimation difficulties, including issues such as nonconvergence and improper solutions, often arise (Lüdtke et al., 2018). Another problem is that parameter estimates are often very unstable, which is reflected by large estimates of standard errors.

As noted above, one possible countermeasure is to use constrained estimation like CML. It is usually implemented by minimizing the $f_{ML}(\boldsymbol{\theta})$ subject to equality and boundary constraints on model parameters. Equality constraints are handled via reparameterization, whereas inequality constraints (e.g., non-negativity of variance parameters) are enforced through boundary-constrained numerical optimization. However, it is empirically known that boundary values can occur in CML and it can lead to biased parameter estimates (e.g., Searle et al., 1992).

### 2.2.2 Bayesian estimation

Lüdtke et al. (2018) introduced a general approach for stabilizing parameter estimation in the STARTS model through a Bayesian framework, making use of MCMC methods with (weakly informative) priors.

Bayesian estimation treats all model parameters as random variables and evaluates their posterior distributions given the observed data. The posterior distribution can be evaluated by

$$p(\boldsymbol{\theta}|\boldsymbol{Y}) \propto L(\boldsymbol{\theta}|\boldsymbol{Y})\, p(\boldsymbol{\theta}), \tag{13}$$

where $L(\boldsymbol{\theta}|\boldsymbol{Y})$ represents the likelihood and $p(\boldsymbol{\theta})$ denotes the prior distribution.

Lüdtke et al. (2018) demonstrate with simulations that the Bayesian approach with weakly informative prior distributions avoided estimation problems and also had desirable properties in terms of the bias and RMSE. However, if a prior distribution is not specified appropriately (i.e., strongly deviates from the true parameter), the Bayesian approach can result in largely biased parameter estimates.

Ideally, a specification of informative priors should be accompanied by a sensitivity analysis that tests how sensitive the resulting parameter estimates are to different specifications of the priors (Lüdtke et al., 2018). Especially when the sample size is small, the prior specification has a greater influence on the estimation results, and researchers should seriously consider conducting a sensitivity analysis (Lüdtke, et al., 2018). However, conducting sensitivity analyses that involve changing various parameter settings can be complex and may lead to an increase in computational cost. They also noted that one limitation of the Bayesian approach was that it showed a tendency to produce coverage rates that were too high.

### 2.2.3 Least squares estimation

Another well-known estimation method in SEM is a weighted LS (WLS). Let $\boldsymbol{s} = vech(\boldsymbol{S})$ and $\boldsymbol{\sigma}(\boldsymbol{\theta}) = vech(\boldsymbol{\Sigma}(\boldsymbol{\theta}))$ denote $T(T+1)/2 \times 1$ vectors that extract the unique (co)variance elements from $\boldsymbol{S}$ and $\boldsymbol{\Sigma}(\boldsymbol{\theta})$, respectively. When mean structure is not considered, the loss function of WLS can be written as:

$$f_{LS}(\boldsymbol{\theta}) = (\boldsymbol{s} - \boldsymbol{\sigma}(\boldsymbol{\theta}))^{\top} \hat{\boldsymbol{W}} (\boldsymbol{s} - \boldsymbol{\sigma}(\boldsymbol{\theta})), \tag{14}$$

where $\hat{\boldsymbol{W}}$ is a weight matrix.

When the weight is removed (i.e., $\hat{\boldsymbol{W}} = \boldsymbol{I}$), this version of estimator is referred to as ULS. There are other types of LS estimators (e.g., Du & Bentler, 2022; Hayakawa & Sun, 2022; Zheng & Bentler, 2021). Although ULS is known to be less efficient than other estimators and is neither scale-free nor scale-invariant (e.g., Kaplan, 2009), it is computationally inexpensive, straightforward to implement, and still yields consistent estimates. In addition, ULS does not require the extremely large sample sizes typically needed for WLS to obtain good quality point estimates, which makes it particularly useful in applications such as ordinal categorical data analysis (e.g., Rhemtulla et al., 2012) and stepwise estimation procedures in which the measurement model part is estimated first (e.g., Rosseel & Loh, 2024).

In research contexts where the STARTS model is applied, sample sizes are not always large, and to the best of the present author's knowledge, no study has systematically compared LS estimator with ML estimator in terms of estimation performance and the frequency of improper solutions in the STARTS model. For these reasons, the present study includes ULS in the comparison as part of an exploratory investigation. Furthermore, the principle of ULS estimation is also incorporated into certain part of the proposed method explained later.

# 3 Proposed MDFA-Based Approach

In this section, we first provide an overview of the MDFA framework. We then describe how this estimation approach can be utilized to the STARTS model, thereby introducing the proposed methodology.

## 3.1 An overview of MDFA

As its name suggests, MDFA has been discussed primarily within the context of factor analysis models. Following Adachi et al. (2019) and Yamashita (2024), we introduce the MDFA framework.

Let $\boldsymbol{Y}$ $(N \times T)$ be a data matrix of $N$ observations with respect to $T$ observed variables (and is now column-centered). When MDFA is applied to $\boldsymbol{Y}$, the method is formulated by minimizing the following (Frobenius norm-based) LS criterion:

$$||\boldsymbol{Y} - (\boldsymbol{F}\boldsymbol{\Lambda}^\top + \boldsymbol{U}\boldsymbol{D})||^2, \tag{15}$$

with respect to the common factor score matrix $\boldsymbol{F}$ $(N \times r)$, the unique factor score matrix $\boldsymbol{U}$ $(N \times T)$, the factor loading matrix $\boldsymbol{\Lambda}$ $(T \times r)$, and the diagonal matrix $\boldsymbol{D}$ $(T \times T)$ whose diagonal elements contain the square roots of the unique variances. Here $r$ indicates the number of assumed common factors. We now assume that the variances of the factor scores in $\boldsymbol{F}$ and $\boldsymbol{U}$ are equal to one, and that these factors are mutually uncorrelated (i.e., $\frac{1}{N}\boldsymbol{F}^\top\boldsymbol{F} = \boldsymbol{I}_r, \frac{1}{N}\boldsymbol{U}^\top\boldsymbol{U} = \boldsymbol{I}_T, \boldsymbol{F}^\top\boldsymbol{U} = \boldsymbol{0}_{r\times T}$). Furthermore, both $\boldsymbol{F}$ and $\boldsymbol{U}$ are column centered.

Let $\boldsymbol{Z} = (\boldsymbol{F}, \boldsymbol{U})$ and $\boldsymbol{B} = (\boldsymbol{\Lambda}^\top, \boldsymbol{D})$. Then, the above criterion can be rewritten as

$$||\boldsymbol{Y} - (\boldsymbol{F}\boldsymbol{\Lambda}^\top + \boldsymbol{U}\boldsymbol{D})||^2 = ||\boldsymbol{Y} - \boldsymbol{Z}\boldsymbol{B}^\top||^2 = ||\boldsymbol{Y} - \boldsymbol{Z}\boldsymbol{S}_{\boldsymbol{YZ}}{}^\top||^2 + N||\boldsymbol{S}_{\boldsymbol{YZ}} - \boldsymbol{B}||^2, \tag{16}$$

which becomes a function of $\boldsymbol{S}_{\boldsymbol{YZ}} = \frac{1}{N}\boldsymbol{Y}^\top\boldsymbol{Z} = [\frac{1}{N}\boldsymbol{Y}^\top\boldsymbol{F}, \frac{1}{N}\boldsymbol{Y}^\top\boldsymbol{U}] = [\boldsymbol{S}_{\boldsymbol{YF}}, \boldsymbol{S}_{\boldsymbol{YU}}]$ (Adachi & Trendafilov, 2018, Theorem 2.1). This expression indicates that only the second term $N\|\boldsymbol{S}_{YZ} - \boldsymbol{B}\|^2$ depends on $\boldsymbol{B}$, and that its solution can be obtained as

$$\hat{\boldsymbol{\Lambda}} = \boldsymbol{S}_{\boldsymbol{YF}}, \quad \hat{\boldsymbol{D}} = \mathrm{diag}(\boldsymbol{S}_{\boldsymbol{YU}}). \tag{17}$$

Let $\boldsymbol{L}$ be the orthonormal matrix of eigenvectors and let $\boldsymbol{\Delta}$ be the diagonal matrix of (positive) eigenvalues obtained from the eigen-decomposition of

$$\boldsymbol{B}^\top\boldsymbol{S}\boldsymbol{B} = \boldsymbol{L}\boldsymbol{\Delta}^2\boldsymbol{L}^\top, \tag{18}$$

where $\boldsymbol{L}^\top\boldsymbol{L} = \boldsymbol{I}$. Adachi & Trendafilov (2018, Lemma 3.1) shows that $\boldsymbol{S}_{\boldsymbol{YZ}}$ can be calculated by

$$\boldsymbol{S}_{\boldsymbol{YZ}} = \boldsymbol{S}\boldsymbol{B}\boldsymbol{L}\boldsymbol{\Delta}^{-1}\boldsymbol{L}^\top. \tag{19}$$

As a result, in MDFA, given appropriate initial values and data ($\boldsymbol{S}$), one can obtain estimates of $\boldsymbol{B}$ by iteratively computing $\boldsymbol{S_{YZ}}$ (as a function of $\boldsymbol{B}$) by the Equation (19) and updating $\boldsymbol{B}$ based on the computed $\boldsymbol{S_{YZ}}$ using the Equation (17) until the convergence criterion is met.

As a notable advantage of MDFA, it has been pointed out that it always provides proper solutions by exploiting eigenvalue decomposition (i.e., no Heywood cases; Yamashita, 2024; Terada, 2025). Moreover, theoretical developments have recently progressed, including extensions to high-dimensional settings and SEM that assumes structural relations among latent variables with $L_2$ penalization (Yamashita, 2024).

Note that the loss functions of MDFA (Equation (15)) and ULS (i.e., $(\boldsymbol{s}-\boldsymbol{\sigma}(\boldsymbol{\theta}))^\top(\boldsymbol{s}-\boldsymbol{\sigma}(\boldsymbol{\theta}))$, where $\boldsymbol{\Sigma}(\boldsymbol{\theta})=\boldsymbol{\Lambda}\boldsymbol{\Lambda}^\top+\boldsymbol{D}^2$) are not equivalent, and the estimates of $\boldsymbol{\theta}$ are not necessarily identical. In other words, MDFA performs fitting in the data space while treating $\boldsymbol{F}$ and $\boldsymbol{U}$ as additional parameters, whereas ULS in the SEM framework estimates the parameters from the perspective of covariance structure fitting. On the other hand, it has been empirically reported that the solutions obtained by MDFA are often very similar to the ML estimates in the context of factor analysis models (e.g., Adachi & Trendafilov, 2018).

Although the statistical properties of the MDFA estimator had remained largely unexplored, Terada (2025) demonstrated that MDFA can be formulated not as a mere matrix-decomposition-based numerical procedure, but rather as a semiparametric ML estimator. Terada (2025) also showed that the loss function of MDFA coincides with the squared Bures–Wasserstein distance between $\boldsymbol{S}$ and $\boldsymbol{\Sigma}(\boldsymbol{\theta})$ (Proposition 3.1), and established both the consistency and asymptotic normality of the MDFA estimator (Theorem 3.4 and Theorem 3.5).

## 3.2 Proposed approach

One key idea of the proposed approach is to reinterpret the STARTS model within the framework of factor analysis, where the relations among latent variables are structured using model parameters. This perspective allows estimates of some parameters ($\phi^2$ and $\psi^2$) to be obtained in a manner analogous to MDFA, while the remaining parameters associated with within-person variability ($\sigma_1^2$, $\beta$, and $\omega^2$) are obtained by fitting the covariance structure corresponding to the auto-regression part

of the model (which represents within-person variability; Equations (6) and (7)) to a covariance matrix as a function of the (submatrix of) $\boldsymbol{S_{YZ}}$, which is calculated in the MDFA step. The details of the procedure are presented below.

### 3.2.1 The STARTS Model as an MDFA representation

From Equations (5) and (8), it follows that $y_{it}$ can be expressed as a total of $(T+2)$ terms related to $s_i$, $y^*_{i1}$, $d_{i2}, \ldots, d_{iT}$ and $\epsilon_{it}$. With this point in mind, we explain how the STARTS model corresponds to the MDFA representation and how its estimation can be carried out.

Once again, let $\boldsymbol{Y}$ denote an $N \times T$ matrix of outcomes. Then, Equation (8) can now be expressed as

$$\boldsymbol{Y} = \boldsymbol{s}\boldsymbol{1_T}^\top + \boldsymbol{Y^*} + \boldsymbol{E}, \tag{20}$$

where $\boldsymbol{s} = (s_1, \ldots, s_N)^\top$, $\boldsymbol{Y^*} = (\boldsymbol{y_1^*}, \ldots, \boldsymbol{y_i^*}, \ldots, \boldsymbol{y_N^*})^\top$, where $\boldsymbol{y_i^*} = (y^*_{i1}, \ldots, y^*_{iT})^\top$, is an $N \times T$ matrix of within-person variability, and $\boldsymbol{E} = (\boldsymbol{e_1}, \ldots, \boldsymbol{e_i}, \ldots, \boldsymbol{e_N})^\top$, where $\boldsymbol{e_i} = (\epsilon_{i1}, \ldots, \epsilon_{iT})^\top$, is an $N \times T$ matrix of measurement errors.

From the relation (4), $\boldsymbol{Y^*}$ can be expressed as

$$\boldsymbol{Y^*} = \boldsymbol{Y^*}\boldsymbol{\Gamma} + \boldsymbol{R}, \tag{21}$$

where $\boldsymbol{\Gamma}$ denotes a $T \times T$ coefficient matrix that includes $\beta$:

$$\boldsymbol{\Gamma} = \begin{pmatrix} \boldsymbol{0_{T-1}} & \beta \boldsymbol{I_{T-1}} \\ 0 & \boldsymbol{0_{T-1}}^\top \end{pmatrix}. \tag{22}$$

$\boldsymbol{R} = (\boldsymbol{r_1}, \ldots, \boldsymbol{r_i}, \ldots, \boldsymbol{r_N})^\top$, where $\boldsymbol{r_i} = (d_{i1}, d_{i2}, \ldots, d_{iT})^\top$, is an $N \times T$ matrix for residuals that are mutually uncorrelated. Note that $y^*_{i1}$ is an exogeneous variable and then the first column of Equation (21) shows the relation $d_{i1} = y^*_{i1}$ (i.e., $\boldsymbol{r_i} = (y^*_{i1}, d_{i2}, \ldots, d_{iT})^\top$).

Assuming that inverse matrix of $(\boldsymbol{I_T} - \boldsymbol{\Gamma})$ exists, from Equation (21) $\boldsymbol{Y^*}$ can be reexpressed as

$$\boldsymbol{Y^*} = \boldsymbol{R}(\boldsymbol{I_T} - \boldsymbol{\Gamma})^{-1}. \tag{23}$$

By substituting this result into the Equation (20), we obtain

$$\boldsymbol{Y} = \boldsymbol{s}\boldsymbol{1_T}^\top + \boldsymbol{R}(\boldsymbol{I_T} - \boldsymbol{\Gamma})^{-1} + \boldsymbol{E}. \tag{24}$$

For estimation, we now reparameterize the factor score (including residuals and measurement errors) matrices as

$$\boldsymbol{s} = \tilde{\boldsymbol{s}}\phi, \quad \boldsymbol{R} = \tilde{\boldsymbol{R}}\mathrm{diag}(\sigma_1, \omega\mathbf{1}_{\boldsymbol{T-1}}), \quad \boldsymbol{E} = \tilde{\boldsymbol{U}}\psi\boldsymbol{I}_{\boldsymbol{T}} = \tilde{\boldsymbol{U}}\tilde{\boldsymbol{D}}, \tag{25}$$

where $\frac{1}{N}\tilde{\boldsymbol{s}}^\top\tilde{\boldsymbol{s}} = 1$, $\frac{1}{N}\tilde{\boldsymbol{R}}^\top\tilde{\boldsymbol{R}}{=}\boldsymbol{I}_{\boldsymbol{T}}$, $\frac{1}{N}\tilde{\boldsymbol{U}}^\top\tilde{\boldsymbol{U}}{=}\boldsymbol{I}_{\boldsymbol{T}}$, and $\tilde{\boldsymbol{D}} = \psi\boldsymbol{I}_{\boldsymbol{T}}$. $\mathrm{diag}(\sigma_1, \omega\mathbf{1}_{T-1})$ denotes the diagonal matrix whose diagonal consists of $\sigma_1$ followed by $T-1$ repetitions of $\omega$. Then $\boldsymbol{Y}$ becomes

$$\boldsymbol{Y} = \tilde{\boldsymbol{s}}\phi\mathbf{1}_{\boldsymbol{T}}^\top + \tilde{\boldsymbol{R}}\mathrm{diag}(\sigma_1, \omega\mathbf{1}_{\boldsymbol{T-1}})(\boldsymbol{I}_{\boldsymbol{T}} - \boldsymbol{\Gamma})^{-1} + \tilde{\boldsymbol{U}}\tilde{\boldsymbol{D}}. \tag{26}$$

$\boldsymbol{Y}$ can be further expressed as

$$\boldsymbol{Y} = \tilde{\boldsymbol{F}}\tilde{\boldsymbol{\Lambda}}^\top + \tilde{\boldsymbol{U}}\tilde{\boldsymbol{D}}, \tag{27}$$

where $\tilde{\boldsymbol{F}} = (\tilde{\boldsymbol{s}}, \tilde{\boldsymbol{R}})$, $\tilde{\boldsymbol{\Lambda}} = [\boldsymbol{\lambda}_{\tilde{\boldsymbol{s}}}, \boldsymbol{\Lambda}_{\tilde{\boldsymbol{R}}}] = [\phi\mathbf{1}_{\boldsymbol{T}}, \mathrm{diag}(\sigma_1, \omega\mathbf{1}_{\boldsymbol{T-1}})(\boldsymbol{I}_{\boldsymbol{T}} - \boldsymbol{\Gamma})^{-1}]$. From this, it follows that the STARTS model can be reformulated in a manner consistent with the MDFA representation (in the case where the relations among common factors are structured by model parameters) by introducing $\tilde{\boldsymbol{F}}$, which consists of $r = T+1$ common factors—namely, one trait factor $\tilde{\boldsymbol{s}}$, the initial within-person variability $y_{i1}^*$ and $(T-1)$ residuals within $\tilde{\boldsymbol{R}}$—, and $\tilde{\boldsymbol{U}}$, which represents the measurement error and is now treated as the unique factor matrix. Moreover, in this formulation, $\tilde{\boldsymbol{\Lambda}}$ contains information relating to variance and covariance for the trait factor and the within-person variability, rather than factor loadings as in the standard factor analysis model.

### 3.2.2 Two-stage parameter estimation using MDFA approach

By considering the Frobenius-norm-based loss function corresponding to Equation (15), solutions of $\tilde{\boldsymbol{\Lambda}}$ and $\tilde{\boldsymbol{D}}$ can be obtained analogously to Equation (17) as:

$$\hat{\tilde{\boldsymbol{\Lambda}}} = \boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{F}}} = [\,\boldsymbol{s}_{\boldsymbol{Y}\tilde{\boldsymbol{s}}},\ \boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{R}}}\,], \quad \hat{\tilde{\boldsymbol{D}}} = \mathrm{diag}(\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{U}}}). \tag{28}$$

$\boldsymbol{s}_{\boldsymbol{Y}\tilde{\boldsymbol{s}}}$ $(T \times 1)$ is a vector that contains information about the variance of the trait factor, whereas $\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{R}}}$ $(T \times T)$ is a matrix that contains information about the within-person variance–covariance structure. The parameters $\phi^2$ and $\psi^2$ are included in $\tilde{\boldsymbol{\Lambda}}$ (i.e., $\boldsymbol{\lambda}_{\tilde{\boldsymbol{s}}}$) and $\tilde{\boldsymbol{D}}$ respectively, without being confounded with other parameters. Therefore, by using arithmetic means, we obtain

$$\hat{\phi}^2 = \left(\frac{1}{T}\mathbf{1}_T^\top\boldsymbol{s}_{\boldsymbol{Y}\tilde{\boldsymbol{s}}}\right)^2, \quad \hat{\psi}^2 = \left(\frac{1}{T}\mathrm{tr}(\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{U}}})\right)^2. \tag{29}$$

In the original MDFA framework, it is formulated based on the standard factor analysis model with the variance of the common factor fixed to one, and $\boldsymbol{\Lambda}$ contains factor loading information. In contrast, within the proposed framework for the STARTS model, the coefficients (factor loadings) associated with the $(T+1)$ common factors are all fixed to one. Consequently, it should be noted that each element in $\boldsymbol{s}_{Y\tilde{s}}$, for example, contains information for the standard deviation of the stable trait factor.

Let $\boldsymbol{\Sigma}^*(\boldsymbol{\theta_1})$, where $\boldsymbol{\theta_1} = (\beta, \sigma_1^2, \omega^2)^\top$, denote the variance–covariance structure at the within-person variability, and partition the full parameter vector $\boldsymbol{\theta}$ as $\boldsymbol{\theta} = (\boldsymbol{\theta_1}^\top, \boldsymbol{\theta_2}^\top)^\top$, where $\boldsymbol{\theta_2} = (\phi^2, \psi^2)^\top$. Given the relation of

$$\begin{aligned}\boldsymbol{\Sigma}^*(\boldsymbol{\theta_1}) &= \boldsymbol{\Lambda}_{\tilde{\boldsymbol{R}}}\boldsymbol{\Lambda}_{\tilde{\boldsymbol{R}}}{}^\top \\ &= (\boldsymbol{I_T} - \boldsymbol{\Gamma})^{-1}\mathrm{diag}(\sigma_1, \omega\mathbf{1_{T-1}})\mathrm{diag}(\sigma_1, \omega\mathbf{1_{T-1}})(\boldsymbol{I_T} - \boldsymbol{\Gamma})^{-1} \\ &= (\boldsymbol{I_T} - \boldsymbol{\Gamma})^{-1}\mathrm{diag}(\sigma_1^2, \omega^2\mathbf{1_{T-1}})(\boldsymbol{I_T} - \boldsymbol{\Gamma})^{-1}, \end{aligned} \tag{30}$$

by computing

$$\boldsymbol{S^*} = \boldsymbol{S}^{\triangle}_{\boldsymbol{Y\tilde{R}}}\boldsymbol{S}^{\triangle}_{\boldsymbol{Y\tilde{R}}}{}^\top, \tag{31}$$

where $\boldsymbol{S}^{\triangle}_{\boldsymbol{Y\tilde{R}}}$ denotes the upper triangular part of $\boldsymbol{S}_{\boldsymbol{Y\tilde{R}}}$ (note that $y_{it}$ and $d_{it'}$ $(t' > t)$ is assumed to be independent in the STARTS model; Figure 1), we can obtain the solution for the variance–covariance structure of the within-person variability $y^*_{it}$ that appears in Equations (9)–(10). Namely,

$$\boldsymbol{S}^* = \{s^*_{tt'}\} = \{\widehat{cov}(y^*_{it},\, y^*_{it'})\}. \tag{32}$$

As shown in Equations (6)–(7), in the STARTS framework variances and covariances for the within-person variability are structured as functions of $\boldsymbol{\theta_1}$, and therefore, unlike Equation (29), the solution for $\boldsymbol{\theta_1}$ cannot be obtained directly. Thus, some method is required to approximate the variance–covariance structure at the within-person variability $\boldsymbol{\Sigma}^*(\boldsymbol{\theta_1})$ to $\boldsymbol{S^*}$. Here, following a Frobenius norm-based criterion in the sense that no distributional assumptions are imposed, we obtain solutions for $\boldsymbol{\theta_1}$ based on the SEM framework using the ULS criterion:

$$(\boldsymbol{s^*} - \boldsymbol{\sigma}^*(\boldsymbol{\theta_1}))^\top(\boldsymbol{s^*} - \boldsymbol{\sigma}^*(\boldsymbol{\theta_1})), \tag{33}$$

where $\boldsymbol{s}^{*} = vech(\boldsymbol{S}^{*})$ and $\boldsymbol{\sigma}^{*}(\boldsymbol{\theta_1}) = vech(\boldsymbol{\Sigma}^{*}(\boldsymbol{\theta_1}))$.

From the preceding discussion, it becomes clear that the proposed method adopts a two-stage estimation procedure in which the model parameters are divided into two subsets, $\boldsymbol{\theta}_1$ and $\boldsymbol{\theta}_2$, and updated separately, because $\boldsymbol{\Sigma}^{*}(\boldsymbol{\theta}_1)$ is structured as a function of $\boldsymbol{\theta}_1$ in the STARTS model. This point differs from the original MDFA framework. As a consequence, even if the parameter updates are iterated in the same manner as in the MDFA algorithm, the loss function:

$$\left\|\boldsymbol{Y} - (\tilde{\boldsymbol{F}}\tilde{\boldsymbol{\Lambda}}^{\top} + \tilde{\boldsymbol{U}}\tilde{\boldsymbol{D}})\right\|^2, \tag{34}$$

or its equivalent and more succinct representation:

$$T_{\mathrm{MDFA}}(\boldsymbol{\theta}) = N\|\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{Z}}} - \tilde{\boldsymbol{B}}\|^2, \tag{35}$$

where $\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{Z}}} = [\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{F}}}, \boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{U}}}]$ (by using the relation $\boldsymbol{S} = \boldsymbol{S}_{\boldsymbol{YZ}}\boldsymbol{S}_{\boldsymbol{YZ}}{}^{\top}$; Adachi & Trendafilov, 2018, Lemma 4.1) and $\tilde{\boldsymbol{B}} = (\tilde{\boldsymbol{\Lambda}}^{\top}, \tilde{\boldsymbol{D}})$, does not necessarily decrease monotonically. Furthermore, once the function value begins to increase, the decrease does not resume in many cases, and a tendency was observed in which certain variance components approach the boundary value of zero.[2]

Based on these considerations, we employed an early-stopping rule in which the iteration terminated if the loss function failed to improve for 10 consecutive steps (i.e., patience = 10). In addition, the optimization was performed using multiple initial starting values like Yamashita (2024), since the loss function in MDFA is intrinsically non-convex, stemming from the presence of two unknown matrices ($\tilde{\boldsymbol{Z}}$ and $\tilde{\boldsymbol{B}}$) that appears jointly, and is therefore characterized by a landscape with many local optima. The final estimate is chosen as the solution that yields the smallest function value in Equation (35) among all attempts.

Summarizing the above explanations, the proposed two-stage estimation algorithm obtains the estimate of $\boldsymbol{\theta}$ in the STARTS model through the following steps:

0. Prepare $M$ distinct initial values for the parameter vector $\boldsymbol{\theta}$, denoted as $\{\boldsymbol{\theta}^{(0,m)}\}_{m=1}^{M}$.

1. Select the $m$-th initial value $\boldsymbol{\theta}^{(0,m)}$ and use it as the starting point of the iterative updates.

[2] In the preliminary stage of this study, we confirmed that this trend was not limited to the use of $T_{\mathrm{MDFA}}(\boldsymbol{\theta})$. A similar pattern was also observed even when an alternative ULS-based criterion corresponding to Equation (14), or its weighted version incorporating information for variances of each variable, was used instead.

2. Update $\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{Z}}}$ using $\tilde{\boldsymbol{B}}$ (that is a function of $\boldsymbol{\theta}$) and the relations in Equations (18)-(19) as

$$\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{Z}}} = \boldsymbol{S}\tilde{\boldsymbol{B}}\tilde{\boldsymbol{L}}\tilde{\boldsymbol{\Delta}}^{-1}\tilde{\boldsymbol{L}}. \tag{36}$$

Here, $\tilde{\boldsymbol{L}}$ and $\tilde{\boldsymbol{\Delta}}$ are calculated from the eigen-decomposition of

$$\tilde{\boldsymbol{B}}^{\top}\boldsymbol{S}\tilde{\boldsymbol{B}} = \tilde{\boldsymbol{L}}\tilde{\boldsymbol{\Delta}}^{2}\tilde{\boldsymbol{L}}^{\top}. \tag{37}$$

3.1. Using the updated $\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{Z}}}$, update the subvector $\boldsymbol{\theta_1}$ by minimizing the ULS criterion in Equation (33).

3.2. Using the same $\boldsymbol{S}_{\boldsymbol{Y}\tilde{\boldsymbol{Z}}}$, update the remaining subvector $\boldsymbol{\theta_2}$ based on Equation (29).

4. Repeat Steps 2 and 3 until convergence criterion (the change in each parameter before and after the update is less than $\varepsilon\,(=10^{-6})$) is met or the loss function $T_{\mathrm{MDFA}}(\boldsymbol{\theta})$ failed to improve for 10 consecutive steps (i.e., patience = 10).

5. Repeat Steps 1–4 for all $m = 1, \ldots, M$. Among the $M$ resulting estimates, select the one that yields the smallest value of the loss function $T_{\mathrm{MDFA}}(\boldsymbol{\theta})$ and adopt it as the final estimates.

# 4 Simulation

## 4.1 Method

The primary objective of this simulation study is to evaluate the performance of the proposed two-stage estimation (hereafter, we refer to this as TS-MDFA) for the STARTS model. Specifically, we assess the frequency of improper solutions, bias and RMSE of estimates, as well as computation time under various conditions, and compare the results with those obtained using ML, CML and ULS estimation in SEM, as well as Bayesian estimation.

The simulation design varied the number of time points as $T = (4, 6, 8)$, the sample size as $N = (200, 1000)$, and the variance of measurement error as $\psi^2 = (0.2, 1.0)$. The variance of the stable trait factor was fixed at $\phi^2 = 0.5$. For the within-person process, we fixed $\sigma_1^2 = 1$, $\beta = 0.3$, and $\omega^2 = 1 - 0.3^2 = 0.91$, assuming a stationary condition where variances of outcomes do not vary

across time points. These settings yielded a fully factorial design with $3 \times 2 \times 2 = 12$ conditions, and 50 replications were conducted per condition.

For each condition, the model-implied covariance matrix was computed based on the true parameter values, and data following the STARTS model were generated under the assumption of multivariate normality. ML, CML and ULS estimations were performed using the `lavaan` package (version 0.6-20; Rossell, 2012) in R (Version 4.5.1; R Core Team, 2025), whereas Bayesian estimation was carried out using `blavaan` (Merkle & Rosseel, 2018), which relies on JAGS and Stan to estimate models via MCMC.

In the Bayesian analysis, the prior distributions of the parameters were specified using the default settings in `blavaan`, as $\phi^2 \sim \text{gamma}(1, 0.5), \psi^2 \sim \text{gamma}(1, 0.5), \omega^2 \sim \text{gamma}(1, 0.5), \beta \sim N(0, 10)$, and $\sigma_1^2 \sim \text{gamma}(1, 0.5)$. Posterior sampling was performed using the No-U-Turn Sampler (NUTS), an adaptive variant of Hamiltonian Monte Carlo (HMC) implemented in Stan. NUTS adaptively tunes step sizes and trajectory lengths to achieve efficient exploration of the posterior without user-specified tuning parameters, providing higher effective sample sizes (a measure of the amount of independent information contained in an autocorrelated Markov chain) per unit time compared with traditional Gibbs sampling or Metropolis–Hastings algorithms. In light of potential non-convergence issues that may arise in the structurally intricate STARTS model, the warm-up phase was set to 1,000 iterations, followed by 10,000 sampling iterations, using two independent Markov chains. Convergence was evaluated using the potential scale reduction statistic $\hat{R}$. The posterior means were used as the parameter estimates.

For comparability and to mitigate potential problem of convergence to local optima—an issue not only for the TS-MDFA but also for competing methods (ML, CML and ULS)—we generated $M = 20$ sets of initial values in each condition and conducted estimation under each set of the same initial values for these methods. Initial values were sampled from $\phi^2 \sim \text{gamma}(3, 4), \psi^2 \sim \text{gamma}(2, 4), \omega^2 \sim \text{gamma}(4, 4), \beta \sim \text{beta}(4, 4)$, and $\sigma_1^2 \sim \text{gamma}(4, 4)$. For each estimation method, estimates were counted as improper if at least one of the estimates of variance parameters $(\phi^2, \psi^2, \sigma_1^2, \omega^2)$ was less than 0.0001.

Following Siepe et al. (2024), here we summarize the computational aspects of the simulation study in greater detail. All analyses were executed on a system running Windows 10 x64 (build

19045), using `R` Version 4.5.1 on the x86_64-w64-mingw32/x64 platform with packages: the `lavaan` and `blavaan` packages to fit structures implied by the STARTS model, the rnorm( ) function included in the stats package (Version 4.5.1; R Core Team) to generate data, the eigen( ) function included in the base package (Version 4.5.1; R Core Team) for eigen-decomposition, the rstan package (Version 2.32.7; Stan Development Team, 2024) for Bayesian estimation via HMC, and the ggplot2 package (Version 4.0.0; Wickham, 2016) to create visualizations. A full `sessionInfo()` output with additional computational details, and all code is available at the Open Science Framework (https://osf.io/**authorsname**/).

## 4.2 Result

Across all conditions, the proportion of cases in which the potential scale reduction statistics $\hat{R}$ for all parameters were below 1.10 under Bayesian estimation was 84.2% on average. Notably, larger values of $\hat{R}$ tended to be observed when the sample size was large ($N = 1000$). For ease of comparison, all results shown below are the ones obtained without excluding these cases, but even if they were removed, it was observed that the overall findings would remain essentially unchanged.

### 4.2.1 Frequency of improper solutions

Table 1 presents, for each estimation method, the frequency of improper solutions evaluated under each condition. First, we focus on ML, CML and ULS, which correspond to the first three columns. Improper solutions occurred for both ML and ULS under all conditions, with ULS exhibiting a slightly higher overall frequency than ML. In contrast, ML and CML yielded improper solutions at approximately similar proportions across conditions. For example, under the condition $T = 4$, $N = 200$, and $\psi^2 = 0.2$, the proportions of improper solutions were 56% for ML, 58% for CML, and 58% for ULS. Moreover, the proportion in which all three methods resulted in improper solutions reached as high as 42%. Improper solutions were most frequently observed in the estimates of $\psi^2$, and this tendency became more pronounced as $T$ and $N$ increased. These results underscore the severity of the improper-solution problem when applying the STARTS model.

Both $N$ and $T$ were associated with reductions in the frequency of improper solutions as they

Table 1: Proportions of improper solutions (cases in which at least one of the variance parameter estimates fell below 0.0001) across estimation methods.

| $T$ | $N$ | $\psi^2$ | ML | CML | ULS | ALL | Bayes | TS-MDFA | TS-MDFA($10^{-2}$) |
|---|---|---|---|---|---|---|---|---|---|
| 4 | 200 | 0.2 | 0.56 | 0.58 | 0.58 | 0.42 | 0.00 | 0.00 | 0.24 |
| 4 | 200 | 1.0 | 0.70 | 0.72 | 0.68 | 0.64 | 0.00 | 0.00 | 0.28 |
| 4 | 1000 | 0.2 | 0.38 | 0.38 | 0.40 | 0.26 | 0.00 | 0.00 | 0.14 |
| 4 | 1000 | 1.0 | 0.42 | 0.44 | 0.44 | 0.30 | 0.00 | 0.00 | 0.14 |
| 6 | 200 | 0.2 | 0.48 | 0.48 | 0.50 | 0.32 | 0.00 | 0.00 | 0.28 |
| 6 | 200 | 1.0 | 0.40 | 0.42 | 0.54 | 0.36 | 0.00 | 0.00 | 0.26 |
| 6 | 1000 | 0.2 | 0.24 | 0.24 | 0.20 | 0.14 | 0.00 | 0.00 | 0.18 |
| 6 | 1000 | 1.0 | 0.24 | 0.24 | 0.24 | 0.22 | 0.00 | 0.00 | 0.22 |
| 8 | 200 | 0.2 | 0.42 | 0.40 | 0.54 | 0.32 | 0.00 | 0.00 | 0.34 |
| 8 | 200 | 1.0 | 0.34 | 0.34 | 0.30 | 0.22 | 0.00 | 0.00 | 0.20 |
| 8 | 1000 | 0.2 | 0.24 | 0.24 | 0.34 | 0.20 | 0.00 | 0.00 | 0.32 |
| 8 | 1000 | 1.0 | 0.06 | 0.06 | 0.08 | 0.00 | 0.00 | 0.00 | 0.02 |

*Note.* "ALL" indicates the proportions in which improper solutions occurred in ML, CML and ULS. "TS-MDFA($10^{-2}$)" indicates the proportions in which improper solutions occurred in the proposed two-stage estimation using MDFA when improper solutions were defined as cases in which at least one of the variance parameter estimates fell below 0.01.

increased. However, the effect of $T$ appeared to be relatively limited when increasing from $T = 6$ to $T = 8$, whereas the impact of $N$ was more pronounced overall. In addition, differences attributable to $\psi^2$ were generally small unless $T = 8$.

Notably, even under conditions such as $T = 8$, which is relatively large in contexts where STARTS models are typically applied, improper solutions still occurred at proportions of approximately 10% to 50% in at least one estimation method. Furthermore, except for the condition with $N = 1000$ and $\psi^2 = 1.0$, the proportion in which all three methods (ML, CML and ULS) yielded improper solutions remained around 20%–30%. Consistent with these findings, Usami et al. (2019) reported high frequencies of improper solutions for the bivariate STARTS model. The present simulation further demonstrates that, even in the univariate case—where risks such as non–positive-definite covariance matrices among multiple trait factors do not arise—improper solutions occur at high frequencies in ML, CML and ULS.

On the other hand, no improper solutions (i.e., cases in which at least one of the variance parameter estimates fell below 0.0001) occurred in TS-MDFA or Bayes. Namely, it can be seen that TS-MDFA avoids improper solutions due to its parameter-updating procedure based on eigenvalue decomposition, while Bayes avoids them due to the specification of prior distributions.

However, it should be noted that although TS-MDFA does not exhibit the same tendency as CML to consistently yield estimates that are stuck at the boundary value of zero, it nevertheless shows a non-negligible tendency to produce relatively small estimates. As a more lenient criterion, when improper solutions are provisionally defined as cases in which the estimate of at least one variance parameter was less than 0.01, TS-MDFA yields improper solutions in approximately 5%–30% of cases, although this proportion is smaller overall than that observed in ML, CML and ULS (see the rightmost column of Table 1). This proportion tends to be higher when $N$ is small ($N = 200$). Furthermore, as with the other estimation methods, most of improper solutions were observed in the estimates of $\psi^2$, and this tendency became more pronounced as $T$ and $N$ increased.

### 4.2.2 Computation time

Table 2 presents the means (standard deviations) of the computation times required to obtain parameter estimates across 50 replications for each condition and each of the five estimation methods.

Table 2: Required computation time across estimation methods.

| | | | ML | | CML | | Bayes | | ULS | | TS-MDFA | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $T$ | $N$ | $\psi^2$ | $M$ | $SD$ | $M$ | $SD$ | $M$ | $SD$ | $M$ | $SD$ | $M$ | $SD$ |
| 4 | 200 | 0.2 | 3.9 | 4.8 | 424.3 | 195.8 | 58.6 | 12.6 | 7.1 | 10.0 | 348.1 | 612.2 |
| | | 1.0 | 5.8 | 5.3 | 526.8 | 364.3 | 49.0 | 13.6 | 11.8 | 11.4 | 555.4 | 841.3 |
| | 1000 | 0.2 | 0.8 | 1.1 | 321.3 | 147.5 | 153.5 | 62.3 | 2.7 | 6.4 | 505.3 | 686.8 |
| | | 1.0 | 4.1 | 5.5 | 296.1 | 151.9 | 185.8 | 74.5 | 9.5 | 14.4 | 733.9 | 910.1 |
| 6 | 200 | 0.2 | 2.6 | 3.9 | 1480.3 | 722.0 | 79.3 | 26.7 | 5.8 | 9.4 | 283.7 | 293.9 |
| | | 1.0 | 2.9 | 3.9 | 1201.6 | 685.9 | 72.8 | 25.8 | 6.9 | 10.5 | 428.4 | 619.8 |
| | 1000 | 0.2 | 0.8 | 0.0 | 1203.7 | 626.7 | 208.7 | 97.9 | 0.9 | 0.1 | 746.8 | 941.9 |
| | | 1.0 | 1.5 | 2.5 | 1109.4 | 380.1 | 267.6 | 138.1 | 1.8 | 6.1 | 870.0 | 1164.0 |
| 8 | 200 | 0.2 | 1.1 | 1.3 | 2806.7 | 1201.9 | 119.8 | 45.0 | 1.7 | 3.1 | 341.4 | 258.8 |
| | | 1.0 | 2.2 | 3.2 | 2338.0 | 825.5 | 147.0 | 57.6 | 3.2 | 6.3 | 351.8 | 361.9 |
| | 1000 | 0.2 | 0.9 | 0.1 | 2613.9 | 914.4 | 254.5 | 126.2 | 1.1 | 0.1 | 910.6 | 1061.8 |
| | | 1.0 | 0.9 | 0.1 | 1859.1 | 581.1 | 420.5 | 237.7 | 1.1 | 0.1 | 647.4 | 474.9 |

*Note.* Results for ML, CML, ULS and TS-MDFA (the proposed method) are based on 20 multiple starts. Results for Bayes are based on 11,000 sampling iterations for each of two independent Markov chains. $M$ = mean; $SD$ = standard deviation.

The computation times reported for ML, CML, ULS and TS-MDFA correspond to the time required to obtain the final estimates under $M = 20$ sets of initial values. For the Bayesian estimation, the computation times represent the time required to run 11,000 sampling iterations for each of two independent Markov chains.

As shown in Table 2, ML was the fastest method overall, with ULS exhibiting a comparable level of computational efficiency. Even with 20 multiple starts, both methods typically completed the whole estimation within approximately 10 seconds in each condition. The Bayesian estimation was the next fastest method; however, when the sample size was larger as $N = 1{,}000$, the average computation time was approximately two to three times longer than that observed in $N = 200$. A similar pattern was also observed for TS-MDFA.

Among the five methods, TS-MDFA and CML were the most computationally demanding. In particular, the computation time for CML increased substantially as $T$ becomes larger. When $T = 8$, CML required on average approximately 40 to 50 minutes, and for $T \geq 6$ its computational cost exceeded that of TS-MDFA. The relatively long computation time observed for TS–MDFA can be attributed to the fact that the parameters related to within-person variability (i.e., $\sigma_1^2$, $\beta$, and $\omega^2$) must be updated through iterative computations based on the ULS criterion. In addition, these two methods exhibited relatively large standard deviations in computation time, indicating that computational cost can vary considerably depending on the properties of the observed data.

When the comparison was restricted to cases in which no improper solutions occurred for each method, computation times tended to be shorter overall for all methods except the Bayesian estimation, while the relative patterns observed across methods remained consistent with those described above (see Table S1 in Online Supplemental Material).

#### 4.2.3 Bias and RMSE of the estimates

Figures 2 and 3 summarize the bias and RMSE of each estimation method across conditions by parameter type under the condition $\psi^2 = 1.0$. The results were restricted to cases in which admissible solutions were observed for all methods. Specifically, in $N = 200$, the numbers of such cases were 12 for $T = 4$, 21 for $T = 6$, and 29 for $T = 8$, whereas in $N = 1{,}000$, these were 21 for $T = 4$, 37 for $T = 6$, and 43 for $T = 8$.

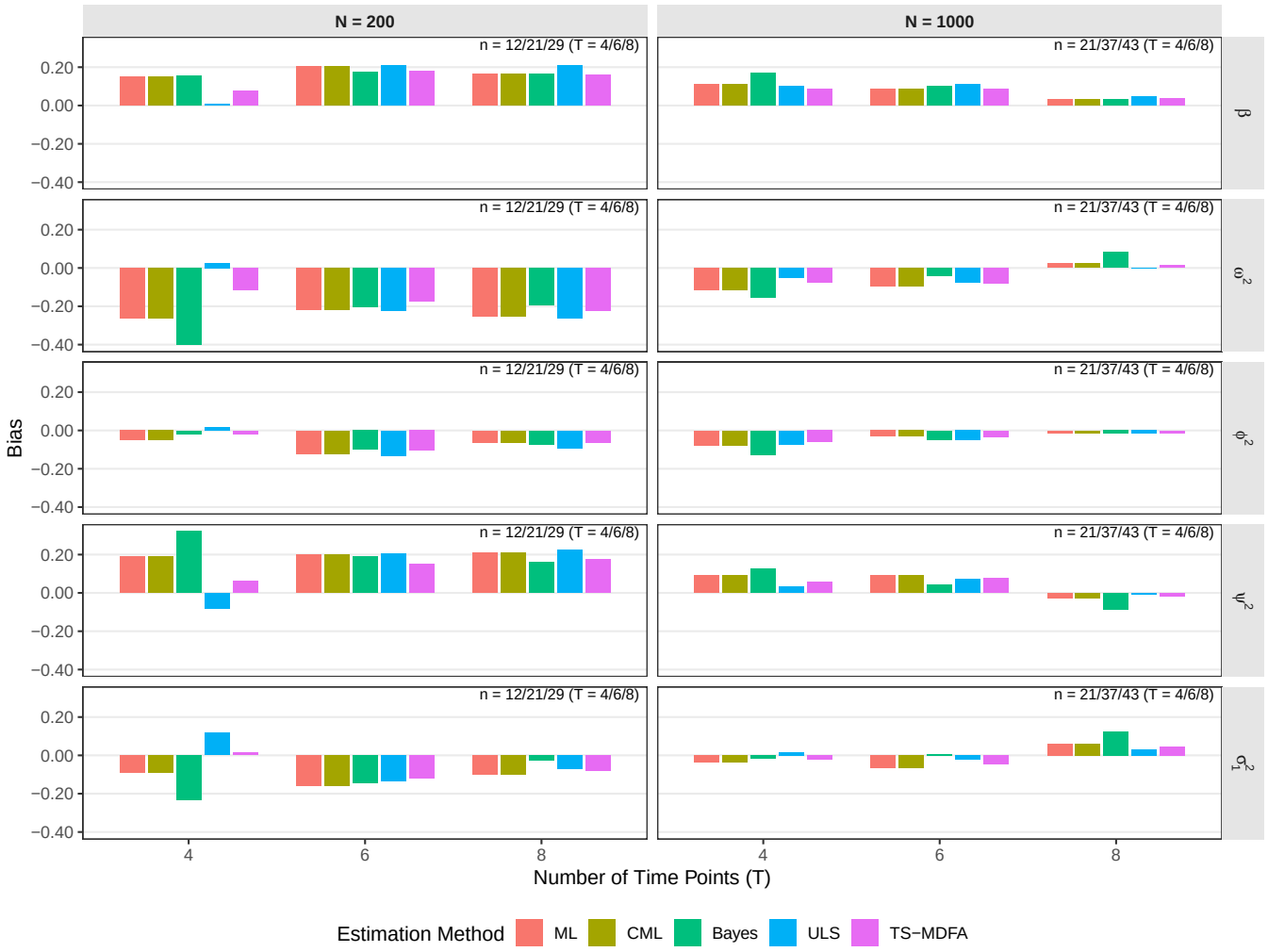


Figure 2: Bias estimates by parameter type across methods ($\psi^2 = 1$). *Note.* The number shown in the upper-right corner of each panel indicates the number of cases used to compute bias, i.e., the number of cases in which admissible solutions were observed for all methods.

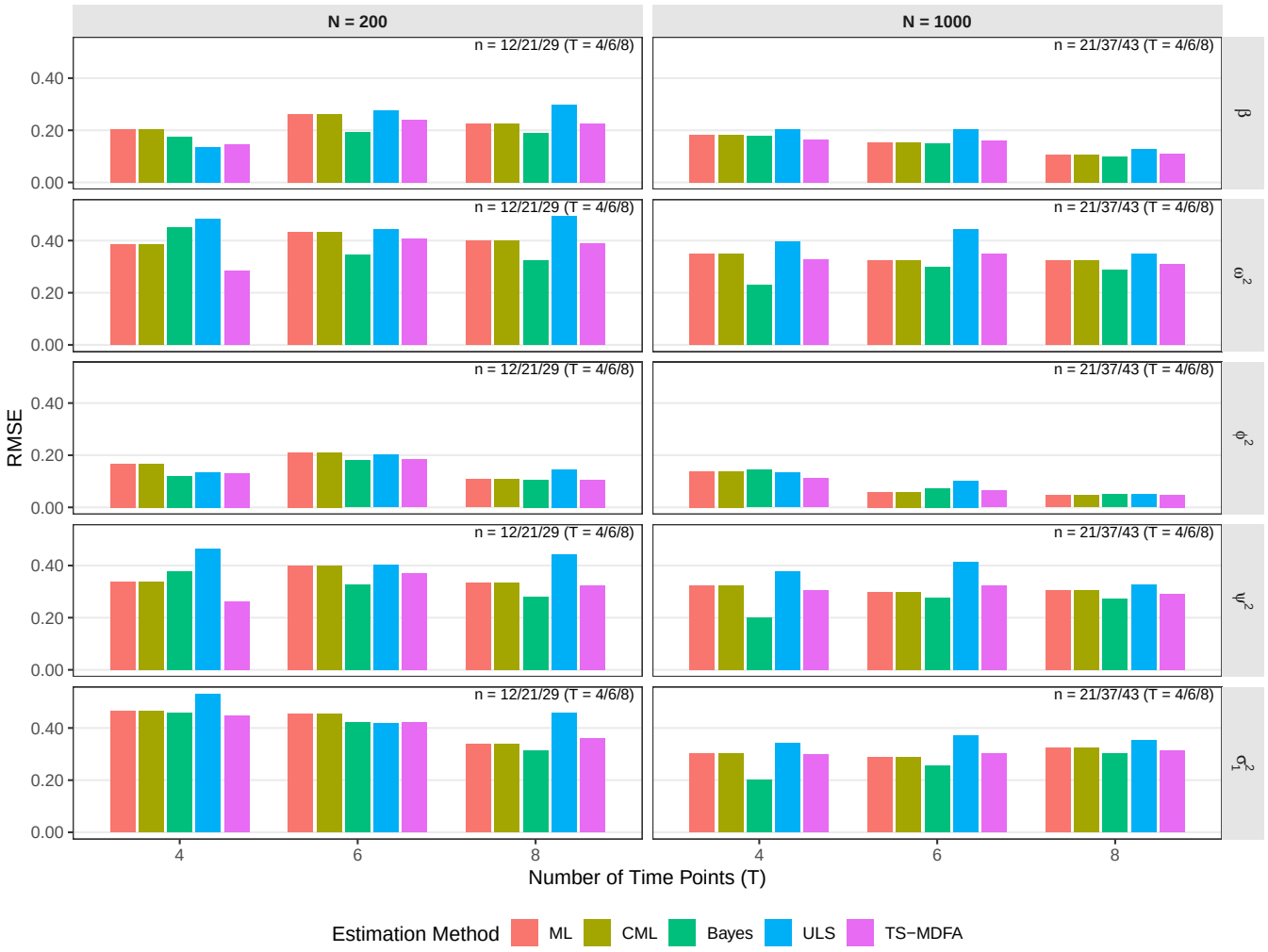


Figure 3: RMSE estimates by parameter type across methods ($\psi^2 = 1$). *Note.* The number shown in the upper-right corner of each panel indicates the number of cases used to compute RMSE, i.e., the number of cases in which admissible solutions were observed for all methods.

As shown in Figure 2, bias estimates tended to decrease across all methods as both $N$ and $T$ increased. In particular, under the condition $T = 8$ and $N = 1{,}000$, bias levels were pragmatically negligible. Among the methods, TS-MDFA exhibited smaller biases than the commonly used ML (and CML) and showed the best overall performance. In contrast, the Bayesian estimation yielded relatively larger biases, especially when $T$ was small, indicating a non-negligible influence of the prior distributions.

With regard to RMSE, Figure 3 indicates a general tendency for RMSE estimates to decrease as $N$ increased. On the other hand, for the measurement error variance parameter ($\psi^2$), the level of RMSE remained non-negligible even under the condition $T = 8$ and $N = 1{,}000$, highlighting the difficulty of achieving stable estimation for this parameter. Again, TS-MDFA exhibited RMSE estimates comparable to those of ML (and CML) across conditions. However, TS-MDFA generally exhibited larger RMSE than the Bayesian estimation. Except for the condition $T = 4$ and $N = 200$, the Bayesian estimation yielded the smallest RMSE overall, indicating that the use of prior distributions helped to mitigate the risk of yielding extreme estimates.

The tendencies observed for the Bayesian estimation—namely, relatively larger biases under the condition $T = 4$ and comparatively smaller RMSE than TS-MDFA—were confirmed even when these estimates were computed using all 50 replications in each condition (see Figures S1 and S2 in Online Supplemental Material).

#### 4.2.4 Correlations among estimates

Figure 4 presents the correlations of parameter estimates across method pairs, restricted to cases in which admissible solutions were obtained for all methods. Because the correlations between ML and CML exceeded 0.999 under all conditions, results for method pairs involving CML are omitted.

Overall, TS-MDFA exhibited high correlations with ML, exceeding 0.90 for many conditions and parameters. This finding is consistent with prior research, such as Adachi et al. (2019), which showed that TS-MDFA yields results that are empirically very similar to ML estimates. In contrast, ULS generally showed lower correlations with the other methods.

Although the Bayesian estimation exhibited higher correlations with TS-MDFA and ML, correlations below 0.8 were observed for some parameters, particularly under the condition $T = 4$. Because

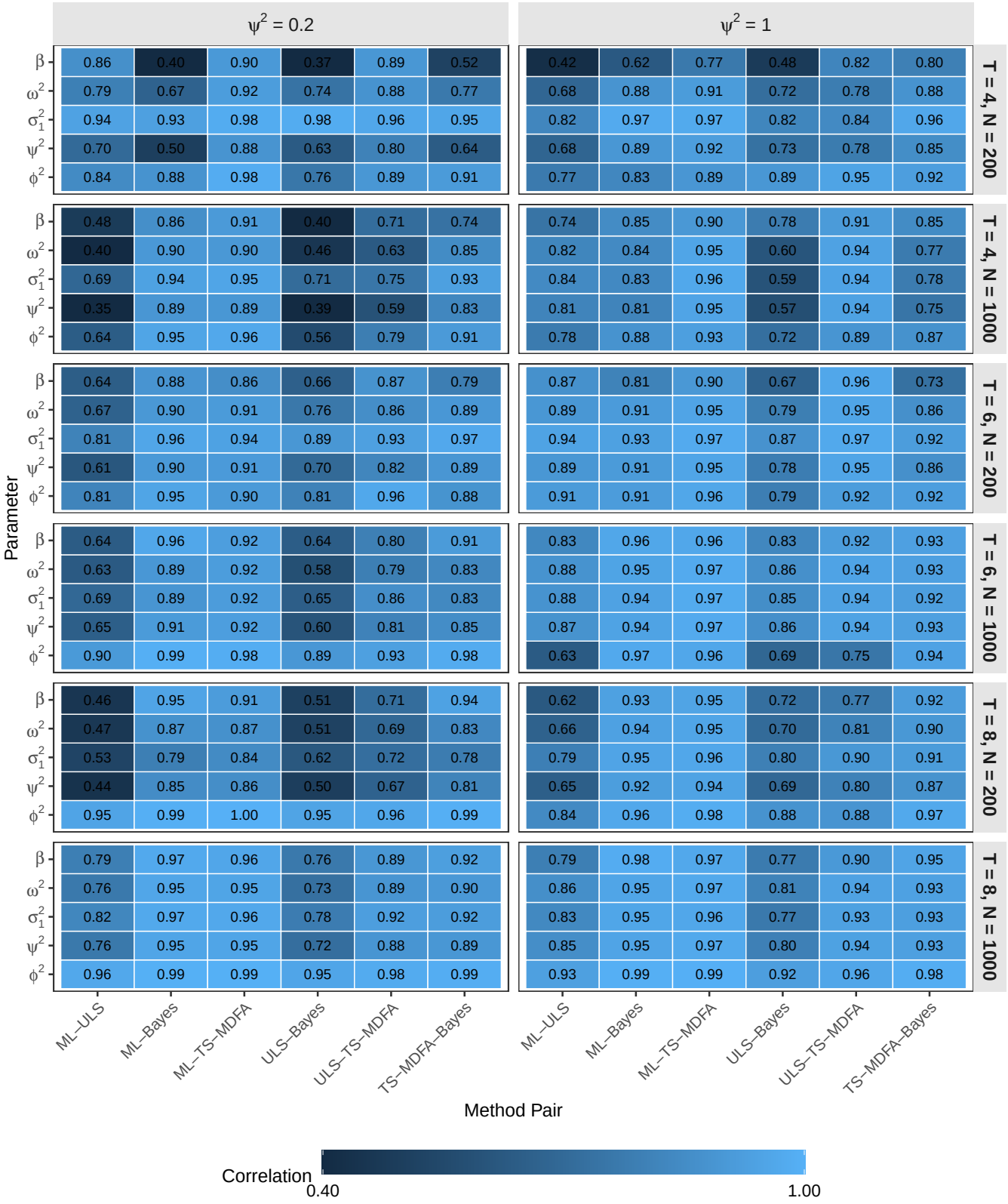


Figure 4: Correlations of parameter estimates across method pairs.

the number of cases in which admissible solutions were obtained for all methods was limited under this condition, these results should be interpreted with caution; nevertheless, when examined by parameter type, the correlations concerning $\beta$ tended to be lower. As $T$ increased, TS-MDFA exhibited correlations with the Bayesian approach that were comparable to those with ML; however, on average, these correlations remained lower than those with ML, indicating that TS-MDFA produces estimates that differ somewhat from those obtained via the Bayesian estimation, which incorporates prior distributions.

### 4.2.5 Summary and discussion

In the estimation of the STARTS model using ML, CML and ULS, improper solutions occurred with a non-negligible frequency. In particular, improper solutions were highly frequent when both $T$ and $N$ were small, exceeding 50%. In contrast, TS-MDFA and the Bayesian estimation were effective in avoiding improper solutions. However, TS-MDFA tended to yield very small variance estimates, especially when $N$ was small (e.g., $\hat{\psi}^2 < .01$), with such cases occurring in approximately 5%–30% of replications. Moreover, the correlations between estimates obtained from TS-MDFA and the Bayesian estimation were not necessarily high, in some cases falling below 0.90.

From a computational perspective, TS-MDFA was computationally demanding, second only to CML. In particular, the computational cost of TS-MDFA tended to increase substantially as $N$ became large. Although TS-MDFA required more computation time than the Bayesian approach on average in the current simulation, it is likely that, under conditions with large $N$ or $T$, comparable results could be obtained with a smaller number of multiple starts ($M$), without substantial differences in estimation performance of TS-MDFA. Furthermore, when sensitivity analyses based on different prior distributions are conducted, the overall computational costs of the Bayesian estimation and TS-MDFA may be of a similar order of magnitude.

In terms of bias and RMSE, reflecting the fact that the use of prior distributions helped to mitigate the risk of yielding extreme estimates, the Bayesian estimation yielded the smallest RMSE overall. However, the Bayesian estimation exhibited relatively larger biases, particularly when $T$ was small (e.g., $T = 4$). In contrast, TS-MDFA showed smaller biases than the commonly used ML (and CML) and exhibited the best overall performance across conditions.

With respect to the correlations of parameter estimates, TS-MDFA exhibited high correlations with ML (and CML), exceeding 0.90 for many conditions and parameters. Correlations with the Bayesian estimates were also relatively high, especially when $T$ was large (e.g., $T = 8$); however, on average, these correlations remained smaller than those with ML (and CML). This indicates that TS-MDFA produces estimates that differ somewhat from those obtained via the Bayesian estimation, which incorporates prior distributions.

Taken together, these results primarily indicate that TS-MDFA can serve as an effective method for the problem of improper solutions that frequently arise with ML, CML and ULS in estimating the STARTS model. Moreover, TS-MDFA may be preferable in situations where bias induced by Bayesian estimation is a concern—such as when $T$ is small—or when it is difficult to specify appropriate (weakly informative) priors. In addition, from the perspective of sensitivity analysis, by referring to estimation results from TS-MDFA, researchers may be better able to delineate a plausible range of conclusions regarding the parameters of the STARTS model.

# 5 Empirical Example

## 5.1 Data

In this section, we present an empirical illustration of the TS-MDFA approach using data from the Tokyo Teen Cohort (TTC) study (Ando et al., 2019), and we also compare the results with those obtained from the other estimation methods (i.e., ML, CML and ULS in SEM, as well as Bayesian estimation). The TTC study is a longitudinal cohort project designed to examine the psychological and physical development of adolescents ($N = 3{,}171$) living in the Tokyo metropolitan region. Data were collected across $T = 4$ measurement waves (ages 10, 12, 14 and 16) beginning in 2012, and a follow-up survey at age 20 has been conducted since 2022.

Here, we fit the STARTS model to the $T = 4$ longitudinal data on sleep duration. Sleep duration in hours was assessed using the question "How long do you usually sleep on weekdays?" Because this item is based on self-reports covering a relatively broad period, it is reasonable to expect that a certain amount of measurement error influences on observations. In the current illustration, we

analyze data from $N = 1{,}294$ adolescents who provided complete responses to the sleep-duration questions across all four waves. The sample covariance and correlation matrix of sleep duration is provided in Table 3.

Table 3: Sample covariance and correlation matrix of sleep duration

| | SD10 | SD12 | SD14 | SD16 |
|---|---|---|---|---|
| SD10 | 0.394 | 0.546 | 0.342 | 0.167 |
| SD12 | 0.253 | 0.546 | 0.480 | 0.219 |
| SD14 | 0.185 | 0.304 | 0.738 | 0.430 |
| SD16 | 0.095 | 0.146 | 0.332 | 0.809 |

*Note.* Diagonal elements and elements below the diagonal represent variances and covariances, respectively, whereas elements above the diagonal represent Pearson correlation coefficients.

## 5.2 Method

As in the simulation study, when fitting the STARTS model, ML, CML and ULS estimations were conducted using the `lavaan` package (version 0.6-20; Rosseel, 2012), whereas Bayesian estimation was implemented with `blavaan` (Merkle & Rosseel, 2018).

In the TS-MDFA, we generated $M = 500$ sets of initial values and conducted estimation under each set. Initial values were sampled from $\phi^2 \sim \text{gamma}(2, 6), \psi^2 \sim \text{gamma}(2, 4), \omega^2 \sim \text{gamma}(2, 4), \beta \sim \text{beta}(4, 4)$, and $\sigma_1^2 \sim \text{gamma}(2, 4)$. Among the 500 resulting estimates, select the one that yields the smallest value of the loss function $T_{\text{MDFA}}(\boldsymbol{\theta})$ and adopt it as the final estimates.

Standard errors of estimates in the TS-MDFA were obtained via a bootstrap procedure. For each of 200 bootstrap samples, the model was re-estimated using a multiple-start with 20 initial values generated from the neighborhood of the previously obtained point estimates. The standard errors were computed as the standard deviations of the resulting 200 bootstrap estimates.

In the Bayesian estimation, prior distributions were specified as: $\phi^2 \sim \text{Gamma}(1, 1)$, $\psi^2 \sim \text{Gamma}(1, 1)$, $\omega^2 \sim \text{Gamma}(1, 1)$, $\beta \sim N(0, 4)$, and $\sigma_1^2 \sim \text{Gamma}(1, 1)$. Posterior sampling was performed using HMC implemented in Stan. The warm-up phase was set to 5,000 iterations, followed

Table 4: Point estimates and standard errors for parameters in the STARTS model obtained from each estimation method. Standard errors in the Bayesian estimation correspond to posterior standard deviations. Standard errors in the TS-MDFA are computed by bootstrap. The values shown in bold indicate improper solutions.

| | ML | | CML | | ULS | | Bayes | | TS-MDFA | |
|---|---|---|---|---|---|---|---|---|---|---|
| Parameter | Est. | SE | Est. | SE | Est. | SE | Est. | SD | Est. | SE |
| $\phi^2$ | 0.114 | 0.015 | 0.091 | 0.017 | 0.015 | 0.056 | 0.089 | 0.019 | 0.054 | 0.019 |
| $\psi^2$ | **−0.304** | 0.124 | **0.000** | NA | 0.134 | 0.055 | 0.013 | 0.012 | 0.035 | 0.012 |
| $\sigma_1^2$ | 0.582 | 0.125 | 0.300 | 0.020 | 0.270 | 0.083 | 0.292 | 0.024 | 0.281 | 0.024 |
| $\omega^2$ | 0.845 | 0.129 | 0.518 | 0.013 | 0.359 | 0.068 | 0.504 | 0.019 | 0.481 | 0.022 |
| $\beta$ | 0.251 | 0.048 | 0.442 | 0.024 | 0.648 | 0.088 | 0.456 | 0.029 | 0.512 | 0.050 |

by 50,000 sampling iterations, using two independent Markov chains. The posterior means were used as the parameter estimates. From the perspective of the potential scale reduction statistic $\hat{R}$, we confirmed that there were no issues. However, we found that HMC sampling frequently encountered divergent transitions, even with high adapt_delta settings (=0.99). Here we will report the estimates for illustrative purposes.

## 5.3 Result

Table 4 presents the point estimates and standard errors for parameters $\boldsymbol{\theta}$ obtained from each estimation method. Under the same criterion as in the simulation study (i.e., estimates smaller than 0.0001), improper solutions occurred in ML and CML, but not in ULS, Bayes or TS-MDFA.

In Bayes, the posterior standard deviations tended to be smaller than the standard errors obtained from ULS, which may be attributable not only to the influence of the prior distributions but also to the `blavaan` warnings indicating frequent divergent transitions encountered in HMC.

For ULS, Bayes and TS-MDFA, in which no improper solutions occurred, estimates exhibiting somewhat different tendencies were obtained. In particular, in Bayes, the estimated measurement error variance was close to zero ($\hat{\psi}^2 = 0.013$), yielding estimates that were overall similar to those obtained by CML, which produced $\hat{\psi}^2$ at the zero boundary. In contrast, $\hat{\psi}^2 = 0.035$ under TS-

MDFA and $\hat{\psi}^2 = 0.134$ under ULS. For example, when considering the case at age 10 ($t = 1$), the proportion of measurement error variance to the observed variance was 8.9% in TS-MDFA and 34.0% in ULS.

As noted above, given the response format in the study (self-report) and the influence of day-to-day fluctuations in sleep duration, it is conceptually reasonable to assume that non-zero measurement error is present in the observations. In this sense, these methods may be considered as providing more natural estimates. Although $\hat{\psi}^2$ estimated by TS-MDFA cannot be regarded as statistically significant given the magnitude of its standard error, ULS yielded a particularly large estimate. On the other hand, in ULS, the estimated variance of the stable trait factor was rather small ($\hat{\phi}^2 = 0.015$). Given that stable individual differences in sleep duration during adolescence are well documented and depend on factors such as constitution and living environment, this result may be interpreted as somewhat implausible.

With respect to the parameters related to within-person variability ($\boldsymbol{\theta_1} = (\beta, \sigma_1^2, \omega^2)^\top$), relatively similar estimates were obtained across TS-MDFA, ULS and Bayes, and it can be found that a substantial proportion of the variance in observations is accounted for by within-person variability at each time point. The similarity between TS-MDFA and ULS is consistent with the fact that these parameters in TS-MDFA were updated under the ULS criterion. The estimates of $\beta$ ranged approximately from 0.45 to 0.65 across these methods, indicating that within-person variability in sleep duration observed at a given time point retain a certain degree of temporal persistence until the subsequent time point (two years later).

To further examine the characteristics of the estimates obtained from each method from the perspective of local fit (e.g., Kline, 2023), Table 5 presents the (Bentler type; both the observed and model implied covariance matrices are rescaled by dividing the elements by the square roots of the corresponding variances of the observed covariance matrix) residual correlation matrices computed from the estimates obtained by TS-MDFA, ULS and Bayes. For the variance elements at ages 10 and 12, ULS yielded values that differed somewhat from those obtained by the other methods. This point is likely to reflect differences in the estimated measurement error variance ($\psi^2$) and the autoregressive coefficient ($\beta$). For the remaining elements, however, differences across methods were small (and absolute values are also relatively small), indicating that these methods yield the similar

model implied covariance matrices, $\boldsymbol{\Sigma}(\hat{\boldsymbol{\theta}})$, despite differences in the parameter estimates.

As a related index, SRMRs in SEM were computed based on the estimates from each method, yielding values of 0.075 for TS-MDFA, 0.077 for Bayesian estimation, and 0.074 for ULS. This result indicates that the STARTS model exhibited an acceptable level of fit under all estimation methods considered, and that there are no substantive differences in the level of fit across methods.

As illustrated in this example, TS-MDFA can flexibly estimate the parameters of the STARTS model even in situations where commonly used methods such as ML produce improper solutions. Moreover, because TS-MDFA allows estimation without requiring the specification of prior distributions while still yielding plausible solutions, it can be used not only as a standalone estimation approach but also as a tool for sensitivity analysis that compares estimation results obtained from different methods.

Table 5: Residual correlation matrices obtained under ULS, Bayes and TS-MDFA. In each element, the residual correlations are provided in the order ULS/Bayes/TS-MDFA.

| | SD10 | SD12 | SD14 | SD16 |
|---|---|---|---|---|
| SD10 | -0.063 / 0.048 / 0.035 | | | |
| SD12 | 0.138 / 0.097 / 0.103 | -0.138 / -0.205 / -0.189 | | |
| SD14 | 0.105 / 0.085 / 0.093 | -0.025 / -0.057 / -0.059 | 0.043 / 0.025 / 0.026 | |
| SD16 | 0.011 / -0.021 / -0.006 | -0.101 / -0.083 / -0.086 | -0.056 / -0.049 / -0.058 | 0.084 / 0.094 / 0.091 |

# 6 General Discussion

In the present study, motivated by the idea of reformulating the STARTS model as a factor-analytic representation in order to apply the MDFA framework, we proposed a new two-stage estimation approach (TS-MDFA). This approach addresses the problem of improper solutions that can arise when estimating the STARTS model via eigen-decomposition, and it may also be effective in mitigating possible estimation bias associated with Bayesian estimation.

TS-MDFA can also be interpreted as an extension of MDFA to SEMs that encompass certain submodels, such as the STARTS model. In contrast to approaches that rely on regularization, such

as the one proposed by Yamashita (2024), TS-MDFA provides a more natural inferential framework without incorporating additional penalty terms.

TS-MDFA adopts a two-stage estimation procedure in which the model parameters are partitioned into two subsets, $\boldsymbol{\theta_1}$ and $\boldsymbol{\theta_2}$, and updated separately. More specifically, the cross-covariance matrix $\boldsymbol{S_{Y\tilde{Z}}}$, which reflects the covariance structure between the observed data $\boldsymbol{Y}$ and the (exogenous) common and unique factors $\tilde{\boldsymbol{Z}}$ in the STARTS model, is updated using eigen-decomposition (Step 2). Based on the updated $\boldsymbol{S_{Y\tilde{Z}}}$, the subvector $\boldsymbol{\theta_1}$, which is associated with within-person variability, is then updated under the ULS criterion (Step 3.1). Subsequently, the remaining subvector $\boldsymbol{\theta_2}$ is updated in a manner analogous to the standard MDFA procedure (Step 3.2). Under the MDFA loss function, these steps are iterated, and the optimal solution is chosen using a multiple-start strategy to mitigate the possible risk of convergence to local minima.

In the simulation study and illustrative example, we demonstrate that the TS-MDFA substantially reduces the occurrence of improper solutions compared with ML and ULS, without requiring the specification of prior distributions. The method can be used not only as a standalone estimation approach but also as a tool for sensitivity analysis that compares estimation results obtained from different methods.

As described above, TS-MDFA can be viewed as an extension of MDFA-based estimation to SEMs that explicitly includes structural equations among observed and latent variables. Consequently, TS-MDFA is applicable not only to a wide range of submodels that can be described within the SEM framework, but also to extended methods built upon those models. As one example, latent growth models (LGMs; Meredith & Tisak, 1990) are empirically known to be prone to improper solutions, particularly when $T$ is small or when the functional form of the trajectory (e.g., linear or quadratic) is misspecified (e.g., Usami, 2026). This problem can be addressed by a new estimation approach like TS-MDFA. Improper solutions in LGMs become an especially serious issue in contexts where model estimation must be repeated a large number of times, such as in SEMTree approaches (e.g., Brandmaier et al., 2013), which aim to identify heterogeneous subpopulations characterized by different parameter values and covariates that explain such heterogeneity. The application of TS-MDFA to SEMTree constitutes an interesting direction for future research, and our research group is currently engaged in the development and empirical validation of such extensions.

In addition, although mathematically simpler than the STARTS model, RI-CLPM, which has seen explosive growth over the past decade in applications particularly for the purpose of inferring reciprocal relations between variables, also tend to suffer from improper solutions. This risk is expected to increase as the number of variables increases, and especially in such cases the application of TS-MDFA is highly promising for the RI-CLPM as well.

In this sense, TS-MDFA offers a new direction for estimation in both the STARTS model and the RI-CLPM, and it is expected to be extendable to and applicable across a wide variety of SEM-based analyses. At the same time, several important issues and potential limitations remain unexamined in the present study and should be addressed in future work. One such issue concerns the asymptotic properties of the proposed two-stage estimation with respect to $T$ and $N$. Under the original MDFA framework, the strong consistency of the estimator has been established (Terada, 2025; Theorem 3.4). It is required to provide a mathematical proof of consistency in TS-MDFA, taking into account comparisons with other estimation methods.

Moreover, although TS-MDFA evaluates candidate solutions based on the loss function given in Equation (35) together with a predetermined patience criterion, alternative evaluation strategies may also be considered. In particular, because TS-MDFA combines the MDFA-based updating for $\boldsymbol{\theta_2}$ with the SEM-based ULS updating for $\boldsymbol{\theta_1}$, it is conceivable to evaluate solutions using alternative loss functions, such as ULS in SEM (Equation (14)). In this case, the resulting estimates are expected to be more similar to those obtained via ULS estimation. Relatedly, compared with the standard ML estimation, TS-MDFA involves several hyperparameters, such as the numbers of patience and multiple starts. Although the required numbers of these hyperparameters are expected to decrease as $T$ and $N$ increase, more principled guidelines for their selection remain an open topic for future investigation. Furthermore, the computational cost can increase substantially—for instance, exceeding one hour—when standard errors are estimated using bootstrap samples as in the empirical example, which indicates a practical limitation of TS-MDFA. In addition, although missing data were not considered in the present study, computational efficiency may become a critical issue when TS-MDFA is combined with multiple imputation procedures to account for missing data assumed to be MAR. Further research aimed at improving algorithmic efficiency should therefore be important.

Next, although extending TS-MDFA to cases involving two or more variables, such as the RI-

CLPM, is technically straightforward, the risk of improper solutions is expected to increase due to potential instability in the estimated covariance matrices associated with stable trait factors (e.g., Usami, Todo et al., 2019). Accordingly, it will be necessary to examine the usefulness of TS-MDFA in multivariate settings.

Both MDFA and TS-MDFA assume that the data $\boldsymbol{Y}$ are continuous. However, in many applications of the STARTS models as well as LGMs, ordinal categorical data are frequently encountered. In such cases, SEM commonly employs a two-stage estimation approach, in which polychoric correlations among variables are first computed and the model parameters are then estimated using (diagonal) WLS criterion based on these correlations (e.g., Rhemtulla et al., 2012). From the perspective of extending (TS-)MDFA to non-metric (TS-)MDFA, it would be a highly interesting research topic to investigate how the frequency of improper solutions and the properties of the resulting estimates differ between such extensions and the above traditional approaches.

Last but not least, due to the substantial computational cost associated with certain conditions—particularly those involving CML, TS-MDFA and Bayesian estimation—the conditions examined in the simulations conducted in this study are still limited. Accordingly, further simulation studies are required to examine their performance in a broader range of conditions.

SEM-based approaches to longitudinal data analysis provide an exceptionally attractive framework that encompasses a wide range of analytical models and empirically testable research hypotheses. At the same time, the potential problem of improper solutions has remained a major obstacle. It is our hope that the proposed TS-MDFA will help mitigate this issue, thereby increasing awareness of the appeal of longitudinal SEM among researchers and practitioners and further expanding its range of applications in the future.

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# Online Supplemental Material

Table S1: Required computation time across estimation methods.

| | | | ML | | CML | | Bayes | | ULS | | TS-MDFA | | $n$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $T$ | $N$ | $\psi^2$ | $M$ | $SD$ | $M$ | $SD$ | $M$ | $SD$ | $M$ | $SD$ | $M$ | $SD$ | |
| 4 | 200 | 0.2 | 0.6 | 0.0 | 310.6 | 85.0 | 58.7 | 12.2 | 0.9 | 0.5 | 298.5 | 516.4 | 13 |
| 4 | 200 | 1.0 | 0.6 | 0.0 | 298.4 | 166.0 | 52.2 | 19.1 | 0.7 | 0.0 | 380.5 | 658.1 | 12 |
| 4 | 1000 | 0.2 | 0.6 | 0.0 | 293.8 | 113.6 | 169.7 | 47.7 | 0.8 | 0.1 | 235.4 | 322.8 | 24 |
| 4 | 1000 | 1.0 | 0.9 | 1.2 | 241.7 | 91.4 | 171.3 | 41.0 | 0.7 | 0.0 | 335.1 | 394.4 | 21 |
| 6 | 200 | 0.2 | 0.8 | 0.0 | 1035.2 | 384.1 | 84.8 | 21.4 | 0.9 | 0.0 | 131.0 | 167.0 | 17 |
| 6 | 200 | 1.0 | 0.8 | 0.1 | 1065.5 | 407.1 | 73.4 | 25.6 | 0.9 | 0.1 | 248.9 | 274.3 | 21 |
| 6 | 1000 | 0.2 | 0.8 | 0.0 | 1030.0 | 349.1 | 238.2 | 97.9 | 0.9 | 0.1 | 337.1 | 344.6 | 35 |
| 6 | 1000 | 1.0 | 0.8 | 0.0 | 1067.4 | 372.8 | 273.4 | 120.7 | 0.9 | 0.0 | 381.2 | 394.2 | 37 |
| 8 | 200 | 0.2 | 0.9 | 0.0 | 2213.1 | 760.4 | 138.6 | 46.3 | 1.1 | 0.1 | 188.0 | 148.5 | 18 |
| 8 | 200 | 1.0 | 0.9 | 0.1 | 1991.7 | 571.1 | 134.0 | 54.2 | 1.1 | 0.1 | 219.0 | 204.9 | 29 |
| 8 | 1000 | 0.2 | 0.9 | 0.0 | 2203.0 | 454.7 | 295.5 | 127.0 | 1.0 | 0.0 | 479.9 | 818.8 | 31 |
| 8 | 1000 | 1.0 | 0.9 | 0.1 | 1811.9 | 546.9 | 433.5 | 245.6 | 1.1 | 0.0 | 624.6 | 467.2 | 43 |

*Note.* Results for ML, CML, ULS and TS-MDFA (the proposed method) are based on 20 multiple starts. Results for Bayes are based on 11,000 sampling iterations for each of two independent Markov chains. $M$ = mean; $SD$ = standard deviation. The column $n$ indicates the number of cases in each condition for which admissible solutions were obtained for all methods.

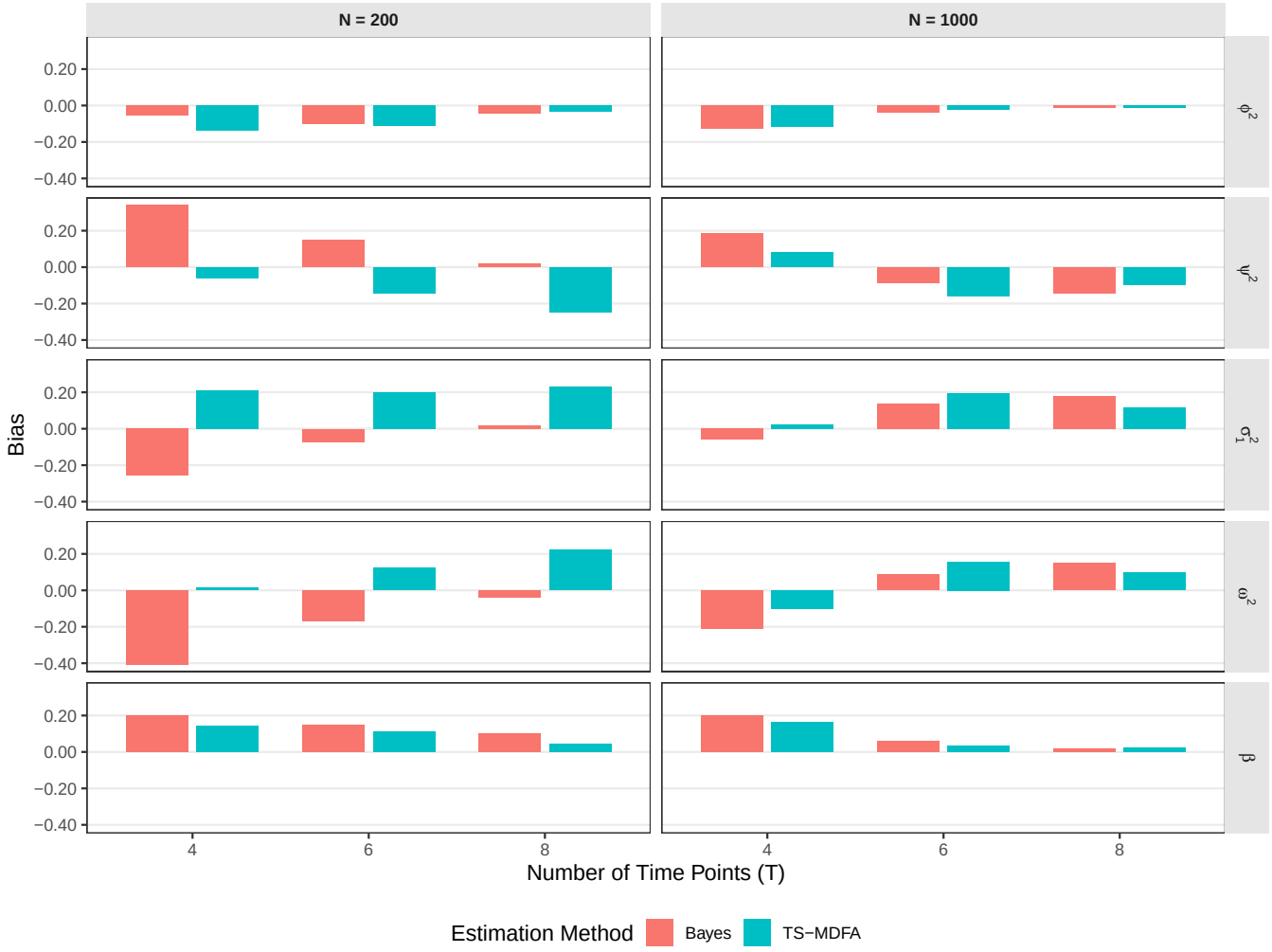


Figure S1: Bias estimates by parameter type in Bayesian estimation and TS-MDFA ($\psi^2 = 1$).

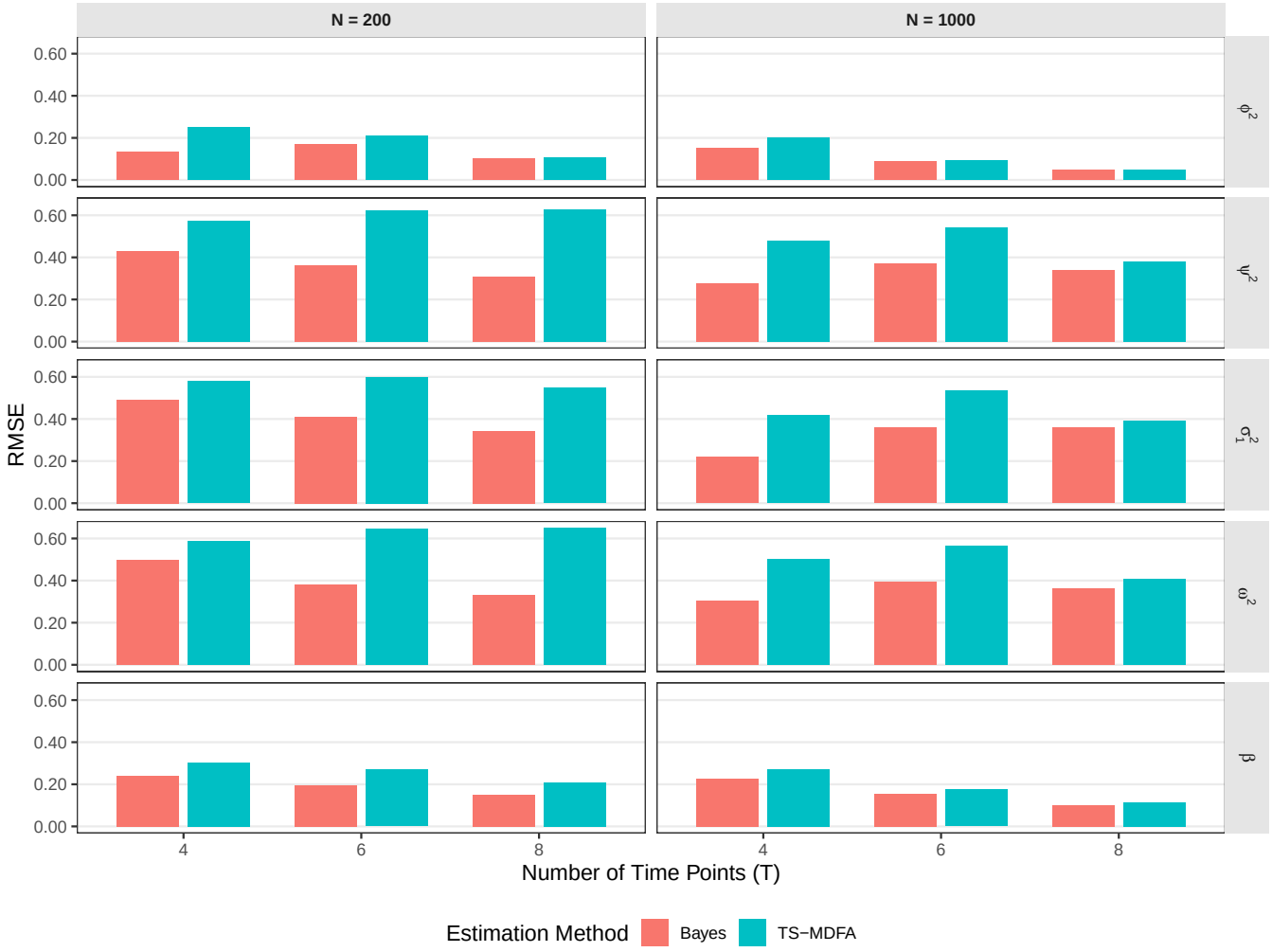


Figure S2: RMSE estimates by parameter type in Bayesian estimation and TS-MDFA ($\psi^2 = 1$).